Bedouin tribe reveals secrets to McGill's GA-JOE

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A Genome Quebec staff scientist prepares GA-JOE for genetic analysis work. Credit: Génome Québec, Montréal

Van Den Ende-Gupta syndrome (VDEGS) is an extremely rare genetic disorder that is characterized by distinctive head and facial features, such as unusual eyelids, narrow and beaked noses, flat nasal bridges, jaw deformities, and a turned out lower lip. As part of McGill's "RaDiCAL" project (Rare Disease Consortium for Autosomal Loci), collaborators in Qatar conducted field research with three patients from biologically interrelated Bedouin families, and sent samples to Canada for analysis by GA JOE - a high-tech genome analyzing machine.

The research effort was led by husband and wife team Dr. Jacek Majewski and Dr. Loydie A. Jerome-Majewska, both of McGill University's Department of Human Genetics and the Research Institute

of the McGill University Health Centre. The team discovered that mutations in the gene SCARF2 are responsible for the condition, and published their findings online today in the American Journal of Human Genetics.

"Why is this interesting? One of my roles at McGill is to implement new genomic technologies in human genetics research," explained Majewski. "Essentially, with a new technique known as exome capture and sequencing, we can now quickly sequence all of the coding portions of the human genome. This approach allows us to identify mutations responsible for rare genetic disorders. While they were too rare to attract much interest, these disorders hold in fact a lot of promise for the identification of the genes and pathways that are involved in generating human diversity. Moreover, knowing the mutations will be essential for future genetic testing and potential therapeutic intervention."

SCARF2 may for instance be involved in DiGeorge Syndrome, a much more common disorder affecting 1:3000 live births. DiGeorge syndrome causes deformities such as congenital heart defects. The researchers caution however that drawing links at this stage amounts to nothing more than "tantalizing speculation."

In anticipation of the fast advances in technology, McGill is identifying as many of the genes responsible for rare disorders as possible. "Over the past couple of years we've been identifying collaborators worldwide and collecting patients and DNA samples for mutation hunting," Majewski said. "This is one of the earliest successes of this project, which is still a hybrid of old and new technologies. In this particular case, although we found the mutation the old fashioned way, we had immediate confirmation using exome sequencing."

"To me the current manuscript is an early example of the enormous power of new exome/genome sequencing approaches and of the

involvement of McGill researchers in this field," Majewski concluded. "It really is a harbinger of more to come."

Provided by McGill University