Special Issue

Historic Genomics: An Emergent Discipline

Message from the Guest Editor

The issue contains papers that show how the diversity of different genetic markers across the world populations may be useful to obtain inferences about their historical-prehistorical interactions. While history often relies on speculation, genomics now provides objective data to challenge traditional views. Technologies like gene amplification enable comprehensive studies of genomes, diseased genes, and population-specific gene diversity. These insights will help confront the historic premises or "dogma" with objective genetic data. Historic genomics is slowly being developed.

HLA alleles, mtDNA, and Y-chromosome variants are all linked to diseases that may have been common in the past or certain populations and are also useful for the historic genomics study. Furthermore, polymorphic genes are currently in use in population genetics: full genome studies, SNPs, and STRs. However, low polymorphic gene markers may be useless for distinguishing populations since "noise" is too high, limiting their usefulness.

We invite you to explore the "Historic Genomics" in the issue.

Guest Editor

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Message from the Editor-in-Chief

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