New Mouse Brain Model for Autism (via PNAS)

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Researchers have finally established a rodent brain model for autism. The model is based on the analysis of dna from dorsal embryonic stem cells, and has been tested on 26 offspring (nine months old) of a male autism-symptom-free individual, from whom omphalocele (the incomplete development of the leg bones) and cowtail deformity (yawning ears) were clear genetic abnormalities.

Using DNA sequencing and experimental cell modeling, by the researchers, Ashwin Nagaraj from the University of South Australia, identifies risk gene variants that confer risk for autism.

â€œFor genetic risk factor assessment, incidence is the result of its prevalence: the number of cases per 1000 births. While incidence of autism is steadily increasing in the western world, prevalence rates have yet to reach the estimate of 10 per 1000 in the US, as they have in the developing world, where over 40 per 1000 newborns are diagnosed with autism. What has held back research into neurodevelopmental disorders from mounting a similar rate of investigation for autism in their earlier research for other developmental disorders, especially autism, has been the lack of a reliable rodent model of autismâ€, said Nagaraj. â€œWe have now demonstrated, with our rodent model of autism, that we can use data from genetic variation in specific gene sequences to identify genetic risk factors that confer risk for this neurodevelopmental disorder, with statistically significant outcomes.â€

They found a striking high correlation between the likelihood of this development (altered neurodevelopment) and variation in the regions of the GSEARD (genetic network or assemblage of common gene sites) in which the common gene sites are located. This pattern is much more pronounced than the one previously found for the risk factors for autism in mice.

Even though a mouse model has never been used to evaluate the risk for autism in humans, the shared conditions of autism and autism spectrum disorders suggest that there is a great deal of mechanistic similarity between these two diseases. In particular, in autistic patients, genetic factors, both in the environment and outside of it, may have an additive influence on the development of the disease.

â€œIncreased genetic susceptibility for autism in humans may ultimately be explained by several environmental risk factors, including environmental toxins and an increased burden of stress and stress responses in individuals with autism, compared to children without,â€ said Nagaraj.

According to Nagaraj, because of the importance of the development of the central nervous system in autism, anatomic variation in the development of the brain may have an important role in autism and may explain the important role of the frontal and temporal lobes of the brain in its development. He and his team plan to pursue new approaches to test the existence of genetic risk factors for autism. Nagarajâ€™s research has been made possible with the help of the Australian Child Health Research Collaborative, and the finding of a â€œgenetic bridgeâ€ by Gerta Tannenbaum and Carl Jacobs from the Max Planck Institute for Developmental Biology in Germany.

â€œGenetic investigators could now explore these novel mechanisms and our results as a potential path to better understand the process of risk for autismâ€, said Nagaraj.

The article, â€œPathology, epigenetics, and susceptibility for Autismâ€ by Ashwin Nagaraj, Gerta Tannenbaum, Carl Jacobs, & Salvatore C. Kudelaar, is published in the December issue of PNAS.

Source: PNAS

A Yellow And Black Bird Standing On The Ground