Audrey Grant, PhD, outlined a highly optimistic and forward-looking approach to investigating the genetic basis of Multiple Chemical Sensitivity (MCS), emphasizing how modern genetic epidemiology can uncover the biological mechanisms underlying the condition. While historical shifts in MCS prevalence over the last two decades point to a prominent environmental component, the distribution of the condition across demographic variables strongly indicates an underlying genetic susceptibility. This points toward complex gene-environment interactions.

To illustrate how genetic architecture operates in complex conditions, Dr. Grant highlighted insights from the well-explored field of chronic pain genomics, serving as a powerful proof of principle for MCS research. In chronic pain, genetic studies have successfully mapped a combination of rare mutations which can have severe effects on phenotype, depending on the environmental input. For example, the TRPV1 gene encodes a receptor that responds directly to volatile organic compounds. Because these chemical triggers are identical to those that trigger MCS, TRPV1 stands out as an excellent, biologically plausible candidate gene for chemical intolerance.

Rather than relying solely on traditional candidate gene methods, Dr. Grant's lab is pioneering an unbiased, comprehensive genome-wide association approach. Her team at the Statistical Pain Genomics Laboratory uses massive reserves of genomic data, such as the UK Biobank, to uncover shared patterns of genes associated with MCS. By using such methods, researchers can improve their statistical power to detect low-frequency MCS variants. Dr. Grant's broad hypothesis is that MCS is driven by a dual architecture featuring both simple Mendelian components and a complex polygenic network of many traits acting together.

The presentation culminated in an exciting call for prospective participant recruitment to build a robust Canadian cohort. Backed by secured funding, the study aims to recruit 500 new adult participants of all genders and ethnic backgrounds through specialized clinical networks and the Environmental Health Association of Québec. To ensure maximum accessibility, the team is using the gold-standard Oragene mail-in saliva collection system. This stable, room-temperature kit allows participants to easily provide DNA samples from home without clinical visits or blood draws. These new cases will be compared against age, sex, and location-matched healthy controls pulled from Canadian databases.

This Canadian data will be integrated into a groundbreaking multi-ancestry meta-analysis conducted in collaboration with an independent cohort from Japan. This global collaboration is designed to reveal convergent, universal genetic signals across diverse populations, greatly accelerating the discovery of novel genetic influences of MCS. Ultimately, this genetic mapping initiative is a transformative step forward for the patient community. Uncovering the genetic blueprint of MCS will decisively legitimize the diagnosis within the clinical establishment, streamline clinical care pathways, guide public health policy, and illuminate clear biological targets for the development of future therapeutic treatments.