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Editorial

Cancer is a leading cause of death in men worldwide and the major cause of cancer related death is drug resistance [1,2]. In past few years, scientists have established tumor heterogeneity as a phenomenon of critical importance in the natural history of individual neoplasms and drug resistance [3-5]. The concept of tumor heterogeneity has a major impact on therapeutic approaches [6-9]. Drug resistance creates difficulty in cancer treatment and is directly linked to the tumor progression and poorer prognosis. As tumor heterogeneity is very common in almost all solid tumors, cancer therapy needs to become more personalized, selective, and specific [10-13]. Understanding the mechanisms of tumor heterogeneity and drug resistance will provide sustenance for the future development of personalized cancer medicine.

Tumor heterogeneity (intra-tumoral) has been well-known for past few decades, as it was said that a single tumor consists of many cell subpopulations [6]. The biggest challenge in tumor heterogeneity is to capture all subpopulations of a solid tumor. If tumor cell subpopulation is not proficiently captured, drug-resistant subpopulations will sporadically emerge [14-16]. Some biomedical techniques (eg. Single-Cell Sequencing, Micromanipulation, Laser-Capture Microdissection, Flow Cytometry Using Fluorescence-Activated Cell Sorting, Whole Genome Amplification, Multi-Regional Sequencing Studies etc.) can be used to detect mutational heterogeneity in solid tumor and to provide personalized therapy [17-19].

In 2012, Gerlinger et al., published an article "Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing" in New England Journal of Medicine. In this article, Gerlinger et al. demonstrated that intratumor heterogeneity can contribute to drug resistance which leads to the treatment failure in renal-cell carcinoma [6]. Recently, our group for the first time demonstrated the difference in mutational

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heterogeneity varying by subsite in Head and neck squamous cell carcinoma (HNSCC). We demonstrated that Larynx and FOM tumors are more heterogeneous than oral tongue tumor [20,21]. The heterogeneity within tumor specimens may adopt resistance to the standard treatment protocols. These kinds of studies on tumor heterogeneity are relevant to the researchers and clinicians in developing personalized cancer therapy based on identification of specific mutations in tumor samples.

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