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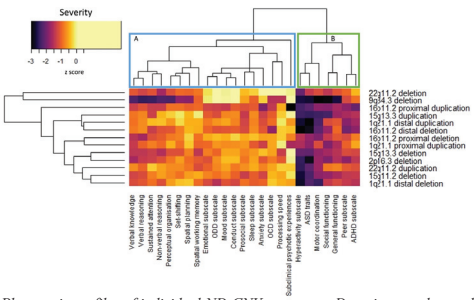
Genotype–phenotype associations in children with copy number variants associated with high neuropsychiatric risk: Case-control analysis of the IMAGINE-ID study data

Statement of the problem: Several genomic disorders caused by micro-deletion or duplication of chromosomal material Copy Number Variants (CNVs) have been associated with high risk of neurodevelopmental and psychiatric disorder (referred to as ND-CNVs). However, it remains unclear to what extent the different genotypes lead distinct and specific patterns of cognitive and behavioural outcomes.

Methodology: Families of 258 children, aged 6–19 years, with at least one of 13 ND-CNVs across 9 loci (1q21.1 [proximal duplication, and distal deletion and duplication], 2p16.3 deletion, 9q34.3 deletion, 15q11.2 deletion, 15q13.3 deletion and duplication, 16p11.2 [proximal deletion and duplication, and distal deletion], and 22q11.2 deletion and duplication) were recruited via the UK National Health Service (NHS) medical genetic clinic network and patient support groups as part of the IMAGINE-ID study. A control sample of 106 siblings of these index children, who did not have these ND-CNVs also took part. All children were assessed for psychiatric disorders and broader traits of neurodevelopmental, cognitive, and psychopathological origin.



Phenotypic profiles of individual ND-CNV genotypes. Domains are clustered into two groups; mental health and cognitive comorbidities (cluster A) and neurodevelopmental traits (cluster B). The lighter colour indicates a Z score difference of zero between the ND-CNV group and controls, with darker colours indicating a deficit in the ND-CNV group compared with the controls. ADHD=attention-deficit hyperactivity disorder. ASD=autism spectrum disorder. ND-CNV=neuropsychiatric disorder-copy number variant. OCD=obsessive-compulsive disorder. ODD=oppositional defiant disorder.

Findings: ND-CNV carriers were impaired across all neurodevelopmental, cognitive, and psychopathological traits compared with controls. 186 (80%) met criteria for one or more psychiatric disorder (OR=13.8, p<.000, compared with controls). Risk of attention-deficit hyperactivity disorder (OR=6.9, p<.000), oppositional defiant disorder (OR=3.6, p=.012), any anxiety disorder (OR=2.9, p=.0146), and autism spectrum disorder traits (OR=44.1, p<.000) was particularly high compared with controls. Only moderate quantitative and qualitative differences in phenotypic profile were found between genotypes. Specific genotype accounted for a low proportion of variance in cognitive and behavioural outcomes (~5–20% depending on the trait).

Conclusion and significance: These ND-CNVs have a similar range of adverse effects on childhood neurodevelopment, despite subtle quantitative and qualitative differences. Genomic risk for neuropsychiatric disorder impacts on multiple processes and neural circuits, indicating that future research should avoid a narrow focus on single phenotypes.

Biography

Marianne B M van den Bree has developed a unique longitudinal research programme of individuals with rare genomic disorders caused by pathogenic Copy Number Variants (CNVs) that are associated with high risk of neurodevelopmental and psychiatric disorder. Detailed and wide-ranging phenotypic assessments are conducted on individuals with these neurodevelopmental risk CNVs (ND-CNVs) and their family members. Her research is elucidating the still poorly understood complex phenotypic presentation of these patients. Her research papers have documented the rate and nature of the neurodevelopmental, psychiatric, neurological, neurocognitive and sleep problems these patients can face. Her longitudinal studies of patients with 22q11.2 deletion syndrome (22q11.2DS), which is associated with high risk of schizophrenia, have contributed to understanding of the childhood predictors of the development of subthreshold psychotic phenomena in adolescence.

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