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Summary

Dissecting the Genetic Architecture of Multiple Chemical Sensitivity
Audrey V. Grant, PhD
Assistant Professor at the Department of Anesthesia, and expert in Genetic Epidemiology at McGill University.

Dr. Audrey Grant's presentation focused on the emerging genetic and epigenetic understanding of Multiple Chemical Sensitivity (MCS), emphasizing the potential for scientific breakthroughs through the application of advanced genomic methodologies. She began by situating MCS in a broader epidemiological context, noting that self-reported chemical intolerance affects up to 16% of the global population, while medically diagnosed MCS affects a smaller percentage (0.5–3.9%). This rarity and severity, she argued, suggest a potential genetic basis for the condition. It is possible that specific genes serve as key factors that increase the propensity for MCS.

Dr. Grant's lab at McGill University conducts genome-wide association studies (GWAS) using large databases, such as the UK Biobank and the Canadian Longitudinal Study on Aging. These efforts are enhanced by machine learning and integrative genomic approaches, which combine GWAS data with tissue-specific gene expression and epigenetic data to better understand the genetic architecture of complex traits, such as pain and potentially MCS. She presented visual data illustrating the high polygenicity of chronic pain, noting a large number of small-effect genetic variants that could inform MCS research. In effect, there are many genes which are implicated in this condition. By acquiring unique combinations of these genes through inheritance and environmental exposure, one could become diagnosed with MCS.

A key part of Dr. Grant's presentation focused on an upcoming research project in collaboration with the Environmental Health Association of Quebec and Genome Quebec. This project aims to collect high-quality DNA samples from participants using saliva kits, which are cost-effective and reliable for genotyping. Due to insufficient representation of MCS in existing biobanks, new cases

will be recruited, with controls drawn from biobanks like Cartagene using careful matching criteria. The project aspires to advance to whole-genome sequencing with additional funding.

Dr. Grant emphasized the goal of identifying both indirect and direct genetic variants associated with MCS, while also using case-control matching strategies to control for confounding variables. She encouraged interested participants to join the study.

Overall, Dr. Grant's presentation showcased how genomic technologies and strategic collaborations are opening new frontiers in understanding MCS, with the hope of uncovering its genetic underpinnings and contributing to more personalized and scientifically grounded approaches to diagnosis and treatment.