High-Resolution Melt

High-Resolution Melt or HRM analysis as it will be referred to herein is a hugely powerful technique for the detection of mutations, polymorphisms and epigenetic differences in double-stranded DNA samples.

Saito et al. examined the efficacy of a pre-screening method for high-resolution melting (HRM) analysis of TP53 mutation before direct sequencing using samples from patients with diffuse glioma. Surgical samples from 64 diffuse gliomas were classified based on the World Health Organization Classification of Tumors of the Central Nervous System 2016 and the cIMPACT-NOW (the Consortium to Inform Molecular and Practical Approaches to CNS Tumor Taxonomy-not official WHO) update. TP53 mutations from exon 5 to exon 8 were assessed by direct sequencing. The results of HRM and p53 immunohistochemistry (IHC) analysis were compared by recording the sensitivity, specificity, and false-negative and false-positive rates. Direct sequencing detected TP53 mutations in 18 of 64 samples (28.1%): diffuse astrocytoma, IDH-mutant (n = 3); diffuse astrocytoma, IDH-wild type (n = 1); anaplastic astrocytoma, IDH-mutant (n = 3); anaplastic astrocytoma, IDH-wild type (n = 4); and glioblastoma, IDH-wild type (n = 7). A total of 22 mutations was detected in the 18 samples; 4 samples exhibited duplicate missense mutations. Sensitivity and specificity were 0.96 and 0.96, respectively, for HRM analysis; they were 0.89 and 0.52, respectively, for p53 IHC. Overall accuracy was 0.98 for HRM and 0.63 for IHC. HRM analysis is a good pre-screening method for the detection of TP53 mutation before direct sequencing [1)].

1)
Saito K, Yokogami K, Maekawa K, Sato Y, Yamashita S, Matsumoto F, Mizuguchi A, Takeshima H. High-resolution melting effectively pre-screens for TP53 mutations before direct sequencing in patients with diffuse glioma. Hum Cell. 2021 Jan 17. doi: 10.1007/s13577-020-00471-2. Epub ahead of print. PMID: 33454902.