and thus one can 'fine-tune' the pharmacological activity of the endogenous ligand. Such compounds could offer not only enhanced CB1R selectivity, but also reduced receptor down-regulation and inter-receptor promiscuity (Kulkarni *et al*, 2016). One such compound GAT211 increases CB1R effects, demonstrates good efficacy in rodent models of chronic pain without demonstrating acute tolerance, rewarding properties or dependence (Slivicki *et al*, 2017). Our preliminary data show that GAT211 also enhances fear extinction in auditory cue-induced fear conditioning model and could potentially provide a novel approach to PTSD drug development.

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Integrating 'Omics' Approaches to Prioritize New Pathogenetic Mechanisms for Mental Disorders

Neuropsychopharmacology research is between a rock and a hard place. The rock is the historical, but slow, hypothesis-driven approach, where discovery occurs by testing candidate mechanisms in already well-known biological models. The hard place is the innovative, but overwhelming, hypothesis-free approach, where 'omics' analyses of everything that is analyzable generates a deluge of data implicating hitherto unknown mechanisms. So, either we have little data on things we already know, or too much data and cannot find the needle in a haystack. One solution is to mix apples and oranges: integrating cross-species and cross-tissues 'omics' data to find mechanisms that recur across different experimental and clinical models. The idea has been used with remarkable success. And yes, we will finish with the proverbs now.

Niculescu *et al* (2000) first developed and used such an approach, which they called convergent functional genomics. More recently, the approach has been used by them to help prioritize genes from genome-wide association studies (GWAS) of bipolar disorder (Patel *et al,* 2010), integrating GWAS findings, transcriptomics data on postmortem human brain and blood, and studies in animal models, to identify top-genes supported by all approaches. They identified six genes (*ARNTL*, *MBP*, *BDNF*, *NRG1*, *RORB*, and *DISC1*), which are involved in relevant biological processes, such as circadian rhythm, connectivity, and neuroplasticity. They used a similar strategy for schizophrenia (Ayalew *et al*, 2012). Interestingly, this strategy could be done with publically available data rather than being based on novel experimental findings.

In 2013, we studied transcriptomics data from the hippocampus of adult prenatally stressed rats (an established animal model of depression with high glucocorticoid levels) and from a human neuronal stem cell line (that we treated with a concentration of cortisol that reduces neurogenesis) (Anacker *et al*, 2013). We found that TGFβ-SMAD2/3 and Hedgehog signaling are reduced in both models: TGFβ-SMAD2/3 promotes neurogenesis (and has been found to be reduced in depressed patients), whereas Hedgehog promotes neuronal differentiation (and has not been studied in depressed patients yet). Similarly, Malki *et al* (2016) studied transcriptomics from the prefrontal cortex of mice bred for high aggressive behavior and from the brain of zebrafish exposed to aggressive social encounters. They identified seven genes shared in both datasets, including HDAC4, which has genetic variants associated with aggressive behavior in mental retardation, and it is targeted by valproic acid, a pharmacological treatment for aggressive behavior. Finally, Luoni *et al* (2016) studied methylome analyses performed in multiple models of early life stress: rats exposed to prenatal stress (prefrontal cortex); human newborns exposed to stress in pregnancy (cells from the umbilical cord); and rhesus monkeys exposed to stressful rearing conditions (peripheral blood and prefrontal cortex). Their top gene was *Ank3*, a gene with a strong association for psychiatric disorders; and they also demonstrated an interaction between functional genetic variants within *Ank3* gene and obstetric complications on working memory in humans. Although these studies are predominantly 'comparative' in their nature, this cross-species and cross-tissues approach can be used to produce 'integrative' findings when it generates

novel lists of overlapping or functionally related genes through statistical or bioinformatic analysis.

With the collapse of R&D in mental health by pharmaceutical companies, convergent/integrative 'omics' approach represents a unique opportunity for the scientific community to mine existing datasets as well as data from experimental and clinical models, to prioritize targets for the psychotropic medications of the future.

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A Translational Model to Assess Sign-Tracking and Goal-Tracking Behavior in Children

Cues or stimuli in the environment can guide behavior in adaptive ways, bringing one in close proximity to valuable resources (for example, food). For some individuals, however, environmental stimuli may acquire inordinate control over behavior and elicit maladaptive tendencies or intrusive thoughts. Thus, the way an individual responds to cues in the environment may be a key determinant of psychopathology. For example, in addiction, relapse is most often triggered by exposure to stimuli (for example, paraphernalia or places) previously associated with the drug-taking experience, and people suffering from post-traumatic stress disorder (PTSD) experience extreme anxiety or flashbacks upon exposure to stimuli reminiscent of a traumatic event. Furthermore, in patients with schizophrenia, psychosis is believed to result from aberrant attribution of motivational salience to environmental stimuli (Kapur, 2003). Such stimuli are able to elicit complex emotional and motivational states via Pavlovian learning, and in recent years we have come to rely on an animal model to better understand these processes (for review see Robinson *et al*, 2014).

When exposed to a Pavlovian conditioning paradigm wherein the presentation of a lever (conditioned stimulus, CS) is followed by delivery of a food reward (unconditioned stimulus, US), some rats, termed 'goal-trackers' (GT), attribute *predictive value* to the lever-cue and go to the location of food delivery upon cue presentation. Others, termed 'sign-trackers' (ST), also attribute *incentive salience* to the lever-cue, as evidenced by their approach towards the cue and the ability of the cue alone to act as a reinforcer (for review see Robinson *et al*, 2014). That is, for ST the reward cue attains excessive incentive motivational value and gains inordinate control, leading to maladaptive behaviors. Indeed, relative to GT, ST have also been shown to be more impulsive, more likely to exhibit cue-induced relapse to drug-seeking behavior after relatively little drug exposure, and more susceptible to abnormal fear responses upon exposure to aversive stimuli (for review see Robinson *et al*, 2014). Thus, examining the translational relevance of the sign-tracker/goal-tracker model may prove critical to our understanding of a number of cue-motivated psychopathologies, including impulse control disorders, addiction and post-traumatic stress disorder.

To-date, little research has directly examined sign- and goal-tracking behavior in humans (Garofalo and di Pellegrino, 2015), and, to our knowledge, none with children. Due to the delayed development of the prefrontal cortex (Casey *et al*, 2000), children may be more likely to exhibit sign-tracking behavior. Indeed, the lack of cortical control and associated attentional deficits and impulsive behavior