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A molecular pathway analysis informs the genetic background at risk for schizophrenia

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Schizophrenia is a complex mental disorder marked by severely impaired thinking, delusional thoughts, hallucinations and poor emotional responsiveness. The biological mechanisms that lead to schizophrenia may be related to the genetic background of patients. A molecular pathway analysis was undertaken to identify the molecular pathways associated with schizophrenia. We collected data of genetic loci previously associated with schizophrenia, identified the genes located in those positions and created the metabolic pathways that are related to those genes' products. These pathways were tested for enrichment in a sample of schizophrenic patients and controls (4486 and 4477, respectively). The molecular pathway that resulted from the identification and analysis of all the genes located in the loci associated with schizophrenia was found to be enriched, as expected (permuted $p(10(6))=9.9999e-06$). We found 60 SNPs amongst 30 different genes with a strong association with schizophrenia. The genes are related to the pathways related to neurodevelopment, apoptosis, vesicle traffic, immune response and MAPK cascade. The pathway related to the toll-like receptor family seemed to play a central role in the modulation/connection of various pathways whose disruption leads to schizophrenia. This pathway is related to the innate immune system, further stressing the role of immunological-related events in increasing the risk to schizophrenia.

Biography

Antonio Drago has completed his PhD from Modena University and Postdoctoral studies from Bologna University. He has published more than 45 papers in reputed journals and has been serving as an Editorial Board Member of repute.

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