This Month in the *Journal*

Genetic Analysis of a Xiongnu Population, *by Keyser-Tracqui et al.* (*p. 247*)

Keyser-Tracqui et al. report the genetic analysis of ancient skeletal remains found in a 2,000-year-old burial site in northern Mongolia. Archaeological data have characterized this site as belonging to the Xiongnu culture, which rose to power in the 3rd century B.C. Because of the climate, these remains were well preserved, and reproducible allelic profiles were obtained from a whopping 49 specimens. Not only that, three types of sequences were analyzed: autosomal short tandem repeats (STRs), STRs on the nonrecombining portion of the Y chromosome, and sequences in the hypervariable region I of mitochondrial DNA. This allows the authors to infer family relationships between the individuals buried at this site and to suggest a social organization for the burial site. A total of nine parent-child pairs were identified, as well as three individuals who are believed to have a common parent. Further, one sector of the burial site was exclusively composed of males of the same patrilineage, a burial practice not previously described in ancient specimens. In addition to providing information on the social organization of the burial site, this analysis also provides population genetic data on the Xiongnu people. The haplogroups found in these samples suggest that contacts between the European and Asian populations occurred prior to the rise of the Xiongnu culture and that a Turkish component in the Xiongnu tribe emerged as the burial site got older.

BRD2 *and JME,* *by Pal et al.* (*p. 261*)

Although mutations have been described in some rare, densely affected epilepsy pedigrees, the same genes do not seem to be mutated in the more common forms of this disorder. Rather than exhibiting Mendelian inheritance, the common epilepsies are thought to result from complex inheritance. A locus at chromosome 6p21 (EJM1) has repeatedly been identified as showing linkage or association to juvenile myoclonic epilepsy (JME), one of the common epilepsies. Pal et al. follow up on these results, using a case-control association design with SNP markers across this region. The markers that are associated with JME in their sample are found in and around *BRD2* (*RING3*). Haplotype analysis identifies a common core haplotype in *BRD2* that is found in 10 of 20 case individuals. Five additional case individuals have a haplotype that differs from the core haplotype by only one allele. Although no definitive *BRD2* mutations were identified in their sample, Pal et al. suggest that polymorphisms in this gene, including two promoter polymorphisms found in their study, may be involved in complex inheritance of JME. Supporting this is the finding that *BRD2* is expressed in human brain and the fact that its homolog in rats seems to be involved in the development of the nervous system.

3.9-cM SNP Map and Screening Set, *by Matise et al.* (*p. 271*)

Although microsatellite markers are generally more informative than SNPs, the abundance of SNPs and the fact that they can be genotyped in high-throughput assays makes this type of marker very attractive for linkage analysis. To make this possible, however, a high-resolution, genomewide SNP map will be required. Matise et al. evaluate >20,000 candidate SNPs to construct a SNP linkage map with an average resolution of 3.9 cM. This map shows high levels of concordance with the genome assemblies from NCBI, Celera, and deCODE Genetics. Further, the average information content of this SNP map is higher than that of the Marshfield microsatellite map. Since expected LOD scores are correlated with information content, this finding implies that the SNP linkage map will provide higher average power to detect linkage, compared with current microsatellite maps. In conjunction with high-throughput technologies, this map should allow genome scans to be completed with greater efficiency than can currently be achieved with microsatellites.

Ascertainment-Corrected LD, *by Clark et al.* (*p. 285*)

The efficacy of genomewide association scans cannot be realistically determined until there is a more-complete picture of the distribution of linkage disequilibrium (LD) across the genome. To begin to address this issue, Clark et al. use SNP data from the first phase of the work by Matise et al. (above), in which >4,800 SNPs across the genome were genotyped in 30 African Americans, 30 European Americans, and 30 Asians. This data set allows them to estimate population recombination rates by use of clusters of SNPs located across the genome. They find a high degree of local variability in the population recombination rate (and therefore LD). Comparisons between populations show significant levels of interpopulation heterogeneity in LD, although regions that have very high LD in one population are more likely to exhibit high levels of LD in another population. This genomewide LD map has implications for the design of ge-

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nomewide association studies; it suggests that tailoring the SNP set for such a study, in terms of the recombination profile, may be more efficient than designs that use randomly or uniformly distributed SNPs.

Genetic Variation of* BDNF *Contributes to OCD, *by Hall et al.* **(*p. 370*)**

Brain-derived neurotrophic factor (BDNF) is a growth factor that is necessary for the survival of striatal neurons in the brain. $Bdnf^{+/-}$ mice have disturbances in their central serotonergic neurons that eventually lead to deterioration of these cells in advanced age. Because obsessive-compulsive disorder (OCD) is thought to result from deficient serotonin neurotransmission, Hall et al. decided to look for an association of *BDNF* with OCD. In their sample of 164 proband-parent trios, they genotyped markers across *BDNF* and found results that suggest an association with OCD. The same haplotype that was undertransmitted to affected individuals in this sample was also undertransmitted to case subjects in two recent studies that reported an association of *BDNF* with bipolar disorder. Although high LD in the *BDNF* region precludes exclusion of neighboring genes as playing a role in OCD, this work does suggest that *BDNF* is a good candidate gene for OCD, in addition to bipolar disorder.

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