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Genetic Epidemiology of Human Complex Diseases

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Message from the Guest Editors

Each human population possesses a unique set of (epi)genetic variants that interact with their specific environmental context. Their frequencies are the result of the evolutionary factors that accompany specific demographic histories, causing sometimes striking epidemiological differences. Unlike disease-associated transgenerational epigenetic variants, which are presumed to exist but are difficult to identify, a large number of disease-associated genetic variants are common and have already been cataloged. These advances were mainly achieved through large-scale genotyping and next-generation sequencing techniques using large sample sizes. The investigation of genetically isolated populations represents a viable alternative. In addition, persistent epigenetic variants may be more easily identified in populations that share a culture and lifestyle over many generations.

Our goal is to publish papers describing the role of (epi)genetic architecture in susceptibility to complex diseases in different populations to establish susceptibility profiles that inform personalized and preventive medicine strategies in public health policies.

Deadline for manuscript submissions:
closed (25 September 2023)

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Special Issue

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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