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Note on genomic ancestry and variation in disease susceptibility

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Motivation and Aim: Human DNA holds the key to uncovering our true ancestral past and determines who we are. A plethora of information stored inside the genome reflects our uniqueness and proximity to different ancestral and modern-day populations. Given the high correspondence between our genetic make-up and the geographical origin of our forefathers, it is possible to glean into precise ancestral origin using the genetic information [1, 9]. Understanding one's ancestry is not only a 'homing' tool bringing someone closer to human evolutionary past but also holds the key in determining population-specific variability in disease susceptibility, drug responsiveness, and other health and fitness related traits. Recently we have organized the Research Topic (special journal issue) at Frontiers in Genetics to collect the papers focused on the ancestry studies [4].

Methods and Algorithms: We have organized special journal issue (Research Topic) in "Frontiers in Genetics" considering genetic background and molecular mechanisms of the human diseases [5]. Understanding one's ancestry can play a monumental role in understanding variation in disease susceptibility across various populations and glean into the complex gene and environment interplay in ancestry-specific disorders [8]. Thus, traditional high fat and protein diets in cold regions of Siberia and North Asia have consequences on obesity and diabetes-related diseases [2]. Understanding one's genomic ancestry can facilitate the development of novel therapeutics or repurposing of existing treatment strategies, particularly aiding in identifying population-specific therapies. Subsequently, our knowledge of ancestry-specific variation in complex disorders can be used towards developing personalized and ancestry-specific precision medicine approaches to ameliorate several complex disorders [9].

Results: We have considered the following themes for this special issue:

• Unravel predisposition of various modern-day populations towards common disorders and conditions, including but not limited to cancers, heart diseases, and infectious diseases.

• The association of alleles with complex disorders, evaluated at a population level; discovery of novel disease marker panels.

• Identification of novel medically relevant genetic variants that can be used as diagnostic markers in genetic diagnostics and healthcare.

• Selection dynamics of the genes. Investigation of the spatial and temporal distributions of positively selected alleles in response to population specific disease susceptibility.

The papers published in the Research Topic correspond to the themes stated above and extend the studies presented in Frontiers in Genetics Topics (see

https://www.frontiersin.org/research-topics/17947/bioinformatics-of-genome-regulation-volume-ii). We had participated in the organization of series of conferences on human population genetics and computational genomics in Russia that allowed formalize the idea of special journal issues [6]. Thus, conference "Century of Human Population Genetics" was held in Moscow in 2019. It was focused on the discussion of the research on gene pools of the world's nations, ancient DNA analysis, possibilities of judicial genetics, population-genetic database development, biobanks, and new genomics technologies [7]. We had series of publications on human ancestry based on new genomics data initially discussed at this meeting [3].

Conclusion: Overall, the Research Topic at Frontiers in Genetics raised actual problems in the genetics studied. The Research Topics in Frontiers in genetics (https://www.frontiersin.org/research-topics/21036/high-throughput-sequencing-based-investigation-of-chronic-disease-markers-and-mechanisms) continues collection of papers on human diseases' markers.

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