Parental consanguinity predicts ASD severity

By Jessica K. Edwards

Earlier this year, Fouad Alshaban and colleagues screened a general school population to estimate the prevalence of autism spectrum disorder (ASD) in Qatar. The researchers identified 1,393 children from medical centres and special needs schools with diagnosed ASD. Then, they screened a further 9,074 children attending 93 different schools using the social communication questionnaire.[1] After combining the datasets, the researchers identified that ASD prevalence in Qatar was ~1.14% among children aged 6-11 years old. While this reported ASD prevalence rate is in line with other recent international studies,[2-4] it is much higher than the results of previous regional surveys. This difference might be due to the more comprehensive methodology used by the researchers to identify those affected by ASD. The level of parental consanguinity (45%) in this cohort was also not significantly different from previously published rates for Qatar and other Arabian Peninsula countries. As such, the researchers conclude that parental consanguinity is unlikely to be a risk factor for ASD. Parental consanguinity could, however, predict ASD severity in this cohort after controlling for the effects of maternal health and developmental indicators. This striking finding suggests that the increased levels of allelic homozygosity in children of consanguineous parents might modulate ASD phenotypes. Other associations with ASD severity included gestational diabetes, delay in walking and developmental regression. Overall, the researchers estimate that 50,500 children <5 years-of-age and a further 137,000 children aged 5-19 years residing within the Arabian Peninsula have ASD. They hope that these figures will help guide health and educational service planning for young people in Qatar.

Referring to:

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References:

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