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Demographic and Lifestyle Characteristics of Parental Occupational Autism Spectrum Disorder

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Abstract

htroduction

A population-based case-control study has previously been described as the Childhood Autism Risks from Genetics and Environment CHARGE study. In a nutshell, the CHARGE study enrolls children selected from birth records maintained by the California State Vital Statistics as well as children selected from the general population. Children between the ages of 2 and 5 who were born in California, reside in the catchment areas of a speci ed list of California Regional Centers that coordinate services for people with developmental disabilities, and live with at least one biological parent who speaks English or Spanish are eligible [1]. Youngsters with mental imbalance are distinguished through the California Branch of Formative Administrations, which manages the Territorial Place framework, and all inclusive community controls from state birth records are recurrence matched to the normal sex dissemination, as well as the age, furthermore, catchment region of developmental imbalance cases. 976 children and their parents who participated in the CHARGE study provided the National Institute for Occupational Safety and Health (NIOSH) with genetic, diagnosis, and basic demographic information. 423 of those were children with typical development (TD) serving as controls. e present study's sample consisted of 711 children, a er excluding 265 participants with

Method

Both the UC Davis MIND Institute and the UCLA Neuropsychiatric Institute evaluated each child. e Autism Diagnostic Observation Schedule-2 (ADOS-2) was used to assess ASD-disabled children, and

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Control center, utilizing the 2-step process suggested in A ymetrix's Accepted procedures. A er calling 175,000 well-characterized SNPs in the rst step, samples with call rates below 95% were eliminated. Genotypes were called on the entire set of SNPs in samples that met the 95% call rate threshold. e mean call rate and number of SNPs were 675,367 prior to any quality control measures being implemented [5]. R and PLINK were used to clean up all of the subsequent data. Based on heterozygosity on the X chromosome, all individuals' reported sex was compared to their likely sex. e samples were eliminated if there was a mismatch between recorded and apparent sex. ree people were eliminated due to extremely low genotyping rates, and 30,601 SNPs were eliminated due to low call rates. Additionally, 12,370 SNPs with p-values below 10-4 that violated the Hardy-Weinberg equilibrium assumption were excluded from the analyses. ere were no samples