Background: Evidence has emerged indicating a role of stress-related disorders in the development of autoimmune diseases. However, it remains unknown whether genetic components contribute to the observed association. We therefore investigated the co-aggregation of stress-related disorders and autoimmune diseases in individuals and their family members in the Swedish population.
Methods: We identified 4,123,631 individuals born in Sweden between 1953 and 1993. Based on information from the Multi-Generation Register, we conducted cohorts of relatives of varying relatedness. Logistic regression was used to estimate the association between clinical ascertained stress-related disorders (i.e., acute stress reaction, posttraumatic stress disorder [PTSD], adjustment disorder, and other severe stress reactions) and autoimmune diseases (36 different types) in individuals and in families, presenting relative risks as odds ratios (ORs).
Results: Individuals with stress-related disorder were at higher risk of having autoimmune diseases compared with individuals who did not have stress-related disorder (OR = 1.66, 95% confidence intervals (CI) 1.63–1.69). Within families, the association seemed strongest between monozygotic twins (OR = 1.47, 95% CI 1.07–2.03), and then decreased with descending dyads of familial/genetic relatednessOR was 1.28 (95% CI 0.97–1.67), 1.16 (95% CI 1.14–1.18), 1.05 (95% CI 1.02–1.09), 1.06 (95% CI 1.03–1.10), 1.05 (95% CI 1.04–1.06), and 1.00 (95% CI 0.98–1.04) for dizygotic twins, full siblings, maternal half siblings, paternal half siblings, full cousins, and half cousins, respectively. Further analyses on PTSD and autoimmune diseases obtained similar estimates.
Conclusion: The pattern of the association across twin zygosity and varying familial relatedness supports the hypothesis of a genetic overlap between stress-related disorders and autoimmune diseases which warrants further exploration.

The moderating role of early-life parent factors on the genetic and environmental contributions to objective sleep duration in middle childhood

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Objective: Early-life parental positive personality and stress can impact offspring health, including sleep. This study examined the moderating role of early-life parental stress and positive parent personality on the heritability of sleep duration.
Methods: A subset of 341 families (30% MZ, 39% same-sex DZ, 31% opposite-sex DZ twins) from the Arizona Twin Project (Lemery-Chalfant et al. 2013, *Twin Research & Human Genetics, 16*, 376–384) were included in this study. Primary caregivers reported on multiple dimensions of stress as well as their own personality when the twins were 12 months. Seven years later (*Mean age* = 8.47), twins (51% female; 57% White, 25% Hispanic) wore actigraph watches on their non-dominant wrist for seven consecutive days to assess their sleep with excellent compliance.
Results: A univariate ACE model indicated sleep duration was moderately heritable. Early-life positive parent personality moderated the genetic contribution on sleep duration where both the moderated C and E paths could be dropped (Δ-2LL = 2.12, Δdf = 2, p = 0.35); as positive parent personality increased the heritability of duration decreased. Early-life parental stress also moderated the genetic contribution on sleep duration and the moderated C and E paths could be dropped (Δ-2LL = 1.75, Δdf = 1, p = 0.42); as parental stress increased the heritability of duration increased. Cross-sectional composites of both positive parent personality and parental stress had the same pattern of findings.
Conclusions: Findings highlight the contribution of parent traits and experiences to the genetic effects on children's sleep and health; therefore, interventions may need to target parental factors in early-life to support children's healthy sleep.

Examining grit and mindset in concurrent and future reading comprehension: a twin study

LaTasha Holden, Florida State University; Kimberly Martinez, Florida State University; Sara Hart, Florida State University; Jeanette Taylor, Florida State University

Early reading difficulties predict a variety of poorer outcomes. Grit and Intelligence Mindset have gained attention as intervention targets for children struggling in school because they predict academic success. Mindset interventions for reading show promise, but less is known about Grit. Twin studies of Mindset, Grit, and achievement suggest genetic and non-shared environmental influences but only focus on concurrent ability. Our twin design addresses how Mindset and Grit relate to reading concurrently and two years later, while examining genetic and environmental influences underlying these relations. Using the Wave 2 and Wave 3 assessments in the Florida Twin Project on Reading, Behavior, and Environment, we conducted multiple regressions and multivariate twin models to investigate these questions. Using one randomly chosen twin, gender, age, Mindset and Grit were regressed onto Wave 2 reading and only Mindset significantly predicted concurrent reading. Gender, age, Mindset and Grit were then regressed onto Wave 3 reading and, again, only Mindset significantly predicted reading (two years later). Finally, gender, age, Mindset, Grit and Wave 2 reading were regressed onto Wave 3 reading, and only Wave 2 reading significantly predicted reading two years later—indicating neither Mindset nor Grit contributed to change in reading. Next, two trivariate and one quadrivariate Cholesky decomposition were applied to the full twin data. Only Mindset and concurrent reading had significant overlap through the non-shared environment. Mirroring regression results, when adding previous reading, this was the only significant predictor of reading two years later, with genetic and shared environmental influences underlying the relation.

Educational attainment polygenic risk scores predict surface area of cortical regions important for language and memory

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Individual differences in educational attainment (EA) correlate with a wide variety of social, health and economic outcomes. Previous studies have uncovered the existence of shared genetic factors influencing both cognitive function and brain structure. Here, we investigate the relationship between brain imaging traits (surface area of cortical regions of interest) and EA, as a proxy for cognitive ability, using a polygenic scoring (PGS) approach. We leverage data from the

largest genome-wide association study (GWAS) of EA to date (EA3, discovery sample) and estimate polygenic scores (PGS) in two independent target samples of young adults with neuroimaging data from Australia (N = 1165) and the USA (N = 723), to examine how the genetic factors underlying educational attainment and cognitive ability relate to brain structure. Higher EA-PGS significantly predicted larger global brain morphometry measures, such as intracranial volume and total surface area (R^2 = 0.006 and 0.016 respectively, $p < 0.001$) in both independent samples. Remarkably, EA-PGS also predicted cortical surface area of three frontal and three temporal regions in both target samples (over and above total surface area). The identified regions have been robustly implicated in language, memory, visual recognition and cognitive processing. Additionally, individuals with higher EA-PGS achieved higher scores in cognitive tests and we demonstrate that these identified brain regions partly mediate the association between EA-PGS and cognitive test performance, accounting for approximately 20% of the variance explained in IQ scores. Altogether, these findings advance our understanding of the neurobiology that underpins educational attainment and cognitive ability and provide focus points for future research.

Update on Australian genetics of depression study

Nick Martin, QIMR Berghofer Medical Research Institute

More than 20.000 depression cases have been enrolled at DNA and GWAS have been obtained on > 16,000 of these. Early results will be presented with a focus on response to anti-depressant medication.

Five ways to analyze 50,000 pairs of related persons in the National Longitudinal Survey of Youth

Michael Hunter, Georgia Tech; Mason Garrison, Vanderbilt University; William Beasley, University of Oklahoma Health Sciences Center; Patrick O'Keefe, Vanderbilt University; David Bard, University of Oklahoma Health Sciences Center; Joe Rodgers, Vanderbilt University

With the rise of molecular genetics methodologies like genome-wide complex trait analysis (GCTA), it becomes critical to viscerally understand how these newer methods relate to the older twin and family methods. Such an understanding informs what novel findings may result from the new methods. This presentation uses the National Longitudinal Survey of Youth (NLSY) to exemplify the techniques. The NLSY is an excellent test-bed for a wide array of biometric analysis methods due to its (a) large, representative sample from the United States, (b) copious number of diverse outcomes, (c) longitudinal data collection, and (d) burgeoning cross-generational structure. We analyze both standard and unconventional outcomes from the NLSY in five related ways. First, we analyze outcomes in the standard form of a structural equation model (SEM). Second, the identical analyses are conducted as a multilevel SEM. Third, multiple large blocks of pedigrees are used to include extended relationships such as cousins. Fourth, the entire data are analyzed as a single genetically-related family using the conventional GCTA software. Fifth, multivariate outcomes are studied for the entire data using the OpenMx software. Each of these ways of structuring the analysis for the NLSY allows certain questions to be answered while forcing the researcher to omit or make assumptions about others.

GWAS on the Internet: systematic review of online news and blog articles about GWAS publications from 2005 to 2018

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In this study, we present a systematic review of news and blog articles on GWAS since its inception, combining statistical analysis with text mining techniques. GWAS publications were identified via the NHGRI-EBI GWAS Catalogue and classified into phenotype categories using the ICD-10. Blog and news articles about these studies were identified using the Altmetric database.

As of 19/09/18, there were 3557 GWAS studies on 1945 different traits. We found 5349 different English language websites that mentioned these publications. Only 41.4% of those websites offered original content (not copied from another website). The most researched areas were non-disease traits (e.g., body mass index, educational attainment, metabolic traits, etc.; N = 1197), neoplasms (N = 462), and mental and behavioral disorders (N = 371). However, only 20.1%, 21.4%, and 15.9% of scientific papers in these areas were mentioned in two or more websites, respectively. Year of publication, number of hits, impact factor, and sample size, were positively and significantly associated with number of online mentions. Non-disease traits generated 2.5 times more mentions than predicted by those variables, while behavioral disorders generated 2 times less, suggesting different patterns in public interest. The Top 5 topics in the news were genetics of Alzheimer's disease, depression, breast cancer, intelligence, and asthma. Finally, readability analysis revealed that more than 95% of all online articles required at least university-level reading skills to understand them. Implications for science communication and genetic literacy campaigns will be discussed.

A cross-country, cross-reporter twin study of oppositional defiant disorder

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Oppositional defiant disorder (ODD) is characterized by a persistent pattern of anger, defiance, or vindictiveness that impairs social functioning. Often beginning during preschool years, temporally it precedes most comorbid disorders. Genetics contributes to the etiology of ODD but research that associates parenting practices with ODD has not been conducted in a genetically sensitive design. We examined the heritability of ODD symptoms in two twin cohorts, one Australian and one Dutch. In Australia, mothers (N = 1281) reported ODD for twins at age ~ 14.3 using the SWAN, and twins self-reported (N = 2210) lifetime incidence of ODD at age ~ 27. An overlapping sample on both measures was available on 246 individuals (110 complete pairs). In the Netherlands, mothers (N = 16,584) and fathers (N = 11,676) reported ODD at age ~ 12.2 using the CBCL12, and twins self-reported (N = 4841) ODD at age ~ 16.9 using the YRS. An overlapping sample on parental and self-report was available for 904 monozygotic and 1138 dizygotic complete