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The "next-generation" knowledge of papillary thyroid carcinoma.

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Abstract

The application of Next-Generation Sequencing for studying the genetics of papillary thyroid carcinomas (PTC) has recently revealed new somatic mutations and gene fusions as potential new tumor-initiating events in patients without any known driver lesion. Gene and miRNA expression analyses defined clinically relevant subclasses correlated to tumor progression. In addition, it has been shown that tumor driver mutations in BRAF, and RET rearrangements - altogether termed "BRAF-like" carcinomas - have a very similar expression pattern and constitute a distinct category. Conversely, "RAS-like" carcinomas have a different genomic, epigenomic, and proteomic profile. These findings justify the need to reconsider PTC classification schemes.

KEYWORDS:

Next generation sequencing; RNA-Sequencing; gene rearrangements; mutations; papillary thyroid carcinoma