Chromosome 10q23 (PTEN Locus) deletion and PTEN mutation (Non-core)

Reason/Evidentiary Support

Chromosome band 10q23 (*PTEN* Locus) Deletion

Hemizygous deletions affecting the *PTEN* gene locus at band 10q23 are detectable in the vast majority of glioblastomas, IDH-wildtype and IDH-mutant, due to monosomy 10 or deletion of 10q.[1,2] Losses of chromosome 10 or chromosome arm 10q have also been reported in smaller fractions of WHO grade II and III diffuse gliomas.[2-4] However, when detected in an IDH-wildtype astrocytic glioma of WHO grade II or III, monosomy 10 or 10q23 deletion may indicate a glioblastoma, IDH-wildtype, in particular when associated with gain of chromosome 7 and other glioblastoma-associated genetic alterations, like *EGFR* amplification and *TERT* promoter mutation.[3-5] Homozygous *PTEN* deletion is less common than hemizygous deletion, and mostly restricted to a small fraction of IDH-wildtype glioblastomas.[1] Detection of 10q23 (*PTEN* locus) deletion is commonly accomplished by FISH or CISH on routine FFPE tissue sections. Other diagnostically useful methods include MLPA, microarray-based DNA copy number profiling, and NGS-based analyses.

PTEN Mutation

Mutations in the *PTEN* tumour suppressor gene at 10q23 are found in approximately 30% of glioblastomas, IDH-wildtype.[1] *PTEN* mutation in IDH-wildtype glioblastomas is usually accompanied by loss of the second allele due to monosomy 10 or deletion of 10q. Mutations are distributed across the entire gene with the highest frequency of mutations seen in exons 5 and 6, which encode the catalytic domain of the PTEN protein.[6] Therefore, diagnostic investigation for *PTEN* mutations requires sequencing of all exons including the flanking intronic regions for detection of splice site mutations. NGS-based approaches represent the most convenient way to detect *PTEN* mutations, while Sanger sequencing is also possible but more laborious.[7-9] Immunohistochemical demonstration of loss of PTEN protein expression does not correlate well with *PTEN* mutation or *PTEN* promoter methylation in glioblastomas, and thus cannot serve as a surrogate marker.[10]

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