Special Issue

Prostate Cancer Genetics and the Emergence of Targeted Therapies Based on Molecular Profiling

Message from the Guest Editors

Our understanding of the genetic basis of prostate cancer has increased considerably over the last decade. Two recent studies have shown that approximately 30% of familial relative risk is explained by common variants, discovered through GWAS and fine-mapping efforts. However, the true clinical utility of these variants is yet to be revealed in terms of patient stratification. To uncover some of the 'missing heritability', NGS methodologies are being used for rare variant discovery, which promises to identify more functionally relevant risk variants. Combined with patient stratification, this approach can also be used to discover rare variants associated with aggressive or fatal prostate cancer. Furthermore, molecular profiling of rare variants at both germline and somatic levels, including circulating tumour cells, can identify biomarkers that predict patient response to targeted therapies (i.e., pharmacogenomics). We extend an invitation for reviews and research articles on the discovery of rare prostate cancer variants, particularly those that can be used to distinguish clinically relevant disease or predict therapeutic efficacies and outcomes.

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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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