Editorial

Current Progress in Cancer Pathobiology Research and Management

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On behalf of the editors, I am pleased to introduce the journal *Cancer Pathobiology and Immunity* (*CPI*)'s debut as "Current Progress in Cancer Pathobiology Research and Management". Our inaugural issue stems from the opportunity today to develop novel treatment strategies for major malignant tumors. The availability of multiple omics technology, single-cell sequencing, artificial intelligence-driven structure modeling, progress in gene therapy, and material innovation for drug delivery have offered an unprecedented era to focus on developing new therapeutic strategies. This approach requires an integrated and coordinated synergy of academia, industry, healthcare system as well as regulatory agencies to discover, to develop, to evaluate, and to approve new therapies and new drugs.

Internationally accepted classifications of malignant tumors, developed by the World Health Organization (WHO) and Union for International Cancer Control (UICC), are based on the histotype/morphology and the spread of cancer throughout the body, including biologic and molecular genetic features, and are the foundation of cancer diagnosis and the starting point of cancer management. Given the advances in cancer genetics and genomics, molecular genetic profiling has been used to refine the current classifications of malignant tumors and to determine the treatment, sometimes (for a small number of cancers) irrespective of histotype [1,2].

Molecular profiling can challenge existing classifications because many tumors share genetic alterations. For example, the *MYC* gene is translocated in lymphomas and amplified in some carcinomas of the breast, ovary, stomach, lung, and skin. In these tumors, *MYC* amplification is associated with resistance to treatment and aggressive disease [3]. Aberrations in this gene can help predict outcomes and guide treatment.

Pathological classification and molecular-genetic profiling can be used together in deciding the treatment strategy. For example, in breast cancer, the standard classification defines the pathologic grade and stage of the tumor, while the molecular–genetic characterization provides information on estrogen receptor expression, *HER2* gene status, proliferative index, and prognostic gene signatures [4]. Furthermore, a chromosomal rearrangement fusing a neurotrophic tropomyosin receptor kinase (*NTRK*) gene with another gene has been observed in more than 20 different tumors; these tumors can be treated with drugs targeting NTRK-fusion kinases [5]. For a small number of advanced or metastatic cancers, the molecular-genetic findings can determine the treatment, irrespective of the morphological-pathological findings [5,6]. The stage is now set for the translation of pathobiologic progresses into new therapeutics which will have an impact on a large number of tumors. Ongoing basket trials will contribute to knowing whether tissue agnostic therapy will be the future strategy in aggressive tumors resistant to therapy [6,7].

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