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The Genomic Impact of Human Migrations

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Deadline for manuscript submissions:
closed (15 September 2021)

Message from the Guest Editors

Anatomically modern humans first appeared in the East African fossil record around 200,000 years ago, and colonized the rest of the world with an unprecedented fast pace, in less than 100,000 years. Their journey was accompanied by various levels of interaction with different species and habitats: a substantial replacement of pre-existing archaic humans, a strong selection drive behind extensive domestication processes, a range of direct and indirect modifications to the landscape which created new niches for commensal and pathogenic species, and finally new challenges for the adaptation to different, and sometimes extreme, environments. After the main colonization dispersal, human genomic variation has been largely shaped by events of localized gene flow of different intensities.

This Special Issue will collect reviews and original contributions about migration dynamics and evolutionary trajectories of our species, and of the species that came into contact with us during our migration journey. This includes studies of human-pathogens interaction and coevolution, human-driven selection, inference of past demographic dynamics and genomic adaptation to new environments.

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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