Ancillary studies (Non-core)

BRAF testing

Based on recent advances in our understanding of the molecular basis of melanoma and the role of the immune system in controlling the disease have led to multiple new therapeutic strategies that have radically transformed the care of melanoma patients, particularly those with advanced stage disease. These treatments were initially shown to be effective in patients with stage IV melanoma but more recently have demonstrated a 50% reduction in the rate of relapse for patients with stage III melanoma and are now being trialled in patients with earlier stage melanoma. Examples of these new effective drug therapies approaches are immunotherapy, using immune system checkpoint inhibitors against CTLA-4^{1,2} and/or PD-1,³⁻⁵ and molecularly-targeted therapy using BRAF inhibitors alone (monotherapy)⁶⁻¹⁰ or in combination with MEK inhibitors¹¹⁻¹⁵ for the approximately 40-50% of patients with metastatic melanoma whose melanoma harbors a BRAF V600 mutation.^{16,17}

BRAF mutations in melanoma are predominantly V600E (73-90%) and V600K (5-20%), but occasionally are other genotypes. There is an inverse relationship between BRAF mutation prevalence and age. Almost all patients <30 years and only 25% of patients ≥70 years had BRAFmutant melanoma. Amongst BRAF-mutant melanoma, the frequency of non-V600E genotypes (including V600K) increase with increasing age. There are various molecular techniques for detecting BRAF and other somatic gene mutations within melanoma and these techniques are associated with varying sensitivity and specificity. With all techniques, careful macrodissection by pathologists to enrich for tumour cells is usually an important pre-analytical step to ensure optimal results of testing. The presence of BRAFV600E mutation can be detected by immunohistochemistry, but there are as yet no validated antibodies available for the detection of BRAFV600K mutations, and hence alternative techniques are required.

Other ancillary testing

In selected circumstances, molecular ancillary studies can be helpful when evaluating melanocytic tumours. In difficult melanocytic tumours, in which accurate characterization of the tumour as benign or malignant is difficult based on routine histopathology, it may be useful to assess for the presence of chromosomal copy number aberrations.

Comparative genomic hybridization (CGH) and fluorescence in situ hybridization (FISH) can be used to detect chromosomal copy number aberrations in formalin-fixed, paraffin-embedded tissue.^{18,19} FISH can be utilized to directly visualize specific chromosomal copy number changes within individual tumour cells. While it has the limitation of being able to test for only a limited number of changes (compared to CGH, which tests for chromosomal aberrations in the entire genome), FISH is more easily applied in routine clinical practice and can be successfully performed on small tumour samples. CGH is generally only available in specialist centres, and is expensive and not applicable to small samples.

Gene expression has also been used to assist in the classification of borderline melanocytic tumours and a number of commercially available tests have been developed utilising this technique. However, these tests need further validation before they can be recommended for routine (i.e., beyond adjunct) use in the clinical setting.^{20,21}

With recent rapid advances in molecular techniques, it is likely that massively parallel next generation sequencing will become widely available in coming years.²² This will provide an opportunity to perform more comprehensive molecular evaluation of a tumour from data generated in a single assay including mutation analysis, copy number changes, structural rearrangements and

mutation burden. Although challenges remain in performing detailed analysis in a timely fashion within the constraints of a diagnostic setting, this will provide an unprecedented opportunity to incorporate molecular data into routine pathological evaluation and provide new insights into diagnosis, and prognostic and predictive biomarkers as well as tumour classification.

While some studies have shown correlation between mutation burden, gene signatures and/or PDL1 expression and response to immunotherapies, at present there are no biomarkers with sufficiently high sensitivity or specificity to be of clinical utility in routine practice.

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