22q11.2 CNVs IN THE GENERAL POPULATION

22q11.2 is a complex and well-studied region because variations within this domain lead to several pathological conditions, including the most frequent human microdeletion syndrome (22q11.2DS - MIM: 188400), caused by Non-Allelic Homologous Recombination (NAHR) triggered by specific Low Copy Repeats. The phenotypic consequences of this microdeletion have been studied mainly in clinical cohorts. These include cardiac defects, changes in the face and palate, immunodeficiencies, endocrine, genitourinary and gastrointestinal disorders, developmental delay, cognitive deficits, and psychiatric disorders, such as schizophrenia. NAHR also generates duplications of 22q11.2, but phenotypic consequences of these are more elusive, in keeping with the idea that deletions are usually more severe than the corresponding duplications. The fact that these studies were performed on patient cohorts implies that mild phenotypes can escape detection. To overcome these biases, Zamariolli et al.[1] (Am. J. Hum. Genet 2023) analyzed data from 500,000 individuals in the UK biobank to unveil associations of CNV 22q11.2 with traits previously implicated by their genetic content. The study allowed a broad view of the phenotype-genotype correlation of the region under study, in which subclinical manifestations were also highlighted.

1-https://www.cell.com/ajhg/pdf/S0002-9297(23)00005-8.pdf