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Dissecting the molecular mechanisms of gene x environment interactions: implications for diagnosis and treatment of stress-related psychiatric disorders

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ABSTRACT
Epidemiological studies indicate a combined contribution of genetic and environmental factors, mainly exposure to adverse life events, in the risk for psychiatric disease. Understanding how adverse life events interact with genetic predisposition on the molecular level to shape risk and resilience to psychiatric disorders may yield important insight into disease mechanism. Using the example of the molecular mechanisms of interaction of functional genetic variants within the stress-regulating gene FKBP5 and early adversity, it is delineated how this interaction could contribute to transdiagnostic disease risk via a combined genetic and epigenetic disinhibition of FKBP5 transcription. This knowledge may now allow to develop biomarkers for a transdiagnostic subset of psychiatric patients and to personalize treatment.

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level, but also on the systemic and brain circuit level, with associated behavioural differences as well as differences in risk for stress- and trauma-associated psychiatric disorders. Indeed, common genetic variants alter the immediate transcriptional response to glucocorticoids (Arloth et al., 2015). These variants were mainly located in GREs, likely modifying the affinity of the DNA binding site to the receptor. These functional genetic variants were associated with risk for schizophrenia and depression when using data from large genetic meta-analyses from the Psychiatric Genomics Consortium. Exposure to adverse life events has been shown to increase risk for both disorders. Additionally, this set of stress-moderating genetic variants is associated with impaired learning of threat-related cues with inappropriately increased reactivity of the amygdala to neutral expressions in young adults. These findings suggest that genetic variants moderating the immediate cellular response to stress may also be associated with differences in stress-processing neural circuits and an increased risk for stress-related psychiatric disorders.

In addition to genetic differences, epigenetic variation can also influence the response to transcription factor. Epigenetic mechanisms modify the accessibility of the DNA to transcriptional regulators. They encompass post-translational modifications of histone proteins as well as chemical modifications of single nucleotides (most commonly in the form of methylation at cytosine guanine dinucleotides [CpGs] = DNA methylation). More condensed chromatin would thus be more prohibitive for binding of GRs and transcriptional regulation of target genes. A series of studies have shown that environmental exposure, especially adversity early in life, can lead to lasting changes in gene function by inducing such epigenetic changes (Fiori & Turecki, 2016; Klengel & Binder, 2015). Exposure to adversity was shown to lead to changes in DNA methylation in both peripheral tissues and post-mortem brains, with complex patterns of increased and decreased DNA methylation emerging with exposure, depending on the region in the genome. Some of these environmentally induced changes may be reversible, although more research is needed. It is likely that a series of different mechanisms will drive these changes, some very specific for certain cell types and brain circuits and likely linked to specific experiences and adaptive coping mechanisms, others more global and possibly linked to system wide effects of the stress response (hormones, catecholamines, immune system). Congruent with the latter type of mechanisms, direct effects of the stress hormone glucocorticoids on the epigenome have been described. GR activation has been shown to induce lasting epigenetic changes at GRE by locally decreasing the level of DNA methylation. This DNA demethylation of GREs subsequently facilitates the transcriptional effects of the GR on the target genes (Kress, Thomassin, & Grange, 2001, 2006). Excessive glucocorticoid release after stress exposure may thus induce long-lasting epigenetic changes and, by this, contribute to the biological embedding of risk trajectories and could sensitize an individual’s response to subsequent stress exposure.

It is also likely that these epigenetic responses to GC are in turn moderated by genetic variants, either by changing the activity or the binding of the GR itself, or the accessibility to molecules that would promote and stabilize such epigenetic changes. The following example will illustrate how genetic and epigenetic changes can moderate and possibly mediate adversity-associated risk for psychiatric disorders.

FKBP5 as an example for mechanisms of gene x environment interactions in psychiatry:

FK506 Binding Protein-5 is encoded by the gene FKBP5. Within the cell, FKBP5 plays a central role in the stress response. It is part of the GR complex (Grad & Picard, 2007). When FKBP5 is bound to the complex, the GR has low affinity to cortisol and does not translocate readily to the nucleus (Davies, Ning, & Sanchez, 2002; Wochnik et al., 2005). FKBP5 is also a target of GR activation, and its mRNA and protein are induced by cortisol. Within a few hours, FKBP5 is strongly upregulated (5–10 fold) by stress or glucocorticoids in a number of tissues, including the brain (Menke et al., 2012; Scharf, Liebl, Binder, Schmidt, & Muller, 2011). This creates an ultra-short negative feedback loop, whereby GR activation induces FKBP5, which then limits GR activity by binding to the GR-complex (Vermeer, Hendriks-Stegeman, van der Burg, van Buul-Offers, & Jansen, 2003). However, FKBP5 not only regulates the function of the GR, but also many other proteins and pathways that are implicated in neuronal function and synaptic plasticity, such as the mTOR and calcium pathways but also autophagy and DNA methyl-transferases (Rein, 2016). FKBP5 would thus serve as a molecular amplifier of the stress response, able to influence a number of downstream pathways, likely in a cell-type specific manner.

Any changes in this upregulation, be it via genetic or epigenetic factors, could thus have important influences on stress-related behaviour. Animal studies show that increased expression of FKBP5 (especially in the amygdala and the hippocampus) is associated with decreased stress coping behaviour, increased anxiety and impaired extinction learning (see Zannas, Wiechmann, Gassen, & Binder, 2016, for review).

On the genetic level, this stress-related induction of FKBP5 mRNA is moderated by common genetic variants (tagged by the functional single nucleotide
polymorphism rs1360780) in the FKBP5 locus (Binder et al., 2004; Klengel et al., 2013). Most humans (about 65% as seen in data from the 1000 genomes project) carry the allele that is associated with a moderate increase in FKBP5 following GR activation; 35% carry the allele that leads to a more exaggerated mRNA response. These genetic effects on the molecular stress response are reflected on the endocrine, behavioural and imaging level. First, the changes in GR sensitivity during the feedback regulation of the HPA axis lead to prolonged stress-related cortisol release in individuals carrying the variant that is associated with higher FKBP5 mRNA induction (Buchmann et al., 2014; Ising et al., 2008; Luijk et al., 2010). Second, the high induction allele is associated with different behavioural responses to threat and trauma such as increased dissociation following trauma, increased bias towards threat and increased intrusions (Cheung & Bryant, 2015; Fani et al., 2013; Koenen et al., 2005). Third, this variant is also associated with both structural as well as functional changes in brain imaging with increased hippocampal and amygdala activity to threat and white matter abnormalities in the posterior cingulum in high expression allele carriers (Fani et al., 2013, 2014, 2016; Hirakawa et al., 2016; Holz et al., 2015).

Overall, these human genetic studies thus agree that high FKBP5 expression is associated with a similar phenotype profile as described in animal studies, including an increased bias towards threat, increased intrusions and delayed normalization of the stress response following psychosocial stressors.

This genetic change in the endocrine, circuit level and behavioural stress response is associated with an altered risk for stress-related psychiatric disorders. Interactions between FKBP5 and stressful life events, especially those occurring in childhood, were found to be associated with a variety of psychiatric disorders, including PTSD, depression, aggression, suicidality and psychosis in a large number of studies including well over 18,000 individuals (for reviews, see Halldorsdottir & Binder, 2017; Zannas et al., 2016). Genome-wide association studies and candidate gene case-control association studies have not found a main effect for this gene in predicting psychopathology, indicating that the effect is dependent on environmental influences. This suggests that additional mechanisms other than the genetic regulation of FKBP5 are necessary to unveil the stress interaction effect.

In the case of FKBP5, genetic and epigenetic changes need to come together. Specifically, changes in DNA methylation of FKBP5 locus glucocorticoid response elements have been implicated that lead to an enhancement of the transcription response of FKBP5 to GC (Klengel & Binder, 2013; Klengel et al., 2013). Only the combination of risk allele carrier status and exposure to child abuse is associated with a reduction in DNA methylation at these response elements. These effects have been observed in DNA from peripheral blood cells and saliva in both adults exposed to early trauma as well as children (Klengel et al., 2013; Non et al., 2016; Tyrka et al., 2015; Yehuda et al., 2016). One possible mechanism here could be that the genetic variants lead to increased FKBP5 expression following GR activation, delaying the negative feedback phase and resulting in prolonged cortisol response to stress and trauma. This in turn would then precipitate GR-induced DNA demethylation at GREs in FKBP5 and a transcriptional disinhibition (Klengel & Binder, 2013). Direct exposure of a hippocampal neuronal progenitor cell line to GC reveals decreased DNA methylation at the same sites that show reduced methylation in peripheral blood in individuals exposed to early trauma and carrying the high-induction allele of FKBP5 (Klengel et al., 2013).

This disruption in regulatory homeostasis of FKBP5 following stress, caused by both a genetic and an epigenetic disinhibition, could result in long-lasting changes in the neural circuits involved in stress and anxiety regulation. This could be driven by changes in GR tone but also by downstream effects of FKBP5 on additional pathways that are relevant for neuronal function and synaptic plasticity. As mentioned above, early trauma x FKBP5 genotype interactions predict risk for a range of psychiatric disorders. It could be possible that patients suffering from such an FKBP5 disinhibition, but presenting with distinct psychiatric symptoms, could benefit from blocking FKBP5 activity. A selective high-affinity antagonist for FKBP5 has been developed, and first experiments in experimental animals show that it has anxiolytic effects and increases stress coping (Gaali et al., 2015; Hartmann et al., 2015).

Dissecting the molecular mechanisms underlying the statistical gene x early trauma association of FKBP5 has identified a combined genetic and epigenetic disinhibition of stress-induced FKBP5 transcription as a possible underlying cause of disease risk. This knowledge may now allow the development of biomarkers for this transdiagnostic subset of psychiatric patients and to personalize treatment. This could include selective inhibition of FKBP5 but also targeted psychotherapy approaches for the underlying risk behaviours such as an increased bias towards threat or increased intrusions observed with increased FKBP5 function (see Figure 1). A study by Wilker et al. shows that FKBP5 genotype moderates long-term effectiveness of exposure-based psychotherapy
for posttraumatic stress disorder, with patients carrying the genotype associated with higher FKBP5 function showing increase relapse rates at 10 months (Wilker et al., 2014). Knowledge about a patients FKBP5 status could thus help guide the type of treatment as well as the frequencies of follow-up visits. The next step will be to expand this set of biomarkers and mechanistic insights to genome-wide approaches.

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