EDITORIAL

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Oman Genome Project is the Future of Using Genomics as the Determinant of Health and Disease in the Society

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Genetics is the science of inheritance and the study of the function and association of a single gene in relation to health and disease, examples include rare Mendelian disorders.[1] While the field of genomics involves the study of all the genes (as a whole) in the cells of an organism and how these genes interact with each other and with environmental factors to affect health and disease status.[2] Consequently, genome variation is one factor of the multi-factorial determinants of health and disease. These factors include lifestyle behaviors, environmental, social, demographic, and cultural factors. These factors interact with each other and determine the prevalence and distribution of diseases globally, but especially genomic variation can influence a specific society's health. Examples of multifactorial disorders include cancer, diabetes, hypercholesterolemia, and heart disease.[3]

Genomic and precision medicine impact is evident in personal health, well-being, and health economics for communities. Other than the rare genetic disorders, presently we see its wide applications in stratifying non-communicable diseases (NCD) like cancer and cardiovascular disease, characterizing genetic risks, and providing information about an individual's likely response to treatment.[4] Globally, genome-wide association studies have advanced our understanding of the genetic determinants of disease risk. However, some populations and regions, like the Middle East, are underrepresented. New genetic loci associated with disease may be evident in some populations and not others, as such genomic studies diversity can provide new opportunities for discovery and translation into therapies.[3] Furthermore, for Oman, it will provide a better understanding of the population-specific disease risks. In Oman, founder effects, endogamy, and autozygosity might provide significant insight. Examples of this pattern of enrichment of certain rare variants include the cardioprotective variant rs76353203 in the *APOC3* gene in the Amish founder population.[5] It is associated with reduced blood triglyceride levels. Additionally, the nonsense variant rs61736969 in the *TBC1D4* gene is observed in high frequencies in the Greenlandic population and is associated with a substantially increased risk of type 2 diabetes mellitus among homozygotes.[6]

Given the recent drastic reduction in the cost of sequencing, there have been numerous studies aimed at generating population genome data.[7] The completed Human Genome Project was the cornerstone of all the current and recent national genomic projects. Yet, much more work is needed in the coming years in order to understand some of the implications of population-specific genetic variation. Establishing Omani genomic data (Human Variome Project) through Oman Genome Project that is linked with representative biobanks and population health resources will be of great value. This will aid to determine the genomic structure, variants, and biological factors that influence the health of our community.

One of the future strategies and investments in healthcare infrastructure is to overcome the NCD challenge, especially in the Gulf Cooperation Council countries.[8] Recently, the Ministry of Health completed a national NCD and their risk factors survey called STEPS 2017.[9] The survey included a sample of 9045 Omani and non-

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Omani families across all the governorates in the Sultanate. It collected comprehensive information and provided essential information on key NCD indicators. These include demographics (e.g., age, gender, and region), physiological data (e.g., blood pressure levels), biochemical factors (e.g., cholesterol, blood glucose, and hemoglobin levels), and behavioral factors (e.g. exercise, smoking, and eating habits). Having country-specific genomic data will have multiple advantages. These include developing variants correlated with traits like blood pressure, hyperglycemia, and hypercholesterolemia. Homozygosity of rare variants might be correlated with extreme biological factors values (harmful or protective); for example, lipid levels, systolic blood pressure, or predisposition to behavioral and psychiatric disorders. Population-specific genetic variants can be targeted for the primary prevention of genetic disorders, such as premarital screening. Generally, unique genomic data that are correlated with biobank data can aid in therapeutic intervention including new drugs designs, start early intervention, and primary preventive measures. This will also help policymakers to draw strategies for enhancing the population's health.

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