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Advances in Genetics and Genomics of Ovarian Cancer

Guest Editor:

Dr. Sohyun Hwang
1. Department of Pathology, CHA Bundang Medical Center, CHA University, Sungnam-si, Gyeonggi-do, Republic of Korea
2. Department of Biomedical Science, Colledge of Life Science, CHA University, Sungnam-si, Gyeonggi-do, Republic of Korea

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Message from the Guest Editor

Ovarian cancer is a leading cause of death among patients with gynecological malignancies and the majority of ovarian cancer cases are high-grade serous carcinomas (HGSCs). The Cancer Genome Atlas (TCGA) also reported that mutations in TP53 are present in more than 96% of HGSCs and homologous recombination (HR) deficiency (e.g. BRCA1 or BRCA2) is present in approximately 50% of the patients. This means that the other half of HGSCs have no apparent defect in HR. Moreover, HGSC is one of the most chromosamally variant malignancies (i.e., genome instability).

In this Special Issue of Genes on "Genetics and Genomics of Ovarian Cancer", we welcome reviews, mini-reviews, new methods, and original research articles that advance our understanding of ovarian cancers. While the new insights driven by 3D chromosome organization on molecular mechanisms or pathways related to HGSC—such as P53 aberration, cellular senescence, immune evasion, and genome instability—will be of special interest, we will also be open to any topic that advances the understanding of ovarian cancers to develop a better therapeutic method.

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Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham, 1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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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Genes Editorial Office
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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