

Pr Mickael Naassila*

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Invited talks

Targeting biased decision making in the treatment of alcohol use disorders

Reinout Wiers (Amsterdam, The Netherlands)

Alcohol Use Disorder (AUD) and other addictions have been characterized as a chronic brain disease from the biomedical perspective and as the unfortunate outcome of adverse social conditions from the social science perspective. We emphasize biased decision making as a central characteristic in (alcohol) addiction. From a therapeutic perspective, the important question is to what extent these biases reverse after successful abstinence, and to what extent they can be reversed through targeted training. Two types of Cognitive Training (CT) can be distinguished: those in which general abilities are trained (e.g., working memory training) and those in which initial motivational reactions to alcohol are targeted, so called cognitive biases (Cognitive Bias Modification, CBM, Wiers 2018). I will review the state of affairs in both. Training of general abilities takes a long time, but does show promise for a subgroup of patients. CBM has shown to increase one-year abstinence in several large clinical trials, with effect sizes similar to medication for alcohol (NNT=12). It is also becoming clear for which individuals CBM shows most promise as an add-on treatment (those with a strong cue-reactivity and/or impulsivity), and we are beginning to understand the neurocognitive mechanisms underlying training effects (e.g., reduced cue-reactivity). CT shows modest but reliable effects as add-on to regular psychosocial treatment, but does not appear to work in the absence of psychosocial treatment, nor in the absence of motivation to change (e.g. in proof-of-principle studies in students). Finally, I will sketch ways

forward, such as combining training with neurostimulation. Together these findings emphasize the malleability of the addicted brain and the promise of targeted CT in the treatment of AUD.

ASH-NASH synergism and its underlying mechanisms

Hidekazu Tsukamoto (Los Angeles, USA)

Alcohol misuse and obesity are two leading independent risk factors for alcoholic and non-alcoholic steatohepatitis (ASH and NASH) around the globe. Synergistic interactions by these factors have also increasingly been recognized. In fact, the emerging evidence indicates the average BMI of some ASH patient populations in the US may be around 30. ASH and alcoholic cirrhosis occur as the consequences of alcohol addiction which dictates heavy drinking and sustained blood alcohol levels (BAL) due to physical dependence. This condition can be reproduced in rodents by intragastric feeding of ethanol diet which also allows precise reproduction of the synergism between sustained BAL and overfeeding-induced obesity. This model exhibits heightened steatohepatitis, M1 macrophage activation, nitrosative stress driven by Notch-dependent mitochondrial metabolic reprogramming. Moderate alcohol intake may also synergistically work with NASH to promote liver cancer development. Evidence suggests social drinking is sufficient enough to promote liver cancer incidence in NASH-cirrhosis patients. This synergism is reproduced in mice injected with the hepatocarcinogen DEN and fed alcohol-containing Western diet. Tumor promotion in this model is dependent on activation of hepatic stellate cells (HSC) driven by Wnt- β -catenin-mediated overexpression of stearyl-CoA-desaturase (SCD), which in turn establishes a SCD-LRP5/6-Wnt positive loop to amplify Wnt-

β -catenin pathway in HSC and tumor microenvironment, leading to tumor-promoting lipid metabolic reprogramming. These findings highlight the causal roles of morphogen-driven metabolic reprogramming in steatohepatitis and liver tumor development promoted by ASH-NASH synergism.

Applying precision medicine to alcohol and drug use disorders

Henry R Kranzler¹ (¹ Philadelphia, USA)

Although most medications approved to treat alcohol use disorder (AUD) and opioid use disorder (OUD) have been shown to be efficacious in placebo-controlled trials, effect sizes vary among them. Even medications with the largest effect sizes, however, are not efficacious for all (or perhaps even most) patients treated with them. Recent efforts to enhance the therapeutic effects of these medications have used a precision medicine approach, including the use of pharmacogenetics (PGx) to identify genetic predictors of treatment response. This lecture will discuss recent developments in the PGx of AUD and OUD. Specific topics to be covered are: 1) a variant in the mu-opioid receptor gene (OPRM1) and response to naltrexone treatment of AUD, 2) a variant in the kainate receptor gene and response to topiramate treatment of AUD, 3) a variant near OPRM1 and usual methadone dose for treating OUD, and 4) a variant in the delta-opioid receptor gene (OPRD1) and response to buprenorphine treatment of OUD. Findings from these studies underscore the potential utility of a precision medicine approach to treating alcohol and drug use disorders and some of the obstacles to be overcome in advancing the field.

The role of CYP2E1 in alcoholic liver disease and alcohol mediated carcinogenesis

Helmut K. Seitz¹, Sebastian Mueller¹ (¹ Heidelberg, Germany)

Various factors are involved in the pathogenesis of alcoholic liver disease (ALD) and ethanol mediated carcinogenesis. In addition to genetic, epigenetic and immunologic mechanisms, acetaldehyde associated toxicity, oxidative stress as well as cytokine mediated inflammation are of major importance. Oxidative stress with the generation of reactive oxygen species (ROS) develops either in inflammation (alcoholic hepatitis) or during oxidation of ethanol via cytochrome P4502E1 (CYP2E1). CYP2E1 is induced by ethanol, oxidizes ethanol to acetaldehyde and generates ROS during this process. ROS results in protein damage, enhanced fibrogenesis and DNA lesions. Furthermore, CYP2E1 induction results in an enhanced activation of various procarcinogens and an increased degradation of retinol and retinoic acid (RA), a compound responsible for cell differentiation and proliferation. An inhibition of CYP2E1 results in an improvement of ALD and chemically induced carcinogenesis in animal experiments. In man, CYP2E1 is induced following the consumption of 40 grams of ethanol per day already after one week. However, the induction varies interindividually. The mechanism for this is still unclear. Patients with ALD show a significant correlation between CYP2E1, the occurrence of highly carcinogenic

etheno DNA-adducts and the severity of fibrosis. First results of the effect of CYP2E1 inhibition by chlormethiazole, a specific CYP2E1 inhibitor on ALD can be expected soon.

Young investigator symposium

Nicotine increases alcohol self-administration via μ -opioid receptor activity in the ventral tegmental area

E. Domi¹, A. Hansson², P. Marvin², E. Barbier¹, Xu Li¹, E. Augier¹, M. Heilig¹ (¹ Linköping, Sweden, ² Mannheim, Germany)

Alcohol and nicotine are the most commonly co-abused drugs, with a large majority of alcoholics diagnosed with a comorbid addiction to nicotine. The endogenous opioid system is involved in the rewarding properties of both alcohol and nicotine. We previously found that CERC-501, a highly selective KOR antagonist reduced escalated alcohol self-administration induced by the intermittent access to alcohol 20%. In here we tested the effect of CERC-501 on escalation of alcohol drinking induced by nicotine. Chronic nicotine elicited a robust and specific escalation of alcohol drinking without affecting saccharin self-administration and locomotion. CERC-501 did not suppress nicotine-induced increased alcohol self-administration in opposite to naltrexone which blocked escalated drinking. Our in situ hybridization data showed a different pattern of expression and functional activation of MORs in alcohol escalation induced by nicotine, while KORs expression and activity was not affected by the combination of the two drugs. Specifically, our data showed an increased expression and a decreased function of MORs in the ventral tegmental area of alcohol-escalated rats. Nicotine induced escalation of alcohol self-administration was also accompanied by decreased p-DARPP32 in nucleus accumbens shell. This suggest that nicotine pretreatment reduces the rewarding value of alcohol and therefore mediates alcohol escalation. In conclusion our results also suggest that targeting μ rather than κ -opioid receptors may represent a promising pharmacotherapeutic approach for the treatment of alcohol use disorders where alcohol consumption is driven by nicotine.

Unveiling the alcohol-dependent alterations of local translation in the prefrontal cortex during adolescence

S. Laguesse, L. Van Hees, L. Nguyen (Liege, Belgium)

Alcohol use disorder (AUD) is a devastating relapsing disease which represents the fourth leading cause of preventable death worldwide. AUD has mainly been considered as a pathological condition in adults, but recent evidence suggests that the roots of alcohol addiction begin to grow during adolescence. Adolescence is a critical developmental period characterized by significant changes in brain architecture and behaviors. Brain maturation begins in posterior regions and progresses towards anterior higher-order regions, including the prefrontal cortex (PFC). The PFC is implicated

in executive functions and its immaturity in adolescents is associated with lack of inhibitory control over behavior, increased impulsivity and desire of risk-taking. It is widely believed that the enhanced ability of the adolescent PFC to undergo experience-dependent changes is associated with heightened vulnerability to exogenous agents, including alcohol. Adolescent Alcohol Exposure (AAE) may interfere with the ongoing maturation of frontal brain circuits, leading to profound long-lasting consequences on PFC structure and function. In addition, AAE is related to serious psychological problems, comorbid psychopathology and detrimental neuro-cognitive consequences, and clinical studies have shown that AAE significantly increases the risk of developing psychiatric and behavioral disorders later in life, including addiction. However, the precise cellular mechanisms underlying the alcohol-induced cognitive and behavioral impairments, the molecular mechanisms underlying defects in PFC maturation, and possible sex differences are still poorly understood. Alcohol addiction is considered as a maladaptive form of learning and memory. Indeed, alcohol is thought to “usurp” the molecular mechanisms underlying those processes, including synaptic plasticity, which depends on the local translation of mRNAs at synaptic sites. It has been shown in adult mice that excessive alcohol consumption modifies synaptic protein composition in brain regions associated with the mesocorticolimbic pathway, promoting the development and maintenance of addiction. Here we use a mouse model of voluntary adolescent binge drinking to study the alcohol-dependent structural and functional defects in the PFC as well as the behavioral consequences. We report that excessive alcohol consumption during adolescence leads to long-lasting behavioral impairments in adulthood, such as increased anxiety and alcohol intake as well as reduced cognitive performances, both in males and females. By using transgenic mouse lines and Ribotag profiling, we are comparing the synaptic transcriptome of specific neuronal populations in the PFC (i.e. glutamatergic neurons and interneurons) in order to identify candidate synaptic mRNAs whose translation levels are modified by AAE.

Neural correlates of implicit emotional processing in binge drinking

Séverine Lannoy¹, Fabien Gierski^{1,2}, Laurence Dricot³, Farid Benzerouk¹, Christophe Portefaix¹, Sarah Barrière¹, Véronique Quaglino², Arthur Kaladjian¹, Mickael Naassila² (¹ Reims, France, ² Amiens, France, ³ Brussels, Belgium)

Binge drinking is a widespread alcohol consumption pattern in young people, defined by occasional but high alcohol intoxications (Courtney and Polich, 2009). It has been related to deleterious consequences such as brain modifications and cognitive dysfunctions (Carbia et al., 2018; Hermens et al., 2013; Maurage et al., 2013b). Recent studies have also underlined a difficulty to process emotions in young binge drinkers (e.g., Huang et al., 2017; Lannoy et al., 2018b), suggesting that this alcohol consumption pattern may also be associated with emotional impairments. Importantly, emotional impairments have been identified as key factors to describe severe

alcohol-use disorders but also explain relapse risk (Rupp et al., 2017). Regarding the binge drinking alcohol consumption pattern (i.e. alternation between high intoxications and withdrawals), research proposed that it would induce similar brain alterations than severe alcohol-use disorders (Stephens and Duka, 2008). This proposal supports the continuum hypothesis, suggesting that binge drinkers would be characterized by qualitatively similar impairments than patients with severe alcohol-use disorders (Enoch, 2006; Sanhueza et al., 2011). Therefore, the existence of emotional impairments in binge drinking could precipitate the development of chronic and severe alcohol-related disorders (e.g., Wills et al., 2016). Accordingly, it appears central that future binge drinking studies explore emotional processing and their brain correlates to precisely determine their role in the maintenance of excessive alcohol use and the possible development of severe alcohol-use disorders. The current literature mainly showed that when binge drinkers had to process emotional contents (e.g., identification, recognition), they performed poorly than control participants (Lannoy et al., 2018b; Maurage et al., 2013a). Disrupted brain activations and electrophysiological activities were also observed during the identification of emotional prosodies (Maurage et al., 2009, 2013a) and emotional crossmodal integration between facial and vocal expressions (Lannoy et al., 2018a). Moreover, altered electrophysiological activities were also found during the view of positive and negative affective scenes (Connell et al., 2015; Huang et al., 2017). Nevertheless, it is unclear whether the simple view of emotions (i.e. when no specific processing is required on emotional stimuli) already lead to alterations at the brain level, as preliminary observed for the processing of affective scenes. In the current study, we explored, beyond the ability to explicitly recognize emotions, the brain activations related to the simple view of emotional stimuli in binge drinkers and controls. Behavioral and neuroimaging findings were combined to explore brain responses during the view of emotional facial expressions (happiness, anger, sadness, fear, contempt) while participants performed a gender categorization task. Preliminary analyses showed specific patterns of activations in binge drinking, such as increased responses in the anterior cingulate cortex during the implicit processing of fear. By highlighting disrupted brain activations whereas no direct emotions processing is required, these results extend the understanding of emotional difficulties in binge drinking. They also support the continuum hypothesis regarding emotional alterations between binge drinking and alcohol-use disorders and reinforce that emotional impairments may be considered a central vulnerability factor in alcohol-related disorders.

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Opposing effects of the hormones leptin and ghrelin on neural alcohol cue-reactivity, craving and relapse in alcohol addiction: two streams merge to one river?

Patrick Bach^{1,2}, Jan Malte Bumb^{1,2}, Rilana Schuster^{1,2}, Sabine Vollstädt-Klein^{1,2}, Iris Reinhard¹, Marcella Rietschel¹, Stephanie H Witt¹, Klaus Wiedemann³, Anne Koopmann^{1,2}, Falk Kiefer^{1,2}
(¹ Mannheim, Germany, ² Heidelberg, Germany, ³ Hamburg, Germany)

Introduction: increasing evidence supports the role of appetite-regulating hormones in the pathophysiology of alcohol addiction. Amongst those, leptin and ghrelin and a “cross-talk” between both hormones were implicated in the pathophysiology of alcohol addiction, both modulating alcohol craving and drug-seeking (Hirth et al., 2016). Preclinical and clinical data thus far indicate that leptin and ghrelin interact with each other and that both modulate the signaling rate of dopaminergic neurons in reward networks (Fulton et al., 2006; Farooqi et al., 2007; Haass-Koffler et al., 2015). However, their role in alcohol addiction is far from being understood, especially the neurobiological underpinnings of their effects remains to be elucidated. To address this issue,

we investigated the association between leptin and acylated ghrelin and mesolimbic brain response to alcohol cues, alcohol craving and relapse risk in a sample of seventy alcohol-dependent patients in the post-acute withdrawal phase.

Methods: a total of seventy abstinent alcohol-dependent patients were recruited from an in-patient setting in the Clinic of Addictive Behavior and Addiction Medicine of the Central Institute of Mental Health (Mannheim, Germany) after having completed detoxification treatment (mean abstinence=11.6 days, range=5–25). All patients underwent a combined psychometric and functional magnetic resonance imaging (fMRI) assessment of alcohol cue-reactivity and alcohol craving using a validated set-up (Vollstädt-Klein et al., 2012). In addition, plasma levels of leptin, total and acetylated, active ghrelin were measured prior to the fMRI session after overnight fasting. Additionally, relapse data was collected during the three months following the assessment using a semi-structured interview, which incorporated the Alcohol Timeline Followback questionnaire (Sobell et al., 1996). Brain imaging data were preprocessed and analyzed using the statistical parametric mapping software for Matlab (SPM), according to standard procedures and previous studies (Bach et al., 2015). Associations between hormone levels and mesolimbic cue-reactivity were tested using multivariate regression models in SPM, using a combined voxel- and cluster-extent threshold that corresponds to a family wise error rate correction of $p_{FWE} < 0.05$. Cox regression analyses were performed to assess the associations between leptin, acylated ghrelin and relapse risk during the three months following the experiment. Results: analyses of psychometric data showed that leptin plasma levels were negatively correlated with the scores of the Obsessive Compulsive Drinking Scale ($r = -0.305$, $p = 0.020$, $p_{FDR} = 0.040$). For ghrelin, there was a positive association between acylated ghrelin levels and changes in the intention to drink alcohol, such that higher acylated ghrelin levels were associated with an increase in the intention to drink alcohol ($r = 0.331$, $p = 0.006$, $p_{FDR} = 0.024$). Multiple regression analyses in SPM showed a significant negative association between leptin plasma levels and alcohol cue-induced activation as the dependent variable in left (77.2% of cluster) and right caudate (18.3% of cluster), with a relevant proportion being located in the dorsal striatum (20.6%), while only a small proportion was located in the ventral striatum (5.1%, combined threshold, corresponding to $p_{FWE} < 0.05$). In addition, mean alcohol cue-induced activation extracted from bilateral caudate, negatively correlated with plasma leptin levels ($r = -0.316$, $p = 0.016$, $p_{FDR} = 0.040$), corroborating the results of the whole brain analyses. In contrast, acylated ghrelin showed a significant positive association to alcohol cue-induced activation in several clusters of brain areas, including the bilateral insulae and parts of the superior and middle frontal gyri, as well as the middle cingulum. Further, the mean functional activation in the left and right insula significantly correlated with acylated ghrelin levels ($r = 0.279$, $p = 0.013$, $p_{FDR} = 0.026$). Cox regression analyses showed a significant association between leptin and time to heavy-relapse, such that high leptin levels during the post-

acute phase of withdrawal were associated with a longer time to first heavy-relapse (Chi² overall model = 4.308, Hazard Ratio = 0.922, 95%CI 0.853-0.996, p = 0.039), while acylated ghrelin and BMI did not contribute to the prediction of time to heavy-relapse (p > 0.684). Conclusion: we could show that leptin and acylated ghrelin showed opposing associations with the extent of alcohol cue-induced mesolimbic cue-reactivity and alcohol craving. Our finding of a negative association between leptin and cue-reactivity in the bilateral caudate and striatum is in line with previous evidence that supplementation of leptin attenuates mesolimbic hyper-activation in the NAc, caudate and putamen of leptin-deficient patients (Baicy et al., 2007; Farooqi et al., 2007). The present results also mirror findings of animal studies showing that leptin modulates firing of dopaminergic neurons in the VTA that project to the striatum (Fulton et al., 2006). We thus suspect that the reduced striatal cue-reactivity might be the neurobiological correlate of leptin's effect on relapse-risk. The findings of a positive association between acylated ghrelin and cue-induced brain response in the left and right insula, harmonize with previous studies that showed that intravenous administration of ghrelin to healthy volunteers during an fMRI food-cue task, increased brain response in the amygdala, orbitofrontal cortex, insula, and striatum (Malik et al., 2008), further supporting the plausibility of BOLD response modulation by ghrelin. The reported results further support the relevance of appetite regulating hormones in the pathophysiology of addiction and their potential role as future treatment targets.

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Altered GABA-signaling in the amygdala contributes to pathological alcohol choice over high value alternative rewards

Eric Augier¹ (¹ Linköping ,Sweden)

Introduction: alcohol addiction is characterized by a progressive shift of decision making, in which alcohol is increasingly chosen over healthy non-drug rewards. Only a subset of people transition from recreational to addictive alcohol use, a pattern that is similar to that of other addictions. By contrast, in commonly used animal models, nearly all rats learn to self-administer addictive drugs, including alcohol and animals have no alternative to drug use. These models fail to capture an important and common feature of human addiction: a continued use of the substance despite the opportunity to engage in important and meaningful social and recreational activities. Purpose: the neurobiological underpinnings of choosing alcohol over a natural reward in the context of developing alcoholism are presently unknown. Here, we set out to identify molecular mechanisms underlying this choice behavior. Methods: we first employed an exclusive choice-based method to identify rats that continue to self-administer alcohol at the expense of a high-value natural reward, a sweet solution, and assessed whether these animals show other characteristics reminiscent of clinical alcoholism. Specifically, we measured their motivation to obtain and take the drug (modeled using an elevated breakpoint on a progressive-ratio schedule) and their continued drug use despite its harmful and negative consequences (here modeled using continued alcohol self-administration despite quinine adulteration or delivery of a shock punishment contingent with drug delivery). We then carried out a discovery effort using gene expression profiling. Results: using this procedure in outbred rats, we were able to identify two populations characterized by distinct patterns of choice behavior. The vast majority of rats stop responding for alcohol when offered the opportunity to access a high-value alternative reward (SP, Saccharin-preferring). However, a subpopulation (15% across multiple batches of outbred Wistar rats, a proportion similar to human alcohol addiction rates) continues to choose alcohol despite the presence of the alternative (AP, Alcohol-preferring). Rats that choose alcohol display a constellation of behavioral traits reminiscent of clinical alcoholism, mimicking key clinical diagnostic criteria for alcoholism. Specifically, they show elevated motivation to obtain alcohol, as measured by progressive ratio breakpoints and continue to take alcohol despite negative consequences that make the majority of rats stop self-administration, namely adulteration with increasing concentrations of the bitter tastant quinine, or pairing of the alcohol delivery with foot-shock. Furthermore, a differential gene expression screen using a custom NanoString nCounter panel found minimal evidence for differential gene expression between alcohol choosing vs non-choosing rats in several brain structures examined, but did identify that a marked dysregulation of a GABAergic pathway within central amygdala

dala (CeA) was associated with addiction-like phenotype. A > 50% down-regulated expression of the *g*-aminobutyric acid (GABA) transporter GAT-3 (Slc6a11) in this structure was accompanied by similarly down-regulated transcripts encoding several GABA_A receptor subunits. This indicated the possibility of elevated inhibitory GABA-tone due to impaired clearance of extracellular GABA by the transporter, a hypothesis that was confirmed using slice electrophysiology. Additionally, a viral-vector mediated knockdown of GAT-3 resulted in increased GABA-mediated inhibition in the CeA in a slice electrophysiology experiment, and converted SP rats into AP rats *in vivo*, demonstrating a causal role of GAT-3 for alcohol choice. Finally, we assessed whether these results may have translational relevance and carried out an RNAseq transcriptome analysis in post-mortem tissue from alcohol dependent people and controls. We found that GAT-3 expression was selectively decreased in the central amygdala of alcohol-dependent people compared to those who died of unrelated causes. Conclusion: our data provide strong support for a causal contribution of neuroadaptations affecting GABA signaling within the amygdala to the development of alcohol addiction. Furthermore, our findings suggest that pre-existing differences in GABAergic gene expression in the CeA may also influence susceptibility to developing alcohol addiction. Collectively, these experiments identify that impaired GABA clearance within the amygdala contributes to alcohol addiction, appears to translate between species, and may offer targets for new pharmacotherapies for treating this disorder.

GPCRs & alcohol-seeking

Andrew Lawrence (Melbourne, Australia)

New lines of experimental evidence on the reducing effects of positive allosteric modulators of the GABA_B receptor on alcohol-motivated behaviors

Giancarlo Colombo¹, Paola Maccioni¹ (¹ Monserrato, Italy)

Among G-protein-coupled receptors, the GABA_B receptor has recently gained considerable interest in the alcohol research field: the prototypic GABA_B receptor agonist, baclofen, has repeatedly been reported to suppress several alcohol-related behaviors in laboratory animals as well as alcohol consumption and craving for alcohol in patients affected by alcohol use disorder (AUD). More recently, preclinical research in the alcohol field has focused on the positive allosteric modulators (PAMs) of the GABA_B receptor, a new class of GABA_B receptor agents with improved safety profile in comparison to baclofen. The present talk will summarize the several lines of experimental evidence unanimously indicating that GABA_B PAMs retain the ability of baclofen to inhibit multiple alcohol-motivated behaviors in rodents; importantly, the effects of GABA_B PAMs are selective for alcohol and occur at doses largely lower than those producing hypolocomotion and sedation. More specifically, all GABA_B PAMs tested

to date (i.e., CGP7930, GS39783, BHF177, rac-BHFF, CMPPE, ADX71441, COR659, and ORM-27669) have invariably been reported to reduce, or even suppress, several alcohol-motivated behaviors in rats and mice. These behaviors include excessive alcohol drinking, alcohol relapse-like drinking, alcohol binge-like drinking, operant oral alcohol self-administration (under both fixed and progressive ratios of reinforcement), reinstatement of alcohol seeking, alcohol-induced locomotor stimulation, and alcohol-induced conditioned place preference. The use of validated animal models of several aspects of AUD confers remarkable translational value to these findings. Among these GABA_B PAMs, COR659 appears to be of particular interest because of a likely dual mechanism of action, involving – beside the positive allosteric modulation of the GABA_B receptor – an action at the cannabinoid CB1 receptor. This results in a unique behavioral pharmacological profile, including suppression of multiple behaviors motivated by alcohol and food (including highly palatable food) in rats. To summarize, data collected to date (i) confirm that the GABA_B receptor is a major part of the neural substrate controlling alcohol drinking and mediating the reinforcing, motivational, stimulating, and rewarding properties of alcohol, and (ii) suggest that positive modulation of the allosteric binding site(s) is an effective mechanism, in addition to activation of the orthosteric binding site, to potentiate GABA_B receptor-mediated neurotransmission and inhibit alcohol-motivated behaviors. The recent transition of the first GABA_B PAMs to the initial steps of clinical testing makes investigation of efficacy of GABA_B PAMs in AUD patients an important and feasible option.

Loss of control over alcohol drinking behaviour is linked to persistent changes in the dopaminergic and opioidergic systems

Valentina Vengeliene¹, Rainer Spanagel², Anita C Hansson²
(¹ Vilnius, Lithuania, ² Mannheim, Germany)

Repeated exposure to deprivation phases in long-term alcohol drinking Wistar rats has proven to be a useful method to induce addictive features, such as loss of control over drinking behaviour. In this study we explored neurobiological mechanisms that underlie transition from controlled to compulsive alcohol consumption. For this purpose male rats were given concurrent ad libitum access to water, as well as to 5%, 10% and 20% alcohol solutions during an observation period of eight months. Loss of control over drinking behaviour was measured during post-abstinence drinking phase by adding quinine hydrochloride to alcohol solutions and by pairing mild foot-shock with instrumental responding for alcohol. Changes in mesocorticolimbic and nigrostriatal neurotransmission induced by long-term alcohol consumption were assessed by means of receptor autoradiography for dopamine and opioid receptor in rats withdrawn from alcohol for three weeks. Our results showed that loss of behavioural flexibility in voluntary alcohol drinking rats are, at least partly, caused by persistent upregulation of μ -opioid receptor, downregulation of dopamine transporter and upregulation of dopamine receptor D1 in the ventral striatum and mPFC. Dopamine

receptor D2 levels were unaffected by long-term drinking procedure. Our findings suggest that development of addictive behaviour could be a result of lost ability of the brain to adapt to a changing environment with respect to alcohol removal and re-exposure, which points at the importance of reversal of the lost brain plasticity in the development of new treatment strategies.

The role of Nociceptin/orphanin FQ NOP receptor system in alcohol abuse

Roberto Ciccocioppo¹, Anna Maria Borruto¹, Yannick Fotio¹, Friedbert Weiss², Alice Ilari¹, Michele Petrella¹, Alessio Masi¹, Nazzareno Cannella¹ (¹ Camerino, Italy, ² La Jolla, USA)

The 17 amino acid peptide Nociceptin/Orphanin FQ (N/OFQ) is the natural ligand for the orphan G protein-coupled receptor (GPCR) Opioid Receptor Like-1 (ORL1), now known as NOP. Earlier studies in genetically selected Marchigian Sardinian (msP) alcohol preferring rats and in alcohol dependent Wistars demonstrated that activation of NOP by selective ligands reduced alcohol drinking and seeking. The effect was particularly pronounced following repeated drug administration. More recently, using selective NOP antagonists our laboratory found that NOP receptor blockade also reduced alcohol intake and relapse elicited by stress or by cues predictive of substance availability. Moreover, in a series of experiments aimed at characterizing the neuro-circuitry mediating the effects of these drugs we found that the central amygdala (CeA) plays a critical role in the effect of NOP agonists. Whereas, the effects of the antagonists involve both the CeA and the ventral tegmental area (VTA). Why both, NOP agonists and antagonists, reduces the motivation for alcohol is still unclear. However, based on evidence that NOP agonists like Ro 64-6198 and MT-7716 reduced alcohol drinking following chronic but not acute administration we propose that multiple dosing of NOP agonists, through receptor desensitization, may reduce N/OFQ transmission. This hypothesis is corroborated by binding data showing that in msP rats repeated injections of Ro 64-6198 down-regulated the expression of NOP receptors in various brain areas. Based on data showing that NOP receptors are upregulated in high alcohol drinking animal like msP and in postdependent Wistars we propose a heuristic model according to which increased activity of N/OFQ system facilitate alcohol use. This view is corroborated by data showing that rats with genetic deletion of NOP receptors drink less alcohol compared to wild type control Grant support (AA017447 and AA014351).

Muscarinic acetylcholine receptors in alcohol use disorder

Aute Leigh C Walker¹, Alice E Berrizi¹, Nicola A Chen¹, Victoria Perreau¹, Patricia Rueda¹, Craig W Lindsley², Carrie K Jones², Christopher J Langmead¹, Andrew J Lawrence¹ (¹ Melbourne, Australia, ² Nashville, USA)

Despite the large socioeconomic burden of alcohol use disorders (AUD), therapeutic treatment options are limited. There is a need to characterize the neurochemistry underpinning

alcohol seeking to aid identifying and evaluating novel targets. AUDs are characterised by a transition to compulsive alcohol seeking, which is hypothesized to involve a shift from ventral to dorsal striatum. In addition, a medial to lateral shift in the dorsal striatum is implicated in the transition from goal-directed to habitual alcohol seeking. Muscarinic and nicotinic acetylcholine receptors (AChRs) are potential targets for AUD treatment as they are expressed within the mesocorticolimbic reward system, including dense expression in the dorsal striatum. Here they modulate dopamine and glutamate release, which may regulate reward processing. To assess the role of AChRs in AUD, we first conducted genome-wide RNA sequencing in the caudate/putamen of 10 human alcoholics and 10 healthy controls and concurrently examined AChR expression in the corresponding regions in rat (dorsolateral and dorsomedial striatum) following chronic alcohol consumption/withdrawal using qPCR. Next we examined the role of select mAChR and nAChR subtypes in alcohol consumption and seeking using selective allosteric modulators. Finally, we probed the role of select mAChR and nAChR subtypes in the dorsal striatum in alcohol consumption and seeking. Collectively, our data show that specific mAChRs are potential novel target pharmacotherapies for the treatment of AUD.

Cellular and extracellular effects of alcohol exposure in liver and extrahepatic organs

Carol Casey (Omaha, USA)

TP-R deletion promotes adipose tissue browning and M2 macrophage polarization with a concomitant reduction in alcohol-associated liver injury in mice

Saraswathi Viswanathan¹, Terrence Donohue¹, Carol Casey¹ (¹ Omaha, USA)

Ethanol (EtOH) administration leads to changes in adipose tissue (AT) lipid storage function and metabolism. In a model of non-alcoholic fatty liver disease (NAFLD), mice lacking thromboxane-prostanoid receptor (TP-R) were protected against NAFLD with a concomitant increase in markers of AT browning. Here, we hypothesized that ethanol would induce AT lipolysis to promote AT browning and that blocking TP-R would enhance EtOH-induced AT browning and attenuate free fatty acid (FFA) flux to liver which would ameliorate alcohol-associated liver disease (AALD). Male TP-R knock out (KO) and wild type (WT) littermate controls were fed Lieber-DeCarli control or EtOH liquid diets for 4 wk. Chronic EtOH feeding increased mRNA for Ucp-1, a marker of AT browning, in visceral AT (VAT) of WT mice ($P < 0.05$) which was further elevated in TPR-KO mice ($P < 0.01$). Moreover, we found a remarkable increase in $\beta 3$ -adrenergic receptor (Adrb3) mRNA expression, which stimulates AT browning, in VAT of KO mice but not in WT

mice after EtOH exposure ($P < 0.01$). RNAs encoding M2 anti-inflammatory macrophages were significantly increased in EtOH fed-KO, but not WT mice. On the other hand, mRNA levels of Ccl2 (encoding MCP-1), an inflammatory marker, rose significantly in EtOH-fed WT, but not KO mice. Plasma MCP-1 levels followed this same trend. Our data show that blockade of TP-R enhances the effect of EtOH in inducing browning markers in AT. Additionally, TP-R deletion leads to AT macrophage polarization and an M2 anti-inflammatory phenotype. Thus, blocking TP-R function in AT may be effective in ameliorating AALD.

Down-regulation of Rab3D: critical role in alcohol-induced liver injury

Carol Casey¹, Karuna Rasineni¹, Terrence Donohue¹, Paul Thomes¹, Armen Petrosyan¹ (¹ Omaha, USA)

The goal of our current work is to examine how ethanol exposure results in impaired function of the Golgi apparatus. The Golgi apparatus (also called the Golgi body or Golgi complex) packages proteins into membrane bound vesicles inside the cell before the vesicles are sent to their destination. As such, this organelle resides at the intersection of the secretory, lysosomal, and endocytic pathways; it is known to be of particular importance in processing proteins for secretion. Previous work from our laboratory has identified multiple defects in endocytosis, protein trafficking, and secretion, after alcohol administration, but we have not until now, examined a role for altered Golgi function in these processes. Of central importance to our study is the role of a small GTPase, Rab3D, which is involved in exocytosis, secretion and vesicle trafficking. We have shown that Rab3D protein content was significantly decreased after alcohol administration, and recently we have obtained exciting new preliminary data that ethanol-impaired Rab3D function plays an important role in Golgi disorganization and fragmentation. We are focusing our examination on a role for Rab3D in transport through the Golgi, and have data showing how alcohol-induced remodeling of Golgi morphology is a significant impairment of post-Golgi trafficking, and may lead to utilization of trans-Golgi membranes for the formation of autophagosomes. With our expertise and experimental models, we hope to provide novel insights as to how alcohol affects trafficking of proteins within the liver cells leading to toxicity.

Complement activation in alcoholic hepatitis: possible association with acute kidney injury

Laura E Nagy¹ (¹ Cleveland, USA)

Complement contributes to liver injury in murine models of alcoholic liver disease (ALD); however, the role of complement in patients with alcoholic hepatitis (AH) is not well studied. Acute Kidney Injury (AKI) is a major predictor of mortality in severe AH. Since complement activation contributes to AKI in other kidney diseases, here we investigated the association between complement activation and AKI in ALD, making use of both murine models and patient samples. When mice are exposed to carbon tetrachloride

(CCl₄) in combination with chronic intra-gastric ethanol feeding, they develop an alcoholic liver fibrosis-associated AKI (10.1016/j.taap.2016.09.011). Using publicly available data, we found that 23 of the 1996 differentially expressed genes in AKI mice were complement genes (GSE83529). Further, when DEGs were filtered into the protein-protein interaction (PPI) network complex, 8 of the top 30 hub DEGs were found to be complement genes. We also find evidence of complement activation in liver explants from patients with AH compared to healthy controls (tissue from the Clinical Resources for AH Investigations at Johns Hopkins University). Further, the concentrations of C5a, a potent anaphylatoxin, and factor Ba, an indicator of alternative pathway activation, were elevated in both the circulation and urine from patients with AH from the DASH consortium compared to healthy controls. Kidney Injury Marker-1 (KIM-1) increased in urine of severe AH patients compared to moderate AH. Taken together, these data suggest that complement activation is associated with AKI in AH and inhibition of complement activation may be a potential target for clinical intervention.

Masked hemolysis as important factor of iron overload in ALD

Vanessa Rausch¹, Inês Silva¹, Teresa Peccerella¹, Sebastian Mueller¹ (¹ Heidelberg, Germany)

Background: 50% of ALD patients develop hepatic iron overload (HIO) and anemia, however, the underlying mechanisms including hepcidin response are poorly understood. Herein, we introduce hemolysis as novel factor in disrupting hepcidin regulation and eventually causing iron overload. Method: we here studied hepcidin, molecular and laboratory iron markers in ALD patients (n=831, mean alcohol consumption 192 g/day). The effect of hemolysis was further studied in C57BL/6 mice using phenylhydrazine (PHZ)-induced hemolysis model. Finally, in vitro erythrophagocytosis model was used to recapitulate in vivo findings and to investigate the underlying mechanisms. Results: indirect evidence for hemolysis (anemia, ferritin, LDH, MCV, CD163) as cause for HIO was found in 16.4% of heavy drinkers. Despite higher ferritin levels as compared to controls, hepcidin was not adequately upregulated in hemolytic patients suggesting a suppressive effect. In confirmation, evere PHZ-induced hemolysis (anemia, transaminases, LDH) suppressed hepcidin in mice leading to anemia, elevated transaminases and transferrin saturation and LDH levels. Phagocytosed erythrocytes were detected in the spleen and iron-loaded Kupffer cells in the liver. In vitro, erythrophagocytosis led also to the suppression of hepcidin at higher pathological levels of oxidized erythrocytes. Conclusion: our data suggest that suppression of hepcidin by masked hemolysis seems to be an important factor contributing to HIO in ALD patients.

Second hits in alcohol-related organ damage

Kusum Kharbanda (Omaha, USA)

Alcohol on fat: worse consequences for liver injuryE. Huang¹, A.M.P. Duly¹, C. Yee¹, S.V. McLennan¹, Devanshi Sethi¹ (¹ Sydney, Australia)

Background and aims: drinkers who are obese are more likely to develop liver cirrhosis than those within a healthy weight range implying the potential for an interaction between alcohol and obesity. Experimental models of alcohol and high fat diet (HFD) alone have proven difficult to induce severe liver injury even after several weeks of treatment. LPS is commonly required as a “second hit” with alcohol to advance steatosis to steatohepatitis and in diet-related obesity models induction of diabetes accelerates liver injury. We studied the interaction between alcohol and HFD in liver injury mouse model comparable to human setting of episodic heavy drinking with fat-rich food. Methods: C57BL6 male mice were fed either chow or high fat diet (HFD) ad libitum for 12 weeks. A sub-set of mice from each group were also given alcohol (2g/kg body weight) twice/week via intra-gastric lavage. Liver injury was examined by histopathology and liver/serum biochemistry. Expression of molecules related to lipid metabolism, inflammation and fibrogenesis were examined (Q-PCR, immunofluorescence). Results: we show that chronic moderate alcohol exacerbates liver injury in a mouse model of HFD compared to either alcohol or HFD alone. Alcohol superimposed on HFD increased serum and liver lipids, triglycerides, cholesterol, circulating insulin, inflammation and several molecules related to lipid processing. In addition, immune cells also increased with Alcohol+HFD. Whereas alcohol alone moderately increased ethno-adducts, Alcohol+HFD fed animals showed a striking elevation of etheno-DNA adducts clusters within the liver suggesting a precancerous profile in our model. Conclusion: alcohol on fat worsens liver injury.

Liver stiffness as a novel prognostic marker in heavy drinkers: first data from a prospective 10-year follow-up studySebastian Mueller¹ (¹ Heidelberg, Germany)

Background and aims: we here present first data on the prognostic impact of liver stiffness (LS) on long-term survival of Caucasian heavy drinkers in a 10 year, prospective single center trial. Method: information of survival status was obtained in 675 (71.6%) of 943 screened patients that had presented for alcohol detoxification over a 10-year period from 2007-2017 with a mean daily consumption of alcohol of 178 g. Mean observation time was 3.7 years and mean duration of heavy drinking was 14.0 years. All patients had LS measurements by transient elastography and routine laboratory tests. Results: during the observation time, 106 patients (15.7%) died. The cause of death could be clarified in 42 patients (39%) and it was liver-related in 16 (38%). Overall death was highest associated with LS ($r=0.291$, $P=1.3E-14$), followed by hemoglobin and alkaline phosphatase (AP). In a multivariate proportional hazard model, LS next to age, AP and serum albumin was the most significant independent predictor of survival with a hazard ratio of 1.013 (1.003 to 1.023, $P<0.05$).

Using ROC analysis, LS was the best predictor of death in general with an AUROC of 0.72 and a cutoff value of 14.0 kPa, followed by AP and albumin. Moreover, LS was the top predictor of death starting from 2 to 5 years. In contrast, LS was preceded by bilirubin and albumin in predicting one-year-survival. Conclusion: we here identify LS as the best long-term prognostic parameter in patients who heavily consume alcohol. LS measurements should become an important parameter for the screening of alcoholics.

Reactive aldehydes from alcohol and cigarette smoke co-exposure impairs lung innate anti-microbial defenseTodd A Wyatt¹ (¹ Omaha, USA)

The vast majority of individuals with an alcohol use disorder smoke cigarettes. Alcohol misuse and cigarette smoking are co-morbidities resulting in the significant susceptibility to lung infections leading to pneumonia. Several innate lung defense mechanisms are altered by the combination of drinking alcohol and smoking cigarettes. Mucociliary clearance is negatively impacted by smoke and alcohol through cilia slowing and ciliated cell detachment caused by the co-exposure-induced activation of protein kinase C epsilon. Malondialdehyde and acetaldehyde are generated via both alcohol metabolism as well as the pyrolysis of tobacco leading to the formation of stable hybrid adducts known as MAA adducts. Lung surfactant protein is altered through MAA adduction resulting in decreased anti-microbial action by the collectin. Lastly, the secretion of lung mucosal immunoglobulin A is decreased through the action of MAA adducts in a TGF beta-dependent manner. Both airway epithelial cells and macrophages bind MAA adducted protein via CD204 suggesting that differential expression of CD204 polymorphisms may govern injury due to co-exposure. Thus, the suppression of lung innate defense is multi-faceted in alcohol misuse due to the comorbidity of cigarette smoking.

Matrix stiffness regulates fibrosis progression in alcohol-induced liver injurySenthilkumar Thulasingham, Michael Moeller, Madhusudanan Narasimhan, Carol Casey, Srivatsan Kidambi¹ (¹ Lincoln, USA)

Liver stiffness (LS) is widely used clinically to monitor, staging and diagnosis, of alcoholic fatty liver diseases (AFLD) and is also believed to predict improved outcome. The regulatory mechanisms of LS in regulating liver function during ALD, specifically, fibrosis, is incompletely understood. This study aims to uncover significant mechanisms underlying the role of increasing matrix stiffness during liver injury in the promoting fibrogenesis induced by alcohol. We hypothesize that LS is just not the readout of fibrosis but also an active contributor of the progression of liver fibrosis and stellate cell activation in AFLD. Using our innovative biomimetic liver fibrosis model that allows modulation of substrate stiffness (2 kPa, 9 kPa 25 kPa and 55 kPa mimicking healthy, early fibrotic, and extremely fibrotic substrates), we investigated the role of liver matrix stiffness in modulating primary

hepatocytes and stellate cell function. In vitro experiments were designed using the conditioned medium (CM) of primary hepatocytes (isolated from alcohol fed rats) cultured on stiffness mimicking healthy and fibrotic environment supplemented to human stellate cells (HSC). A significant increase in HSC proliferation, and expression of fibrosis-related genes were observed in cells treated with CM from stiffer matrix. Together, all these data demonstrates the plausible role of stiffness in regulating hepatocytes function and contribute to stellate cells activation and progression of liver fibrosis during alcohol liver disease. Understanding the impact of stiffness on hepatocytes biology will provide significantly more nuanced data to aid drug development for AFLD and liver fibrosis.

What can we learn from epidemiology in alcohol research? Recent findings from large population-based cohorts

Guillaume Airagnes (Paris, France)

Do addictive behaviors explain social inequality regarding depression? Findings from the Constances cohort

Joane Matta¹, Nicolas Hoertel, Guillaume Airagnes, Emmanuel Wiernik, Frédéric Limosin, Marcel Goldberg, Marie Zins, Cédric Lemogne (¹ Villejuif, France)

Objective. To examine the associations between depression and alcohol, tobacco and cannabis, taking into consideration socioeconomic status (SES). **Methods.** We applied mediation and moderated mediation models stratified for sex to a nationally representative sample (N=37,192) of French men and women from the Constances cohort with baseline and follow-up measures regarding depressive symptoms. The structural equation model tested the associations between low SES status (income and education, separately) and depressive symptoms at follow-up mediated by alcohol, smoking and cannabis, while taking into consideration age and depressive symptoms at baseline. A second set of analyses tested the mediation and moderation models with interactions between SES and substances. **Results.** Mediation analyses using low education or low income did not explain the association between SES and depressive symptoms in either men or women. Mediation and moderation models showed that direct effects were not significant in the presence of interactions and that the moderation effect was largely significant. Direct associations between substances and SES or depressive symptoms were only retained for tobacco use. In the low education models, the estimate of moderation was 0.278 ± 0.076 and 0.182 ± 0.09 in men and women respectively. Strong moderation effects were also found in the low income models (0.348 ± 0.076 and 0.247 ± 0.08 in men and women, respectively). **Conclusion.** Prevention strategies targeting at risk subgroups should consider SES and substance use not only as a cumulative risk factor but take into account their

interplay; particularly regarding tobacco use, whatever the underlying mechanisms. Future studies should investigate mechanisms related to the observed associations.

Development of a predictive clinical tool of alcohol-related consequences: results from the Epidemiologic Survey on Alcohol and Related Conditions

Nicolas Hoertel¹, Marie Dosquet, Hugo Peyre, Carlos Blanco, Géraldine Ducoutumany, Philip Gorwood, Henri Leleu, Guillaume Airagnes, Cédric Lemogne, Henri-Jean Aubin, Frédéric Limosin (¹ Paris, France)

Objective. To develop an individualized risk calculator tool of the 3-year risk of 6 important alcohol-related medical, psychological and social adverse outcomes based on predictor variables that are easily and routinely collected in primary healthcare settings. **Material.** A nationally representative sample of US adults aged 18 years or older was interviewed 3 years apart in the National Epidemiologic Survey on Alcohol and Related Conditions (wave 1, 2001-2002; wave 2, 2004-2005). Analyses concerned 22,009 respondents interviewed in both waves and using alcohol in wave 1. This sample was randomly split into a construction (N=11,013) and a validation sample (N=10,996). **Methods.** The 3-year risk of 6 important alcohol-related adverse outcomes (i.e., alcohol use disorder, withdrawal symptoms, occurrence of tremors or seizures, interpersonal relationship problems and legal problems) was modeled in the construction sample using logistic regression, with age, sex and the 3 AUDIT-C variables as predictors. Scoring was used to combine information derived from predictors and quantify alcohol-related risks for each subject. Discrimination and calibration were assessed in the validation sample based on the C-index and the Hosmer and Lemeshow (H-L) test. **Results.** The predictive values of the risk equations were good (C-index ranging from 0.75 to 0.83) and calibrated well (all H-L test p-values > 0.44) in the validation sample, showing potential clinical usefulness. **Conclusions and Relevance.** This clinician-friendly individualized risk calculator can be useful to identify individuals with a short-term risk of developing alcohol-related adverse outcomes, encourage at-risk drinkers to cut down their drinking and facilitate the implementation of focused preventive interventions.

Associations of depressive symptoms with alcohol use: findings from the Constances cohort

Emmanuel Wiernik¹, Nicolas Hoertel, Guillaume Airagnes, Joane Matta, Frédéric Limosin, Marcel Goldberg, Marie Zins, Cédric Lemogne (¹ Villejuif, France)

Background. It remains unclear whether the risk of alcohol use is related to specific depressive symptoms (e.g. poor appetite), to specific dimensions underlying depression (e.g. somatic symptoms), to a general depression factor representing the shared effect of all depressive symptoms, or to a combination of these explanations. In addition, these effects could be specific to alcohol or common to other substances. **Methods.** From 14,117 men and 14,629 women included from January

2015 to December 2016 in the French Constance cohort, we applied structural equation modeling to examine the shared and specific effects of depressive symptoms (Center for Epidemiological Studies-Depression) on alcohol, tobacco, e-cigarette and cannabis use, while taking into account the co-occurrence between those substances. Analyses were stratified by sex and adjusted for age and education. Results. Heavy alcohol use was significantly associated with depression and this association was mostly mediated through a general depression factor (i.e. shared effect of all depressive symptoms). This was also the case for the other substances. Beyond and above the effect of that general factor, reduced positive symptoms (e.g. anhedonia) had an additional effect on heavy alcohol use, particularly in men. Somatic symptoms had an additional effect on cannabis use. Conclusions. Because the association between depressive symptoms and substance use was mainly mediated through a general depression factor, a better knowledge of biological and psychological mechanisms underlying this dimension may help reduce the burden of substance use. In addition, the importance of particular substance-specific dimensions of depression could help to better identify at-risk individuals.

Do personality traits predict alcohol consumption decades after their assessments? Findings from the Gazel cohort

Guillaume Airagnes¹, Cédric Lemogne, Alice Gueguen, Nicolas Hoertel, Marcel Goldberg, Frédéric Limosin, Marie Zins (¹ Paris, France)

Background. Hostility has been found to be positively associated with alcohol intake in cross-sectional studies. Our aim was to examine prospectively the long-lasting association of hostility with alcohol consumption. Methods. We included 10,612 men and 3,834 women from the French Gazel cohort with mean ages in 1993 of 48.6 (SD=2.9) and 45.7 (SD=4.2), respectively. Hostility (i.e. total, cognitive and behavioral) was assessed in 1993 with the Buss and Durkee Hostility Inventory. Alcohol consumption was self-reported annually from 1994 to 2014. Hostility scores were introduced successively in general linear mixed models with annual alcohol consumption in drinks per week as dependent variable. Multivariable analyses were adjusted for age, occupational status, marital status, retirement status and depression score. All the analyses were stratified by sex. Results. Among men(women), 83.0%(76.2%) completed at least 75% of all annual assessment of alcohol consumption over a 21-year follow-up. In univariate analysis, alcohol consumption was associated with total and behavioral hostility in both sex (all $p < 0.001$). In multivariable analyses, these associations remained significant with a greater size effect for behavioral hostility. Estimated means of alcohol consumptions ranged from 10.50[95%CI:10.01-10.92] drinks per week to 13.32[95%CI:12.90-13.74] in men and from 4.09[95%CI:3.71-4.46] to 5.78[95%CI:5.39-6.17] in women, for the first and last quartiles respectively (p trends < 0.001 and all pairwise comparisons < 0.01). Similar effects were observed among participants with at-risk alcohol consumption at baseline. Conclusions. In both men and women, behavio-

ral hostility predicted alcohol consumption over a 21-year follow-up. Interventions aiming at modulating behavioral hostility may help reducing its long-lasting influence on alcohol consumption.

Beyond cognition: neuroscience correlates of affective and motivational processes in binge drinking

Pierre Maurage (Louvain-la-Neuve, Belgium)

The role of interoception and emotional impulsivity in binge drinking

Aleksandra Herman¹ (¹ Brighton, UK)

Despite our increasing knowledge of the cognitive as well as emotional alterations in binge drinking, the factors that actually predispose to binge drinking remain unclear. More recently the role of interoception, defined as the sense of the physiological state of the body, is being investigated in alcohol use and misuse. The talk will present our recent neuroimaging as well as behavioural findings focusing on the role of emotional impulsivity and interoception as well as emotional recognition alterations as driving factors for alcohol use in non-dependent binge drinkers. A model will be presented of how these factors interact with each other in the context of identifying potential endophenotypes associated with risk for the development of alcohol addiction.

Emotional impairments in binge drinking: insights through a behavioral and neuroscientific approach

Severine Lannoy¹ (¹ Reims, France and Stanford, USA)

Binge drinking is a widespread alcohol consumption pattern in young people. It has been related to deleterious consequences such as brain modifications and cognitive dysfunctions. Recent studies have also proposed that binge drinking may be associated with emotional difficulties. The talk will present behavioral, electrophysiological, and neuroimaging findings supporting this proposal. It will underline the existence of emotional deficits in binge drinkers as well as the heterogeneity of this population. Electrophysiological and neuroimaging results related to distinct paradigms involving the processing of emotional stimuli will also be presented to extend the understanding of emotional difficulties in binge drinkers. These results reinforce the importance of emotional processes in binge drinking and open new research avenues in the field of alcohol-use disorders.

How do binge drinkers inhibit alcoholic images? A functional magnetic resonance imaging study

Sónia S Sousa¹ (¹ Braga, Portugal)

Binge Drinking (BD) is characterized by the consumption of large amounts of alcohol in a short time followed by a period of abstinence or very low consumption. This pattern of alco-

hol consumption is highly prevalent among adolescents and young adults, especially college students, and an important risk factor for substance abuse. Although BD is not considered an addictive disorder per se, binge drinkers (BDs) display cognitive deficits similar to addicted individuals. Namely, deficits in executive functions, such as in inhibitory control, impulse control and delay of gratification, in addition to functional alterations of the frontal networks involved in addictive behaviours. Thus, while behavioural differences are not usually observed between BDs and light social drinkers, increased activation in the BDs' frontal or fronto-parietal regions during the performance of executive-related tasks is relatively consistent across studies. This greater neural activation seems to reflect a brain compensatory mechanism that enables BDs to maintain task performance levels similar to controls. However, current knowledge on the BDs' neurofunctional response when inhibiting a motor response to alcoholic stimuli is scarce. In this sense, the main purpose of the present study was to assess functional activity in the brain networks associated with motor response inhibition to alcoholic stimuli in young BDs. Twenty College BDs and 16 age-matched non-alcohol consumers (NACs) (18-23 years-old) underwent a functional magnetic resonance imaging (fMRI) acquisition while performed a stop signal task with alcohol-related and non-alcohol-related stimuli. At the behavioral level, BDs exhibited lower reaction times than NACs in response to alcoholic stimuli. When analyzing neural activation, BDs displayed increased activity over the right dorsolateral prefrontal cortex during response inhibition to alcoholic stimuli. In addition, BDs showed augmented activation in limbic regions such as the parahippocampal gyrus, when observing alcoholic stimuli. Finally, brain activity of visual regions for alcoholic drinks was superior relative to non-alcoholic beverages in the BD group only. Overall, our results suggest that BDs may need additional cognitive resources to perform similar to NACs when inhibiting a response to alcoholic stimuli. These findings are in agreement with the only fMRI study conducted to date on motor inhibition to alcoholic stimuli in BDs (Ameza et al., 2014), pointing to a compensatory neurofunctional mechanism that may allow BDs to perform efficiently in inhibitory control-related tasks. Additionally, BDs seem to be more impulsive in their responses to alcoholic stimuli and to be attentionally biased towards this type of stimulus, which in turn could be activating emotional memories contributing to alcohol consumption reinforcement.

Neural correlates of an alcohol-cued Go/NoGo task: a dual process approach to binge drinking in college students

Javier Blanco-Ramos (Santiago de Compostella, Spain)

Dual-process models have been proposed as an explanation of substance abuse and other risky behaviours, with inefficient decision-making abilities as the central core. Decision making abilities result from the balance between a reflective system and an automatic or affective system. The adolescent brain, in comparison with normal adults, presents an imbalance between earlier developed motivational systems and a still

immature cognitive control system. As a result, adolescence is characterized by elevated risk-taking behaviours and seeking of novelty and rewarding sensations, associated with inefficient decision-making abilities. As the adolescent brain is still under critical development, alcohol misuse has serious deleterious effects, which may exacerbate the problem. To explore brain activity associated with inhibitory control in motivational alcohol-related contexts in young binge drinkers (BD), a sample of college students performed a Go/NoGo task with beverage (alcohol vs. non-alcohol) stimuli while ERPs (80 controls, 71 BD) and fMRI (36 controls, 32 BD) were recorded. Differences between BD and controls were found in the anterior N2 ERP wave and in the inferior frontal cortex activity during response inhibition. These differences were modulated by the alcohol-related content of stimuli. The results will be discussed in the frame of the dual-process models, providing new evidence on the understanding of excessive drinking habits in youth.

Don't stress the amygdala – the role of pro- and anti-stress systems in AUDs

Sophia Khom (La Jolla, USA)

Corticotropin releasing factor binding protein in the amygdala: the good, the bad and the ugly

Carolina L Haass-Koffler¹ (¹ Providence, USA)

To investigate the causal link between corticotropin releasing factor binding protein (CRFBP) in the central nucleus of the amygdala (CeA) and alcohol-seeking behaviors, we utilized a rat model trained to self-administer ethanol, designed with controlled regional expression of CRFBP in the CeA and electrophysiology data in transgenic mice expressing green fluorescence protein (GFP) in CRF Receptor 1 expressing neurons in chronic ethanol exposure. In rats, we found that CRFBP downregulation in the CeA reduces ethanol self-administration and CeA hemodynamic activity but does not attenuate yohimbine-induced ethanol self-administration. In mice, preliminary data suggest that CRFBP inhibition decreases postsynaptic GABAA receptor function through CRF R2 in the CeA. All these data support our hypothesis that CRFBP is not only a sequestering protein, but it may possess additional functions.

Dysregulated endocannabinoid signaling in the central nucleus of the amygdala (CeA): role in anxiety and excessive alcohol consumption

Antonia M Serrano¹ (¹ Málaga, Spain)

The endogenous cannabinoid system is a neuromodulatory system that plays a homeostatic role in the constraint and termination of stress responses. Disrupted endocannabinoid signaling is linked to maladaptive stress responses and affective disorders such as anxiety and depression. These negative emotional symptoms are associated with alcohol dependence

and abstinence and may contribute to relapse drinking and excessive alcohol intake. We have shown that stress- and alcohol-induced increases in the endogenous levels of 2-arachidonoylglycerol (2-AG) in the CeA were blunted in rodents with a history of alcohol dependence. This effect was associated with anxiety-like behaviors and excessive alcohol consumption, and these dependence-associated behavioral effects were alleviated by enhancement of 2-AG tone. These results suggest that dysregulated 2-AG signaling in the CeA may contribute to dependence-related affective disorders and excessive alcohol intake.

A role for amygdalar endocannabinoid signaling in excessive alcohol intake and comorbid anxiety in genetically selected Marchigian Sardinian alcohol preferring rats

Nazzareno Cannella¹ (¹ Camerino, Italy)

Addiction is a chronic disease characterized by compulsive drug seeking and taking. Transition from recreational drug use to excessive consumption and eventually drug addiction is shaped by the interaction of excessive drug consumption with genetic, stress, and environmental factors. The Marchigian Sardinian alcohol-preferring (msP) rat line, genetically selected for excessive alcohol consumption, have a hyperactive amygdalar corticotropin releasing factor (CRF) to CRF receptor-1 signaling resulting in increased Fatty Acid Amide Hydrolase (FAAH) activity and reduced N-arachidonylethanolamine (AEA) levels, compared to non-selected Wistar controls. MsP rats show innate traits resembling generalized anxiety and post-traumatic stress disorder (PTSD) in humans. Negative environmental conditions exacerbate this disorder, which can be attenuated by voluntary alcohol drinking or by enhanced endocannabinoid transmission. Here we provide evidences that FAAH inhibition in the central amygdala (CeA) decreases alcohol self-administration and stress-induced anxiety in msP but not in non-preferring Wistar rats. We also compared alcohol intake and comorbid anxiety in male and female msP and Wistar rats demonstrating that female msPs consume a larger amount of alcohol than male. Negligible alcohol consumption and no sex differences were observed in Wistars. Both male and female msP show comorbid anxiety, however, while in male alcohol alleviates generalized anxiety assed by an elevated plus maze paradigm, in female alcohol reduces the expression of a PTSD-like syndrome in a fear conditioning paradigm. In addition, inhibition of FAAH activity mimic the effect of alcohol reducing PTSD-like behavior in female msP rats. Considering the link between reduced endocannabinoid transmission, excessive stress response, and expression of PTSD-like traits, our data suggest that msP rats consume high amounts of alcohol to normalize their amygdalar endocannabinoid transmission in the attempt to medicate their innate negative state.

Aberrant central amygdala Substance P/neurokinin receptor 1 signaling in rodent models of alcohol dependence and anxiety

Sophia Khom¹ (¹ La Jolla, USA)

Substance P (SP) and its preferred target – neurokinin 1 (NK-1) receptors – have emerged as critical players in stress-elicited alcohol seeking and alcohol consumption. However, the underlying cellular mechanisms are still poorly understood. SP and NK-1 receptors are widely expressed in the brain and SP is released in response to stressful or painful stimuli. Here, we will discuss the effects of SP and a specific NK-1 receptor antagonist on GABAA receptor-mediated neurotransmission in the CeA of different rodent models of alcohol dependence as well as innate anxiety. Briefly, SP increases transiently frequency and amplitudes of spontaneous inhibitory postsynaptic currents (sIPSCs) in the CeA of alcohol-naïve rats suggesting increased GABA release and enhanced postsynaptic GABAA receptor-mediated neuronal inhibition. The NK-1 receptor antagonist decreases sIPSCs frequency indicative of SP release into the CeA under basal conditions and a SP participation in regulating neuronal activity. Most notably, SP effects on CeA GABA transmission are more pronounced and more sustained in alcohol-dependent rats. These functional effects are accompanied by decreased SP and NK-1 receptor expression pointing towards increased NK-1 receptor sensitivity. Similarly, larger and more sustained SP-induced increases of CeA GABAergic transmission are observed in rats undergoing alcohol withdrawal. Collectively, these data support the hypothesis that both alcohol dependence- and withdrawal-associated stress sensitize SP/NK-1 receptor signaling.

The endocannabinoid system and alcohol-related outcomes: genes, brain and behavior

Christian S Hendershot (Toronto, Canada)

Endocannabinoid genes and alcohol-induced reward phenotypes

Vijay A Ramchandani¹, Matthew E Sloan¹, Emily L Vogt¹, Melanie L Schwandt¹, Hui Sun¹, Peter Herscovitch¹, Markus Heilig¹, Nancy Diazgranados¹, David Goldman¹ (¹ Bethesda, USA)

Background: previous studies indicate that endocannabinoid (eCB) signaling may be related to the etiology of alcohol use disorder (AUD). Preclinical studies indicate that eCB administered during alcohol intake increases mesolimbic dopamine release. Cannabinoid receptor (CNR1) and fatty acid amyl hydrolase (FAAH) gene variations have been associated with alcohol response and AUD severity. However, the broader relationship between eCB and alcohol use has yet to be elucidated in humans. Aim: the aim of this study was to examine the impact of endocannabinoid system polymorphisms CNR1 rs2023239 and FAAH rs324420 following IV alcohol infusion on striatal dopamine release measured using [¹¹C]-raclopride position emission topography (PET). Methods: twenty-six healthy males underwent two, randomized PET scans with [¹¹C]-raclopride, one concurrent with intravenous

alcohol (target breath alcohol level of 80mg%) and the other with placebo. The difference in [¹¹C]-raclopride binding potential between alcohol and placebo sessions was used to quantify alcohol-induced dopamine release. Results: results show that CNR1 T/T homozygotes had significantly greater alcohol-induced dopamine release in the posterior ($p=0.001$) and anterior ventral striatum ($p=0.025$) than C-allele carriers. There was no impact of the FAAH polymorphism on alcohol-induced dopamine release. To explore interactions between eCB and opioidergic mechanisms, a linear model combining CNR1 and OPRM1 A118G genotype demonstrated a significant additive effect of both genotypes on alcohol-induced dopamine release ($R^2=0.43$). Conclusion: these results suggest an additive effect of opioid and cannabinoid systems on striatal dopamine release following alcohol. Future studies should explore the effect of eCB polymorphism on alcohol measures across the spectrum of AUD.

A laboratory-based investigation of FAAH C385A and alcohol-related phenotypes in youth

Christian S Hendershot¹, Jeffrey D Wardell¹, Laura M Best¹, Rachel F Tyndale¹, Isabelle Boileau¹ (¹ Toronto, Canada)

Background: the FAAH gene encodes the fatty acid amide hydrolase (FAAH) enzyme, which metabolizes the endocannabinoid anandamide. The A allele of the FAAH C385A variant (rs324420) has been linked to reduced enzyme activity, higher anandamide, and increased severity of alcohol use in adults. Aims: to extend this finding to a younger sample, we investigated associations of C385A with alcohol-related phenotypes among heavy-drinking youth. Methods: participants ($N=283$, mean age=19.74 years) completed a self-report battery. A subset of participants completed alcohol administration sessions involving the alcohol clamp (target BrAC=80mg%; $n=88$) and intravenous alcohol self-administration (IVASA) ($n=61$). Results: relative to youth with the C/C genotype, those with the A allele (37%) reported greater alcohol consumption (AUDIT-C; $p=0.047$), hazardous use (AUDIT; $p=0.075$), and stronger coping motives for drinking ($p=.014$). Coping motives mediated the association of genotype with consumption and alcohol-related problems. During the alcohol clamp, within-subjects analyses of subjective responses revealed a significant, positive association between sedation and craving for A allele carriers ($p=0.045$), but not CC participants ($p=0.138$). Among CC participants, within-person increases in sedation during IVASA predicted within-person decreases in craving, which in turn predicted lower self-administration (indirect effect $p=0.002$). This effect was not observed for A allele carriers. Between-subjects analyses showed no genotype differences on peak BrAC during IVASA. Conclusion: findings support an association of the C385A variant with self-reported consumption in young drinkers. Results also implicate negative reinforcement processes, including the motivational salience of acute sedative effects, as candidate behavioral mechanisms for this association. Funding: supported by the Canadian Institutes of Health Research, the Ontario Mental Health Research Foundation, and NIH P60AA007611.

Endocannabinoid-mediated effects of acute alcohol administration in healthy humans

Leah M Mayo¹, Elisabeth Paul¹, Robin Kämpe¹, Niclas Stensson¹, Bijar Ghafouri¹, Markus Heilig¹ (¹ Linköping, Sweden)

Background: chronic alcohol use is associated with dysregulation of the endocannabinoid system (eCB), a neuromodulatory system implicated in stress and reward processing. However, little is known regarding the acute effects of alcohol on the eCB system in humans. Aims: our goal was to assess the consequence of acute alcohol administration on circulating eCBs and subsequent relationship to the anxiolytic and rewarding effects of alcohol as assessed via functional magnetic resonance imaging (fMRI). Methods: thirty-two healthy adults (16 each men, women) participated in a within-subject pharmacological fMRI study consisting of two sessions (placebo, alcohol) on separate days. After drink consumption, they completed an fMRI scan assessing threat reactivity and reward processing. Blood samples were collected at baseline and before, during, and after the scan to assess plasma eCB levels. Breath-alcohol concentrations (BrAC; target=0.06g%) and subjective mood and drug effects were assessed repeatedly throughout sessions. In addition, participants were genotyped at eCB-relevant loci (e.g. FAAH rs324420 and CNR1 rs2023239). Results: alcohol significantly influenced circulating eCBs, but this effect differed between sexes. Specifically, alcohol consumption increased eCBs in women, but decreased eCB levels in men. Preliminary analyses indicate that the anxiolytic effects of alcohol (e.g. attenuation of amygdala reactivity to threat cues) appear to be mediated, in part, by eCB levels. Current analyses are underway to determine if eCBs similarly modulate reward processing during alcohol intoxication. Conclusion: these data provide insight into acute biochemical consequences of alcohol that may contribute to individual differences in alcohol use and misuse.

Are deficits in brain endocannabinoid metabolism linked to heavier alcohol use? Neuroimaging studies of the enzyme fatty acid amide hydrolase

Laura M Best¹, Bernard Le Foll, Esmaeil Mansouri, Richard Bazinet, Dina Lagzdins, Pablo Rusjan, Rachel F Tyndale, Christian S Hendershot, Markus Heilig, Junchao Tong, Stephen J Kish, Isabelle Boileau (¹ Toronto, Canada)

Background: fatty acid amide hydrolase (FAAH) is the catabolic enzyme for the major endocannabinoid neurotransmitter anandamide and a target for medication development. Preclinical and genetic studies of a functional polymorphism in the FAAH gene (C385A, rs342240) suggest that lower FAAH levels might be associated with risk for alcohol use disorder (AUD). Aim: to investigate whether lower brain FAAH level is associated with AUD, family history of AUD and/or behavioural phenotypes related to risk for AUD. Methods: FAAH brain levels were measured with positron emission tomography using the FAAH radioligand [¹¹C]CURB in healthy controls ($n=25$), in heavy-drinking youth with positive ($n=14$) or negative family history of AUD ($n=17$) and in subjects with AUD at two time points (~5

and ~25 days of monitored abstinence: n=14; n=11). Heavy-drinking youth completed an intravenous alcohol infusion session and blood samples were taken in all participants to assess FAAH C385A genotype and plasma endocannabinoid levels at multiple time points. Results: [¹¹C]CURB binding was globally lower than controls during early but not protracted abstinence and significantly correlated with drinks per week and with plasma concentrations of anandamide. Family history of AUD did not affect [¹¹C]CURB binding, however higher alcohol consumption and hazardous use (Alcohol Use Disorders Identification Test (AUDIT)) in heavy-drinking youth, as well as lower sedative effects of alcohol during intravenous administration (Biphasic Effects of Alcohol Scale) was related to lower [¹¹C]CURB binding. Conclusion: in line with preclinical studies our findings that lower FAAH is related to higher alcohol consumption (in AUD and in non-AUD heavy drinking youth) may be an acute consequence of recent chronic alcohol use (in AUD) and or a preexisting factor increasing vulnerability for hazardous use. Although clinical significance of low FAAH in AUD remains to be established, treatment approaches targeting FAAH should consider that increased endocannabinoid tone during early abstinence could drive drinking however some aspects could be beneficial. Funding: supported by the Canadian Institutes of Health Research, the Ontario Mental Health Research Foundation, and NIAAA 1R21AA022246-01A1.

Insights into alcohol-associated cancers

Sebastian Mueller (Heidelberg, Germany)

Alcohol and cancer: the epidemiological evidence

Elisabete Weiderpass¹, Carolina Espina¹, Pietro Ferrari¹ (1 Lyon, France)

Alcohol consumption is one of the top-10 health risks, contributing to circa 3.9% of worldwide burden of disease and 3.3 million annual deaths. Alcohol use increases overall cancer incidence and overall and cancer-specific mortality. The 2012 IARC Monograph reviewed the epidemiological evidence on the possible association between alcoholic beverage consumption and cancer risk at 27 anatomical sites, and reported that cancers of the upper digestive tract (UADT; oral cavity, pharynx, larynx, esophagus), liver, colorectum and female breast are causally related to the consumption of alcoholic beverages. In 2018 the World Cancer Research Fund/American Institute for Cancer Research (WCRF/AICR) report additionally showed that alcohol intake was inversely associated with the risk of kidney cancer and described a suggestive positive relationship with pancreatic cancer. There are several mechanisms through which alcohol induces cancer: a direct effect on the cells where conversion to acetaldehyde such as primarily in the liver cells, where it can induce cirrhosis; conversion also occurs in the saliva and the large intestine. Ethanol promotes production of highly reactive oxygen species, which can damage DNA, alter DNA methylation, and

has hormonal effects, including increasing oestradiol levels, which may affect the risk of breast cancer. Ethanol facilitates uptake of carcinogens in the mouth and throat, thus also increasing the risk of tobacco-induced cancers. It may also propel already existing cancers through immunosuppression, angiogenesis, and decrease the effect of chemotherapeutics. Alcohol use increases overall cancer incidence and overall and cancer-specific mortality. Epidemiological and experimental research on alcohol and cancer remains limited. Research priorities include 1) investigation of the role of alcohol in a wider list of cancers; 2) better analytical strategies to elucidate the role of drinking patterns and of specific alcoholic drinks; and 3) elucidation of the role of smoking in alcohol-related carcinogenesis, particularly in those cancer sites that are tobacco-related.

Role of adaptive immune system, particularly IgA⁺ and CD8⁺ T cells, in alcoholic steatohepatitis and its progression to hepatocellular carcinoma

Shabnam Shalapur¹ (1 La Jolla, USA)

Hepatocellular carcinoma (HCC) is one of the most prevalent malignancies worldwide and a leading cause of cancer-related deaths. Despite major growth in fighting hepatitis virus B and C, the epidemic of liver disease continues to grow with clear links to obesity and alcohol abuse. Non-alcoholic and alcoholic steatohepatitis (NASH/ASH) are the major drivers of HCC, but the mechanisms underlying the progression to HCC are poorly known. Progress in this field depends on the availability of reliable preclinical models amenable to genetic and functional analyses and exhibiting robust NASH-to-HCC progression. Using MUP-uPA mouse models, we found that accumulation of IgA⁺PD-L1⁺CD138⁺IL-10⁺ plasmacytes in NASH-afflicted human and mouse livers results in localized immunosuppression that fosters HCC development by attenuating the activation of a protective, tumor-directed cytotoxic CD8⁺ T-cell response. Moreover, we found that alcohol feeding increases tumor development through a profound induction of gut barrier disruption, and systematic changes in adaptive immune cells' development and responses. Although high fat diet (HFD) supports CD8⁺ T cell infiltration in the liver, alcohol suppresses it. Our work provides new insights on how HFD and alcohol regulate adaptive immune cells and thereby affect fibrosis and the response to immunotherapy. Specifically, consumption of alcohol or HFD regulates the response to anti-PD(L)1 therapy in a different manner, namely due to its distinct ability to regulate CTL function and induction of dysbiosis, both locally and systemically.

Molecular mechanisms of alcohol-associated cancers: from metabolism and oxidative stress to stem cells and genomic instability

Vasilis Vasilou¹, David C Thompson² (1 New Haven, USA, ² Aurora, USA)

Chronic ethanol abuse is associated with, and may be involved with the development of, several types of cancers

in humans, including liver, colon, pancreas and, in women, breast. Although the exact cause of alcohol-induced cancer is currently unknown, several possible underlying mechanisms have been suggested and are currently under investigation. It is well established that alcohol metabolism promotes oxidative stress. Of the many molecules formed during ethanol metabolism, the aldehydes exhibit activities that can promote cancer. Acetaldehyde and lipid peroxidation aldehydes (generated by reactive oxygen species during CYP2E1-mediated alcohol metabolism) can form DNA adducts, and thereby cause genetic mutations, inhibit DNA repair, and disrupt DNA replication processes, all of which cause genomic instability – a hallmark of cancer. In addition, aldehydes may adduct proteins and inhibit cellular processes, such as folate and retinoid metabolism. They can also regulate redox-sensitive signaling pathways and transcription factors that sustain inflammation. Alcohol consumption affects the composition and function of the gut microbiome, leading to inflammation and changes in the function of the immune system, both of which are known to promote and exacerbate cancer. Importantly, gastrointestinal bacteria can produce acetaldehyde from ethanol. Finally, reactive oxygen species and lipid aldehydes may also affect immunometabolism that is now recognized as an important factor in cancer. As such, there are many mechanisms by which aldehydes can contribute to alcohol-associated cancers. As the primary enzymes responsible for detoxifying aldehydes, aldehyde dehydrogenases (ALDHs) have the potential to influence alcohol-associated carcinogenesis. Indeed, we and others have shown ALDHs to be involved in the pathophysiology of cancer and cancer stem cells. We now propose two novel hypotheses regarding the role of ALDHs in alcohol-mediated carcinogenesis. First, ALDHs may shield tumor-initiating or tumor cells against genomic instability by protecting their DNA repair mechanisms from damage by acetaldehyde and lipid-derived aldehydes. Second, ALDH-derived acetate could serve as a precursor of acetyl-CoA, a fuel used to form biomolecules in cancer cells. In conclusion, the mechanisms by which alcohol metabolites and associated oxidative stress may contribute to carcinogenesis are complex and often interconnected. Their elucidation provides new opportunities for the prevention or mitigation of alcohol-associated cancers.

Local acetaldehyde – its key role in alcohol-related upper gi tract carcinogenesis

Mikko Salaspuro¹ (¹ Helsinki, Finland)

Ethanol molecule is neither genotoxic nor mutagenic. However, its first metabolite acetaldehyde (ACH) associated with the consumption of alcoholic beverages is classified as carcinogenic in humans. ACH concentrations present in saliva instantly after alcohol drinking result in the generation of mutagenic ACH-DNA adducts in human mouthwash samples and in oral mucosa of rhesus monkeys. Recently, similar ACH levels have been shown to play a key role in ethanol-dependent telomere shortening in primary human foreskin fibroblasts. Strongest evidence for the local carcinogenicity of ACH in man provides a point mutation in

the aldehyde dehydrogenase 2 gene, which has randomized millions of alcohol consumers to markedly increased ACH exposure via saliva and gastric juice. This novel human cancer model is associated with a manifold risk for upper GI tract cancer and proves conclusively the causal role of local ACH in alcohol-related upper digestive tract carcinogenesis. Most importantly, the model minimizes the role of confounding factors hampering most epidemiological studies on alcohol and cancer. Normal human saliva does not contain measurable levels of ACH. However, alcohol ingestion results within seconds in a concentration-dependent accumulation of ACH in saliva, which continues up to 10-15 minutes after each sip of alcoholic beverage. The prominent instant increase of salivary ACH level is followed by a long-term phase lasting for as long as ethanol stays in the saliva. Bacteria and yeasts representing normal upper GI tract microbiome play a major role in local ACH formation from ethanol. This is contributed locally by organ specific expression and gene polymorphisms of ethanol- and ACH-metabolizing enzymes.

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Novel concepts in the evaluation of fibrosis in alcohol-related liver disease

Carolin Lackner (Graz, Austria)

Non-invasive fibrosis assessment in compensated and decompensated alcohol-related liver disease and clinical implications

R. Stauber¹ (¹ Graz, Austria)

Alcohol-related liver disease (ALD) is the most common liver disease in the Western World. Especially in Europe ALD is a substantial burden as the European population has the highest per capita alcohol consumption world-wide. However, awareness about the risks of heavy drinking is low among patients with ALD and they usually present at an advanced stage with clinical symptoms such as jaundice and/or ascites. Early/compensated ALD does not manifest itself clinically and patients rarely seek medical advice, unless ALD is detected during work-up of other illnesses. Screening for early ALD is warranted since it is readily reversible under abstinence and treatment is available (psychological interventions, anti-craving drugs). Recent data show that prognosis of early ALD, apart from abstinence, is mainly determined by histological fibrosis stage; advanced fibrosis (F3, bridging fibrosis; F4, cirrhosis) carries dismal outcome (10-year mortality 45%). However, due to the high prevalence of ALD, universal liver biopsy is not feasible. Noninvasive fibrosis tests have shown high diagnostic accuracy for advanced fibrosis in a variety of liver diseases including ALD. Among these, simple fibrosis tests such as FIB-4 are based on routine clinical and laboratory parameters and provide relatively high

diagnostic accuracy at low cost. Proprietary fibrosis panels based on direct fibrosis markers including Enhanced Liver Fibrosis (ELF™) test, FibroMeter™ and FibroTest show improved diagnostic accuracy. Vibration-controlled transient elastography (VCTE, FibroScan®) enables noninvasive estimation of liver stiffness (LS) and has shown superior diagnostic accuracy in comparative studies. However, LS is not only determined by fibrosis but also inflammation, cholestasis and/or hepatic congestion. Importantly, several studies have demonstrated a rapid decline of LS during alcohol detoxification, which presumably reflects the resolution of steatohepatitis. A recent comparative study showed best performance for VCTE (per protocol) and ELF score. While the latter tests are mostly restricted to referral centers, simple tests such as FIB-4 are suitable for screening in primary care. The clinical impact of noninvasive fibrosis tests in decompensated ALD is rather limited since most patients already have clinical signs of cirrhosis.

Staging of alcohol-related liver disease and clinical implications

C. Lackner¹ (¹ Graz, Austria)

Histological stage has emerged as one of the most important predictors of outcome in most chronic liver diseases including non-alcoholic fatty liver disease (NAFLD), chronic viral hepatitis and autoimmune liver diseases. Surprisingly, despite the fact that ALD is among the most frequent liver diseases, to date no universally accepted histological staging system has been devised. Because NAFLD and ALD share broad morphological overlap, also with respect to type of fibrosis and its centrilobular predominance, several authors have proposed that histological staging systems for NAFLD may also be used for ALD. However, there are points of concern with such an approach. Firstly, most patients with compensated as well as decompensated ALD are cirrhotic at first presentation. There are different histological stages of severity of cirrhosis which are not reflected in most staging systems used in NAFLD. Secondly, there are data suggesting that pericellular and septal fibrosis types may have different impact on outcome in patients with ALD. An ALD-specific staging system has recently been devised by the Consortium for the Study of Alcoholic LiVer Disease in Europe (SALVE) Histopathology Group. This ALD-specific staging system (SALVE stage) reflects different histological stages of severity of cirrhosis and the degree of pericellular fibrosis in ALD. The potential clinical implications of SALVE staging will be discussed.

Histologic fibrosis patterns associate with disease severity and short-term mortality in patients with acute decompensation of cirrhosis

Yan Wang¹ (¹ Guangzhou, China)

Histologic fibrosis has an important prognostic value in natural history of chronic liver disease. However, there are few evidences for its role in the end stage of liver disease. For the purpose of fully describing the morphologic features

of cirrhotic fibrosis with diverse etiology, we developed a dual-photon microscopy-based computerized image analysis tool to detect collagen architectural features including both collagen geometry and collagen spatial network within septa, nodule, and sinusoidal regions of interest. A profile of these collagen features composed the quantitative collagen pattern (QCP) of the detected biopsy specimen. By using this tool, we analyzed a retrospective cohort, which included 225 hospital patients diagnosed with acute decompensation of biopsy-proven cirrhosis, with clinical collaboration from the Institute of Liver and Biliary Science, New Delhi, India. We found that QCP faithfully captured the morphologic difference in fibrosis patterns between etiologies of fatty liver diseases and viral hepatitis and between Laennec stages. It also related to MELD and HVPG. When using for predicting the short-term mortality in these patients, QCP had a robust prognostic performance superior to MELD, CTP, Laennec stage and collagen proportionate area. On multivariate regression, it was identified as an independent prognostic factor. All the data indicate that histologic fibrosis captured by QCP could have an important prognostic value even in the end stage of liver disease. In addition, because by using the same measurement strategy, we previously found that cirrhosis remodeling in viral hepatitis can be detected in high accuracy, we would propose that QCP may be helpful for assisting the investigation of undiscovered meaning of histologic fibrosis with diverse chronic liver disease.

Ethanol-induced neuroinflammation and oxidative stress: chronic ethanol intake and binge-like intoxication – translational options

Yedy Israel (Santiago, Chile)

It is well accepted that chronic alcohol intake or its administration lead to neuroinflammation; seen as morphological changes in astrocytes and microglia. These are clearly seen in alcohol-consuming rodents, while microglial changes in humans presenting alcohol-use-disorders (AUD) may depend on the noninvasive detection method employed. Neuroinflammation and oxidative stress are self-perpetuated for prolonged periods in a vicious-like cycle and appear to be the basis for protracted increases in chronic ethanol intake and relapse-like binge drinking. The presentations in this Symposium show (i) clear microglial changes, as determined by PET imaging in AUD patients; (ii) demonstrate marked reductions in ethanol intake induced by antioxidant N-acetyl cysteine both in operant and chronic ethanol administration paradigms in rodents, including the abolition of binge-like drinking in the post-deprivation and re-access condition (ADE) (iii) show that N-acetyl cysteine normalizes the both oxidative stress and the glial changes induced by ethanol, in line with the vicious cycle hypothesis (iv) demonstrate that the systemic or intranasal administration of mesenchymal stem cells (MSC) or MSC-products, presenting marked anti-inflammatory and antioxidant properties, strongly inhibit

ethanol-induced and relapse drinking. These studies further show that MSCs normalize the ethanol-reduced levels of the glial glutamate transporter GLT-1. Overall the Symposium ties neuroinflammation/oxidative-stress/hyper-glutamatergic conditions as the likely mechanism that perpetuates chronic alcohol intake and promotes intoxicating relapse. Translational options are envisioned.

TSPO PET imaging to study the dynamics of ethanol-induced neuroinflammation

Wadad Saba¹ (¹ Orsay, France)

Imaging techniques play an important role for the non-invasive determination of the effects of alcohol in vivo, mainly focusing on brain structure and neuronal function. Positron Emission Tomography (PET) imaging using radioligands of the translocator protein 18 kDa (TSPO), a biomarker of glial activation, is useful to address the importance of neuroinflammation in various pathophysiological states and offers a unique tool to study the dynamics of the neuroimmune impact of alcohol exposure on the brain. In adolescent monkeys, TSPO PET imaging using ¹⁸F-DPA-714 revealed that an acute and initial ethanol exposure (0.7-1.0 g/L) induced an immediate and prolonged (7-12 months) glial activation, suggesting a priming of glial function after initial alcohol exposure. In rats chronic alcohol exposure over a 14-day period induced an increase in the binding of ¹⁸F-DPA-714 which was reduced by nalmefene (0.4 mg/kg, s.c, 1 hour prior to ethanol injection). This unexpected effect could be linked to the antagonist property of nalmefene on Toll-like receptor 4 (TLR4). Our results are consistent with neuroinflammation associated with acute/chronic alcohol exposure. This contrasts with the decreased binding of ¹¹C-PBR28, another TSPO ligands, observed in the brain in patients with alcohol use disorders, which is consistent with a blunted peripheral proinflammatory response compared with controls. TSPO PET imaging provides a novel insight into the dynamics of glial function related to alcohol exposure and may be useful to i) address the neuroimmune component of alcohol-related neurotoxicity and addiction and ii) evaluate immunotherapeutic strategies for neuroprotection or the treatment of alcohol dependence.

Evaluation of N-acetylcysteine effects on two preclinical rat model of Alcohol Use Disorders: the operant binge drinking model and the "post-dependent" state rat model

Catherine Vilpoux¹, Sophie Lebourgeois¹, María Carmen González-Marín¹, Mickael Naassila¹ (¹ Amiens, France)

Many components of ethanol addiction such as reinforcement, withdrawal, extinction, and relapse are known to involve glutamate transmission, and N-acetylcysteine (NAC) is thought to counteract glutamatergic dysregulation underlying ethanol addiction. We tested NAC effect on two different rat models of Alcohol Use Disorders (AUD). In a rat model of operant binge drinking, we demonstrated the efficacy of acute 100 mg/kg NAC treatment to reduce ethanol alcohol self-

administration, alcohol-seeking behavior and to reduce relapse on rats that were abstinent for 17 days. In a "post-dependent" state rat model (induced by chronic intermittent ethanol (CIE) vapour exposure for 10 weeks in male Wistar rats), we evaluated the effects of NAC during acute withdrawal, 8 hours after inhalation chambers were turned off. We showed that a lower dose of NAC (25 mg/kg) was enough to reduce ethanol self-administration and motivation to consume ethanol, evaluated in a progressive ratio paradigm, while the 50 mg/kg NAC reduced extinction responding and reacquisition of self-administration after 1 month abstinence. Overall, our results demonstrate that NAC is able to limit rat's ethanol self-administration, extinction responding, and relapse, making it a potential new treatment for the maintenance of abstinence via an anti-craving effect. We will discuss further the possibility to evaluate NAC potential as a new treatment of AUD in patients.

Administration of anti-inflammatory mesenchymal stem cells or its secretome inhibits alcohol self-administration and blocks relapse intake. Mechanisms and translational opportunities

Fernando Ezquer¹, Maria Elena Quintanilla¹, Paola Morales¹, Daniela Santapau¹, Pablo Berrios-Cárcamo¹, Marcelo Ezquer¹, Mario Herrera-Marschitz¹, Yedy Israel¹ (¹ Santiago, Chile)

Chronic alcohol consumption leads to neuroinflammation and brain oxidative stress, which inhibit the astrocyte Na-glutamate transporter (GLT-1), proposed to perpetuate alcohol intake and relapse. Mesenchymal stem cells have been postulated as a therapeutic option for the treatment of different diseases since they can produce potent anti-inflammatory molecules and reduce oxidative stress. Studies presented evaluate the addictive-like suppression exerted by (i) intracerebroventricular administration of anti-inflammatory mesenchymal stem cells (MSCs), (ii) intravenous administration of MSC-spheroids or (iii) intranasal administration of MSC-derived secretome in a rat model of chronic ethanol intake and relapse drinking. Studies show that administration of a single intracerebroventricular or intravenous dose of MSCs or the administration of three intranasal doses of MSC-derived secretome: (a) inhibited chronic ethanol intake and relapse binge drinking by 80-90%, displaying protracted effects over 4-5 weeks; (b) fully normalized alcohol-induced neuroinflammation, shown as a reduced astrocyte and microglia activation in hippocampus; (c) reduced brain oxidative stress evidenced by the restoration of the normal hippocampal GSH/GSSG ratio and (d) markedly increased the levels of the GLT-1 transporter in prefrontal cortex and nucleus accumbens. Knockdown of GLT-1 transporter by administration of an antisense oligonucleotide fully abolished the inhibitory effect of MSC-derived secretome on ethanol intake, suggesting that the glutamate transporter GLT-1 mediates the addictive-like MSCs inhibitory effects. Overall, studies indicate that the administration of anti-inflammatory mesenchymal stem cells or its secretome affords translational opportunities for the treatment of alcohol-use disorders. Supported by FONDECYT #1180042 to YI.

Translational studies on ethanol effects in adolescence

Cindy L Ehlers (La Jolla, USA)

Neurophysiological synchrony and sleep are both disrupted in young adult humans and rats with a history of adolescent alcohol exposure

Cindy L Ehlers¹ (La Jolla, USA)

The present study aimed to document the young adult consequences of adolescent alcohol exposure, in humans and rodents, as assessed by waking EEG and sleep. Synchrony of phase (phase-locking, PL) of event-related oscillations (EROs) between frontal and parietal cortex and sleep data, were evaluated. The human participants were young adults (age 18-30 yrs, n=1041), with and without a history of adolescent binge drinking (5 drinks for boys 4 for girls per occasion at least once per month), and 74 young adult rats with and without a history of 5 weeks of adolescent alcohol vapor exposure (PD 23-55). Human binge drinkers were found to have lower PL in the beta and theta frequencies between frontal and parietal cortex. PL was also decreased in the rats exposed to ethanol vapor in the theta band across the two cortical regions. A history of adolescent regular binge drinking was also associated with reduced sleep quality as indexed by: longer sleep latencies, more problems with breathing, bad dreams and an overall higher Pittsburgh sleep quality index total score. Adolescent vapor exposure in the rat was found to result in decreases in theta power (4-8 Hz) and delta (1-4 Hz) and theta (4-8 Hz) power during slow wave sleep (all $p < 0.05$). These findings suggest that alcohol exposure during adolescence may result in deficits in sleep quality in humans and slow wave sleep in animals and decreases in synchrony between cortical neuronal networks, in both species. Supported by R37 AA010201, AA026248, RO1 AA027316, U01 AA019969.

Adolescent alcohol exposure alters adult neurobiology through neuroimmune and epigenetic signaling

Fulton Crews¹ (Chapel Hill, USA)

Adolescence brain develops in parallel with maturation of self-control. To investigate the impact of adolescent binge drinking on brain development Wistar rats were exposed to adolescent intermittent ethanol (AIE, 5gm/kg/day-2 days on-2 off) across puberty and assessed in adulthood for cognitive deficits and changes in neurobiology. Post-mortem human brain of controls or AUD patients were also determined. AIE increased adult brain expression of innate immune genes HMGB1, CCL2, Toll-like receptors, and RAGE. AIE also increased activation of the transcription factor NFkB and altered glial morphology in parallel with increases in histone methylation, H3K9me2, a marker of epigenetic silencing. AIE also increased adult risky decisions and blunted behavioral flexibility in parallel with reduced

adult hippocampal neurogenesis, reduced forebrain cholinergic and midbrain serotonergic neurons as well as increases in markers of neurodegeneration. Post-mortem AUD human brain also indicated increases in HMGB1, toll-like receptors, RAGE, interferon, CCL2 and other signaling genes. Further, increases in human AUD brain gene expression correlated with age of drinking onset and lifetime alcohol consumption. Emerging studies find exercise, indomethacin, donepezil and galantamine prevent and/or reverse AIE pathology. These findings support the hypothesis that adolescent alcohol exposure increases expression of HMGB1, TLR, RAGE, NFkB, and other genes are modified through epigenetic gene silencing or enhancing signals that persist into adulthood long after alcohol exposure ends, but are in some cases are reversible. These findings identify targets for consideration of treatment of adolescent onset AUD. Supported by NIAAA AA020024, AA020023, AA011605.

Impulsive action and decision making in young adults binge drinkers; brain mechanisms

Theodora Duka¹ (Brighton, UK)

Binge drinking is associated with increased impulsivity. Data will be presented to elaborate on the role of impulsivity facets and brain function in alcohol abuse. In young adult binge drinkers (BD; aged 18 to 25) the relationship between “motor” impulsivity in the form of “can’t stop” and “can’t wait” as well as “temporal” impulsivity (failure to delay gratification) is examined. In parallel, “can’t wait” impulsivity is tested in two inbred strains of mice known to differ in alcohol intake (alcohol preferring and alcohol averse mice). In addition functional brain activity and resting state functional connectivity is tested in BD. Binge drinkers showed robust impairments in “can’t wait” impulsivity under increased attentional load; alcohol preferring mice also showed impairments in “can’t wait” impulsivity compared to alcohol-averse mice before any exposure to alcohol. Brain imaging revealed that higher BD severity is associated with enhanced activation in precentral gyrus and superior parietal lobule during successful stop responses, indicating a compensatory mechanisms. Delayed gratification was associated with lower frontopolar activation. Resting-state functional connectivity revealed that the higher the incidence of BD, the lower the coupling of the right supramarginal gyrus to the Ventral Attentional Network (VAN). These findings support the assumption that aspects of cognitive impairments seen in binge drinkers in particular those associated with “can’t wait” impulsivity may precede drinking behaviour. Disrupted functional connectivity within the Ventral Attention Network in more bingeing individuals may suggest disrupted attentional processing providing supporting evidence for the brain signature associated with binge drinking.

Epigenetic, neuroinflammation and GluN2B participate to cognitive deficits after ethanol binging in adolescent rat

Olivier Pierrefiche¹ (Amiens, France)

Binge drinking induces memory impairment and recently, we showed that only Two Ethanol Binge-like Exposure (TEBE) in adolescent rats are sufficient to transiently abolish long-term synaptic depression (LTD) in the hippocampus leading to mnesic deficits after 48h. To understand the mechanism of such long-lasting action of EtOH, we investigated the role of epigenetic and neuroinflammation after TEBE in the hippocampus of young adult rats. Neuroinflammation was revealed through an increase in TLR4 immunolabelling in CA1 area and in vimentin + GFAP co-labelling showing astrogliosis in the dentate gyrus (DG). Neurogenesis was revealed with an increase in doublecortin labelling in the subgranular zone of the DG. In stratum oriens of CA1, synaptic pruning probably occurs since synaptophysin labelling decreased. Expression level and activity of Histone Deacetylase 2 (HDAC2), involved in epigenetic, increased while acetylated Histone 4 (Ac-H4) decreased. Further, TEBE increases mRNA level for GluN2B subunit of the NMDA receptor while ChIP analysis revealed that HDAC2 modulates the GluN2B gene promoter. Further, TEBE altered GluN2A/GluN2B balance in synaptic transmission. Finally all cellular effects of TEBE were prevented with sodium butyrate, an HDAC inhibitor. In conclusion, two EtOH exposures induces long-lasting memory-impairment because it overexpressed HDAC2 resulting in GluN2A/GluN2B imbalance that leads to LTD blockade. In parallel, neuronal injury and altered morphologic plasticity in the hippocampus take place. It is now important to study the link between inflammation and epigenetic in the effects of ethanol since this would help developing new therapeutic strategy.

New arguments for a role of the gut microbiota and inflammation in alcohol-use-disorders

Philippe de Timary (Brussels, Belgium)

The gut microbiome in binge alcohol drinking: recent translational efforts

Lorenzo Leggio¹ (¹ Providence, USA)

We provided the first descriptive analysis of the gut microbiome in a unique non-human primate model of alcohol binge-drinking. We analyzed the gut microbiome on fecal samples from male baboons chronically exposed to either alcohol or a non-alcoholic isocaloric beverage (tang). There were three treatment groups: G1=tang (controls); G2="short-term" alcohol binge drink (2-3 years); G3="long-term" alcohol binge drink (10 years). Fecal samples were collected in two conditions: A=early abstinence (days 3-5) and B=during 3 days of ongoing drinking. Microbial alpha-diversity was significantly lower in the G3 group vs. the G1/G2 groups. The two genera *Lactobacillus* and *Streptococcus* showed high relative abundances in G3. *Fecalibacterium* was reduced in G3 only. For G2, the order Clostridiales and the family Ruminococcaceae showed high relative abundances compared to G1 and G3. Cohort G1 showed members of

the family Anaeroplasmataceae to be more abundant. No significant difference was found between Conditions A and B. Our findings suggest that in alcohol binge drinking baboons, long-term exposure to alcohol binge drinking (G3) leads to significant changes in the gut microbiome, whereas short-term (G2) does not. These changes were not affected by acute short-term forced abstinence. This was confirmed in a rat model of binge alcohol drinking, where we see similar reduction in microbiome diversity after prolonged exposure, and this whether the rats were knock-out or not for the receptor of the feeding-related hormone ghrelin. Our result support a role for the gut microbiome in binge drinking.

Implication of the gut microbiota in the behavioral changes linked to alcohol-dependence: mechanistic approach

Sophie Leclercq¹, Tiphaine Le Roy¹, Laure Bindels¹, Caroline Quoilin¹, Audrey Neyrinck¹, Peter Stärkel¹, Philippe de Timary¹, Nathalie M Delzenne¹ (¹ Brussels, Belgium)

It is well established that alteration of the gut microbiota composition can disturb many aspects of host physiology, including metabolism, immunity and peripheral and central nervous system with consequences for brain functions and behavior. In a previous study, we showed that alterations of the gut microbiota composition of alcohol-dependent (AD) patients were associated with high score of depression, anxiety and alcohol craving, suggesting the existence of a gut-brain axis in AD patients. Here, we demonstrated the causal role of the gut microbiota in the development of the psychological symptoms associated with alcohol dependence, by using fecal microbiota transplantation. The microbiota of AD patients and healthy controls (CT) were transferred into two groups of mice which were subsequently tested for behavior. We found that mice transplanted with the gut microbiota of AD patients exhibited increased depression-like behavior and decreased social behavior compared to CT-recipient mice. Furthermore, AD-recipient mice showed increased inflammatory cytokines and activated microglia markers in the striatum, decreased expression of myelin-related genes in the frontal cortex and unbalance of GABA/glutamate neurotransmission. Metabolomics analysis revealed that a specific metabolite might be responsible for these changes in brain functions and behavior observed in AD-recipient mice. These results strongly reinforce the existence of gut-brain interactions in mental disorders, and highlight the gut microbiota as a new potential target in the management of alcohol addiction.

The gut microbiota as a new target in the treatment of disinhibition in alcohol-dependence: a clinical study

Caroline Quoilin¹, Julie Duque¹, Philippe de Timary¹, Sophie Leclercq¹ (¹ Brussels, Belgium)

Alcohol dependence is usually seen as a disinhibitory disorder, notably characterized by a state of central nervous system hyperexcitability and a lack of inhibitory control. In parti-

cular, by applying transcranial magnetic stimulation (TMS) over primary motor cortex (M1) to assess the excitability of the motor corticospinal pathway during action preparation, we have shown that alcohol-dependent (AD) patients suffer from a deficit in physiological motor inhibition when planning a behaviour. Recently, among the potential mechanisms underlying this inhibitory deficit, an alteration of the gut microbiota composition has been identified as a promising candidate. Here, we aimed at determining whether a treatment with prebiotics, by restoring the microbiota, modifies motor cortex excitability and inhibitory abilities of AD patients. To do so, 50 AD patients participated in a randomized, double blind, placebo-controlled clinical trial, in which they received a supplementation with dietary fibers (inulin) or a placebo during a 3-week detoxification program. Motor cortex excitability was examined at the end of the treatment, using a range of TMS measures, including the resting motor threshold, recruitment curve, short and long intracortical inhibition and intracortical facilitation within M1. Moreover, physiological motor inhibition was assessed during action preparation by applying TMS in a choice reaction time task. Finally, all patients completed questionnaires and performed neuropsychological tasks to evaluate their level of impulsivity and behavioral response inhibition. This double-blinded clinical study will allow to elucidate whether the gut microbiota is an effective target in the treatment of a core symptom of alcohol dependence.

Does inflammation lead to changes in brain anatomy in alcohol use disorder (AUD)? The effects of alcohol withdrawal in MRI scans

Philippe de Timary¹, Géraldine Petit¹, Laurence Dricot¹, Sophie Leclercq¹, Pierre Maurage¹ (¹ Brussels, Belgium)

AUD is characterized by large brain morphological alterations. Alcohol-withdrawal, is attended by large behavioral and inflammatory changes that have been related to altered microbiota composition. Here we tested by MRI scans the hypothesis of a drinking related edema that would resolve during withdrawal. 19 AUD inpatients undergoing a detoxification, were tested on the first and 18th day of withdrawal, for MRI brain anatomy and DTI. Results: using paired T tests, alcohol withdrawal was attended by significant decreases in volume of 4th ventricle, choroid plexus, white matter, while the cortical volume was increasing. In parallel to these changes, we also observed a decrease in mean diffusivity in all the white matter regions tested, and these decreases were significant in 21 out of the 36 regions tested. A decrease in mean diffusivity was also observed in grey matter in 160 of the 180 regions tested and significant in 50 of these regions, but globally significant changes were observed in regions corresponding to the central executive, motor, salience, auditory, and most significant in the visual and default-mode grey matter regions. In only one region we observed a significant increase in mean diffusivity : the right pallidum. Conclusion: alcohol withdrawal is related to changes in brain anatomy and mean diffusivity in both white and grey matter regions. These changes will be compared

to plasma inflammatory markers, to evaluate whether these changes could express brain inflammation and to changes in functional connectivity and behavior.

CIFASD advances in the pathophysiology and diagnosis of FASD

Michael E Charness (Boston, USA)

Molecular mechanisms underlying ethanol teratogenesis and its antagonism

X. Dou, J.Y. Lee, Michael E Charness¹ (¹ Boston, USA)

Ethanol teratogenesis is caused in part by ethanol disruption of the L1 neural cell adhesion molecule (L1). Ethanol inhibits L1 adhesion by interacting with a binding site in the extracellular domain of L1 at the Ig1-Ig4 interface. NAPVSIPQ (NAP) an octapeptide, blocks ethanol inhibition of L1 adhesion and prevents ethanol teratogenesis in mouse embryos at femtomolar concentrations by an unknown mechanism. Ethanol inhibition of L1 adhesion requires L1 binding to ankyrin-G and the spectrin/actin cytoskeleton. Dephosphorylation of selected residues on the L1 cytoplasmic domain (L1-CD) leads to uncoupling of L1 from ankyrin-G, rendering L1 insensitive to ethanol. Polymorphisms in the genes that encode p90^{rsk}, a kinase that phosphorylates the L1-CD, and ankyrin-G were associated with facial dysmorphism in children with heavy prenatal alcohol exposure. Ankyrin-G binding to L1 requires dephosphorylation of tyrosine in the FIGQY¹²²⁹ ankyrin-binding motif of the L1-CD. Femtomolar concentrations of NAP activated the phosphorylation of L1-Y1229 and the dissociation of L1 and ankyrin-G. NAP phosphorylation of L1-Y1229 was mediated by EphB2, and knockdown of EphB2 abolished ethanol inhibition of L1 adhesion. Thus, NAP antagonizes ethanol inhibition of L1 adhesion by activating the phosphorylation of L1-Y1229, inducing the dissociation of L1 and ankyrin-G, and stabilizing an ethanol-insensitive conformation of L1. Supported by NIAAA Grant R01AA012974; U24AA014811 (CIFASD); VA Merit Review 5I01BX002374; and DoD W81XWH-12-2-0048 Subaward 8742sc.

Synergistic gene-environment interactions in a zebrafish model of Fetal Alcohol Spectrum Disorders

J.K. Eberhart¹, S. Tucker, Y. Fernandes¹, N. McCarthy¹ (¹ Austin, USA)

Susceptibility to FASD is genetically modulated, but the nature of these modifying loci is poorly understood. We have used genetic screens to identify mutants that are sensitive to normally sub-teratogenic doses of ethanol. Embryos mutant or heterozygous for platelet-derived growth factor receptor alpha (pdgfra) are exquisitely sensitive to ethanol-induced facial defects. Under control conditions, proper

neural crest cell migration, but not survival, requires *Pdgfra* function. Following ethanol exposure, *Pdgfra* promotes the survival of neural crest cells. The PI3K pathway is the major *Pdgfra* effector, and the PI3K/mTORC1 pathway modulates ethanol teratogenesis. We have used CRISPR/Cas-9 to generate mutants altering mTORC1 function and are currently assaying the ethanol sensitivity of these mutants. Disruption of the essential mTORC1 complex member rapTOR sensitizes embryos to ethanol-induced defects, whereas elevating mTORC1 function by disrupting *tsc1a* restores facial development in ethanol-treated *pdgfra* mutants and heterozygotes. The mTORC1 pathway is also associated with social behavior, and ethanol alters social behavior in zebrafish. Consistent with our findings in the face, reduced *tsc1a* gene dosage appears to protect against ethanol-induced social behavioral reductions. Collectively, our findings implicate the mTOR pathway in multiple aspects of FASD. This work is supported by NIH/NIDCR R01DE020884, NIH/NIAAA and NIH/NIAAA U01AA021651 as a component of the Collaborative Initiative on Fetal Alcohol Spectrum Disorders (CIFASD) to J.K.E.

Ethanol and cannabinoids interact to induce birth defects through a mechanistic pathway converging on primary cilia

S.E. Parnell¹, E.W. Fish¹, K.E. Boschen¹ (¹ Chapel Hill, USA)

Ethanol has long been known to be teratogenic, inducing significant craniofacial and brain abnormalities during embryogenesis. We have shown that exposure to both synthetic cannabinoids and the natural cannabinoids found in cannabis – THC and cannabidiol (CBD), during early gestation in mice results in abnormalities similar to those caused by ethanol, including midfacial hypoplasia, holoprosencephaly, and cleft lips/palates. These effects are synergistically produced by the combination of small doses of ethanol and cannabinoids. The teratogenic effects of these drugs are mediated through reductions in the sonic hedgehog (Shh) signaling pathway within the neural tube and can be ameliorated in two ways: amplification of Shh signaling; or inhibition of cannabinoid signaling with cannabinoid receptor 1 (CB1) antagonists. Ethanol inhibits Shh signaling through disruptions of primary cilia function (Shh requires cilia for normal signaling). We also show that cannabinoids inhibit Shh signaling through inhibition of smoothened (Smo), the main effector molecule of the Shh pathway, and CB1 binds to Smo in the primary cilium, acting as an endogenous regulator to fine-tune Shh signaling and downstream mTOR pathway activity. Together, these data demonstrate a mechanistic pathway through which ethanol and cannabinoids act synergistically to impair embryonic development. Supported by NIAAA grants R01AA026068 and U01AA021651 as a component of the Collaborative Initiative on Fetal Alcohol Spectrum Disorders (CIFASD) (S.E.P.).

Utilising 3D facial analysis for the early identification of fasd associated facial dysmorphism at neonatal and infant stages

Michael Suttie¹, Peter Hammond¹, Neil Aiton², CIFASD³
(¹ Oxford, UK, ² Brighton, UK, ³ Collaborative Initiative on Fetal Alcohol Spectrum Disorders, USA)

At the most severe end of the FASD spectrum is Foetal Alcohol Syndrome (FAS), where diagnosis is reliant on the identification of a complex set of neurocognitive deficits and identifiable facial features. To attain diagnosis, individuals would typically have been brought to the attention of care professionals or by guardians or parents at early stages of education when behavioural and neurodevelopmental deficiencies become apparent. Individuals with FAS facial criteria make up only a small proportion of those prenatally exposed to alcohol, and cases are often missed. At the neonatal stage, cognitive assessment is not possible, and an individual without the characteristic facial features will not receive diagnosis until later on in childhood. Previous studies in adolescent populations have utilised 3D imaging, accurately identifying FAS individuals, and objectively recognising subtle facial dysmorphism across the FASD spectrum. For this study, 3D images of infants taken at one month and one year were collected from a South African population, and neonatal images were obtained from a Caucasian population from a clinic in Brighton, UK. Using surface-based analysis of facial form, we observe subtle changes in dysmorphism that occur at the two time points. In addition, we identify subtle dysmorphism in those with a record of prenatal alcohol-exposure in the neonatal population. At neonatal and infant stages, 3D imaging may accurately and objectively assist facial analysis in those exposed prenatally to alcohol, particularly where features are subtle and more challenging to identify. Early diagnosis is paramount to providing early support and improving outcomes. Supported by NIAAA Grant U01AA014809 as a component of the Collaborative Initiative on Fetal Alcohol Spectrum Disorders (CIFASD).

Gut microbiota and alcohol: present and future

Jose Antonio López-Moreno (Madrid, Spain)

Gut microbiome may predispose to alcohol use disorder in rats

Kshitij S Jadhav¹, Veronica L Peterson², John F Cryan², Benjamin Boutrel¹ (¹ Lausanne, Suisse, ² Cork, Ireland)

Alcohol use represents a significant public health cost, accounting for 4.5% of global disease burden. With current pharmacotherapies largely unsatisfying, discovering novel alternatives to prevent alcohol use disorder becomes a priority. Hence, identifying biological markers predicting vulnerability to develop excessive alcohol consumption may lead to a real improvement of clinical care. With converging evidence suggesting that gut microbiota is capable of influencing brain and behavior, we aimed at investigating the gut microbiome in rats exhibiting uncontrolled alcohol seeking behaviors defined as: 1) inability to abstain during a signaled period

of reward unavailability, 2) increased motivation assessed in a progressive effortful task and 3) persistent alcohol seeking despite aversive foot shocks. Based on addiction criteria scores, rats were assigned to either Vulnerable or Resilient group. Not only Vulnerable rats displayed increased impulsive and compulsive behaviors, but also displayed increased relapse after abstinence and increased sensitivity to baclofen treatments compared to resilient animals. Following a 2-month wash out period, rats were sacrificed; dorsal striatum was collected to assess dopamine receptor mRNA expression, and 16S microbiome sequencing was performed on caecal contents. Analyses revealed significant correlations between gut microbiome and impulsivity measures, as well as augmentations in striatal Dopamine 1 receptor (D1R) and reductions in D2R as vulnerability to AUD increased. Therefore, using a singular translational approach based on biobehavioral dispositions to excessive alcohol seeking without heavy intoxication, our observations suggests an association between gut microbiome composition and the vulnerability to lose control over alcohol seeking behaviors. Acknowledgements: this work was supported by APC Microbiome Ireland and Science Foundation Ireland (SFI) [Grant No. 12/RC/2273], the Swiss National Science Foundation (Grant No. 310030_185192) and the Department of Psychiatry, Lausanne University Hospital. KSJ is recipient of a Swiss Government Excellence Scholarship.

Translational studies in alcohol-induced changes in gut microbiota

Jose Antonio López-Moreno¹, I. Rincón-Pérez¹, V. Echeverry-Alzate^{1,2}, K. Bühler¹, J. Calleja-Conde¹, L. Segovia¹, E. Giné¹, F. Rodríguez de Fonseca^{1,2}, J. Albert¹, J.A. Hinojosa¹ (¹ Madrid, Spain, ² Málaga, Spain)

The intestinal microbiota is an own ecosystem within our body that evolved with us and that changes with our diet and other environmental influences. In a sample of 507 university students we have found that the consumption of alcohol during weekends is associated with a change in the composition of feces and intestinal bacteria. The most plausible hypothesis would be to consider that alcohol changes the intestinal microbiota although a second hypothesis cannot be ruled out: that the differences in the composition of our gut microbiota would explain, at least in part, individual differences in the amounts of alcohol consumed. To verify this second hypothesis, we conducted a series of experiments with animal models (Wistar rats). A group of rats were subjected to alcohol intoxications and another group of rats were treated only with water. These two groups of rats were donors of fecal microbiota transplantation. Other groups of rats received the fecal microbiota transplantation. Animals that received the fecal microbiota transplantation from animals treated with alcohol drank more alcohol than animals that received the microbiota transplantation from animals treated with water or treated with vehicle. We also found that the use of a cocktail of antibiotics to sterilize the intestine produced a reduction in alcohol consumption. During the presentation we will show the main changes that we found in the popu-

lation of intestinal bacteria analyzed by Next Generation Sequencing and the similarities / differences found between humans and animals. Acknowledgements: this work was supported by the Ministerio de Sanidad, Consumo y Bienestar Social (Plan Nacional sobre Drogas 2018/050 to J.A.L.M) and the Fondo de Investigación Sanitaria (Red de Trastornos Adictivos, FEDER, RD16/0017/0008 to J.A.L.M).

Gut microbiota in alcohol related disease

Ali Keshavarzian¹, Christopher B Forsyth¹, Robin M Voigt¹, Garth R Swanson¹, Faraz Bishehsari¹, Maliha Shaikh¹, Stefan Green¹ (¹ Chicago, USA)

The gut microbiota is currently one of the most active research areas in medicine, including alcohol-related diseases. However, this has not always been the case. Our laboratory has been a leader in investigating the complex relationship between the gut microbiota and diseases related to alcohol consumption/abuse. In early studies from our lab we demonstrated that increased intestinal permeability to gut microbial contents was associated with development of alcoholic liver disease (ALD) in human patients. We then went on to carry out studies in rats to show that disruption of the normal pattern of the gut microbiota (so called dysbiosis) by chronic alcohol feeding was associated with intestinal hyperpermeability and ALD in those models. In addition we went on the show that dietary microbiota-directed therapy with probiotics and prebiotic fiber could reverse the changes in the gut microbiota as well as prevent intestinal hyperpermeability and ALD. We then published the first comprehensive study of the gut microbiota in alcoholics with and without liver disease and found an association of specific microbiota dysbiosis with ALD in human subjects. Our lab was also the first one to show that disruption of circadian rhythms resulted in dysbiosis of the gut microbiota. Significantly, we went on to show that disruption of circadian rhythms together with chronic alcohol feeding exacerbated intestinal hyperpermeability to gut microbial contents and resulted in increased liver inflammation and steatosis. Using the APC mouse model of colon cancer, we showed that circadian disruption increased chronic alcohol feeding promotion of colon polyps and invasive polyps in that model and that microbiota directed intervention with prebiotic fiber feeding reversed these effects. We then went on the show that human shift workers with disrupted circadian rhythms exhibit dysbiosis and are more susceptible (than day workers) to alcohol-induced gut leakiness with only moderate consumption of alcohol. Finally in our most recent studies we utilized intestinal organoids from chronic alcohol fed mice to show that decreased colonic microbiota short chain fatty acids (dysbiosis) is associated with epigenetic changes in colonic stem cell fate and junctional proteins resulting in intestinal hyperpermeability and liver inflammation. Our current studies are focused on further investigating these circadian and intestinal stem cell effects of the microbiota and alcohol related diseases and on how microbiota directed therapies can be used to treat and prevent alcohol-related disease.

Intestinal microbiota in alcoholic patients

Dragos Ciocan¹ (¹ Clamart, France)

Chronic harmful alcohol consumption can induce a large spectrum of conditions including liver, pancreatic, neurologic and psychiatric diseases. The intestinal microbiota is recognized as an important player in the development and the severity of different diseases related to alcohol. Alcohol induces changes in the composition and functions of microbiota (called dysbiosis). Also, alcohol increases the intestinal permeability which allows translocation of bacteria, bacterial components, and bacterial metabolites (such as short chain fatty acids, bile acids and tryptophan metabolites) into the portal and the systemic circulation. These elements can reach the liver or the brain, establishing a gut-liver or gut-liver-brain axis, and can trigger local and systemic inflammation. Targeting microbiota has been shown to improve liver injury both in animal models of diseases. Different strategies were tested: live bacteria (probiotics), microbiota transplantation, or the consumption of dietary fibres, such as pectin. All these methods can alter the ratio of bacterial species and thus their functions. But although the connections between the microbiota and the host are well established, the underlying mechanisms, including key components that might serve as potential therapeutic targets, remain to be elucidated. From a clinical perspective, well-designed studies that target microbiota in order to modify the clinical course, reverse disease or prevent complications are needed in patients with harmful alcohol consumption.

From alcohol initiation to disorder: perspectives and treatment across the lifespan

Marisa M Silveri (Boston, USA)

Adolescent neurobiology and the impact of alcohol use initiation

Marisa M Silveri¹ (¹ Boston, USA)

Early initiation of alcohol use is considered an important risk factor for the later development of an alcohol use disorder. While behavioral and neurobiological alterations have been observed in relation to early onset alcohol use, it has not been fully elucidated whether differences reflect antecedents to, or consequences of, early alcohol initiation. In our longitudinal study, alcohol- and drug-naïve adolescents (n=81, 13-14 years-old) completed neuroimaging at baseline, magnetic resonance imaging (MRI) and functional MRI during spatial navigation and emotional response inhibition task performance. Based on quarterly follow-up assessments of alcohol use, those who initiated use by age 16 exhibited smaller hippocampal volumes and larger posterior cingulate and superior frontal volumes than non-initiators. During fMRI, hippocampal activation during memory retrieval was negatively correlated with age of first use, while hippocampal activation during negative response inhibition trials was positively correlated with

age of first use. These findings suggest that distinct regional brain volumes in areas involved in learning and memory (hippocampus) and adaptive decision-making (frontal lobe), and functional differences in hippocampal efficiency and sensitivity across emotional contexts may be important predictors for the timing of alcohol use initiation. Characterizing brain structure and function may therefore be useful in the search for biomarkers of risk for hazardous adolescent behaviors, such as alcohol consumption. Further, such neurobiological patterns, established early in the second decade of life, may then escalate into adulthood, conferring neurobiological risk of developing an alcohol use disorder later in life.

Evaluating combined treatment versus single-focused treatment for depression and heavy episodic drinking in college students

Paola Pedrelli¹ (¹ Boston, USA)

Heavy Episodic Drinking (HED) and depressive symptoms often co-occur among college students and are associated with significant personal and societal problems. However, evidence-based treatments are not available for these comorbid conditions. The current study compared the effectiveness of a treatment combining Cognitive-Behavioral-Therapy for Depression and Brief Motivational Interviewing (CBT-D+BMI) and CBT-D alone among 94 college students with depressive symptoms and HED. Both treatment programs were associated with significant reduction in HED, alcohol-related problems (ARP), and depressive symptoms, at the end of treatment and at one-month follow-up, of similar magnitude. Moderators of outcomes were also examined. Among students with fewer depressive symptoms at baseline CBT-D was associated with greater preservation of gains relative to CBT-D+BMI long-term. Furthermore, among students with higher baseline frequency of HED, those who received CBT-D+BMI had a higher ARP reduction between baseline and the end of treatment than their peers receiving CBT-D. While the study did not include a no-treatment condition, the magnitude of improvement during treatment was higher than usually observed with time, suggesting a benefit of psychosocial treatments for this population. Depending on the main focus of treatment, HED or depression, different approaches may be implemented.

Mindfulness-based relapse prevention for drinking reduction among community-dwelling older adults seeking treatment for alcohol use disorder

Katie Witkiewitz¹ (¹ Albuquerque, USA)

Treatments for alcohol use disorder (AUD) have progressed considerably over the past 30 years. Yet, relatively few studies have been conducted to evaluate treatments that target drinking reduction for less severe drinkers who are interested in reducing alcohol consumption and even fewer studies have examined treatments for older adults interested in drinking reduction. Mindfulness-based relapse prevention is a treatment for addiction that holds considerable promise for targeting cognitive and affective processes, and has recently been found in

two randomized clinical trials to be superior to gold standard cognitive behavioral treatment in reducing heavy drinking and drug use days. Yet, prior work has not examined mindfulness-based relapse prevention (MBRP) for heavy drinking reductions as primary outpatient treatment and has not examined MBRP in older adults. In the current study, we examined the effectiveness of rolling group MBRP among treatment seeking individuals (n=84) with alcohol use disorder who were interested in reducing their heavy drinking. We also examined the effects of treatment among older adults (age 60+, n=25). Results indicated a significant effect of treatment on drinking reductions. The magnitude of drinking reductions also correlated with the number of MBRP group sessions attended. Results from the subgroup analyses indicated the effects were also significant in those over the age of 60. Taken together, these results suggest drinking and craving reductions are achievable among people with AUD, including older adults. The current findings also suggest a dose response relationship between MBRP sessions attended and drinking reductions.

Pharmacological treatments for alcohol use disorder: riding the waves of medications development

Lorenzo Leggio¹ (¹ Baltimore and Providence, USA)

Harmful alcohol use is a risk factor in more than 60 diseases and injuries resulting in approximately 2.5 million deaths per year worldwide, therefore effective treatments for alcohol use disorder (AUD) are needed. Among them, medications development represents a high priority in the alcohol field. However, only a few medications (“first wave”) are currently approved by the appropriate regulatory bodies (e.g., FDA, EMA) for AUD. Research has been conducted with the goal of testing medications already approved for other clinical indications as potential effective treatments for AUD (“second wave”). Among several medications that may be mentioned in this group, two examples include GABA_B receptor agonism via baclofen, a medication already approved for spasticity; and alpha-1-blockade via prazosin and doxazosin, two medications already approved for hypertension and benign prostatic hyperplasia. More recently, additional efforts have been made toward the identification of new neurobiological pathways involved in the development and maintenance of AUD and possibly useful as new therapeutic targets (“third wave”). Among them, neuroendocrine pathways such as ghrelin, GLP-1 and oxytocin seem promising and are currently under investigation. The overall goal of the clinical and translational research in the field of medications development for AUD is to increase the armamentarium of effective pharmacological treatments that health care providers may use to treat patients with AUD and provide evidence toward patient-oriented precision medicine.

The changing face of clinical trials for alcohol use disorders

Henri-Jean Aubin (Villejuif, France)

Precision medicine in alcohol dependence: matching phenotypes to pharmacotherapy

Henry Kranzler¹ (¹ Philadelphia, USA)

Early efforts to identify predictors of response to alcohol use disorder (AUD) treatment focused largely on patient characteristics that moderate the response to psychotherapy. Although some significant moderators were identified in Project MATCH, a large, multi-center trial that examined a series of features as predictors of response to three different psychotherapies for AUD, the findings have not substantially altered clinical care. More recent efforts have examined genetic predictors of medication response, with the most widely studied gene variant-medication pair being the Asn40Asp single nucleotide polymorphism in the mu-opioid receptor gene as a moderator of naltrexone treatment response. In a recent meta-analysis of that literature, we found no effect of the Asp40 variant on the response to naltrexone. Mann et al. recently reported that a subgroup of individuals from the PREDICT Study identified as reward drinkers showed an 83% reduction in the likelihood of any heavy drinking when treated with naltrexone compared to placebo. In a secondary analysis of a randomized trial of naltrexone among problem drinkers, reward drinkers treated with naltrexone reported significantly less frequent and less heavy drinking, and desire to drink mediated the effect of naltrexone on daily drinking. If validated prospectively, the reward drinker phenotype could serve as a clinically useful self-report measure that predicts the subgroup of AUD patients who benefit most from naltrexone treatment.

Harm reduction: an alternative avenue for alcohol use disorder pharmacotherapy

Karl Mann¹, Katie Witkiewitz¹, the ACTIVE group¹ (¹ Mannheim, Germany)

Only 10-20% of individuals with a diagnosis of alcohol dependence subscribe to a specific treatment. Empirical data show that the most important reason for this treatment gap is the requirement to subscribe to total abstinence. The scientific discussion of this issue gained significant momentum when the European Medicines Agency accepted Reductions in alcohol consumption as an interim harm reduction strategy in the treatment of alcohol use disorder. Earlier studies have found that significant reductions in alcohol use are common among individuals with alcohol use disorder, however it remained unclear whether reductions in drinking risk levels are associated with significant improvements in health, quality of life, and other consequences of alcohol use disorder, and also whether reductions in drinking are stable over time. The goal of our approach was to examine the correspondence between levels of alcohol consumption and experiences of drinking-related consequences, mental health, blood pressure, and liver function tests during treatment among individuals receiving treatment for alcohol dependence in the COMBINE study. Results indicated reductions in WHO drinking risk levels were associated with significantly fewer alcohol related consequences, greater mental health, and improvements in

physical health functioning, including reduced blood pressure and better liver function. Importantly, reductions in risk levels were also stable over time. The results provide evidence of reductions in WHO risk levels as a viable alternative to abstinence as an endpoint for alcohol clinical trials associated with meaningful reductions in alcohol related consequences and improvements in mental and physical health.

Placebo response in clinical trials for alcohol use disorders: can we improve clinical trial designs?

Henri-Jean Aubin¹, Claire Farina¹ (¹ Villejuif, France)

The placebo response in Alcohol Use Disorder (AUD) trials has been shown to be negatively correlated to the treatment effect size. This systematic meta-analytic approach gives insight on how the choice of various endpoints and time points affect the placebo response in AUD trials. Moderator and meta-regression analyses can provide valuable information regarding the impact of variables such as patient characteristics and trial design options on the placebo response. Depending on endpoints and time points, placebo response effect size (standardized mean difference) may vary from values as high as 1.5 to 2.2. Return to any drinking at 12 weeks was observed in more than 70% individuals in trials selecting abstinent subjects at baseline. Placebo response moderators differed according to endpoints. Nevertheless, journal impact factor appeared to be consistently related to a lower placebo response. Interestingly psychiatric comorbidity did not appear to significantly affect the placebo response effect size. Also, studies published in recent years showed a higher placebo response effect size for alcohol reduction-related endpoints, whereas earlier studies showed a higher placebo response effect size for abstinent-related endpoints. Some of these findings can be valuable for future AUD randomized clinical trials protocols.

Examining psychosocial predictors of alcohol outcomes: implications for etiology, prevention, and treatment

Matthew R Pearson (Albuquerque, USA)

An ecological test of stress- and cue-induced alcohol craving

Matthew R Pearson¹, Katie Witkiewitz¹, Eric Claus¹
(¹ Albuquerque, USA)

A sample of 68 participants were recruited and randomized to a mindfulness-based intervention (n=24), attentional bias modification (n=21), or a health education/attentional bias assessment control condition (n=23). Our design included the collection of drinking data for 2 weeks via ecological momentary assessment (EMA) before, during, and after the intervention. Our hypotheses were built from a craving-based model of drinking such that both exposure to alcohol cues

and experience of negative affect/stress are expected to predict increased alcohol craving, which in turn leads to alcohol use. Although our data EMA data failed to support expected intervention-specific effects, we found independent effects of self-reported stress (2 items: stressed and overwhelmed), reports of experiencing specific stressors (financial/job-related, relationship, health-related, daily hassles), and negative affect on craving. For example, we found that relationship-related stressors and daily hassles predicted level of craving at the within-subject level, whereas financial/job-related stressors and health-related stressors predicted level of craving at the between-subject level. These kinds of nuanced associations between stress-related factors and alcohol-related outcomes have yet to be examined using ecologically valid data. Further, we found independent effects for four out of five cue exposure measures. Specifically, at the within-subjects level, we found that exposure to alcohol advertising, seeing alcohol, being proximal to a drinking establishment, and hearing conversations about alcohol were all uniquely predictive of alcohol craving (though being around other individuals with whom they have consumed alcohol was not).

Alcohol use among college students: lessons learned from the Protective Strategies Study Team

Protective Strategies Study Team¹ (¹Albuquerque, USA)

Protective behavioral strategies (PBS) are specific behaviors one can utilize to minimize the harmful consequences of alcohol consumption. There has been an increasing amount of interest in use of PBS among college students, especially as an intervention target. In 2013, Pearson reviewed all PBS studies conducted at that time. This review demonstrated that despite the fact that a large number of studies have been conducted on PBS, there have been few replication attempts. To advance the PBS field, the Protective Strategies Study Team (PSST) was formed to conduct large multisite studies investigating PBS. In our first study, we collected over 7,307 across 10 different states in the United States. In this presentation, we highlight our major findings to date. Chiefly, we replicated and extended past findings by exploring a wide range of more distal antecedents (i.e., mental health symptoms, drinking motives, impulsivity-like traits) that may affect alcohol-related outcomes via PBS use (i.e., mediation) as well as a number of factors that interact with PBS use to predict outcomes (i.e., moderators). We also compare and contrast alcohol PBS findings with cannabis PBS findings. Finally, we discuss the implications of these findings for prevention and intervention efforts.

Beyond one size fits all: deviance regulation theory-based interventions targeting use of alcohol protective behavioral strategies

Robert D Dvorak¹ (¹ Orlando, USA)

The prototypical college student alcohol intervention is norm-based. Most of these interventions use personalized normative feedback to correct college students' overestimations of their peers' alcohol use. Unfortunately, these inter-

ventions tend to have small, short-lived effects on alcohol use. Protective behavioral strategies (PBS) are behaviors one can engage in before, during, or after drinking to help reduce alcohol use, intoxication, and/or alcohol-related harms. PBS have been shown to be directly related to lower alcohol consequences even when controlling for levels of use, making it a promising intervention target. There is reason to suspect that traditional normative feedback will not translate well to targeting PBS use. In this presentation, we review a social psychological theory, deviance regulation theory (DRT), that posits individuals engage in behaviors to stand out in positive ways or avoid standing out in negative ways. We review the findings from 5 studies conducted to date evaluating DRT-based interventions targeting alcohol PBS. Taken together, these interventions have been shown to increase alcohol PBS use, which in turn reduces alcohol use and/or alcohol-related problems. We discuss the implications of matching intervention content (in our case, positively framed vs. negatively framed messages) to individuals' preexisting beliefs (in our case, their normative perceptions) in the broader context of alcohol interventions.

I am what i am: defining the nomological network of alcohol identity using meta-analysis

Kevin S Montes¹, Matthew R Pearson² (¹ Carson, USA, ² Albuquerque, USA)

Alcohol identity refers to the centrality of alcohol use to an individual's self-concept (e.g., the extent to which alcohol use is important to one's self-image or self/personal identity). Theory (e.g., PRIME theory of motivation; social identity theory, theory of planned behavior) suggests that alcohol identity may serve as an important source of motivation that guides alcohol use. Empirical research has also been conducted to examine the associations between alcohol identity and alcohol-related outcomes (e.g., frequency, quantity, consequences, and dependence). Traditionally, alcohol identity has been assessed using self-report measures although more recent investigations have assessed alcohol identity using implicit measures (e.g., implicit alcohol identity). Over 40 studies have been conducted to examine the associations between alcohol identity and alcohol-related outcomes along with narrative reviews that summarized findings from many of these studies. Missing from this extant literature is a systematic review that includes a meta-analytic component that synthesizes effect size estimates across these studies in order to derive a single, weighted effect size estimate between alcohol identity and each alcohol-related outcome. In the current study, we meta-analytically examined the associations between alcohol identity and alcohol-related outcomes. We also examined the associations between alcohol identity and known correlates of alcohol use (e.g., motives, expectancies, negative affect, norms, cravings). In addition, we summarize measurement approaches used in the assessment of alcohol identity. Finding from this meta-analytic study will inform a discussion surrounding opportunities to improve the measurement of alcohol identity as well as how best to target alcohol identity in future prevention/intervention efforts.

**Do you feel your body or your emotions?
Drinking alcohol in the context of body-mind communication**

Marcin Wojnar (Warsaw, Poland)

Drink until you cannot feel feelings: the role of physical pain in predicting relapse to alcohol use following treatment for alcohol use disorder

Katie Witkiewitz¹ (¹ Albuquerque, USA)

Identifying factors that predict a return to heavy drinking (i.e., relapse) following alcohol treatment is critical for the development of relapse prevention interventions. Physical pain is common among individuals with alcohol use disorders (AUDs), yet few studies have examined associations between pain and alcohol relapse. Data from the COMBINE study (n=1383) and the United Kingdom Alcohol Treatment Trial (n=743) were used to examine the associations between physical pain and alcohol relapse in randomized clinical trials for alcohol use disorders. Results indicated a significant association between physical pain and alcohol relapse, which was mediated by experiences of negative affect. Targeting acceptance and management of physical pain in the treatment of alcohol use disorder may help reduce relapse risk.

Can you feel your own body? The role of interoception in alcohol use disorder

Andrzej Jakubczyk¹ (¹ Warsaw, Poland)

It has been suggested that interoception (which reflects the way one perceives somatic stimuli from the body) may contribute to alcohol use disorder (AUD) as it relates to the body's experience of substance use or withdrawal. Moreover, there is growing evidence that interoceptive responses are associated with immediate, discrete emotions. However, only a few studies have directly investigated associations between interoception, emotion regulation and alcohol use. The study conducted in a group of sober alcohol-dependent individuals showed that when controlling for level of anxiety, sleep problems, age, sex and education, individuals with AUD scored significantly higher on self-reported interoceptive sensibility and lower on interoceptive accuracy in comparison to healthy controls. Moreover, in the group of subjects with AUD measures of emotional utilization remained a significant correlate of interoceptive accuracy, whereas lack of own emotional awareness, difficulties controlling impulsive behaviors when experiencing negative emotions, and appraisal of emotions remained significantly associated with interoceptive sensibility. These results have to be treated as preliminary and need to be replicated; however, findings indicate that interoception may present a novel therapeutic target for treatment of AUD.

Can you feel what I am feeling – childhood adversity, alcohol use and mentalization

Maciej Kopera¹ (¹ Warsaw, Poland)

Although theoretical link between childhood trauma and mentalization has been established empirical evidence for it is still limited. Current data shows that the direction of this relationship might be individually shaped in selected at-risk populations. Childhood trauma is highly prevalent in treatment-seeking subjects with AUD and may play a significant role in the development and severity of AUD. The first goal of the presented studies was to see if the presence of risky alcohol use during the developmental age would influence the relationship between childhood adversity and mental states recognition in early adulthood (Study 1). Additionally, we wanted to see if the transgression from risky alcohol use to AUD would influence the trauma-mentalization relationship in another treatment seeking AUD sample (Study 2). Our findings highlight an important and lasting role for variations in early life stress on individual differences in adult social cognitive functioning.

Heavy drinking, depression, and treatment seeking for mental health concerns in physicians

Kirk J Brower¹ (¹ Ann Arbor, USA)

Introduction: the relationship between heavy drinking and depression in physicians is worthy of further study. A large survey of U.S. physicians found that 15.3% screened positive for an alcohol use disorder using the AUDIT-C, which correlated significantly with depression. The objective of this study was to look at the influences of heavy drinking (HD) and depression on treatment seeking for mental health concerns in physicians. It was hypothesized that each would have independent effects and reduce the likelihood of treatment seeking. Methods: a faculty and physician health survey was sent by an email link to 3657 faculty members at a medical school. Anonymity was assured by using an external survey center, so that only de-identified data were analyzed. A total of 1710 (46.8%) of surveys were returned, including 1089 physicians who constituted the study group. The sample consisted of 46% females with a modal age group between 36 to 45 (34.5%). The NIAAA single question screen and criteria for HD, and the PHQ9 for depression were used. Results: rates of any HD and for at least monthly HD during the past year were 23.1% and 7.3%, respectively. Moderate-to-severe depression and any suicidal ideas during the past 2 weeks were endorsed by 13.6% and 3.7%, respectively. Physicians with at least monthly HD had significantly increased severity of depression. Frequency of suicidal thoughts were significantly correlated with both any HD and at least monthly HD. Those who drank heavily at least monthly were less willing to seek treatment for a mental health concern (60.8% vs. 67.2%, $p=0.02$). Conclusion: frequent heavy-drinking physicians had greater depression severity, but were less willing to seek treatment for a mental health concern than other physicians. Possible reasons for these findings will be discussed.

Social cognition in severe alcohol-use disorders: from emotional decoding to dehumanization experience

Pierre Maurage (Louvain-la-Neuve, Belgium)

It's complicated: different tasks lead to different conclusions as to the severity of the impact of severe alcohol-use disorder upon social cognition

Sharon Cox¹ (¹ London, UK)

Severe alcohol-use disorder (SAUD) is associated with deficits in social cognition, frequently evidenced by errors in emotional facial recognition and a lesser ability to theorise about another's state of mind. To date, little evidence exists on the clinical impact of these deficits, including how they influence treatment outcomes and are perceived by others. Findings from two studies will be presented; the first study (N=123) highlights the impact of poor social cognition on treatment outcomes (completion versus drop out), and how different tasks (binary versus non-binary responses) generate varying conclusions as to the extent of the deficits caused by SAUD. Results suggest that non-binary tasks which are non-time defined allow adults with SAUD scope to explore their answers and self-correct, leading to lower error rates. In the second study (N=89), how apparent these problems are to professionals who support these individuals is explored through the correlation of estimates of deficits to experimental data. Professionals' ability to recognise these deficits is contained to those who clients presenting with SAUD and other clinical symptoms (e.g., anxiety, psychosis). Taken together, results suggest that the nature of the experimental tasks affects the degree to which we can estimate the severity of the impact of SAUD upon social cognition.

Self-evaluative emotions in severe alcohol use disorders

Delphine Grynberg¹ (¹ Lille, France)

Guilt and shame have been very little explored in severe alcohol-use disorder (SAUD). Although previous findings suggest that the experience of shame may play a major role in the maintenance of SAUD, they do not allow to determine (1) whether proneness to experience guilt and shame is associated with the experience of the emotions in the context of their consumption, (2) whether SAUD and healthy controls (HC) differ in terms of guilt and shame concerning their alcohol consumption, and (3) whether these later are associated with alcohol use severity. The present study examined these hypotheses in 40 patients diagnosed with SAUD according to DSM-V criteria and 54 HC (AUDIT scores < 7). Participants were instructed to complete the Test of Self-Conscious Affect-3, the Personal Feelings Questionnaire-2 (PFQ-2), the Hospital Anxiety and Depression Scale, the Alcohol Use Disorders Identification Test (AUDIT) and a questionnaire that has been developed for the present study,

the “Substance Shame and Guilt” (SSG). Main results show (1) PFQ-2-shame and PFQ-2-guilt are moderately associated with SSG-guilt and SSG-shame, (2) SAUD report higher SSG-guilt and SSG-shame than HC and (3) SSG-guilt is positively associated with the AUDIT in SAUD only. These results suggest that patients with SAUD experience greater shame and guilt associated with their consumption and that the consumption severity is associated with greater guilt in SAUD. This study thus emphasized the importance to consider shame and guilt in the maintenance of SAUD.

Clinical impact of social cognition in treatment seeking patients with severe alcohol-use disorders

Claudia Rupp¹ (¹ Innsbruck, Austria)

Past years research witnessed growing evidence that cognitive deficits in patients with severe alcohol-use disorder (SAUD) include social cognition, most prominently deficits in (facial) emotion recognition. Until now, less is known about the clinical relevance of these impairments in SAUD. In our prospective research studies, we were interested whether deficits in social cognition (1) contribute to less successful treatment outcome (relapse/dropout), and (2) recover “naturally” (with abstinence) during (about 8-week) SAUD treatment, or are persistent cognitive problems. Main results of our studies are that (1) patients with SAUD presenting poorer (facial) emotion recognition showed less successful treatment outcome with respect to relapse and/or early dropout. In addition, (2) patients with SAUD showed no recovery with controlled abstinence during treatment in social cognition deficits, including impaired (facial) emotion recognition ability, compared with healthy controls. Our findings evidence the clinical impact of social cognition deficits, particularly emotion recognition deficits on treatment success in SAUD. Moreover, our findings indicate that clinically relevant social cognitive deficits are rather persistent cognitive problems in SAUD that would need special (e.g., neurocognitive rehabilitation) treatments. New research focusing on the improvement of these deficits in SAUD seems warranted.

Dehumanizing experiences of patients with severe alcohol-use: links with fundamental needs and important clinical outcomes

Sullivan Fontesse¹ (¹ Louvain-la-Neuve, Belgium)

Dehumanization, the denial of one’s humanness, has important negative consequences for social interactions. Dehumanization from the dehumanizer’s perspective has been widely studied in social psychology. However, victims’ perspective has been neglected. Moreover, despite dehumanization being described as endemic in medicine, no study has investigated dehumanizing experiences (i.e the feeling of being dehumanized by others) in psychiatric populations. To address these gaps, dehumanizing experiences of 120 patients with severe alcohol-use disorder (SAUD) were investigated. We argue that because patients with SAUD are rejected and stigmatized against, two known antecedents of dehumanization, they might feel dehumanized by others.

Our model proposed that dehumanizing experiences would be associated with fundamental needs thwarting. These needs are the psychological equivalent of thirst or hunger: shared by all and causing important negative health consequences when thwarted. Additionally, it was hypothesized that dehumanizing experiences and fundamental needs thwarting would together be linked to patients’ emotions, cognitions, and behaviors. Results supported that dehumanizing experiences were associated with increased fundamental needs thwarting. Dehumanizing experiences were also associated with negative emotions, negative self-esteem, and dysfunctional coping strategies, such as alcohol use. Our results suggest that dehumanizing experiences might play a crucial role in the vicious circle leading to SAUD.

Novel concepts in alcoholic liver disease

Sebastian Mueller (Heidelberg, Germany)

Systemic inactivation of hypoxia-inducible factor prolyl 4-hydroxylase 2 in mice protects from alcohol-induced fatty liver disease

Anna Laitakari¹, Teemu Ollonen¹, Thomas Kietzmann¹, Gail Walkinshaw², Daniela Mennerich¹, Valerio Izzi¹, Kirsi-Maria Haapasaaari¹, Johanna Myllyharju¹, Raisa Serpi¹, Elitsa Y Dimova¹, Peppi Koivunen¹ (¹ Oulu, Finland, ² San Francisco, USA)

Alcoholic fatty liver disease (AFLD) is a growing health problem for which no targeted therapy is available. We set out to study whether systemic inactivation of the main hypoxia-inducible factor prolyl 4-hydroxylase, HIF-P4H-2 (PHD2/Egln1), whose inactivation has been associated with protection against metabolic dysfunction, could ameliorate it. HIF-P4H-2-deficient and wild-type (WT) mice or HIF-P4H inhibitor-treated WT mice were subjected to an ethanol diet for 3-4 weeks and their metabolic health, liver and white adipose tissue (WAT) were analyzed. Primary hepatocytes from the mice were used to study cellular ethanol metabolism. The HIF-P4H-2-deficient mice retained a healthier metabolic profile, including less adiposity, better lipoprotein profile and restored insulin sensitivity, while on the ethanol diet than the WT. They also demonstrated protection from alcohol-induced steatosis and liver damage and had less WAT inflammation. In liver and WAT the expression of the key lipogenic and adipocytokine mRNAs, such as Fas and Ccl2, were downregulated, respectively. The upregulation of metabolic and antioxidant hypoxia-inducible factor (HIF) target genes, such as Slcs 16a1 and 16a3 and Gclc, respectively, and a higher catalytic activity of ALDH2 in the HIF-P4H-2-deficient hepatocytes improved handling of the toxic ethanol metabolites and oxidative stress. Pharmacological HIF-P4H inhibition in the WT mice phenocopied the protection against AFLD. Our data show that global genetic inactivation of HIF-P4H-2 and pharmacological HIF-P4H inhibition can protect mice from alcohol-induced steatosis and liver injury, suggesting that HIF-P4H inhibitors, now in clinical

trials for renal anemia, could also be studied in randomized clinical trials for treatment of AFLD.

Modeling of fibrosis pattern formation: from mouse models to human patients of chronic liver diseases

Seddik Hammad^{1,2}, Jieling Zhao^{3,4}, Jan G Hengstler³, Sebastian Müller⁵, Dirk Drasdo^{3,4}, Steven Dooley¹ (¹ Mannheim, Germany, ² Qena, Egypt, ³ Dortmund, Germany, ⁴ Paris, France, ⁵ Heidelberg, Germany)

Fibrosis is a consequence of repetitive liver injuries, e.g. alcohol consumption. Liver fibrosis develops in different patterns according to the etiological factor i.e. pericellular to septal pattern in alcoholic hepatitis. The mechanism behind the generation of the different “scar” patterns is still elusive. Furthermore, this scar pattern is considered an early stage of cirrhotic nodules in the advanced disease stage. We aim to define (a) molecular driver(s) of fibrosis pattern formation. We exposed mice to acute or chronically repeated doses (twice/week for 6 weeks) of CCl₄, which like alcohol is metabolized by CYP2E1, but presents with more severe liver damage in a shorter time frame. Spatial distribution of fibrosis formation and metabolic enzyme expression, namely CYP2E1, were analyzed in liver tissues. We found that recovery of CYP2E1⁺ hepatocytes after acute CCl₄ form exactly the same septal pattern of collagen scar walls that form upon chronic injury, suggesting that CYP2E1⁺ hepatocytes are the trigger of the fibrotic pattern. To study this hypothesis, we assumed a dynamic activator/inhibitor CYP2E1 mathematical model. The current model already partially captures the aforementioned CYP2E1/ECM pattern. We are currently challenging the model by mechanistic studies. These include i) crosstalk between activated/reverted HSCs and LSECs differentiation; ii) communication between ECs lining the CV and metabolically zoned hepatocytes; iii) testing a potential diffusible inhibitor in the portal compartment, i.e. the bile acid concentration. We are targeting the WNT/ β -Catenin pathway (CYP2E1 regulator) by monoclonal antibodies against R-spondin1/2/3 in the fibrosed liver, and iv) test the mechanical role of ECM deposited by HSCs. Clinical application of the suggested model will be iteratively investigated in F1, F2, F3 and F4 cohorts of patients with alcoholic liver disease.

The characteristics of alcoholic liver disease in Japan

Tomomi Kogiso¹ (¹ Tokyo, Japan)

Aim: the clinical features of alcoholic liver disease (ALD) including the genetic background were not fully identified in Japan. Here, we investigated that the clinical characteristics, hepatocellular carcinoma (HCC), and the single nucleotide polymorphisms (SNPs) associated with alcohol, glucose, and fat metabolism in patients with ALD compared to non-alcoholic fatty liver disease (NAFLD). Methods: 1) ALD (n=118; male, 86%; median age, 62 years; liver cirrhosis, 58%; HCC, 31%) and NAFLD (n=200; male, 55%; age, 61

years; cirrhosis, 19%; HCC, 12%) patients were evaluated. 2) The survival and recurrence rates of HCC were examined in the patients of multi-center in Japan (532 ALD-HCC and 209 NAFLD-HCC). Results: 1) Comparing with NAFLD, ALD were predominantly male and lower body mass index and the complication of lifestyle-related diseases. As the genetic background, the ADH1B genotype GG and ALDH2 genotype GG were observed more frequently and the MTP genotype GG was decreased in ALD (ALD vs. NAFLD, ADH1B, 16% vs. 4%; ALDH2 84% vs. 44%; MTP 62% vs. 72%, respectively; all p<0.01). Comparing with and without HCC, the KCNJ15 genotype GG were identified as the risk factors of ALD-HCC. 2) The patients showed 5-year survival rates of ALD-HCC 43.7% vs. NAFLD-HCC 49.1%; 5-year recurrence rates of 65.4% vs. 69.6 %, respectively. Conclusion: the SNPs for the enzymes of alcohol metabolism were associated with ALD and the risk of diabetes were co-related to ALD-HCC. The survival and recurrence rates of HCC were equally shown in ALD and NAFLD.

The role of intestinal microbiota in alcoholic liver disease

Ryuta Kitagawa¹, Kazuyoshi Kon¹, Maiko Suzuki¹, Kenichi Ikejima¹ (¹ Juntendo, Japan)

Emerging attention has been paid for gut microbiota in the human health and disease. Indeed, gut microbiota is dynamically altered by dietary factors, lifestyle, and alcohol intake. Gut microbiota-dependent activation of hepatic innate immunity is important in the pathogenesis of steatohepatitis caused by both alcohol and metabolic syndrome. Chronic alcohol exposure, as well as dietary overload, compromises gut barrier function causing increases in intestinal permeability, thereby aggravating translocation of bacterial products into the portal blood. Pathogen-associated molecular patterns (PAMPs) derived from gut microbiota elicit production and release of inflammatory cytokines through multiple innate immune signaling pathways, resulting in the exacerbation of steatohepatitis. The comorbidity of alcoholic liver disease and metabolic syndrome has become an emerging clinical problem worldwide. We have recently applied the mouse model of chronic-binge EtOH liver injury (NIAAA model) for obese KK-A^y mice, mimicking alcoholic liver injury comorbid metabolic syndrome. For therapeutic approach, we investigated the effect of rifaximin (RFX), an oral non-absorbed antibiotic, in this model. EtOH-feeding/binge caused more severe hepatic steatosis, oxidative stress, and induction of inflammatory cytokines in KK-A^y mice as compared to BI/6 controls, which were markedly prevented by RFX treatment. RFX dramatically modified the small intestinal microbiota following chronic EtOH feeding, decreasing the relative abundance of the order Erysipelotrichales and increasing the order Bacteroidales, without affecting EtOH-induced increase of net amount of viable bacteria. It is postulated that the modulation of small intestinal microbiota is critical for the prevention of alcoholic liver injury comorbid metabolic syndrome.

Natural history of alcoholic liver disease: risk factors, early disease detection and prognostic markers

Maja Thiele (Odense, Denmark)

Epidemiology and natural history of alcohol-related liver disease

Gro Askgard¹ (¹ Copenhagen, Denmark)

End-stage alcohol-related liver disease is a rare disease in the general population (0.06% per year or lower in men > 45 years) and knowledge of risk factors is needed to target screening for early liver disease in individuals of high risk of the disease. In this session we will focus on risk factors for alcohol-related liver disease. We will discuss the influence of alcohol amount (recent and earlier in life), alcohol drinking patterns (binge drinking/daily drinking, wine/beer/liquor, meal-related alcohol consumption) and age, smoking, and obesity as risk factors of alcohol-related disease. Will cutting down on alcohol amount decrease the risk of further progression in liver disease? Individuals at particular high risk for end-stage liver disease may be found at specialized alcohol treatment centers or as hospital patients given an alcohol problem diagnosis. These populations have a risk for end-stage alcohol-related liver disease of 7 to 16% after about 10 years. Moreover, some studies suggest half of patients with end-stage alcohol-related liver disease had healthcare contacts in general practice or at the hospital before their diagnosis with obvious alcohol problems. This indicates that there may be opportunities to reach about half of patients with end-stage alcohol-related liver disease with preventive interventions before diagnosis.

Current state-of-the-art prognostic and diagnostic markers including genetic traits

Maja Thiele¹ (¹ Odense, Denmark)

This talk will include an overview of the current best-in-class non-invasive markers for diagnosis of fibrosis and prognostication in alcohol-related liver disease patients. These markers include ultrasound elastography techniques and serum markers that reflect extracellular matrix formation, so called direct fibrosis markers. Beyond the marker's diagnostic role in an outpatient hospital setting, they may be used for case-finding or screening at a population level. However, due to the lower prevalence of advanced fibrosis in at-risk populations, compared to patients referred to secondary healthcare, preselection of patients using risk scores may be used to increase true-positive rate and decrease false-positives, thereby minimizing risk of overdiagnosis. Such risk scores are likely to include genetic traits, co-occurrence of metabolic risk factors, alcohol drinking history and drinking pattern.

Pathophysiology of alcoholic liver disease

Kenichi Ikejima (Chiba, Japan)

Alcoholic liver disease: impact of the type of alcoholic beverage

Ina Bergheim¹ (¹ Vienna, Austria)

Alcohol intake is still among the leading causes of chronic liver diseases world-wide. Despite marked efforts made in many countries around the world to increase the awareness in the general population regarding the negative effects on health associated with chronic and especially elevated chronic intake of alcohol, the global proportion of the alcohol consumers has not markedly dropped throughout the last decades. Indeed, alcohol consumption still accounts for nearly 10% of global deaths among populations aged 15-49. Epidemiological studies also suggest that per capita consumption of alcohol from various alcohol beverages e.g. the beer, wine, spirits and other alcohol containing beverages including palm wine, or fermented beverages made of banana, sorghum or maize differs markedly between different areas of the world. Epidemiological but also clinical and animal studies further suggest that different alcoholic beverages may impact the development of alcoholic liver disease differentially. These findings along with possible molecular mechanism involved will be reviewed and discussed.

Vinyl chloride-induced interaction of nonalcoholic and toxicant-associated steatohepatitis: protection by the ALDH2 activator Alda-1

Juliane I Beier¹ (¹ Pittsburgh, USA)

The abundant environmental toxicant vinyl chloride (VC) shares similar metabolic pathways in the liver to alcohol. Specifically, VC is metabolized via CYP2E1 and aldehyde dehydrogenase dependent pathways to produce the corresponding alcohol (chloroethanol, CE) and aldehyde (chloroacetaldehyde, CAA). VC causes steatohepatitis at high levels, but is considered safe at lower (i.e., sub-OSHA) levels. However, we have previously shown that even lower VC levels exacerbate experimental fatty liver disease caused by high-fat diet (HFD). Mitochondrial oxidative injury and subsequent metabolic dysfunction appeared to play key roles in mediating this interaction. Mitochondrial aldehyde dehydrogenase 2 (ALDH2) serves as a key line of defense against endogenous and exogenous reactive aldehydes. The current study therefore tests the hypothesis that allosteric activation of ALDH2 with Alda-1 will protect against VC-enhanced fatty liver disease. Mice were exposed to low VC concentrations (<1 ppm), or room air for 6 hours/day, 5 days/week for 12 weeks, while on HFD or low-fat control diet (LFD). Some mice received Alda-1 (20 mg/kg i.p., 3x/week) for the last 3 weeks of diet/VC exposure. Indices of liver injury, oxidative stress, metabolic and mitochondrial (dys) function were measured. As observed previously, low-dose VC did not cause liver injury in control mice; while liver injury caused by HFD was enhanced by VC. VC decreased hepatic ALDH2 activity of mice fed HFD. Alda-1 attenuated oxidative stress, liver injury, and dysmetabolism in mice exposed to HFD+VC under these conditions. Importantly, alterations in mitochondrial function caused by VC and

HFD were diminished by Alda-1. Previous studies have indicated that liver injury caused by HFD is mediated, at least in part, by enhanced mitochondrial autophagy (mitophagy). Here, Alda-1 suppressed PINK1/PARKIN-mediated mitophagy. Taken together, these results support the hypothesis that ALDH2 is a critical defense against mitochondrial injury caused by VC in experimental fatty liver disease. The ALDH2 activator Alda-1 conferred protection against liver damage under these conditions, most likely via increasing clearance of aldehydes and preserving mitochondrial respiratory function.

The liver matrisome and inflammatory liver injury in ALD

Gavin E Arteel¹ (¹ Pittsburgh, USA)

The strategic location of the liver between the intestinal tract and the rest of the body makes it a critical organ for clearance of xenobiotics and toxins that enter the portal blood. As the main detoxifying organ in the body, the liver has a high likelihood of toxic injury. It is therefore not surprising that the liver has tremendous ability to heal and regenerate from injury. The complex and synchronized regenerative response in the liver can be perturbed and thereby can impact normal tissue recovery from injury or damage, leading to progressive injury, and potentially liver failure. The extracellular matrix (ECM) consists of a diverse range of components that work bi-directionally with surrounding cells to create a dynamic and responsive microenvironment that regulates cell signaling, recruitment, and tissue function. The basic definition of the ECM comprises fibrillar proteins (e.g., collagens, glycoproteins and proteoglycans). More recently, groups have extended the definition to include ECM affiliated proteins (e.g., collagen-related proteins), ECM regulator/modifier proteins (e.g., lysyl oxidases and proteases) and secreted factors that bind to the ECM (e.g., TGF β and other cytokines); this broader definition has been coined the "matrisome" (1). The ECM not only provides structure and support for the cells in a tissue, but also acts as a reservoir for growth factors and cytokines and as a signaling mechanism by which cells can communicate with their environment and vice-versa (2). Quantitative and qualitative changes to the ECM structure and superstructure can impact overall health of the organ and organism. Remodeling of the hepatic ECM/matrisome in response to injury is well understood in some contexts. For example, changes to the extracellular matrix associated with fibroproliferative diseases (i.e., fibrosis/cirrhosis) are considered almost synonymous with hepatic ECM changes. Proteomic-based studies in other organs have demonstrated that the matrisome responds dynamically in composition after insult well before fibrotic changes to the organ (3, 4). These changes to the ECM may not alter overall ECM architecture and are therefore histologically undetectable. Nevertheless, these changes have potential to alter hepatic phenotype and function (5). These acute responses can be viewed as an arm of the wound healing response and facilitate recovery from damage, which resolves once the damage is repaired. However, under conditions of

chronic injury, these changes likely contribute to activation of a significant remodeling response that leads to scar formation (i.e., fibrosis). This presentation will discuss some of the salient processes and players involved in the acute phase response of the ECM to liver injury after alcohol and other insults.

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Endoplasmic reticulum stress and oxidative stress in alcoholic liver injury comorbid metabolic syndrome

Kazuyoshi Kon¹, Maiko Suzuki¹, Kenichi Ikejima¹ (¹ Tokyo, Japan)

The endoplasmic reticulum (ER) is a multifunctional organelle required for the regulation of calcium homeostasis, lipid metabolism, and protein synthesis. A number of cellular stress conditions lead to the accumulation of unfolded or misfolded proteins in the ER and disruption of the ER homeostasis, which can trigger ER stress. ER stress activates the unfolded protein response (UPR). The UPR pathway includes induction of several molecular chaperones that restore cellular homeostasis by promoting the folding or degradation of unfolded proteins; however, if ER stress is prolonged or too severe, the signaling switches from pro-survival to pro-death, leading to ER stress-induced apoptosis. Several studies have shown that ER stress contributes to the development of alcoholic liver disease. Here we investigated the role of ER stress in chronic-binge ethanol (EtOH) model using obese KK-A^y mice. Chronic-plus-binge EtOH intake induced massive hepatic steatosis along with hepatocyte apoptosis and inflammation, and increased ER stress markers including binding immunoglobulin protein (Bip), unspliced and spliced forms of X-box-binding protein-1 (uXBP1 and sXBP1, respectively), inositol trisphosphate receptor (IP3R), and C/EBP homologous protein (CHOP), and also enhanced oxidative stress markers heme oxygenase-1 and 4-hydroxynonenal. Administration of 4-phenylbutyric acid, the chemical chaperone, during chronic EtOH exposure ameliorated steatohepatitis after chronic-binge EtOH, and completely inhibited both ER and oxidative stress markers. These findings indicated that binge EtOH intake after chronic consumption induces massive ER stress-related oxidative stress followed by liver injury, and inhibition of ER stress by chemical chaperone is a potential preventive therapy for alcoholic liver injury especially in obese subjects.

Genetics of alcohol dependence

Joel Gelernter (West Haven, USA)

The Genetics of antisocial personality disorder in the context of alcohol dependence

Andrew McQuillin¹ (London, UK)

Antisocial personality disorder (ASPD) is characterised by impulsive, irresponsible and criminal behaviour. These personality traits begin in childhood or early adolescence and continue into adulthood. The prevalence of ASPD in the general population is 2-3%, with estimates of 3% in men and 1% in women. The rates are higher in certain populations with ASPD rates of 47% amongst male prisoners. ASPD is highly comorbid with substance use disorders (SUD) and studies have reported that 80-85% of individuals with ASPD also meet criteria for a substance use disorder. Alcohol use disorder in particular is highly comorbid with ASPD and in one study 71% of ASPD patients abused alcohol. We have conducted a GWAS of ASPD symptom scores in two alcohol dependence cohorts from the UK and the US (n=3,223). This analysis produced a genome wide significant finding for a SNP located close to the *SLCO3A1* gene on chromosome 15 ($p=3.77 \times 10^{-08}$). *SLCO3A1* is a member of a family of organic anion transporter genes. Previous studies have reported association of this gene with AUD comorbid with bipolar disorder, with smoking behaviour and with inattentive symptoms in ADHD. Polygenic risk score analyses provided evidence for shared risk of ASPD in AUD subject with smoking behaviour, educational attainment and reproductive traits. We report the first genome-wide significant finding for ASPD and evidence for shared genetics risk for ASPD in AUD across a range of behavioural traits.

Polygenic contributions to alcohol use and alcohol use disorders across population-based and clinically ascertained samples

Emma Johnson¹, Sandra Sanchez-Roige², Arpana Agrawal¹, Toni-Kim Clarke³, Alexis C Edwards⁴, The Collaborative Study on the Genetics of Alcoholism, The Avon Longitudinal Study of Parents and Children (1 Saint Louis, USA, 2 La Jolla, USA, 3 Edinburgh, UK, 4 Richmond, USA)

Recent studies suggest that alcohol consumption and alcohol use disorders (AUD) have distinct genetic architecture. We examined polygenic risk scores (PRS) from a genome-wide association study of the consumption and problem subscales of the Alcohol Use Disorders Identification Test (AUDIT-C and AUDIT-P) in four independent samples: an ascertained cohort, the Collaborative Study on the Genetics of Alcoholism (COGA); and three population-based cohorts, the Avon Longitudinal Study of Parents and Children (ALSPAC), Generation Scotland (GS), and a subset of the UK Biobank (UKB). Regression models examined the correlation between the AUDIT-C and AUDIT-P PRS and a variety of alcohol-related phenotypes. Cox proportional

hazards models determined whether the PRS increased risk of onset of hazardous drinking and dependence. In COGA, the AUDIT-P PRS was strongly associated with alcohol dependence, symptom count, and maximum drinks, while AUDIT-C PRS was not an independent predictor of any phenotype. In ALSPAC, both PRS were strongly associated with alcohol dependence, whereas AUDIT-P PRS was a superior predictor of maximum drinks. In GS, AUDIT-C PRS was a better predictor of weekly alcohol use, whereas AUDIT-P PRS was strongly associated with CAGE scores. AUDIT-P PRS was also associated with ICD-based alcohol-related disorders in the UK Biobank sample. Lastly, AUDIT-P PRS was associated with increased risk of onset of alcohol dependence in COGA, whereas AUDIT-C PRS was associated with increased risk of onset of hazardous drinking in ALSPAC. Our findings demonstrate that AUDIT PRS could dissect genetic influences across alcohol use to misuse in both population-based and ascertained cohorts.

Genetics of alcohol dependence in a family sample

Howard J Edenberg¹ (Indianapolis, USA)

There is clear evidence that genetic variants affect the risk for alcohol dependence (AD), but few specific variants have been identified to date. The Collaborative Study on the Genetics of Alcoholism (COGA) conducted genome-wide association studies (GWAS) on AD, with secondary analyses looking at DSM-IV criteria endorsed. The primary analyses were among European Americans (EA), followed by trans-ancestral meta-analysis with an African American (AA) sample. In the GWAS of the EA sample, the functional SNP in *ADH1B*, rs1229984, was genome wide significant (GWS) for DSM-IV criterion count and 2 of the 7 criteria. Trans-ancestral analysis strengthened the signal for criterion count ($p=2.6e-13$) and 2 criteria, and elevated the signal for DSM-IV AD to GWS. Other GWA findings from the trans-ancestral GWAS were rs61826952 on chromosome 1 for AD, and rs7595960 on chromosome 2 for "time spent drinking". Adding in data from several independent GWAS supported most of these findings. A polygenic risk score (PRS) derived from the EA discovery GWAS significantly predicted a small amount of variance in other EA datasets (SAGE-EA, OZALC-EA). A promising endophenotype related to the risk for alcoholism is the sensitivity to alcohol (SRE). Individuals who need to consume more alcohol to feel its effects are at higher risk for heavy drinking and problems. GWAS and meta-analysis of SRE showed some novel associations on chromosomes 6, 11, and 13. A PRS derived from the EA SRE significantly predicted alcohol dependence and criterion count in the independent SAGE-EA subset, and one from the AA SRE did in the SAGE-AA subset. Further progress will require substantially larger samples, including non-European populations, and will benefit from detailed characterization of AD and its symptomatology.

Alcohol GWAS results in different populations – AA, EA, Asian – and attendant implications

Joel Gelernter¹, Hang Zhou¹, Daniel Levey¹, Henry Kranzler², Murray Stein³ (¹ West Haven, USA, ² Philadelphia, USA, ³ San Diego, USA)

Alcohol-related phenotypes – alcohol use disorder, quantity-frequency measures such as AUDIT-C, and maximum habitual alcohol use – are moderately heritable; as is the case for other complex traits, the specific risk variants and overall genetic architecture differ somewhat between populations. In some cases, as for the trait of “maximum habitual alcohol use,” the interpopulation differences are very useful in a practical sense for fine mapping of risk variants, because of differences in linkage disequilibrium between populations. At least one high odds ratio protective variant is almost entirely specific to certain Asian populations (ALDH2 rs671). Notwithstanding these differences and the general recognition of the importance of studying major world populations, the available characterized samples for European-ancestry subjects are much larger than those for African- and Asian-ancestry. The US Million Veteran Program (MVP) presently includes samples of European-ancestry subjects in the hundreds of thousands, and African-ancestry, in the tens of thousands. The largest reported studies of Asian ancestry barely reach the thousands. This presentation will review available results in these three populations; emphasize knowledge that has been gained only through the study of multiple populations; and prospects for the future.

Epigenetic effects of alcohol exposure in brain and in blood: an implication of methylation biomarker for alcohol use disorder

Ke Xu (New Haven, USA)

Fetal alcohol exposures promote the development of aggressive tumors in the endocrine glands

Dipak K Sarkar¹ (¹ New Brunswick, USA)

There have been several studies demonstrating that alcohol abuse promotes development of aggressive tumors in breast, prostate, pancreas, and colon tissues in human patients. Whether fetal alcohol exposures promote development of aggressive tumors in the offspring during adult period are not well studied. Using rat animal model of fetal alcohol exposure, we studied the susceptibility of the growth of aggressive tumors in the mammary, prostate and the pituitary glands during the adult period. Pregnant laboratory rats were fed between gestational days 7 and 21 with a liquid diet containing alcohol, pair-fed with isocaloric liquid diet, or fed ad libitum with rat chow. Between 50 to 90 days of age, fetal alcohol-exposed and control rats were given a dose of N-Nitroso-N-methylurea (NMU) to induce mammary cancer growth in female offspring, NMU and testosterone to induce prostate tumor in male offspring, or ovariectomized and implanted with an estrogen capsule to induce pituitary tumors in female offspring. Mammary glands, prostate

glands or pituitary tissues were processed for determination of biochemical changes and histopathologies for tumor characterization. In the case of mammary tumor development, overall tumor multiplicity was greater in the offspring from the alcohol-fed group compared to the control groups, indicating a decrease in tumor latency. Alcohol-exposed animals developed more malignant tumors and more estrogen receptor- α -negative tumors relative to the control groups. In the case of prostate tumorigenesis, prenatal alcohol-exposed rats showed histological evidence for high-grade prostatic intraepithelial neoplasia (PIN) primarily in the ventral prostate, whereas control animals showed only low-grade PIN. Prenatally ethanol-exposed rats treated with carcinogen and testosterone also showed increased number of proliferative cells and androgen receptor with concomitant decreased levels of tumor suppressor proteins in the ventral prostate. Our results also show that pituitaries of fetal alcohol-exposed rats upon estrogen challenge developed prolactin-secreting tumors (prolactinomas) that were hemorrhagic and often penetrated into the surrounding tissue. Pituitary tumors of fetal alcohol-exposed rats produced higher levels of hemorrhage-associated genes and proteins and multipotency genes and proteins. Cells of pituitary tumor of fetal alcohol exposed rat grew into tumor spheres in ultra-low attachment plate, expressed multipotency genes, formed an increased number of colonies, showed enhanced cell migration, and induced solid tumors following inoculation in immunodeficient mice. These data suggest that fetal alcohol exposure programs some of the endocrine tissue to develop aggressive tumors. Although the exact mechanism for the tumor promotion effect of fetal alcohol is not clearly established, but our preliminary studies suggest the possibility that fetal alcohol programs some of these endocrine cells acquire stemness that enhances neoplastic properties for developing aggressive tumors.

Genome-wide DNA methylation in PFC of AUD subjects: insights on the epigenetic regulation of the glucocorticoid receptor

Eleonora Gatta¹, Dennis R Grayson¹, James Auta¹, Vikram Saudagar¹, Erbo Dong¹, Ying Chen¹, Harish R Krishnan¹, Jenny Drnevich¹, Subhash C Pandey¹, Alessandro Guidotti¹ (¹ Chicago, USA)

Individual vulnerability to develop psychiatric disorders depends on an intricate interplay between the genetic background and the environment. Environmental factors, including substance abuse and stress, cause long-lasting changes in the regulation of gene expression in the brain via epigenetic mechanisms, such as DNA methylation. Similar to stress, alcohol stimulates glucocorticoids release that bind to specific receptors, i.e., the glucocorticoid receptor (encoded by NR3C1). The human NR3C1 gene is comprised of nine untranslated alternative first exons (1_{A-J}) and eight translated exons (2 to 9). Seven of the exons 1 variants are embedded within a CpG island known to be susceptible to epigenetic regulation via DNA methylation. These epigenetic changes have been associated with psychopathological conditions in adulthood. However, little is known on the

role of DNA methylation mechanisms in the expression of stress-responsive genes in the brain of alcohol use disorders (AUD) subjects. Using a genome-wide DNA methylation approach (Infinium® MethylationEPICBeadChip, Illumina) followed by the identification of 5-methylcytosine (5mC) and 5-hydroxymethylcytosine (5hmC) by specific immunoassay, we identified a differential pattern of DNA methylation in AUD. Post-mortem brain samples were obtained from 25 controls and 25 AUD subjects from the New South Wales Tissue Resource Centre (University of Sydney, Australia). Bioinformatic analyses of differentially methylated genes highlight biological processes containing genes related to stress adaptation, including NR3C1. We validated some of these data and observed that chronic alcohol drinking results in a significant increased methylation of the NR3C1 exon variant 1H, with a particular increase in the levels of 5hmC over 5mC. These changes in DNA methylation were associated with reduced NR3C1 mRNA and protein expression in PFC as well as other cortico-limbic regions of AUD subjects when compared to controls. Furthermore, we show that the expression of several stress-responsive genes (e.g., CRF, POMC, FKBP5) is altered in the PFC and hippocampus of AUD subjects. These data suggest that alcohol-dependent aberrant DNA methylation of NR3C1 and consequent changes in other stress-related genes might be fundamental in the pathophysiology of AUD and lay the groundwork for treatments targeting the altered epigenetic regulation of NR3C1 in AUD. Supported by the P50AA022538 NIAAA-NIH grant to SCP and AG.

DNA-methylation abundantly associates with fetal alcohol spectrum disorder and its sub-phenotypes

I.M. Krzyzewska¹, J.M. Cobben¹, A. Venema¹, A.N. Mul¹, A. Polstra¹, A.V. Postma¹, R. Smigiel², K. Pesz², J. Niklinski³, M.A. Chomczyk³, P. Henneman¹, M.M.A.M. Mannens¹ (¹ Amsterdam, The Netherlands, ² Wroclaw, Poland, ³ Bialystok, Poland)

Aim: Fetal Alcohol Spectrum Disorder (FASD) involves prenatal growth delay, impaired facial and central nervous system development and causes severe clinical, social-economic burdens. Here we aim to detect DNA-methylation aberrations associated with FASD and potential FASD diagnostic and prognostic biomarkers. **Patients and methods:** FASD diagnosis was established according to golden-standard protocols in a discovery and independent replication cohort. Genome-wide differential methylation association and replication analyses were performed. **Results:** we identified several loci that were robustly associated with FASD or one of its sub-phenotypes. Our findings were evaluated using previously reported genome-wide surveys. **Conclusions:** we have detected robust FASD associated DMPs and DMRs for FASD in general and for FASD sub-phenotypes, i.e. on growth delay, impaired facial, and CNS development.

A rapid methylation sensitive digital PCR test that can sensitively and specifically assess heavy alcohol consumption and monitor alcohol treatment using DNA from blood or saliva

Robert Philibert¹, Meeshanthini Dogan¹, Jeffrey Long¹, James Mills¹ (Coralville, USA)

Background: alcoholism is the third largest preventable cause of morbidity and mortality. Uniquely, in the absence of acute intoxication, there is no readily employable test for assessing unhealthy levels of alcohol consumption. In 2014, we published the first genome wide study of heavy alcohol consumption (HAC). In this presentation, we expand on those earlier findings using data and biomaterials (both saliva and whole blood DNA) from 143 participants with current HAC and 200 abstinent controls. **Results:** using DNA from whole blood, we show that a set of four methylation sensitive digital PCR assays have a Receiver Operating Characteristic (ROC) area under the curve (AUC) of 0.96 for detecting those with HAC using DNA from whole blood with similar findings being obtained. After a mean of 21 days of inpatient enforced abstinence, methylation status at one of these markers, cg04987734, began to revert to baseline values. Re-examination of methylation data from our 2014 study with respect to this locus demonstrated a similarly significant reversion pattern at cg04987734 in association with treatment enforced abstinence. When the saliva DNA is used in place of whole blood, similar findings with respect to AUC and methylation reversion are observed. **Conclusions:** we conclude that clinically implementable dPCR tools using DNA from blood or saliva can sensitively detect the presence of HAC and monitor alcohol treatment results. These digital PCR tools will be useful to clinicians and researchers in monitoring those enrolled in substance use disorder treatment, employee wellness programs and insurance underwriting.

Novel alcohol-induced epigenetic signaling: neuroimmune genes and miRNAs

Fulton T Crews (Chapel Hill, USA)

Neuronal-glia signaling through miRNA let7 and Toll-like Receptor 7 induce interferons and negative affect

L.G. Coleman¹, J. Zou¹, L. Qin,¹ S.S. Moy¹, F.T. Crews¹ (¹ Chapel Hill, USA)

Neuroimmune activation is a prominent feature of alcoholic neuropathology. This includes activation of neuroimmune Toll-like Receptors (TLRs) with release of their endogenous agonists. Neuronal-glia interactions likely mediate neuroimmune responses to alcohol, however specific intercellular signaling mechanisms associated with alcoholic behavioral pathology need to be identified. We found a novel glial to neuronal signaling pathway, involving TLR7 and its endogenous agonist, miRNA let-7, which contributes to neuronal cell death, interferon (IFN) induction, and negative affect. Ethanol causes the secretion of let-7 in media microvesicles from microglia and astrocytes, which can activate TLR7 in neurons. In postmortem human alcoholic cortex, TLR7

and its downstream signaling components IRF7 and IFNs were induced. In mice, chronic binge ethanol induced let-7, TLR7, and pIRF7, and sensitized to immune responses and degeneration due to the TLR7 agonist Imiquimod (IMQ). In primary ex-vivo slice culture, ethanol caused secretion of miRNA let-7 in media microvesicles, and inhibition of TLR7 with siRNA or a novel small molecule antagonist prevented ethanol-induced cell death. The TLR7 antagonist also blocked neurodegeneration to chronic binge ethanol in mice. Using immortalized neuronal (SH-SY5Y), microglial (BV2), and astrocyte (U373MG) cell lines, and conditioned media transfers, we found ethanol induced glial secretion of miRNA let-7 and IFN induction in neurons. Microglial depletion ex-vivo blunted ethanol or IMQ-TLR7 induction of TNF α and IL-1 β , but not IFNs suggesting neuronal or astrocytic responses. In a 5-week binge model, ethanol caused persistent negative affect (anxiety-like behavior, and conditioned fear memory), with IFN β expression correlating with persistent conditioned fear memory.

Neuroimmune and epigenetic mechanisms regulate adolescent binge ethanol-induced loss of basal forebrain cholinergic neurons and hippocampal neurogenesis

Ryan Vetreno¹ (¹ Chapel Hill, USA)

Adolescence is a critical period of neurotransmitter system refinement and neuroplasticity that coincides with development of adult cognition. Binge drinking and alcohol abuse are common during adolescence causing lasting pathology. We find adolescent intermittent ethanol (AIE), which models human binge drinking, persistently decreases basal forebrain cholinergic neuron (BFCN) populations and hippocampal neurogenesis. Reciprocal connections between the basal forebrain and hippocampus are critical for maintenance of BFCNs and neurogenesis. We linked proinflammatory signaling to loss of BFCNs and neurogenesis as treatment with lipopolysaccharide mimics and anti-inflammatory treatments prevent AIE pathology. An imbalance between neuroimmune/neurotrophic signaling might contribute to persistent AIE-induced loss of BFCNs and neurogenesis through epigenetic mechanisms. In the basal forebrain, AIE increases histone 3 lysine 9 dimethylation (H3K9me2) occupancy at Chat and Trka gene promoters, which is associated with silencing of gene transcription. Exercise and acetylcholinesterase inhibitor (AChEI) treatment post-AIE reversed the loss of BFCNs, and restored the neuroimmune/hippocampal NGF balance and increased histone methylation. These data suggest AIE-induced loss of BFCNs might involve silencing of cholinergic phenotype and not cell death. Similarly, we find AIE increases H3K9me2 and reduces H3K9 acetylation in the adult hippocampus, the latter associated with diminished BDNF expression. Treatment with an AChEI and the histone deacetylase inhibitor TSA post-AIE reversed the AIE loss of hippocampal neurogenesis, and restored the neuroimmune/BDNF neurotrophic balance and epigenetic modifications. Together, these data suggest that an imbalance of neuroimmune/neurotrophic signaling might contribute to

persistent AIE-induced neuropathology through epigenetic mechanisms that can be reversed in adulthood.

Glia-to-neuron transfer of inflammatory proteins and miRNAs via extracellular vesicles: a new mechanism underlying ethanol-induced neuroinflammation

F. Ibáñez¹, M. Pascual¹, J. Ureña¹, C. Guerri¹ (¹ Valencia, Spain)

Extracellular vesicles (EVs) participate in intercellular signaling, and in the regulation and amplification of neuroinflammation. We have shown that ethanol activates glial cells through Toll-like receptor 4 (TLR4), triggering neuroinflammation. We evaluate if ethanol and the TLR4 response change the release and the inflammatory content of astrocytes-derived EVs, and whether these vesicles are internalized by neurons, spreading neuroinflammation. Cultures of cortical neurons and astrocytes were used. EVs were isolated from the extracellular medium of WT and TLR4-KO astrocytes, treated or untreated with ethanol (40 mM) for 24 h. The EVs content in inflammatory proteins, mRNA and miRNAs was analyzed by Western blot and RT-PCR in astrocyte-derived EVs and in neurons incubated or not with these EVs. A functional analysis of the miRNAs was also performed. We show that ethanol increases the number of secreted nanovesicles and alters their content by raising the levels of both inflammatory-related proteins (TLR4, p65, IL-1R, caspase-1, NLRP3) and miRNA (mir-146a, mir-182 and mir-200b) in the EVs from WT-astrocytes compared with those from the untreated WT cells. Ethanol did not change the number and the content of TLR4-KO astrocytes-EVs. We further showed that astrocytes' EVs were internalized by naïve neurons, changing their physiological functions and increasing inflammatory markers and miRNAs (e.g. mir-146a) levels, along with miRNAs-target genes (Traf6, Mapk14, Stat1 and Foxo3) in neurons treated with ethanol-treated WT astrocyte-derived EVs. These results suggest that astrocyte-derived EVs could act as cellular transmitters of inflammation signaling by spreading and amplifying the neuroinflammatory response induced by ethanol through TLR4 activation.

Role of microRNA 137 mediated changes in histone methylation in adolescent alcohol-induced anxiety and alcohol drinking behaviors in adulthood

Subhash C Pandey¹, Evan J Kyzar¹, J. Peyton Bohnsack¹, Huaibo Zhang¹ (¹ Chicago, USA)

Binge drinking during adolescence increases risk for psychiatric disorders later in life. Epigenetic mechanisms such as microRNAs (miRNAs) may contribute to this increased risk via molecular changes in the amygdala. Here, we investigated the role of miR-137 and its targeting of the epigenetic enzyme lysine-specific demethylase 1 (LSD1) in the adult amygdala after adolescent intermittent ethanol (AIE) exposure. Rats were exposed to 2g/kg ethanol (2 days on/off; AIE) or intermittent n-saline (AIS) during postnatal days (PND) 28-41 and allowed to grow to adulthood for analysis of behavior and biochemical measures. Some adult rats were

cannulated in the central nucleus of amygdala (CeA) and infused with miR-137 antagomir with or without concurrent Lsd1 siRNA infusion prior to analysis. AIE increases miR-137, decreases Lsd1 expression, and decreases LSD1 occupancy at the brain-derived neurotrophic factor exon IV (Bdnf IV) promoter in adult amygdala. Infusion of miR-137 antagomir into the CeA rescues AIE-induced alcohol drinking and anxiety-like behaviors. miR-137 antagomir infusion in the CeA also normalizes the decreased Lsd1 expression, decreased LSD1 occupancy, and decreased Bdnf IV expression due to increased H3K9me2 occupancy seen in the amygdala of AIE adult rats. Finally, co-infusion of Lsd1 siRNA into CeA prevents the miR-137 antagomir-induced rescue of molecular changes and anxiety-like behaviors. These results suggest that increased miR-137 in the CeA play an important role in chromatin remodeling and adult psychopathology caused by adolescent alcohol exposure. Supported by the NIAAA-NIH U01AA-019971, U24AA-024605 & P50AA022538 grants and senior VA career scientist award to SCP and F30AA024948 to EJK.

Alcohol-related cognitive impairment (ARCI): Korsakoff, Alzheimer, and friends

Florence Vorspan (Paris, France)

Epidemiology: early-onset dementia is mostly related to alcohol use disorders

Michaël Schwarzingier¹ (¹ Paris, France)

We conducted a nationwide retrospective cohort of all adult (≥ 20 years) patients admitted to hospital in metropolitan France between 2008 and 2013. Of all 81,958 cases of early-onset dementia (<65 years), 39,206 (47.8%) were related to alcohol use disorders. Early-onset dementia was more frequently recorded in men (51,339 [62.6%]) than women (30,619 [37.4%]), with stronger association with alcohol use disorders (29,944 [58.3%] vs. 9,262 [30.2%]). This nationwide study suggests that the burden of early-onset dementia could be substantially alleviated by reinforcing alcohol policies.

Clinical care: diagnosis and prognosis of Wernicke-Korsakoff disease and severe alcohol-related cognitive impairment: Alcomemo cohort

Julien Azuar¹, Frank Questel¹, Virgile Clergue-Duval¹, Thomas Barré¹, Florence Vorspan¹ (¹ Paris, France)

Cognitive disorders are common in patients with alcohol-related disorders (AUD). They must be screened and characterized in order to obtain appropriate care. An observational cohort of patients with AUD and severe cognitive impairment is being constructed from 2013 in our Addictology Department, with the help of a multicenter network called Resalcog. This network helps to keep a patient off alcohol for several months. We will describe the characteristics of this cohort of 124 patients, including clinical description of

comorbidities and evolution, circuit care, anatomic and functional brain imaging (IRM, 18-FDG-PET), nutritional status, CSF biomarkers (tau, beta-amyloid peptides, neurogranin, neurofilament light chain). We will insist on the prevalence of multifactorial origin of cognitive disease in this population. For the patients with strictly alcohol-related cognitive disorder, we will identify items correlated with a better prognosis of this disease.

Neuropsychological Impairments and brain alterations in “uncomplicated” patients with Alcohol Use Disorder

Anne-Lise Pitel¹, Alice Lanièpce¹, Nicolas Cabé¹, Laurent Coulbault¹, Géraldine Rauchs¹, Shailendra Segobin¹ (¹ Caen, France)

Alcohol Use Disorder (AUD) is associated with altered brain structure and function well before the development of neurological complications. Two brain circuits are mainly affected in “uncomplicated” AUD patients: the frontocerebellar circuit involved in motor abilities as well as working memory and executive functions; and the Papez circuit implicated in episodic memory. However, the pathophysiology of the brain dysfunction observed in AUD remains unclear since the nature and extent of cerebral damage and cognitive deficits do not seem to be directly related to the duration or severity of the alcohol history. Other factors including associated malnutrition potentially resulting in altered thiamin metabolism or deficiency, liver disease, or sleep disturbances may favor the development or exacerbate alcohol-related neuropsychological deficits and brain abnormalities. The role played by these factors must be further investigated since they are potential therapeutic targets that could prevent or reduce brain dysfunction in AUD.

Biomarkers in ARCI: what can we learn from the past 20 years of Alzheimer’s disease research and care?

Emmanuel Cognat¹ (¹ Paris, France)

Cognitive neurodegenerative disorders are slowly progressive brain diseases with overlapping clinical features and limited access to brain pathology in living patients. Thus, important efforts have been made during the past decades to develop diagnostic biomarkers that reflect pathological processes and prognostic markers that could predict the course of the disease. Research in this field has been most active in Alzheimer’s disease, the most frequent cause of cognitive disturbance in older patients but recent advances have been made in the past few years in other neurocognitive disorders such as frontotemporal lobar degeneration. Alcohol-related cognitive impairment (ARCI) is a complex condition with frequent multifactorial origin and difficulties to predict prognosis. Co-existing neurodegenerative pathology does not seem rare. Thus there is a crucial need for both diagnostic and prognostic biomarkers useable in patients with ARCI. Development of such biomarkers may take advantage of the lessons learnt from past and current research and use in clinical practice of biomarkers in AD and other neurodegenerative disorders.

Alcohol use disorders in context of dual diagnosis: did DSM make us lose the MATCH?

Georges Brousse (Clermont-Ferrand, France)

Dimensional perspectives for a pragmatic therapeutic approach

Maurice Dematteis¹ (¹ Grenoble, France)

Dual disorders are common and polydrug use is the norm. In patients combining both, the clinical presentation results from a mixture that makes a categorical diagnosis as well as a specific and stepped care difficult to establish. However complex the clinical picture, its deconstruction by elementary functional dimensions and endophenotypes (e.g. impulsivity) allows for pragmatic, gradual and integrative holistic treatment suited to the patient's needs, resources and ecology. There are currently no validated strategies in the literature. According to our experience and the Research Domain Criteria approach, we propose a framework that provides functional understanding (drug's functions in the psychic economy) and treatment of addictions which are considered to be dysfunctional adaptive strategies. Motivation- and education-based treatment aims at restoring functional autonomy and quality of life in accordance with the patient's needs, and combines dimensional pharmaco-psychotherapy, including: 1. substitutive strategies of harm reduction: substitution of consumption modalities and/or substances and/or behaviours (e.g. how to cope differently, starting from strategies applied by the patients and reinforcing what intuitively better works for them); 2. an integrative psychotherapy based on psychosocial rehabilitation modalities and introduced gradually, to first address the most basic functions (life rhythms, negative emotions, etc.) then the more and more complex issues (social processes, cognitions); 3. and a behavioral pharmacology according to medication's mechanism of action (neuroscience-based nomenclature) allowing for treatment of elementary dimensions and endophenotypes, complemented by specific treatments when categorical diagnosis is possible. In our experience, such an integrated and integrative approach allows for efficient treatment of the most complex patients in an outpatient setting.

Mechanisms underlying binge drinking and compulsive alcohol use

Heidi MB Lesscher (Utrecht, The Netherlands)

Behavioural traits and neurobiological mechanisms underlying loss of control over alcohol use in rats

Johanna AS Smeets¹, A. Maryse Minnaard¹, Geert MJ Ramakers¹, Roger AH Adan¹, Louk JMJ Vanderschuren¹, Heidi MB Lesscher¹ (¹ Utrecht, The Netherlands)

Alcohol use disorder (AUD) is characterized by loss of control over alcohol use, but only a minority of individuals

who drink alcohol develop AUD. Importantly, the mechanisms underlying loss of control over alcohol use and an individual's risk to develop AUD remain incompletely understood. Age of onset of alcohol use and certain personality traits are thought to play an important role in the risk for AUD. Neurobiologically, exaggerated involvement of the dorsolateral striatum (DLS) has been proposed to contribute to habitual alcohol seeking and loss of control over alcohol use. We assessed the contribution of these factors to the propensity to lose control over alcohol seeking in rats. Our studies showed that conditioned suppression of alcohol seeking, as a measure for alcohol use in the face of adversity, was less pronounced in rats with adolescent-onset alcohol consumption, compared to adult-onset animals. Further, rats that show high levels of social play behaviour as juveniles consumed more alcohol but showed intact conditioned suppression of alcohol seeking, unlike rats that displayed low levels of social play, reflecting a lack of control over alcohol seeking. Furthermore, preliminary analysis of optically-induced excitatory neurotransmission in cortical-DLS projection neurons showed increased facilitation of paired-pulse responses in the DLS in rats with a high alcohol drinking phenotype. These data suggest a complex relationship between age of onset, social development and DLS plasticity the development of AUD-like behaviour in rats.

Brain-wide functional architecture remodeling by alcohol dependence and abstinence provides evidence for the three-stage hypothesis

Olivier George¹, Daniel J Lurie², Andres Collazo³, Max Kreifeldt¹, Harpreet Sidhu¹, Mark D'Esposito², Candice Contet¹, Adam Kimbrough¹ (¹ La Jolla, USA, ² Berkeley, USA, ³ Pasadena, USA)

The identification of the psychological constructs and neurobiological mechanisms underlying the transition to addiction remains one of the most critical steps to better understand and treat alcohol and drug addiction. Converging lines of evidence suggest that multiple neurobiological modules processing reward, incentive salience, habits, stress, pain, and executive function may explain the vulnerability to alcohol addiction, and three major theories – incentive salience, hedonic allostasis and habit – have been proposed to contribute to addiction. However, because of technical limitations, we have been unable to directly test these hypotheses and visualize changes throughout the whole brain at single-cell resolution in subjects that are dependent on alcohol to validate the existence of these modules. The present study used an unbiased single-cell whole-brain imaging approach to map neuronal activity in alcohol-dependent mice and found that alcohol abstinence resulted in whole-brain reorganization of functional architecture and a pronounced decrease in modularity not observed in moderate drinkers. Structuring of the alcohol abstinence network revealed that addiction is driven by three major brain modules, reminiscent of the three-stage theory of addiction. Many hub brain regions controlling this pathological network were identified, including several that have been typically overlooked in addiction research. Further, a handful of the hub regions identified were predictive of

addiction-like behavior. These results provide a single-cell resolution map for addiction and demonstrate that alcohol dependence remodels brain-wide functional architecture to decrease modularity similarly to other brain disorders. Such neuroadaptations strongly reinforce the brain disease model and may explain why addiction is such a pervasive disease and why relapse is so common.

Face and predictive validities of a new preclinical model of operant binge drinking

Jérôme Jeanblanc¹, Pierre Sauton¹, Maria del Carmen Gonzalez-Marin¹, Alessia D'Ippolito¹, Virginie Jeanblanc¹, Mickael Naassila¹ (¹Amiens, France)

Binge drinking has multiple definitions in Humans (OMS, NIAAA, binge score for research...) making it difficult to define it accurately in animal models. Here we developed an animal model in outbred rats (Long Evans males and females) based on an operant ethanol self-administration paradigm. Rats were trained to self-administer a 20% ethanol solution under a FR1 (fixed ratio 1) then FR3 schedule for 1 hour. Slowly, the duration of the session was reduced first to 30 minutes then to 15 minutes and the levels of consumption reached on average 1.2g/kg within 15 minutes sessions. We found that such high consumption is associated with a higher motivation for the drug and for highly concentrated alcohol solutions (30% vs. 10%). Moreover, we showed that the speed of consumption is the factor that can differentiate heavy drinkers compared to binge drinkers. We also found that prolonged binge drinking leads to a decrease in decision making in a gambling task and that poor decision making is associated to lower dopamine release in the nucleus accumbens. We then tested drugs used in the treatment of alcohol use disorders (Acamprosate, (R)-Baclofen, GHB, Nalmefene and Naltrexone) and we found that all of them reduced binge drinking and all of them but acamprosate decreased both the motivation to consume and the relapse after prolonged abstinence. We thus demonstrated the face and predictive validities of our model and further neurobiological and behavioral studies are in progress to better characterize this damaging behavior.

Targeting GABAB receptors to treat AUD: recent advances in clinical and preclinical models

Eric Augier (Linköping, Sweden)

The use of baclofen for patients with alcohol use disorder: where do we stand?

Lorenzo Leggio¹, Mehdi Farokhnia¹, Roberta Agabio²
(¹ Bethesda, USA, ² Cagliari, Italy)

Baclofen, a selective gamma-aminobutyric acid-B (GABA-B) receptor agonist, has emerged as a promising drug for Alcohol use disorder (AUD). This talk will provide an overview of the clinical work done with this medication in patients with

AUD. Baclofen may be particularly advantageous in those with liver disease, due to its limited hepatic metabolism and safe profile in this population. Baclofen is mostly used off-label in some European countries and Australia, and in particular, for patients who have not benefitted from the currently used and approved medications for AUD. In France, baclofen has been extensively studied and was recently approved at the dose of up to 80 mg per day, by the French authority that regulates drugs approval and marketing (see Dr. Benjamin Rolland's talk). However, the use of this drug remains controversial, in part due to uncertainty regarding dosing and efficacy, alongside concerns about safety. A recent Consensus Statement among 26 international experts in the field was developed and published (Agabio et al. *Lancet Psychiatry* 2018) where the current state-of-the-art was briefly summarized and the need for future research was emphasized. On the latter point, human laboratory studies may shed light on the biobehavioral and other mechanisms how baclofen may work in some individuals with AUD (see Dr. Mehdi Farokhnia's talk). Finally, beyond baclofen, positive allosteric modulation of the GABA-B receptor may represent a better pharmacological approach towards the development of novel treatments for patients with alcohol and substance use disorders (see Dr. Eric Augier's talk).

Biobehavioral mechanisms underlying baclofen's effects on alcohol seeking and consumption: lessons learned from a human laboratory study

Mehdi Farokhnia¹, Sara Deschaine¹, Armin Sadighi², Melanie Schwandt¹, Lisa Farinelli¹, Mary Lee¹, Fatemeh Akhlaghi², Lorenzo Leggio¹ (¹ Bethesda, USA, ² Kingston, USA)

The GABA-B receptor agonist baclofen has been broadly studied and used as a pharmacotherapy for alcohol use disorder. The biobehavioral mechanisms underlying baclofen's effects are, however, not well understood. Human laboratory studies provide an informative platform to shed light on this domain. In the present randomized, double-blind, placebo-controlled study, thirty-four alcohol-dependent individuals received baclofen (30 mg/d) or placebo for a week, and then participated in a laboratory experiment consisting of three procedures: alcohol cue-reactivity, priming, and self-administration. Repeated blood samples were also collected for pharmacokinetic measurements. Group analyses showed that baclofen, compared to placebo, did not significantly attenuate cue-elicited craving or the amount of alcohol self-administration. However, baclofen disrupted the link between alcohol priming and self-administration, as indicated by significant interaction effects between drug condition (baclofen vs. placebo) and some of the priming variables (alcohol craving: $F_{3,9}=6.03$, $p=0.01$; alcohol sedation: $F_{3,6}=7.16$, $p=0.01$; breath alcohol concentration: $F_{1,25}=5.22$, $p=0.03$) on the total amount of alcohol self-administered. Considerable interindividual variability in baclofen pharmacokinetic parameters was observed. Maximum plasma concentrations of baclofen negatively correlated with cue-induced alcohol craving ($r=-0.57$, $p=0.03$) and priming-induced ratings of 'like more' ($r=-0.59$, $p=0.02$). These data suggest that baclofen may work by disso-

ciating the link between an initial drink and subsequent alcohol consumption. Considerable pharmacokinetic variability is an important factor to take into account when employing baclofen as a treatment for alcohol use disorder.

France and the recent approval for baclofen in AUD

Benjamin Rolland¹ (¹ Lyon, France)

In October 2018, the French Drug Agency granted an approval to the GABA-B receptor agonist baclofen for Alcohol Use Disorder (AUD). Baclofen is thus now labeled for “supporting drinking reduction in AUD”, up to the dose of 80 mg per day, and after failure of other drugs approved for AUD. This regulatory decision results from a long story of off-label use, sometimes at doses exceeding 300 mg per day. The French practice consists of using baclofen in patients who are still displaying heavy drinking. As baclofen is a sedative drug, interaction with alcohol can raise safety concerns. In 2019, many uncertainties remain with respect to the efficacy and tolerability features of baclofen in AUD. Despite this, France is now the first country in which baclofen is officially labeled for AUD. The French drug agency explained that this decision was not based only on scientific considerations, but also on the pragmatic statement that more than 60,000 patients were still treated with baclofen for AUD in France. As such the country will thus constitute an interesting real-life laboratory regarding the public health impact of this medication in AUD patients.

Effect of the novel GABA_B PAM ADX74441 on preclinical models of AUD and pathological alcohol choice

Eric Augier¹, Russell Dulman¹, Gaëlle Augier¹, Markus Heilig¹
(¹ Linköping, Sweden)

Alcohol effects on gamma-aminobutyric acid (GABA) transmission are key for the development and maintenance of alcohol addiction. Previous research indicate that GABA_B receptor agonists such as baclofen can affect addiction-related behaviors in preclinical models of alcoholism. More importantly, baclofen has also shown promise in clinical studies, in particular in severely alcohol-dependent patients. However, despite promising results in both clinical and preclinical models, baclofen itself has inherent limitations as a therapeutic for alcohol addiction, and failed to obtain an approval for this indication. An attractive alternative approach to targeting the same mechanism is offered by positive allosteric modulators (PAM:s) of the GABA_B receptor, which have the potential to achieve mechanistic and therapeutic effects similar to GABA_B agonists, while avoiding tolerance and overdose toxicity. In this symposium, I will present recent data obtained with ADX71441, a novel GABA_B PAM that has entered Phase 1 clinical testing, on several alcohol-related behaviors in rats that model important aspects of human alcoholism. In particular, ADX71441 dose-dependently decreased alcohol self-administration, with a higher efficacy in animals with a history of dependence. Furthermore, both cue- and stress-induced alcohol seeking were blocked by the GABA_B

receptor PAM. Importantly, these effects are observed in the absence of significant sedative side effects. Finally, I will show new data evaluating the potential of positive allosteric modulation of GABA_B receptors to rescue pathological alcohol choice over high value alternative rewards.

Neuroimaging in addiction: recent advances in the monitoring and prediction of pharmacological effects

Patrick Bach (Heidelberg, Germany)

Effects of High-dose baclofen on neural and behavioural cue-reactivity in alcohol dependence

Anne Beck¹ (¹ Charité, Berlin)

Increased functional brain response towards alcohol-associated stimuli (“cue reactivity”) is a neural hallmark of alcohol dependence and a promising target for pharmacotherapy. In this study, we assessed the effects of individually titrated high-dose baclofen on cue-induced brain activation in alcohol-dependent (AD) patients in a randomized controlled trial (RCT). Patients receiving baclofen showed a significant stronger decrease in cue-elicited brain activation in left orbito-frontal cortex (OFC), bilateral amygdala and left VTA than patients receiving placebo and had significantly reduced relapse rates. Thus, our data suggest the modulatory capacity of high-dose baclofen on alcohol-associated cue reactivity on a neuronal level, thereby potentially contributing to the relapse preventive effects of this compound in alcohol dependence.

The ICCAM platform: using fMRI to characterize brain responses in addiction and their pharmacological modulation

Anne Lingford-Hughes¹ (¹ London, UK)

This talk will describe the ICCAM platform which uses 3 fMRI tasks to characterise brain responses in alcoholism and polydrug (alcohol, opiate, cocaine) addiction. The study explored how any dysregulation is modulated by a range of pharmacological probes, e.g. a DRD3 antagonist, a NK1 antagonist, opiate antagonists and if this is consistent with likely therapeutic benefit.

Comparison of the effects of naltrexone on cue reactivity across different substance use disorders

Joar Guterstam (Stockholm, Sweden)

The opioid antagonist naltrexone is often used in the treatment of alcohol and opioid use disorders, and some clinical trials have also shown that it might reduce the risk of relapse in amphetamine dependence. In recent years, a number of fMRI studies have investigated the effects of naltrexone on drug cue reactivity in individuals with these different substance use disorders. Several studies have reported that nalt-

rexone attenuates neural responses to alcohol cues in alcohol dependent patients, and there is also preliminary evidence of a similar effect in patients with opioid use disorder. Recent studies of amphetamine users have found that they often exhibit strong neural and behavioral cue reactivity, but these reactions do not seem to be significantly affected by naltrexone pre-treatment. These divergent findings might point to differences in the pathophysiology of craving in alcohol, opioid and stimulant use disorders.

Identifying neurobiological predictors for pharmacological treatment response in addiction: results from the recent TRANSALC study

Patrick Bach¹ (¹ Mannheim, Germany)

Despite the high prevalence of alcohol use disorder (AUD), only a few medications are approved for its treatment and meta-analyses point towards a modest overall effect size of available medications, such as Naltrexone. Understanding the neural and behavioral mechanisms underlying the highly variable treatment response to anti-relapse medications therefore seem to be a key factor for improving individual treatment success and enhancing impact on clinical practice based on the principles of precision medicine. We will present data of a recent longitudinal open-label trial, investigating whether Naltrexone (NTX) could block increases in alcohol craving and neural alcohol cue-reactivity (CR) in patients with alcohol use disorder, compared to standard treatment using longitudinal combined neuroimaging and psychometric assessments. At baseline (before treatment initiation), all participants underwent baseline psychometric testing and fMRI assessment of mesolimbic alcohol CR. Following this, patients participated in a standard treatment program with the option of adjuvant NTX. After 2 weeks of treatment, AUD patients underwent a second combined neuropsychological and fMRI assessment of alcohol craving and mesolimbic CR. Results show higher mesolimbic CR in AUD patients vs. healthy controls at baseline. Over the treatment episode of 2 weeks, mesolimbic CR significantly increased in the standard treatment group (n=13), but not in the NTX group (n=22, $F_{(1,12)}=23.526$, $p=0.001$). Only NTX treated patients showed significant attenuation of CR in the left putamen over time (interaction time x medication: $F_{(1,33)}=6.823$, $p=0.013$) that was associated with a reduced relapse risk to heavy-drinking within three months of treatment (interaction treatment x time: Hazard Ratio=0.255, 95%CI=0.084-0.775, $p=0.016$). Further, NTX treated patients compared to patients receiving standard treatment reported a significantly higher proportion of abstinent days during follow-up ($t_{(33)}=1.834$, $p=0.042$). In conclusion, NTX blocked increased in mesolimbic CR that was observed in the standard treatment group. NTX was most effective in the patients with high baseline CR in the left putamen, reflecting in a number needed to treat of 1.8 [95%CI=1.3-6.2] to prevent one heavy relapse. While the results from our naturalistic study await further confirmation from prospective randomized trials, they support the role of neural CR as a biomarker in the development of precision medicine approaches with NTX.

From Fetal alcohol syndrome to Korsakoff syndrome through binge drinking: a neuroscientist/neuropsychological perspective

Anne-Lise Pitel (Caen, France)

Evaluating and training executive functions in binge drinking: a combined neuroscience approach

Pierre Maurage¹, Valérie Dormal¹, Séverine Lannoy^{1,2} (¹ Louvain-la-Neuve, Belgium, ² Stanford, USA)

Binge drinking, constituting the most frequent alcohol consumption pattern among adolescents and young adults, is characterized by a repeated alternation between intense consumption episodes and abstinence periods. The neuro-cognitive deficits related to this drinking pattern have been widely explored during the last decade. Executive functions deficits have been specifically identified as key factors in the emergence and maintenance of such habit. This talk will present new neuropsychological, electrophysiological and neuromodulation data allowing to better understand the specific executive impairments associated with binge drinking. We will centrally underline that binge drinkers (1) present a differential impairment across executive functions, with a preserved performance for shifting and updating abilities, but impaired inhibition processes; (2) show a dissociation, observed at the electrophysiological level, between impaired error-related processing and preserved feedback processing; (3) have a sufficiently preserved brain plasticity to benefit from neurostimulation-based rehabilitation of executive functions. The theoretical, experimental and clinical impact of these new insights will then be discussed, notably to underline the potential usefulness of joint neuropsychological/neuromodulation interventions among people presenting binge drinking habits.

Why we should ask bingers if they smoke cannabis?

Hélène Beaunieux¹, Virginie Bagnoux¹, Ludivine Ritz¹, Ingrid Banovic², Anaëlle Bazire¹, Nicolas Cabé¹, Caroline Cheam-Bernière¹, Laure Marine Houel¹, Denis Jacquet¹, Reynald Le Boisselier¹, Pascale Leconte¹, Jean-Baptiste Marchand¹, Nicolas Margas¹, Maxime Mauduy¹, Fabrizio Scrima², Cécile Sénémeaud¹, Jessica Mange¹ (¹ Caen, France, ² Rouen, France)

Studies focusing on college students' consumptions of psychoactive substance and their consequences have mainly focused on alcohol use and more recently on binge drinking (BD). Distinct BD patterns associated with specific psychological profiles have been identified (Lannoy et al., 2017; Gierski et al., 2018). Based on its effects on various psychological parameters, cannabis use, which frequently co-occurs with BD, may modulate these differentiated psychological profiles. Further, in contrast to the wide evidence of neuropsychological deficits associated with the use of cannabis or alcohol separately, few studies have investigated the risk of alcohol

use disorder and neuropsychological deficits related to the combined consumption of alcohol and cannabis. The aims of the present study were to examine the effect of cannabis on (1) the risk for alcohol use disorder and (2) the neuropsychological deficits observed in bingers. First, students of the University of Caen consuming alcohol and/or cannabis were screened through an internet survey-based study focusing on alcohol and cannabis experiences. Results showed that compared to bingers, students who both binged and smoked cannabis had an earlier onset of alcohol consumption, drank more and were more at risk of alcohol use disorder. Motivation and socio-normative parameters associated with alcohol consumption were significantly higher in this group than in binge drinkers who did not smoke cannabis. The neuropsychological evaluation revealed that compared to bingers, students who binged and smoked cannabis had more severe neuropsychological impairments, especially for episodic memory. These results suggest that cannabis consumption associated with BD is a risk factor for alcohol use disorder and episodic memory deficits. Those findings reinforce the idea that BD prevention programs may gain efficacy if considering its frequent combination with cannabis.

Decorticating the pathophysiological mechanisms underlying alcohol use disorder with and without Korsakoff's syndrome: a neuroimaging review and future directions

Shailendra Segobin¹, Alice Laniece¹, Nicolas Cabé¹, François Vabret¹, Francis Eustache¹, Anne-Lise Pitel¹ (¹ Caen, France)

Alcohol Use Disorder (AUD) exists in two main clinical forms. The first one, often referred to as “uncomplicated AUD”, is associated with mild-to-moderate deficits of episodic memory, executive functions, working memory and motor abilities. Some, but not all, uncomplicated AUD patients develop the second clinical form that is Korsakoff's syndrome, characterized by severe and irreversible amnesia, resulting from long-term excessive alcohol consumption and thiamine deficiency. Clinically, it is extremely relevant to identify uncomplicated AUD patients at risk of developing Korsakoff's syndrome. In this talk, the contribution of neuroimaging biomarkers towards understanding the pathophysiological mechanisms underlying these two clinical forms will be reviewed. More precisely, the brain circuits predominantly affected in both clinical forms, namely the frontocerebellar and Papez circuits will be discussed in terms of alterations to their macrostructural and microstructural integrity. The thalamus, a key region consisting of several nuclei is shared by these two brain circuits. Consolidating evidence showing that the loci and nature of structural alterations occurring within the thalamus potentially defines the specificity of Korsakoff's syndrome will be presented. To conclude this talk, current and prospective biomarkers in the field of cognition, neuroimaging and biology will be discussed based on how they bring incremental value towards the global understanding of the pathological mechanisms underlying Korsakoff's syndrome. Such a better understanding will ultimately enable clinicians to identify patients at risk for

such a severe and debilitating neurological disease in order to provide appropriate prevention treatment.

Genetics/genomics in alcohol induced liver injury – what next?

Vanessa Rausch (Sydney, Australia)

Genetics of hepatic steatosis and fibrosis

Marcin Krawczyk¹ (¹ Homburg, Germany)

Fatty liver disease (FLD) belongs to the most frequent conditions in hepatology. Indeed, more than 20% of adult Europeans suffer from fatty liver and the incidence of this condition is predicted to increase even further. A subgroup of patients with FLD will also develop liver fibrosis, which is a common hallmark of chronic liver diseases. Both hepatic lipid accumulation as well as liver scarring have for long been expected to be modulated by the inherited predisposition. In the recent years genetic variants in several genes, for example PNPLA3, TM6SF2 and MBOAT7, have been linked to the progression of chronic liver diseases. Prosteatotic and/or profibrotic variants in these genes were first detected in large genome wide association studies (GWAS) and afterwards these associations were replicated in the following candidate gene analyses. In particular carriers of the PNPLA3 p.I148M variant have been proven to be at risk of severe liver steatosis, fibrosis, cirrhosis and hepatocellular carcinoma (HCC) rendering variant PNPLA3 a common genetic risk factor for progressive liver injury. Interestingly, the same variant also seems to modulate the response to the FLDh therapies. The most recently detected splice variant rs72613567 in hydroxysteroid 17 β dehydrogenase 13 (HSD17B13) seems to, in turn, reduce the risk of FLD. Here we will summarize the current knowledge on the genetic background of hepatic steatosis and fibrosis, discuss the effects of the known variants on the disease progression as well address the potential use of genetic analyses in the clinical work up of patients with FLD.

An exploratory genome wide analysis of patients with alcoholic hepatitis

Suthat Liangpunsakul¹ (¹ Bloomington, USA)

An exploratory genome wide association study (GWAS) was conducted comparing patients with alcoholic hepatitis (AH) and heavy drinking matched controls without liver disease in order to identify variants or genes associated with risk for AH. Individuals were genotyped using the multiethnic genotyping array, after which the data underwent conventional quality control. Using bioinformatics tools, pathways associated with AH were explored on the basis of individual variants, and based on genes with a higher ‘burden’ of functional variation. Although no single variant reached genome wide significance, an association signal was observed for PNPLA3 rs738409 (p=0.01, OR 1.9, 95%CI 1.1h

3.1), a common single nucleotide polymorphism that has been associated with a variety of liver related pathologies including alcoholic cirrhosis. Using the improved gene set enrichment analysis for GWAS tool, it was shown that, based on the single variants' trait association p values, multiple pathways were associated with risk for AH with high confidence (false discovery rate [FDR]<0.05), including several pathways involved in lymphocyte activation and chemokine signaling, which coincides with findings from other research groups. Several Tox Functions and Canonical Pathways were highlighted using Ingenuity Pathway Analysis, with an especially conspicuous role for pathways related to ethanol degradation, which is not surprising considering the phenotype of the genotyped individuals. This preliminary analysis suggests a role for PNPLA3 variation and several gene sets/pathways that may influence risk for AH among heavy drinkers.

Contribution of common SNPs in explaining genetic variability in alcoholic cirrhosis

Devanshi Seth¹ (1 Sydney, Australia)

Genetic pathways contributing to the pathophysiology of liver cirrhosis in drinkers are fundamentally important to understand this disease. There is limited comprehension of the genetic basis of variation in Alcoholic Liver Cirrhosis (ALC) susceptibility as only up to 20% of heavy chronic drinkers progress to cirrhosis. Cirrhosis is the major medical consequence and health problem of excessive alcohol abuse with high morbidity and mortality. Genetics of ALC is poorly understood despite several candidate gene studies and a single GWAS reporting a strong association with PNPLA3. Other reported SNPs, e.g. TM6SF2, MBOAT7 and HSD17B13, only show modest GWAS level association with ALC. Our multinational GenomALC Consortium also performed GWAS in the world's largest collection of drinkers in a case-control study design. Age, gender and ethnicity matched Cases (drinkers with cirrhosis) and Controls (drinkers with no liver disease) were subjected to GWAS (Infinium GSA Array). Our data showed increased risk of alcoholic cirrhosis in offspring of parents with alcohol problems who died of liver disease, underscoring the heritability of this disease. We confirmed PNPLA3 (rs739409) and HSD17B13 (rs4607179) that strongly associated with alcoholic cirrhosis. However, all these common variants identified from GWAS approach only account for about 20% of the overall genetic variance leaving much of the genetic contribution to ALC unexplained. Due to typical GWAS array design, which focuses on common variants, protein coding exonic and rare variants, as well as other non-genetic factors are yet to be for ALC.

The role of PNPLA3 and MBOAT7 polymorphisms during alcohol detoxification – identification of different mechanisms for fibrosis development

Vanessa Rausch¹ (1 Heidelberg, Germany)

The PNPLA3 rs738409 and MBOAT7 rs626283 polymorphisms are genetic risk factors for ALD progression; however, their molecular mechanisms are still poorly understood. We

investigate the impact of these variants on important clinical parameters in response to alcohol withdrawal. Therefore, we prospectively enrolled 516 ALD patients for alcohol detoxification. Patients were genotyped and CAP, LS and ultrasound as well as laboratory markers were assessed before and after detoxification. In 105 patients, liver biopsy was also obtained and histologically analyzed. Carriers of MBOAT7 CC and PNPLA3 GG showed a strong and combined effect on fibrosis development ($P<0.05$), however display striking differences with regard to inflammation, fibrosis and steatosis in response to alcohol withdrawal. Inflammation was not different and resolved equally in all MBOAT7 genotypes during detox (AST, $P<0.001$), whereas PNPLA3 GG carriers presented with significantly enhanced liver injury after detoxification and with delayed resolution of inflammation (M30 and AST, $P<0.001$). Finally, steatosis resolved equally in both polymorphisms and genotypes to the same extent and no differences prior and after detoxification have been observed. In the histology cohort, PNPLA3 GG was significantly associated with inflammation (steatohepatitis, ballooning and lobular inflammation) and steatosis and MBOAT7 CC with fibrosis. In summary, both variants are associated with fibrosis progression, but the response of steatosis and liver injury to alcohol withdrawal is remarkably different. While PNPLA3 is associated with liver injury and steatosis, MBOAT7 is not affecting liver injury. Interestingly, both variants did not alter the resolution of steatosis during alcohol withdrawal.

Alcoholic liver cirrhosis, beyond single variant analysis

Tae-Hwi Linus Schwantes-An¹ (1 Bloomington, USA)

In the posth GWAS era, much of the genetic underpinnings of complex diseases such as alcoholic liver cirrhosis (ALC) remain unexplained. Missing heritability, the large unexplained portion of genetic heritability after discoveries from GWAS studies, spurred adaptation of next gen sequencing to identify genetic variations that are not captured by GWAS arrays. In parallel, statistical genetic methods have evolved from simple single variant analysis (e.g. assessing effect of each genetic variant one at a time) to polygenic risk scores that include more than several tens of thousands of common variants to stratify risk for disease. In this talk, using examples from GenomAlc Consortium analyses, examples of recent statistical genetic methods will be highlighted.

The role of Cytochrome P4502E1 in alcoholic liver disease and cancer

Helmut K Seitz (Heidelberg, Germany)

Ethanol metabolism in the liver: the role of CYP2E1

S. Zakhari¹ (1 Washington, USA)

About 95-98% of ingested alcohol is metabolized in the liver in a two-stage, enzymatically-catalyzed oxidation process;

the remainder is excreted in breath, urine and sweat. A small proportion of alcohol metabolism occurs via non-oxidative metabolic pathways resulting in the formation of fatty acid ethyl esters and phosphatidyl ethanol. A smaller portion undergoes conjugation with glucuronic acid or sulphate, and these conjugates are excreted in urine. The major pathway of oxidative metabolism of ethanol in the liver involves cytosolic alcohol dehydrogenase (ADH) to produce acetaldehyde. The cytochrome P450 isozymes, including CYP2E1, 1A2 and 3A4, also contribute to ethanol oxidation to acetaldehyde in the liver, particularly at elevated alcohol concentrations. CYP2E1 is induced by chronic ethanol consumption. It also metabolizes numerous medications such as acetaminophen, and other xenobiotics. The catalase enzyme can also metabolize alcohol to acetaldehyde; however, this pathway appears to play a minor role in alcohol oxidation by the liver. This presentation focuses only on CYP2E1 and will address its role in: health and disease; ethanol-mediated oxidative stress; drugs, xenobiotics and procarcinogens metabolism; fatty acid metabolism; and ethanol-induced hepatotoxicity and carcinogenesis. Discussion will also focus on hepatic CYP2E1 in pathological conditions such as obesity, diabetes and chemical inducers, as well as on drugs that inhibit ethanol-induced CYP2E1 and their role as protective agents against ethanol-mediated liver injury.

Alcohol and drug interaction: the role of CYP2E1

Rolf Teschke¹ (1 Frankfurt/Main, Germany)

Following the discovery of the hepatic microsomal ethanol-oxidizing system (MEOS) by Charles S Lieber and Leonore M DeCarli in 1968 and its subsequent purification and isolation from alcohol dehydrogenase and catalase through column chromatography in 1972, additional studies identified the microsomal cytochrome P450 (CYP) with its isoenzyme CYP2E1 as its major constituent. CYP2E1 metabolizes not only ethanol but also other short chain alcohols and various drugs and chemicals. Among these are paracetamol, halothane, and carbon tetrachloride. Consequently, the broad substrate specificity explains molecular interactions at the level of CYP2E1. In particular, a few substrates such as disulfiram, diallylsulfide, and clomethiazole are known for their inhibitory effect on CYP2E1, whereas the use of many other chemicals and drugs including acetone and isoniazid upregulate CYP2E1 gene expression. Most importantly, prolonged ethanol consumption upregulates CYP2E1 and thereby induces MEOS activity through a process involving reduced degradation of CYP2E1 by inhibition of hepatic proteasome peptidase activities. This induction of MEOS activity explains the adaptive increase of alcohol metabolism in individuals with prolonged alcohol abuse. In addition, upregulation of CYP2E1 and associated production of toxic intermediates is responsible for increased acute liver injury by paracetamol or carbon tetrachloride in patients with a past history of alcohol abuse. Ethanol-related upregulation of CYP2E1 is also observed in the intestinal tract, modifying thereby the intestinal microbiome, considered as mechanistic contributor to alcoholic liver injury, and facilitating the acti-

vation of carcinogens and potential tumor development in the gastrointestinal tract of patients with an alcohol problem. In essence, microsomal CYP2E1 plays an essential role in drug-alcohol interactions, increased risk of toxicity in the liver, and potential tumor development in the gastrointestinal tract.

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CYP2E1, ethanol and carcinogenesis

Gary J Murray¹ (1 Bethesda, USA)

Although there is a strong association between chronic and excessive consumption of alcohol and increased risk of various cancers, the causative role and the specific mechanisms involved remain a subject of ongoing research. Cytochrome P450E1 (CYP2E1) is induced in the liver after chronic alcohol consumption. As a consequence, in addition to alcohol, there is increased oxidation of many toxic and carcinogenic xenobiotics, including a variety of drugs, steroids, and other compounds. The oxidation and reduction reactions catalyzed by most P450 class enzymes are important mechanisms for detoxification of these xenobiotics but these same processes may lead to the creation of damaging products including the direct activation of carcinogens by oxidation of less toxic precursors. Another important pathway involves the generation of reactive oxygen species (ROS) including lipid peroxidation products and 4-hydroxynonenal that react with DNA resulting in the formation of exocyclic etheno DNA-adducts. These highly carcinogenic adducts contribute to the development of more serious pathology in liver and other tissues. There remains some controversy on the specific role of CYP2E1 in the production of ROS and of oxidative damage, and the significance of the observations that microsomes and purified P450s generate ROS, has been questioned. This is countered by observations in liver biopsies from patients with alcoholic liver disease (ALD) that the generation of these adducts were correlated with the induction of CYP2E1 in the liver after chronic alcohol consumption. Newer data has also emerged to implicate mitochondrial CYP2E1 in the production of ROS. The causative role of increased CYP2E1 activity in the development of alcohol-related cancers will be discussed.

The role of CYP2E1 in alcoholic liver disease and alcohol mediated carcinogenesis

Helmut K Seitz¹, Sebastian Mueller¹ (1 Heidelberg, Germany)

Various factors are involved in the pathogenesis of alcoholic liver disease (ALD) and ethanol mediated carcinogenesis. In addition to genetic, epigenetic and immunologic mechanisms, acetaldehyde associated toxicity, oxidative stress as well as cytokine mediated inflammation are of major importance. Oxidative stress with the generation of reactive oxygen species (ROS) develops either in inflammation (alcoholic hepatitis) or during oxidation of ethanol via cytochrome P450E1 (CYP2E1). CYP2E1 is induced by ethanol, oxidizes ethanol to acetaldehyde and generates ROS during this process. ROS

results in protein damage, enhanced fibrogenesis and DNA lesions. Furthermore, CYP2E1 induction results in an enhanced activation of various procarcinogens and an increased degradation of retinol and retinoic acid (RA), a compound responsible for cell differentiation and proliferation. An inhibition of CYP2E1 results in an improvement of ALD and chemically induced carcinogenesis in animal experiments. In man, CYP2E1 is induced following the consumption of 40 grams of ethanol per day already after one week. However, the induction varies interindividually. The mechanism for this is still unclear. Patients with ALD show a significant correlation between CYP2E1, the occurrence of highly carcinogenic etheno DNA-adducts and the severity of fibrosis. First results of the effect of CYP2E1 inhibition by chlormethiazole, a specific CYP2E1 inhibitor on ALD can be expected soon.

Drugs with novel mechanisms for the treatment of alcohol dependence

Robert Swift (Providence, USA)

Effect of the mGluR5 modulator GET 73 on alcohol pharmacokinetics and pharmacodynamics and alcohol craving and consumption in a human laboratory model

Robert Swift¹, Carolina Haas-Koffler^{1,2}, Lorenzo Leggio², Roberto Cacciaglia³ (¹ Providence, USA, ² Bethesda, USA, ³ San Remo, Italy)

GET 73 is a novel, small molecule compound that reduces alcohol consumption and has anxiolytic and anti-stress activity in animals. GET 73 acts as a negative allosteric modulator (NAM) at the mGluR5 receptor and could reduce the high glutamatergic allostatic state associated with alcohol use disorders. To establish safety/tolerability and to determine whether GET 73 reduces alcohol craving and alcohol drinking, we conducted a placebo-controlled, within-subjects crossover study with GET 73 in twenty non-treatment seeking alcohol dependent persons. After screening for medical and psychiatric suitability, eligible subjects were randomized to the 14-day inpatient study, receiving 3 days of treatment with GET 73 or placebo, followed by a 7-day outpatient washout, followed by 3 days of the alternate medication. Under each condition (GET 73 or placebo), on Day 2 and Day 12, participants received an oral dose of alcohol to bring BAC to 0.12 g/L. Alcohol and GET 73 pharmacokinetics and pharmacodynamics (intoxication, impairment, mood, etc.) were monitored and compared between drug and placebo conditions. On Day 3 and Day 13, participants received an alcohol cue-reactivity (craving) session, followed by alcohol self-administration. The results showed that GET 73, was safe and did not affect alcohol pharmacokinetics. GET 73, compared to placebo, increased alcohol sedation on the BAES but did not affect performance. GET73 did not affect subjective craving or alcohol self-administration in the

laboratory. However, GET73 appeared to reduce naturalistic alcohol consumption during the outpatient washout period.

Probenecid reduces alcohol drinking in rats: is pannexin1 a novel therapeutic target for alcoholism?

Pietro Paolo Sanna¹, Brendan J Tunstall², Sam A McConnell², Katrina L Gazo², Lia J Zallar^{2,3}, Carolina Haas-Koffler⁴, Vez Repunte-Canonigo¹, George F Koob², Leandro F Vendruscolo² (¹ La Jolla, USA, ² Baltimore, USA, ³ Bethesda, USA, ⁴ Providence, USA)

The development of novel and more effective medications for alcohol use disorder (AUD) is a pressing unmet medical need. Approved medications for AUD generally have limited efficacy and are prescribed for fewer than 10% of US patients with AUD. Drug repositioning or repurposing is an appealing strategy to bring new therapies to the clinic because it greatly reduces the overall costs of drug development and expedites the availability of treatments to those who need them. We recently found that the glycyrrhetic acid derivative carboxolone (CBX; 3 β -hydroxy-11-oxoolean-12-en-30-oic acid 3-hemisuccinate), a medication that was previously approved for the treatment of gastritis and peptic ulcer, reduces both dependent and nondependent alcohol intake in rodents, suggesting that it is a candidate for drug repositioning for the treatment of AUD. Carboxolone is a multi-target drug that shapes cellular responses to glucocorticoids by inhibiting 11 β -hydroxysteroid dehydrogenase (11 β -HSD) isozymes. It also inhibits pannexin1 channels, which contribute to adenosine triphosphate release, in the extracellular space. Probenecid is a medication that is used clinically primarily to increase uric acid excretion in the urine in hyperuricemic conditions, such as gout, through its activity as a competitive substrate for anion-transporting polypeptides in the kidney. Probenecid was also shown to inhibit pannexin1 channels. Therefore, we tested its effects on alcohol intake in rats. Similar to CBX, probenecid reduced alcohol intake in both dependent and nondependent rats. These results raise the possibility that pannexin1 may be a novel therapeutic target for the treatment of AUD. The clinical use of probenecid has been found to be generally safe, suggesting that it may be a candidate for drug repositioning for the treatment of AUD.

ANS-6637, a selective reversible inhibitor of ALDH2, suppresses alcohol consumption and cue-induced alcohol self administration in the absence of alcohol and acetaldehyde

Ivan Diamond¹, Stephanie O'Malley², Maria Arolfo, Lina Yao³, Peidong Fan³, Brent Blackburn¹ (¹ Los Angeles, USA, ² New Haven, USA, ³ Redwood City, USA)

According to prevailing clinical concepts Disulfiram discourages drinking because of adverse symptoms caused by increased acetaldehyde as a consequence of irreversible inhibition of hepatic ALDH2. However, Daidzin, a known ALDH2 inhibitor derived from Kudzu extracts, suppresses Golden Syrian hamster drinking without increasing ace-

aldehyde. This suggested that inhibiting ALDH2 in brain might reduce urges to drink alcohol. We used highly selective reversible inhibitors of ALDH2 to prevent excessive self-administration of alcohol. Paradoxically, these inhibitors also inhibited cue-induced reinstatement of drinking in the absence of alcohol and acetaldehyde. We soon discovered that ALDH2 inhibition in VTA prevents dopamine surges underlying craving/drug-seeking for alcohol, cocaine and other addictive drugs. Here we demonstrate that expression of viral ALDH2 antisense in the VTA also suppresses drinking, independently confirming ALDH2 as a CNS target. Transient ALDH2 antisense expression correlates directly with transient reduction of alcohol drinking. We then developed ANS-6637, a safe highly selective reversible inhibitor of ALDH2. We studied the dose-response of ANS-6637 interaction with alcohol in subjects consuming 5 standard drinks in 2.5 hours. There were virtually no adverse effects from ANS-6637 except an insensitive flushing reaction. We know ANS-6637 only targets ALDH2. In contrast, Disulfiram has recognized broad toxicity. The adverse alcohol-dependent adverse effects of Disulfiram are likely due to strong inhibition of hepatic ALDH1, not merely ALDH2. Our findings suggest that ANS-6627 holds great promise for treating alcoholism and preventing relapse by attenuating craving/alcohol seeking behavior without immediate adverse effects.

An evaluation of the Peroxisome proliferator receptor-alpha (PPAR- α) agonist, fenofibrate, in a human laboratory model of alcohol use disorder

Barbara J Mason¹ (¹ La Jolla, USA)

The PPAR- α agonist, fenofibrate, has been shown to decrease alcohol consumption and preference in rats and mice, and a human genome-wide association study showed an association of a single nucleotide polymorphism in PPAR- α with alcohol withdrawal. Taken together, these data provide a compelling rationale for testing fenofibrate for therapeutic potential in a human laboratory model of AUD. We hypothesized that fenofibrate would significantly attenuate craving in response to in vivo alcohol cue exposure in the laboratory and reduce drinking under natural conditions during treatment and post-treatment follow-up. Fifty non-treatment-seeking, cue-reactive volunteers with AUD (39 males, 11 females; aged 37.6 ± 11.8 years) were randomized to 9 days of treatment with fenofibrate (145mg/d) or matched placebo, and were followed for 1-week post-treatment. Subjects were required to be abstinent for 3 consecutive days prior to testing on Day 9; abstinence was verified by alcohol glucuronide testing. On Day 9, subjects were exposed to standardized mood induction procedures and in vivo beverage cues (alcohol or water). Subjects consistently showed significantly greater craving in response to alcohol cues relative to water cues, but no differences in craving between fenofibrate and placebo were observed. Similarly, no pre-post treatment differences were found for drinking. Fenofibrate concentration in plasma did not correlate significantly with alcohol cue reactivity or drinking measures. These data do not show an advantage in therapeutic potential for fenofibrate over placebo in individuals

with AUD. This research was supported by U01AA025476 and P60AA006420.

Recent advances in probing the link between alcohol and neuroendocrine pathways

Carolina L Haass-Koffler (Providence, USA)

The effects of oral and intravenous alcohol administration on appetitive and stress-related hormones: results from human laboratory experiments

Mehdi Farokhnia¹ (¹ Bethesda, USA)

A growing body of evidence from preclinical and clinical research suggest that endocrine pathways play important roles in the pathophysiology of addictive behaviors, including alcohol use disorder (AUD). A number of these pathways, especially appetitive and stress-related hormones, are currently under investigation as potential targets to develop novel treatments for AUD. To this end, it is also important to understand whether and how alcohol consumption and dependence may affect endogenous concentrations of endocrine markers. In a series of human laboratory experiments, we examined the effect of alcohol administration on blood concentrations of different endocrine markers in heavy-drinking alcohol-dependent individuals. Four separate sessions were conducted across these studies: oral self-administered (variable dose) alcohol, oral fixed dose alcohol, intravenous self-administered (variable dose) alcohol, and intravenous fixed-dose alcohol. Repeated blood samples were obtained during each session and the following hormones were measured: total ghrelin, acyl-ghrelin, leptin, glucagon-like peptide 1, GLP-1, insulin, amylin, pancreatic polypeptide (PP), peptide YY, gastric inhibitory peptide (GIP), insulin-like growth factor 1 (IGF1), growth hormone (GH), prolactin, Adrenocorticotrophic hormone (ACTH), cortisol, and aldosterone. The results of alcohol administration, via different routes and with different dosing schedules, on each endocrine marker will be discussed.

Dysregulations of glucocorticoid and mineralocorticoid receptor systems in alcohol dependence: converging evidence from rats and humans

Leandro F Vendruscolo¹ (¹ Baltimore, USA)

Alcohol consumption and withdrawal in alcohol use disorder (AUD) activate the hypothalamic-pituitary-adrenal (HPA) axis to release corticosteroids (corticosterone in rats or cortisol in humans), which binds to glucocorticoid receptors (GRs) and mineralocorticoid receptors (MRs). We hypothesized that excessive activation of the HPA axis by alcohol intoxication and withdrawal dysregulates GR and MR systems and that these changes contribute to negative emotional states that drive compulsive alcohol drinking. We found that GR expression and function were altered in cortical and subcortical brain

regions in dependent rats compared with nondependent rats. Systemic and intracerebral (central nucleus of the amygdala, ventral tegmental area, and nucleus accumbens) GR antagonism blocked the enhanced alcohol drinking and the motivation for alcohol in alcohol dependent rats. In a translational proof-of-concept human laboratory study, we found that GR antagonism decreased cue-induced alcohol craving and alcohol drinking in humans with alcohol use disorders. Additionally, we found that levels of MR in the CeA were negatively associated with anxiety-like behavior and compulsive-like alcohol drinking in dependent rats. In non-abstinent patients with AUD, the levels of aldosterone, an MR agonist, positively correlated with alcohol drinking, craving and anxiety scores, suggesting a potential functional role of MR in AUD. These findings provide converging evidence from rats and humans for dysregulations of GR and MR systems in AUD.

Effect of GLP-1 analogue and desacyl ghrelin administration on alcohol cue reactivity in humans: the gut hormone in addiction study

Tony Goldstone¹ (¹ London, UK)

Common neurobiological mechanisms underlie addictive behaviours, including alcohol use disorder (AUD), drug dependence and overeating. Recent pre-clinical research has shown that gut-brain hormonal signals regulating food intake play an important role in non-food reward behaviours, and that the role for the appetitive hormones, glucagon like peptide-1 (GLP-1), and acyl ghrelin (AG), extends beyond food intake regulation to include reward behaviour and consumption of alcohol. Although desacyl ghrelin, the precursor for AG (active at the GHSR1a receptor), is not an antagonist or inverse agonist at GHSR1a, it has opposite metabolic effects to AG in some pre-clinical and clinical studies, and reduced sugar intake in humans. Furthermore, in clinical studies a DAG analogue, AZP-531, reduces body weight and improves glycaemic control in adults with obesity and type 2 diabetes mellitus. Dr. Goldstone will present novel results from his MRC-funded experimental medicine, Gut Hormone in Addiction study, examining the effects of acute infusion of the GLP-1 analogue, Exendin-4, and DAG on brain responses to evaluation of alcohol pictures using functional magnetic resonance imaging in 3 groups: adults with obesity, ex-smokers and abstinent alcohol dependence (<http://clinicaltrials.gov/ct2/show/NCT02690987>). This will reveal the possible benefits of targeting the GLP-1 and ghrelin systems for treatment of alcohol use disorder, and potential underlying mechanisms for reductions in alcohol consumption by attenuating alcohol cue reactivity.

Intravenous administration of ghrelin increases serum cortisol and aldosterone concentrations in heavy-drinking alcohol-dependent individuals

Carolina L Haass-Koffler¹, Mehdi Farokhnia², Lorenzo Leggio¹
(¹ Providence, USA, Bethesda, USA)

Increasing evidence supports the role of appetite-regulating hormones, including ghrelin, in alcohol use disorder (AUD).

Effects of ghrelin administration on cortisol and aldosterone concentrations have been observed in ghrelin-exposed tissues or cells, rodents and healthy volunteers, however whether these effects replicate in individuals with AUD is unknown. Here we tested the hypothesis that intravenous administration of ghrelin leads to increase in endogenous serum cortisol and aldosterone concentrations in alcohol-dependent heavy drinking individuals, and that these changes may predict ghrelin-induced alcohol craving. This was a double-blind, placebo-controlled human laboratory study in non-treatment-seeking, heavy-drinking alcohol-dependent individuals randomized to receive either placebo, 1 mcg/kg or 3 mcg/kg of intravenous ghrelin. Then, participants underwent a cue-reactivity procedure in a bar-like setting, which included exposure to both neutral (juice) and alcohol cues. Repeated blood samples were collected and used to measure endogenous cortisol and aldosterone serum concentrations in response to exogenous ghrelin administration. Furthermore, cortisol and aldosterone serum concentrations were used to develop a model to predict the effect of exogenous ghrelin administration on alcohol craving. Intravenous ghrelin administration increased endogenous cortisol and aldosterone serum concentrations. While the effects on cortisol were greater than those on aldosterone, only the ghrelin-induced changes in aldosterone serum concentrations predicted alcohol craving. These findings provide evidence of ghrelin effects on glucocorticoids and mineralocorticoids in individuals with AUD, thereby providing additional information on the potential mechanisms how the ghrelin system may play a role in alcohol craving and seeking in AUD. Funding: Dr. Haass-Koffler is supported by the National Institute on Alcohol Abuse and Alcoholism (K01AA023867; PI: Haass-Koffler). Drs. Farokhnia and Leggio are supported by the National Institute on Alcohol Abuse and Alcoholism Division of Intramural Clinical and Biological Research and the National Institute on Drug Abuse Intramural Research Program (ZIA-AA000218, Section on Clinical Psychoneuroendocrinology and Neuropsychopharmacology; PI: Leggio). The parent study was funded by the National Institute on Alcohol Abuse and Alcoholism (R21AA019709; PIs: Leggio and Kenna). The content of this article is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health or the Department of Veterans Affairs. Conflict of interest: the authors report no biomedical financial interests or potential conflicts of interest.

Free oral communications

In vivo longitudinal study of risky alcohol consumption effects on the brain

A. Lanquetin¹, A. Drieu¹, C. Freyssainge¹, D. Vivien¹, A.L. Pitel¹,
M. Rubio¹ (¹ Caen, France)

Introduction: neuroimaging and neuropsychological studies revealed structural and functional brain alterations associated with Alcohol Use Disorder (AUD). In 50 to 80 % of AUD

patients, these brain alterations result in cognitive and/or motor impairments. However, the consequences of risky alcohol consumption (not reaching AUD but superior to the recommendations) have been less studied in both humans and rodents. In this longitudinal study, we aimed at studying the effects of risky alcohol consumption in mice at different time points. Materials and methods: mice were divided into 3 groups: control (drinking water), risky alcohol consumption (10% ethanol solution ad libitum) and risky alcohol consumption with repeated periods of abstinence (ethanol replaced by water before and during the test week). From 6 weeks to 12 months alcohol exposure, every 3 months, and we conducted i) a battery of behavioral tests to measure motor abilities (balance beam), anxiety (open field) and memory (Y-maze, fear conditioning); ii) MRI examinations to study regional brain volumes. Beverage intake and body weight were measured all along the experiment and did not show any difference between groups (~6 ml/mouse/day). Results: behavioral alterations were significant after 6 months of risky alcohol consumption, as revealed by persistent memory impairments. After 9 and 12 months of alcohol exposure, balance abilities were gradually altered in the two groups with risky alcohol consumption. Anxiety levels did not differ between groups at any time. Brain volumes in various regions classically affected by alcohol consumption did not show any between-group difference after 6, 9 or 12 months of alcohol exposure. Conclusion: our results show that risky alcohol consumption, even when not reaching AUD, drives a series of behavioral alterations which are less severe but compatible with the deficits described in AUD patients. Interestingly, these deficits do not seem to be related to macrostructural brain alterations. Microscopic analyses to study neuronal density, microgliosis and astrogliosis that could explain the behavioral deficits observed are ongoing.

BEARNI as screening tool for neuropsychological impairments and brain shrinkage in alcohol use disorder and Korsakoff's patients

Ludivine Ritz¹, Shailendra Segobin¹, Coralie Lannuzel¹, Céline Boudehent¹, François Vabret¹, Anne-Lise Pitel¹, Héléne Beaunieux¹ (¹ Caen, France)

Chronic and excessive alcohol consumption results in Alcohol Use Disorder (AUD) without neurological complications and Korsakoff's syndrome (KS) when combined with thiamine deficiency. These two clinical forms are accompanied by widespread structural brain damage in both the fronto-cerebellar and Papez circuits as well as in the parietal cortex. Grey matter (GM) shrinkage in these brain regions is in agreement with the neuropsychological impairments observed in AUD patients early in abstinence including notably executive and motor deficits as well as episodic memory disorders. AUD and KS can be distinguished on the severity of the brain damage and cognitive deficits. The main specificity of KS is a disproportionately encoding deficit in episodic memory, whose severity allows distinguishing KS from AUD. BEARNI is a screening tool especially designed to detect neuropsychological impairments in AUD. But the relevance of BEARNI for

the detection of KS patients and its relationships with brain damage remain unknown. Ten KS patients, 26 AUD patients and 16 healthy controls (HC) underwent the BEARNI and a 3T-MRI examination. On BEARNI, KS had lower performance than AUD patients (who did not differ from HC) for the episodic memory and fluency scores. The specificity of KS deficits on the memory subtests suggests that BEARNI is sensitive to amnesia. Statistical cluster analysis revealed that several AUD patients were classified within the same cluster as KS patients based on the BEARNI episodic memory results. Thus, a low score on this subtest (inferior or equal to 1.5 points/6) would enable the detection of patients at risk for developing KS. Multiple regression analyses conducted between GM volume and performance on each BEARNI subtest revealed correlations with the FCC, the PC and parietal cortices. The comparison between KS and AUD regarding the GM volume in the FCC and parietal cortices revealed that they were atrophied to the same extent, suggesting that BEARNI is sensible to the severity of alcohol-related GM abnormalities. Within the PC, the volume of the parahippocampal gyrus correlated with the fluency score and was the only region to be specifically atrophied in KS, suggesting that BEARNI is sensible to specific brain abnormalities occurring in KS. It is worthwhile noting that BEARNI remains a screening test and should not be considered as a sufficient tool to diagnose KS. An extensive neuropsychological assessment associated with a follow-up examination (in order to confirm the persistence of the neuropsychological impairments) is required for a confirmed KS diagnosis.

Is impulsivity related to executive deficits in patients with Alcohol Use Disorder?

Nicolas Cabé¹, Alice Laniepcé¹, Céline Boudehent¹, Francis Eustache¹, François Vabret¹, Héléne Beaunieux¹, Anne-Lise Pitel¹ (¹ Caen, France)

Introduction: impulsivity, strongly associated with Alcohol Use Disorder (AUD), is a multidimensional construct encompassing various different cognitive and behavioral components. Impulsivity is involved in the induction of the first alcohol consumption, reactivity to alcohol stimuli, loss of control over alcohol consumption, development of dependence, risk of relapse, and craving (1, 2). Anxiety and depression are also associated with craving and risk of relapse and may be related to impulsivity (3, 4). In clinical practice, impulsivity is assessed by self-questionnaires such as the Barratt Impulsiveness Scale (BIS), which has been designed to measure trait impulsiveness and their dimensions. Some authors rather consider impulsivity as a result of an executive dysfunction and more particularly as an inhibition failure. Chronic and excessive alcohol consumption is indeed known to be associated with cognitive impairments and especially with executive deficits such as altered planning, flexibility or inhibition (5). Impulsivity observed in AUD patients may thus reflect the behavioral consequences of impaired executive abilities related to a history of excessive and chronic alcohol consumption. A better understanding of the cognitive substrates of impulsivity is crucial to offer appropriate care when impulsivity is considered as a therapeutic

target. Our aim was to investigate the relationships between impulsivity and executive functions in AUD patients, taking patients' alcohol history, as well as anxiety and depression, into account. Considering that impulsivity is a consequence of the dysexecutive syndrome, we would expect the impulsivity score to be related to executive abilities and alcohol exposure. If we rather consider impulsivity as a matter of personality or emotions, we would expect it to be related to thymic variables such as anxiety and depression, as well as early alcohol consumption. Method: eighty-five recently detoxified AUD patients and sixty-three healthy controls (HC) matched for age, education, and sex were included. Sociodemographic data and information about patients' alcohol consumption history were collected. Anxiety was measured by the State-Trait Anxiety Inventory (STAI), and depression by the Beck Depression Inventory (BDI). Executive functions were assessed with an extensive neuropsychological battery, which explored flexibility, inhibition, manipulation of information stored in working memory, organization and strategy. Impulsivity was measured by the Barratt Impulsiveness Scale 10 (BIS10) which is the latest validated version of this questionnaire in French. Parametric statistical analyses (Student's T-tests) and chi-square tests when appropriate were used to compare AUD and HC groups. We then conducted correlational analyses (Bravais-Pearson) to investigate the relationships between BIS 10 total score, cognitive abilities including executive functions, anxiety and depression, and alcohol history or clinical variables. Results: compared to HC, AUD patients were significantly more anxious and depressed and presented a more frequent alcohol family history. Moreover, AUD patients were significantly more impulsive than HC as indicated by their BIS 10 total score. AUD patients were impaired on all the executive tests used in the study except on the verbal fluency task. Their speed processing was significantly lower than in HC. Correlations revealed that in AUD patients, the BIS 10 total score correlated with none of the executive and alcohol history measures. By contrast, impulsivity correlated with higher anxiety and depression. Discussion: AUD patients presented a high level of impulsivity, which was related neither to their executive deficits nor to their history of alcohol consumption. Our findings indirectly indicate that impulsivity, as evaluated by the BIS 10, does not seem to be a consequence of an alcohol-related dysexecutive syndrome. Impulsivity could rather be a vulnerability factor, linked to affective parameters (anxiety, depression) and potentially favoring the development of excessive and chronic drinking, which in turn would result in altered executive functions. These unexpected results could be interpreted within the theoretical framework of the neurocognitive dual-process model, which proposes that addictions may be the product of an imbalance between 1) a "reflective system", involved in the cognitive evaluation of the stimuli by means of memory and executive functions, responsible for controlled-deliberate responses and 2) an "affective-automatic system", involved in the emotional evaluation of the stimuli, initiating automatic-appetitive responses. The imbalance between these two systems would account for rapid decision making, prioritizing short-term reward irrespective of the long-term consequences (6). Our

findings suggest that impulsivity would correspond to the hyperactivation of the affective system rather than to the alteration of the reflective system. Another explanation could be that AUD patients have difficulty to self-evaluate their level of impulsivity when asked through questionnaires (7). Further studies are required to explore whether our findings could be replicated using other impulsivity questionnaires (like UPPS or BIS 11) and executive tasks targeting other functions such as decision-making or planning. Clinically, these results suggest that impulsivity and executive abilities should be evaluated and managed separately and in complementary perspective to prevent or reduce the relapse risk in AUD patients.

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A smartphone App to assess alcohol consumption behaviours: development, validity, compliance, and reactivity

Antoinette Poulton¹, Jason Pan¹, Loren Richard Bruns¹, Richard O Sinnott¹, Robert Hester¹ (¹ Parkville, Australia)

Background: Although research into problem drinking often relies on retrospective measures to assess alcohol intake, such methods have been found to distort actual consumption levels/patterns. Real-time electronic protocols in the form of smartphone apps are consequently advocated. There is limited research pertaining to the development, validity, compliance, and reactivity of using such apps in the experimental arena. Methods: an iterative process guided the development of the CNLab-A app. Healthy individuals (N=671) completed demographic questions and a 21-day Timeline Followback before using CNLab-A for 21 days. We considered the size and diversity of the sample; compared data reported via retrospective measures with that captured using CNLab-A; and, assessed the data for evidence of compliance and reactivity as a function of hazard versus non-hazard drinker status. Results: CNLab-A yielded a large and diverse sample. On average, participants submitted data on 20.27 out of 21 days. Compared to Timeline Followback, a significantly greater percentage of drinking days (24.79% vs. 26.44%) and signi-

ificantly higher total intake (20.30 vs. 24.26 standard drinks) was recorded via the app. Both hazard and non-hazard drinkers were highly compliant with app protocols. Linear growth analyses revealed hazardous drinkers decreased their alcohol intake by 0.80 standard drinks over the 21-day experimental period. There was no change to the drinking of non-hazard individuals. Both hazard and non-hazard drinkers showed a slight decrease in responding (“yes”) to drinking behavior over the same period. Conclusions: smartphone apps appear an effective and methodologically sound means of obtaining alcohol consumption information.

Affect regulation training (ART) program in alcohol abstinence consolidation

Caroline Claisse¹, Marie-Charlotte Gandolphe¹, Lydie Defrance¹, Mickael Naassila², Jean-Louis Nandrino¹ (¹ Lille, France, ² Amiens, France)

Background: this study aimed at exploring the evolution of emotion regulation strategies and abilities with training remediation program in abstinent patients suffering from severe alcohol use disorders (AUD). The main objective of this project is the consolidation of abstinence with the acquisition or reinforcement of new emotion regulation strategies. In the Adaptive Coping with Emotions Model (ACE Model, Berking & Whitley, 2014), adaptive emotion regulation is conceptualized as a situation-dependent interaction between emotion regulation skills. To this end, the Affect Regulation Training (ART, Berking & Whitley, 2014) was conceptualized in six training modules (psycho-education, muscle and breathing relaxation, non judgmental awareness, acceptance and tolerance, compassionate self-support, analyzing emotions and modifying emotions) related to these emotion regulation skills. Each unit focuses on one emotion regulation skill. Method: 117 alcohol-abstinent individuals abstinent from two weeks to several years were recruited in day hospitals and groups of Alcoholics Anonymous association. 87 individuals participated in the ART program and were compared to 30 alcohol-abstinent individuals who do not have the program. The ART program consisted of six weekly 3-hour therapy sessions in a group of 5 to 8 persons. In control group (n=30), evaluations were proposed within therapy session. For all individuals, the evaluation consisted of two parts: a clinical questionnaire (concerning their current situation, alcohol use and context) and a cognitive and emotional assessment. Drinking history and emotion regulation processes were assessed using the Difficulties in Emotion Regulation Scale (DERS-F) and the Cognitive Emotion Regulation Questionnaire (CERQ). Anxiety and depression scores were assessed using Hospital Anxiety Depression Scale (HADS). Finally, mindfulness levels were assessed with Five Facets Mindfulness Questionnaire (FFMQ). For the experimental group, the same evaluation was performed before ART program (T0 ART), after the ART program (T1 ART) and six months later (T2 ART). In control group, the evaluation was performed twice, one at (T0 control) and six weeks later (T1 control). Result: differences in emotion regulation strategies were found according to the participation in ART remediation program. The results

showed less difficulties in emotion regulation (DERS-F) for all individuals immediately after (T1 ART) or six months after the end of therapy (T2 ART) than before ART session (T0 ART). Compared to control group, individuals with emotion training partially recovered on DERS-F subscales especially for strategies and emotional clarity. In addition, individuals had higher levels of non-adaptive strategies for emotion regulation (CERQ) before (T0 ART) than after therapy session (T1 ART, T2 ART). In comparison to control group (T0 control), they had less non-adaptive strategies after ART session (T1 ART). Finally, mindfulness total score was higher after therapy session in ART group (T1 ART) than in control group (T0 control, T1 control). Conclusion: these results demonstrated a recovery of emotion regulation abilities after emotional training in a sample of abstinent alcohol individuals. Compared to Control group, the ART group presented less difficulties in emotional abilities and regulation strategies, and higher levels of mindfulness. The ART program allows greater flexibility in the emotion regulation strategies involved in consolidating abstinence and should be used both initially at the beginning of withdrawal but also in individuals in the process of maintaining their abstinence.

Effect of inflammatory pain on alcohol induced dopamine release in the NAc and alcohol relapse in rats

Yolanda Campos-Jurado¹, Jose Luís González-Romero¹, Jesús Lorente¹, Ana Polache¹, Luis Granero¹, Teodoro Zornoza¹, Lucía Hipólito¹ (¹ València, Spain)

Epidemiologic data have shown a relationship between pain and addiction especially to opioids and alcohol. Indeed, a recent clinical study undercovered that the correct management of pain in patients with a previous history of alcohol use disorder decreases the risk of relapse in alcohol drinking, suggesting that in this prone population, pain may increase the vulnerability to relapse in alcohol consumption. Previous data in rats revealed that inflammatory pain desensitizes mu opioid receptors (MORs) in the ventral tegmental area (VTA) and increases intake of high doses of heroine. Due to the relevant role of MORs in alcohol effects, we hypothesize that this desensitization may also alter the pattern of activation of the mesocorticolimbic system exerted by alcohol and therefore have an effect on alcohol relapse. In our study, we evaluated the effect of inflammatory pain on accumbal increase of dopamine release elicited by 1.5 g/kg of ethanol (s.c.). This microdialysis study showed that the presence of inflammatory pain blunted the increase of extracellular dopamine levels in the Nucleus Accumbens induced by ethanol. Later on, we evaluated the effect of inflammatory pain on the alcohol deprivation effect (ADE) in long-term ethanol-experienced rats. After four cycles of free ethanol intake and abstinence periods, inflammatory pain did not affect to the magnitude of the ADE. These data further support the impact of pain on the neurochemical events on the dopaminergic mesocorticolimbic system following alcohol administration and also underscore the necessity of finding an appropriate paradigm to determine the behavioral consequences.

Emotional memory in young binge drinkers

Carina Carbia¹, Montserrat Corral², Francisco Caamaño-Isorna², Fernando Cadaveira² (¹ Cork, Ireland, ² Santiago de Compostela, Spain)

Background: college binge drinking (BD) has been linked to persistent cognitive difficulties, especially in episodic memory. However, despite impairments in emotional functioning have been associated with the development of alcohol use disorders, the emotional sphere has been relatively unexplored in BDs. The purpose of this study is to examine the effects of BD in emotional episodic memory. Methods: a cohort of 180 (96 ♀) healthy college students was followed during two years (18-20 years old) and their alcohol use was recorded. In the last assessment, participants completed an adaptation of the Emotional Verbal Learning Test (EVLTL). Generalized linear mixed models were applied. The models were adjusted by psychopathological symptoms (BSI-18). The neuropsychological analyses were carried out separately for males and females, in accordance with sex differences in the development of emotion circuitry in adolescents. Results: in females, BD was associated with poor performance in the emotional memory task, in particular lower recall of neutral words and greater recall of negative versus neutral words. Whereas in males, no alcohol-related effects were found. Conclusions: females binge drinkers present difficulties in emotional episodic memory linked to the interference of negative content. This is in line both with sex-related differences in the recall of emotional memory and an alcohol-related aberrant processing for emotionally salient stimuli, which might result in greater vulnerability to affective disturbances among women. Further research is needed to understand the role of emotional functioning in the escalation of alcohol abuse, from a gender perspective.

Methylation profiles during acute alcohol withdrawal in a clinical sample

Lea Sirignano¹, Stephanie H Witt¹, Josef Frank¹, Jens Treutlein¹, Fabian Streit¹, Ulrich Frischknecht¹, Jerome C Foo¹, Franziska Degenhardt², Gabi Koller³, Ulrich Preuss⁴, Peter Zill³, Kristina Adorjan³, Markus Nöthen², Rainer Spanagel¹, Falk Kiefer¹, Marcella Rietschel¹ (¹ Mannheim, Germany, ² Bonn, Germany, ³ Munich, Germany, ⁴ Herborn and Halle-Wittenberg, Germany)

Withdrawal is a serious and sometimes life threatening event in alcohol-dependent individuals. It has been suggested, that epigenetic processes may play a role in this context. Identification of genes involved in such processes may hint to relevant mechanisms underlying withdrawal. In the present study we sought to longitudinally investigate epigenome-wide methylation patterns in 100 severely alcohol-dependent patients during alcohol withdrawal and after 2 weeks of recovery, and also in 100 matched controls. More than 850,000 methylation sites were assessed using Illumina EPIC bead chips. Reflecting the high quality of our methylation data, we found – consistent with earlier reports – that correlation of methylation age with biological age of assessed individuals was very high ($r=0.9$). We found pronounced genome-wide

significant differences between patients in withdrawal and after 2 weeks, among them in genes which have been reported to play a role in withdrawal symptomatology in previous studies (SLC29A1, FYN). As expected, methylation between patients and controls differed considerably, also in genes implicated in withdrawal (FKBP5, BDNF, EFNA5). Search for differentially methylated regions and gene ontology based gene set analysis revealed involvement of apoptotic processes in acute withdrawal. This has been also shown in other assessments with alcoholic patients. This epigenome-wide longitudinal methylation study conducted in the so far largest sample of severely alcohol-dependent individuals suffering from withdrawal symptoms replicates known and suggests novel genes, which may play a crucial role in alcohol withdrawal.

Alcohol consumption during pregnancy: preliminary data on the effects of environment enrichment on transcriptional regulation of relevant key genes in mothers and offspring

F. Bellia¹, A. Wille-Bille², M. Pucci¹, R.S. Miranda-Morales², R.M. Pautassi², C. D'Addario^{1,3} (¹ Teramo, Italy, ² Córdoba, Argentina, ³ Stockholm, Sweden)

Introduction: the consumption of alcohol by mothers during pregnancy may lead to mental or physical issues for the newborn, as well as be potentially dangerous to themselves after delivery. possibly increasing the risk of alcohol use due to heightened stress. The different phenotypes occurring in both mothers and offspring might involve the epigenetic regulation of genes transcription. Using an animal model of prenatal ethanol exposure, we here studied in mothers postpartum and in their offspring the effects of brain transcriptional regulation of target genes and how environmental enrichment might modulate possible alterations. Methods: the dams were given one daily intragastrically administration of 0.015 ml/g of a 16.8% v/v ethanol solution or a similar volume of vehicle (gestational days 17-20). After delivery litters were divided in two groups to distinguish infancy from adolescence. Starting from PD14 in both infants and adolescents were evaluated anxiety-like behavior and exploratory activity together with risk-taking behavior in the light-dark box and in the concentric square field test respectively. Mothers were sacrificed 21 days after delivery by decapitation, offspring were sacrificed one day after the behavioral tests (PD32), brain dissected and nucleic acids extracted for genes expression studies and genes promoter evaluation of DNA methylation/hydroxymethylation. Results and discussion: our findings so far show selective altered expression for BDNF and prodynorhin genes in the VTA of adolescent rats prenatally exposed to alcohol and of dams exposed to alcohol during pregnancy, whereas environmental enrichment partially reverted these changes at least in adolescent offspring. Moreover, altered methylation at specific CpG sites at both gene promoters was observed consistently with the changes in genes transcription. These data, even if preliminary, might be promising in order to understand the protective role of environmental switch on the effects evoked by alcohol also suggesting molecular mechanisms accounting for it.