

News Release

Title

Comparative analyses of copy number variation in autism spectrum disorder and schizophrenia

~Discovery of overlap of genetic risk variants and pathogenesis in the two psychiatric disorders~

Key Points

- We performed large-scale comparative analyses of copy number variation (CNV) in autism spectrum disorder (ASD) and schizophrenia (SCZ) in a Japanese population
- Pathogenic CNVs were identified in around 8% of both patient groups and their overlap was observed between the two disorders.
- Overlap of biological pathways was also confirmed between the two disorders.
- Patients with pathogenic CNVs have a higher prevalence of intellectual disability.
- Disease-relevant genes were identified in well-known ASD/SCZ-associated CNV loci (e.g., 22q11.2 and 3q29) using a bioinformatics approach.

Summary

Prof. Norio Ozaki (Department of Psychiatry) in Nagoya University Graduate School of Medicine (Dean: Kenji Kadomatsu, M.D., Ph.D.) and Itaru Kushima in Nagoya University Institute for Advanced Research (Director: Yoshiyuki Suto) and collaborators performed comparative analyses of copy number variation (CNV) in autism spectrum disorder (ASD) and schizophrenia (SCZ) in a Japanese population and found evidence for overlap of both genetic risk variants and pathogenesis between the two disorders.

In the present diagnostic criteria based on psychiatric symptoms, ASD and SCZ are defined as two distinct disorders. However, recent epidemiological studies suggested that there might be etiological overlap between them. Therefore, we examined CNV in patients with ASD or SCZ and controls (total samples >5500) and found that around 8% of both patient groups had known pathogenic CNVs. CNVs in 29 loci were common to both patient groups, confirming overlap of genetic risk variants. Phenotypic analysis revealed that patients with pathogenic CNVs have a higher prevalence of intellectual disability. Furthermore, we observed overlap of biological pathways involved in pathogenesis of these disorders, including oxidative stress response, genomic integrity, and lipid metabolism. Finally, we identified multiple disease-relevant genes in well-known ASD/SCZ-associated CNV loci (e.g., 22q11.2 and 3q29).

These findings should be useful for development of novel diagnostics and therapeutics, as well as elucidation of pathophysiology of these disorders. In addition, the finding of etiological overlap between ASD and SCZ may influence the diagnostic concept of these disorders. This work was published online in Cell Reports on September 11, 2018.

Research Background

In the present diagnostic criteria (DSM-5) based on psychiatric symptoms, ASD and SCZ are defined as two clinically distinct disorders. However, recent epidemiological studies suggested that there might be etiological overlap between the two disorders. Molecular genetic studies on Caucasian populations also identified multiple pathogenic CNVs associated with the risk for both ASD and SCZ. However, genetic studies on other populations including a Japanese population are lacking, and few studies have directly compared CNVs between ASD and SCZ. Thus, direct comparative analyses of CNVs in a Japanese population are crucial to clarify the relationship of the two disorders and the pathophysiology of these disorders.

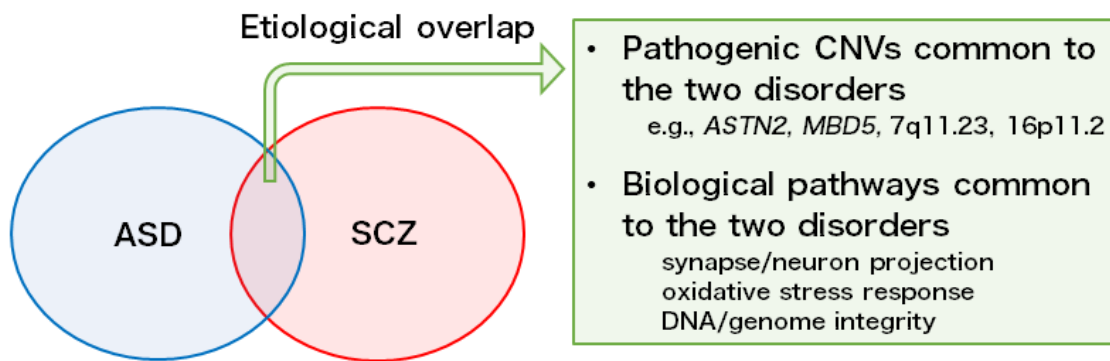
Research Results

Using array comparative genomic hybridization, we performed genome-wide analyses of CNVs in Japanese patients with ASD or SCZ and controls (total samples >5500). As a result, we found that around 8% of both patient groups had known pathogenic CNVs associated with the risk for developmental or psychiatric disorders. These CNVs were widely distributed in the human genome and those in 29 loci (*ASTN2*, *MBD*, 7q11.23, 16p11.2) were common to both patient groups, confirming overlap of genetic risk factors. For individual CNVs, we obtained evidence for significant associations between 1) 22q11.2 duplication and ASD, and 2) 22q11.2 deletion, 1q21.1 deletion, 47,XXY/47,XXX and SCZ. We also identified novel pathogenic CNVs in 12 genes. Phenotypic analysis revealed that patients with pathogenic CNVs have a higher prevalence of intellectual disability.

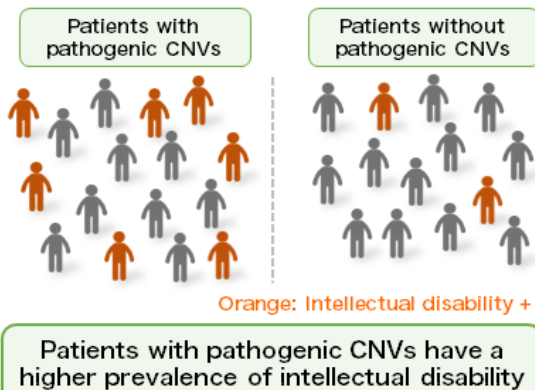
Next, we examined which biological pathways were preferentially affected by patient CNVs. Gene set analysis based on the CNV dataset identified multiple biological pathways relevant to the pathogenesis of each disorder. We found evidence for overlap of pathogenesis between them, such as synapse, small GTPase signaling, gene expression regulation, oxidative stress response, genomic integrity, and lipid metabolism. Finally, we set out to identify disease-relevant genes in eight well-known ASD/SCZ-associated CNVs (e.g., 22q11.2 deletion, 3q29 deletion). These CNVs are large (>500 kb) and include many genes, preventing identification of responsible genes for the disorders. We performed bioinformatics analysis based on the findings of biological pathways, identified multiple disease-relevant genes in these CNVs.

These findings should be useful for development of novel diagnostics and therapeutics, as well as elucidation of pathophysiology of these disorders. In addition, the finding of etiological overlap between ASD and SCZ may influence the diagnostic concept of these disorders.

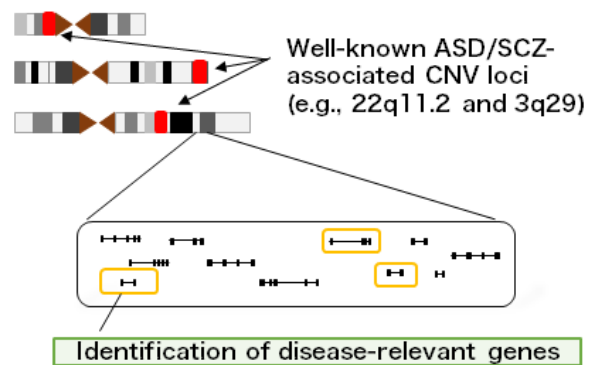
Comparative analyses of CNV in ASD and SCZ



Phenotypic analysis



Bioinformatics analysis



Research Summary and Future Perspective

The present study suggests etiological overlap of ASD and SCZ and provides novel insights into the pathogenesis of these disorders. The results will be applied to genomic medicine including diagnosis and treatment of patients. In fact, such efforts have already begun in patients with 22q11.2 deletion, the most important genetic factor for SCZ. In the near future, more studies will be conducted using iPSCs derived from patients with pathogenic CNVs. The establishment and analysis of animal model based on pathogenic CNVs will also become more popular. Studies using iPSCs and model animals will contribute to the elucidation of molecular network and neuronal circuit dysfunction relevant to psychiatric disorders. Finally, as how the same CNVs produce different psychiatric disorders remain unknown, more studies on this point are also required.

Publication

Comparative Analyses of Copy Number Variation in Autism Spectrum Disorder and Schizophrenia Reveal Etiological Overlap and Biological Insights

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