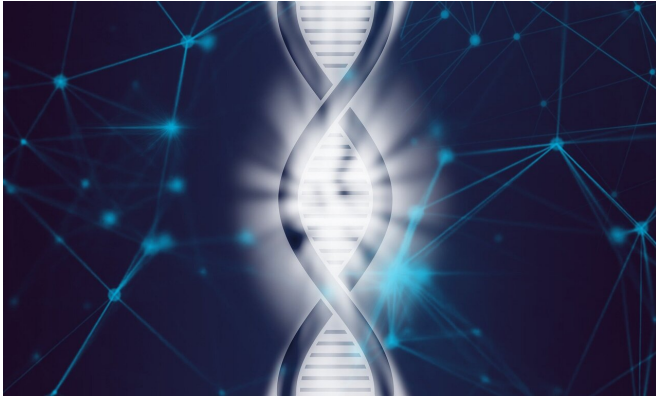


Largest comprehensive Middle East GWAS reveals Arab genetic risk factors

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A group of researchers at Qatar Foundation have reported the first and largest genetic association study in the Middle East, that has been published online in *Nature Communications*—a leading a peer-reviewed, open access, scientific journal published by Nature Research.

The study titled "Whole genome sequencing in the Middle Eastern Qatari population identifies genetic associations with 45 clinically relevant traits" highlights a vital piece of information wherein now there is a better understanding of the genetic risk factors that are specific to the Arab population, including those that are shared with other ethnicities.

Qatar was among the first countries to launch its own large-scale, national genome project. Qatar Genome combines whole genome sequencing data with comprehensive phenotypic resource collected at Qatar Biobank, and is considered the first, largest and most ambitious population-based projects of its kind in the Middle East.

This kind of studies can be considered as experiments conducted by nature, where the

natural variation found in the genomes of thousands of Qataris is linked to variations in their respective blood tests. The results from this project are shared publicly, ensuring that the specificities of the Arab genomes will be taken into consideration in future research on new treatments and therapies.

The study—led by researchers at Qatar Foundation's (QF's) Hamad Bin Khalifa University (HBKU) and QF's partner university Weill Cornell Medicine—Qatar (WCM-Q), along with other scientists from the Qatar Genome Research Consortium—includes over 6,000 Qatari individuals with whole genome sequence data.

By performing detailed assessments of genetic variants across the whole genome in 6,218 individuals, comprising data from 45 clinically relevant traits, this study identified about 300 independent genetic signals. Some of these signals were predominantly found in the Qatari population. This observation was then confirmed in a further 7,768 subjects from QF's Qatar Biobank.

Omar Albagha, Principal Investigator from HBKU's College of Health and Life Sciences, says: "The study provides new insights into the genetic architecture of clinical laboratory tests and identifies for the first time genetic variations that are specific to the population of Qatar. The study also shows that findings from genetic studies in European populations don't translate well when applied to our population in the Middle East. This argues for further studies to define the genetic architecture of diseases in our region. We are excited because the study represents a foundation for the implementation of precision medicine in the Middle East."

Karsten Suhre, Director of Bioinformatics Core at Weill Cornell Medicine—Qatar and joint senior author on the paper, says: "It has been a long but successful journey from the first patient recruitments to Qatar Biobank to analyzing the

resulting enormous genetic data set for associations with clinically relevant traits, and we as a consortium are proud to contribute with this paper to the international effort of obtaining an even better understanding of our human genome."

"Qatar Genome Research Consortium gave research groups the platform to study whole [genome](#) sequencing and other omics data to empower the genetic discoveries in this part of the world, which otherwise would be under-represented," said Professor Said Ismail, Director of QF's Qatar Genome, part of QF Research, Development, and Innovation.

More information: et al, Whole genome sequencing in the Middle Eastern Qatari population identifies genetic associations with 45 clinically relevant traits, *Nature Communications* (2021).
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