Conclusions The present data suggest that the psychosocial stress response is a multidimensional physiological event that is affected by a variety of factors as diverse as 5-HTTLPR genotype, personality profile, BMI, and age.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0181

Skin conductance response to emotional stimuli and injury location in patients with single right hemisphere damage

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Introduction Right hemisphere damage (RHD) has been related to alterations in emotion processing. However, results regarding physiological responses are limited and inconsistent. More research regarding specific brain areas involved in emotional physiological responses is needed.
Objectives To examine the skin conductance response (SCR) to emotion eliciting images in patients with single RHD. To explore the relationship between SCR and brain injury location in patients with single RHD.
Aims To examine the relationship between SCR and cortical and subcortical damage in RH regarding emotional processing.
Method Forty-one individuals with RHD due to stroke were assessed (mean age 68.5, SD 12.2, 51.1 males). The amplitude of event-related SCR was registered through a biofeedback system while observing 54 photographs from the international affective picture system (IAPS). Emotional images were classified using two different approaches: emotional valence (pleasant, unpleasant, neutral) and social vs. non-social content. Brain damage location, determined through medical records, included cortical (frontal, parietal, temporal and occipital lobes) as well as sub-cortical (caudate nucleus, thalamus, lenticular nucleus, insular cortex, basal ganglia and limbic system) structures.
Results Amplitude of SCR to emotional images was significantly lower in individuals with occipital cortex injury compared to those with damage in other brain locations ($P < 0.05$). These results were consistent through all stimuli categories but non-social pictures, which presented the same pattern though, did not reach statistical significance.
Conclusions Results show a relationship between occipital areas in HD and SCR to emotional eliciting stimuli, suggesting occipital right lobe involvement in physiological emotional processing.
Disclosure of interest The authors have not supplied their declaration of competing interest.

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EW0182

The use of polygenic risk scores to inform aetiology of mood and psychotic disorders

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Introduction Polygenic risk scores (PRS) incorporate many small genetic markers that are associated with conditions. This technique was first used to investigate mental illnesses in 2009. Since then, it has been widely used.
Objectives We wanted to explore how PRS have been used to the study the aetiology of psychosis, schizophrenia, bipolar disorder and depression.
Aims We aimed to conduct a systematic review, identifying studies that have examined associations between PRS for bipolar disorder, schizophrenia/psychosis and depression and psychopathology-related outcome measures.
Methods We searched EMBASE, Medline and PsychInfo from 06/08/2009 to 14/03/2016. We hand-searched the reference lists of related papers.
Results After removing duplicates, the search yielded 1043 publications. When irrelevant articles were excluded, 33 articles remained. We found 24 studies using schizophrenia PRS, three using bipolar PRS and nine using depression PRS. Many studies successfully used PRS to predict case/control status. Some studies showed associations between PRS and diagnostic sub-categories. A range of clinical phenotypes and symptoms has been explored. For example, specific PRS are associated with cognitive performance in schizophrenia, psychotic symptoms in bipolar disorder, and frequency of episodes of depression. PRS have also demonstrated genetic overlap between mental illnesses. It was difficult to assess the quality of some studies as not all reported sufficient methodological detail.
Conclusions PRS have enabled us to explore the polygenic architecture of mental illness and demonstrate a genetic basis for some observed features. However, they have yet to give insights into the biology, which underpin mental illnesses.
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EW0183

Identification of biological pathways to Alzheimer's disease using polygenic scores

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Introduction Single nucleotide polymorphisms (SNPs) contribute small increases in risk for late-onset Alzheimer's disease (LOAD). LOAD SNPs cluster around genes with similar biological functions (pathways). Polygenic risk scores (PRS) aggregate the effect of SNPs genome-wide. However, this approach has not been widely used for SNPs within specific pathways.
Objectives We investigated whether pathway-specific PRS were significant predictors of LOAD case/control status.
Methods We mapped SNPs to genes within 8 pathways implicated in LOAD. For our polygenic analysis, the discovery sample comprised 13,831 LOAD cases and 29,877 controls. LOAD risk alleles for SNPs in our 8 pathways were identified at a *P*-value threshold of 0.5. Pathway-specific PRS were calculated in a target sample of 3332 cases and 9832 controls. The genetic data were pruned with $R^2 > 0.2$ while retaining the SNPs most significantly associated with AD. We tested whether pathway-specific PRS were associated with LOAD using logistic regression, adjusting for age, sex, country, and principal components. We report the proportion of variance in liability explained by each pathway.
Results The most strongly associated pathways were the immune response (NSNPs = 9304, $= 5.63 \times 10^{-19}$, $R^2 = 0.04$) and hemostasis (NSNPs = 7832, $P = 5.47 \times 10^{-7}$, $R^2 = 0.015$). Regulation of endocytosis, hematopoietic cell lineage, cholesterol transport, clathrin and