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Long non-coding RNAs in cancer

It is now well established that long non-coding RNAs (lncRNAs) are key regulators in various biological processes such as development, metabolism and immune response. LncRNAs control these processes via several mechanisms including 1) directing epigenetic modifiers or transcription factors to their target genes, 2) functioning as sponges for endogenous RNAs, 3) regulating mRNA decay, 4) mediating inter-chromosomal interaction and etc. As a consequence, aberrant expression of lncRNAs is often associated with several diseases including cancer [1].

This special issue "long non-coding RNA in cancer" includes six excellent reviews on recent advances on our understandings of the role for lncRNA in cancer development and progression. First of all, a review by Balas and Johnson discusses general mechanisms by which lncRNAs control cancer pathways and provides a list of lncRNAs that are associated with specific types of cancer. In addition, the authors discuss functions of three lncRNAs including HOTAIR (Hox transcript antisense intergenic RNA), TUG1 (taurine upregulated gene 1) and MEG1 (maternally expressed gene 3) as well as detailed mechanisms of their action in cancer development and progression [2].

In the review by Aird et al., the authors summarize 34 lncRNA that are associated with prostate cancer [3]. Specifically, they emphasize the role for these lncRNAs in the AR (androgen receptor) pathway. In addition, they discuss involvement of lncRNAs in EMT (epithelial to mesenchymal transition). In relation to this review, Helsmoortel et al. [4] discuss potential use of some of these lncRNAs as biomarkers in prostate cancer.

Furthermore, Distefano provides an excellent review on the lncRNAs in tumorigenesis, progression, and metastasis of hepatocellular carcinoma, focusing on the function of HULC (highly upregulated in liver cancer) and HOTAIR and potential use of MALAT1 (metastasis-associated lung adenocarcinoma transcript 1), UCA1 (urothelial carcinoma associated 1), and HULC as biomarkers in hepatocarcinoma [5]. The review by Samson and Dean provides comprehensive overview on the role for BC200 (BCYRN1), previously known to be brain-specific, in several types of cancer [6].

Aforementioned discovery was only made possible by technological advances on sequencing and analysis of lncRNAs. Teipathi et al. provide timely overview on recent advances on the RNA sequencing and analysis techniques [7].

Together, the articles published in this special issue provide not only excellent reviews on lncRNAs in cancer but also future direction of the lncRNA research. LncRNAs have high potential to be used as biomarkers and furthermore as therapeutic targets in several types of cancers.

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