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SNP panel can help clarify breast cancer risk in non-*BRCA* families

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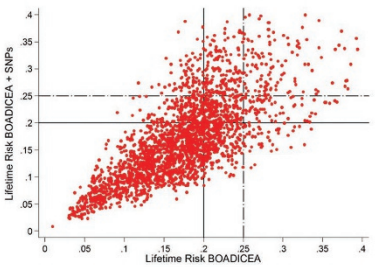

For families in which cases of breast cancer appear to be inherited but don't fall neatly into a *BRCA*-associated high-risk group, increased screening frequency has been the only clinical recommendation. In this issue, Li *et al.* describe a multi-institutional effort to prospectively assess the value of a single-nucleotide polymorphism (SNP) panel in fine-tuning risk assessment in this group of women. There is an increasing number of common SNPs, each of which is associated with a relative risk of 1.05 to 1.3 of developing breast cancer. These relatively common alleles, each with a small effect, explain less than half of familial breast cancer, but their cumulative value has never been prospectively assessed. Investigators evaluated 1,608 women from 488 families in either the Breast Cancer Family Registry or the Kathleen Cuningham Consortium Foundation for Research into Familial Breast Cancer (kConFab) cohort. These women had been assessed to be at increased familial risk but were unaffected at enrollment. The women were followed for more than seven years. During this time, 205 of them were diagnosed with breast cancer. Based on the SNP panel analysis, the research team determined that clinical management of up to 23% of women in the study might have been altered due to genomic testing results. They concluded that an SNP panel could provide more accurate risk prediction than family history alone and might influence recommendations for cancer screening for high-risk women. —*Karyn Hede, News Editor*

Assessment of newborn genomic screening for progressive hearing loss

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The most common sensory defect in children—hearing impairment—is typically screened for via auditory modalities. But auditory screening misses one to two cases per thousand in which hearing loss starts later and progresses through childhood. Wu et al. describe their experience with newborn genetic screening in Taiwan. The study included 5,173 infants born at a tertiary hospital between 2009 and 2015. Newborn genetic screening identified 82 (1.6%) babies with conclusive genotypes. The investigators then used serial audiometric results to follow infants with conclusive genotypes up to 6 years of age. The study confirmed the utility of newborn genetic screening in identifying infants with late-onset or progressive hearing impairment undetectable by current audiology-based newborn hearing screening. The results, they suggest, can help inform evidence-based cost-effectiveness analysis to justify population-wide genetic screening. However, they caution that implementing newborn genetic screening for deafness could raise ethical issues, including raising the risk of discrimination or stigmatization, respect for personal autonomy, and undue parental anxiety for the health of their children. —*Karyn Hede, News Editor*

NEWS BRIEFS

The ants go marching one by one, hurrah!

The Isthmus of Panama, that thin ribbon of land connecting the Americas, has served as a gateway for species migration between the continents since its formation in a distant epoch. But the timing of its emergence from the sea has been unclear, with the current best guess set at 3 million years ago. Now, a genomic study of army ants is pushing back the date of closure by millions of year. Army ants found strictly in Central America diverged from their South American sister lineages between 4 million and 7 million years ago, according to biologists from Chicago's Field Museum of Natural History and the University of Chicago. Their study, published in *Molecular Ecology* in October 2016, used genomic sequencing to determine that three of the lineage pairs in Costa Rica and Nicaragua show no evidence of gene flow, suggesting at least two waves of army ant dispersal into Central America separated by millions of years. The research team chose army ants for the study because

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