

Special Issue

Genomic Aberrations in Hematologic Malignancies

Message from the Guest Editors

Recurrent chromosomal abnormalities are very common in a variety of hematological malignancies, such as translocations and/or inversions related to the formation of fusion genes such as t(9;22)(q34.1;q11.2) and related BCR::ABL1; t(8;21)(q22;q22.1) and related RUNX1::RUNX1T1; inv(16)(p13.1q22)/(16;16)(p13.1;q22) and related CBFB::MYH11; t(15;17)(q24;q21) and related PML::RARA; t(12;21)(p13.2;q22.1) and related ETV6::RUNX1; and a wide spectrum of 11q23 abnormalities/KMT2A(MLL) gene rearrangement and related fusion genes in both myeloid and lymphoid neoplasms. They are widely applied as biomarkers for the diagnosis of specific entities and/or sub-entities of hematological malignancies, targeted therapies, and prognostic predictions in the field of hemato-oncology. Attributed to the widespread application of advanced next-generation sequencing (NGS)-based technologies and genome-wide comprehensive studies, tremendous novel fusion genes as well as chromosomal abnormalities have been identified in hematological malignancies in the past several decades. They all play important roles in the era of precision medicine.

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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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Editor-in-Chief

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