

Molecular Diagnostics in Melanocytic Tumors: The Pathologist's Perspective

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During the last 15 years, molecular techniques have led to a fast gain in our knowledge on the development of melanocytic tumors. The potential implications of these advances for prognosis and therapy of melanoma patients are outstanding. There is, however, an even greater problem which has to be raised: since the histopathological diagnosis of melanoma is matter of considerable disagreement even among experts [1]. Pathologists have been increasingly asking for a molecular 'key to the code' in order to overcome the diagnostic limitations of conventional morphology. Table 1 summarizes the main molecular techniques and their expected results in melanoma [2], are these data meaningful also for the histopathological differential diagnosis between 'nevus' and 'melanoma'?

Whole exome sequencing performed on metastatic tumor tissue has demonstrated that melanoma has the highest mutation rate among all human cancer types (16.8 mutations/Mb) [3]. However, these data do not necessarily apply to primary cutaneous tumors. Of the latter, over 80% of cases harbor mutations involving the RAS-RAF-MEK-ERK pathway which is also affected in nevi [4]. In the field of Spitzoid melanocytic tumors, fluorescence in-situ hybridization with break-apart probes demonstrate kinase fusions of ROS1, NTRK1, ALK, BRAF, and RET; but these chromosomal rearrangements are present along the entire spectrum of Spitzoid tumors (55% of Spitz nevi; 56% of atypical Spitz tumors; 39% of Spitzoid melanomas) [5], a finding that clearly hampers the diagnostic usefulness of such a molecular signature. The same is also true for homozygous BAP1 (3p21) mutations, which can be found in

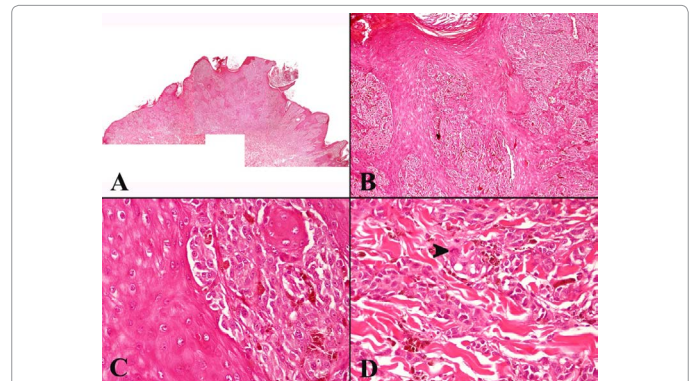


Figure 1: A) A verrucous melanocytic tumor of the arm in a 7-year-old boy. B) A confluent junctional proliferation of melanocytes with a strikingly irregular epidermal hyperplasia. C) Relatively monomorphic epithelioid cells at the dermoepidermal junction. D) The deep dermal component of the tumor with a mitosis (arrow). The lesion was diagnosed as atypical Spitz tumor, but, unlike atypical Spitz tumors, it harbored the BRAF^{V600E} mutation and behaved as a 'conventional' melanoma.

a subset of syndromic and sporadic atypical epithelioid (Spitzoid) cell nevi but also in morphologically clear-cut melanomas [6]. Despite early claims about 11p gains or mutations of the HRAS exon 3 as a hallmark of benignity in Spitzoid neoplasms [7], cases of melanoma with HRAS mutations can be found as well [8]. One could therefore conclude, along with Dummer et al. [9] that the expectations on molecular biology in the differential diagnosis of melanocytic lesions have been overestimated.

In our opinion, a completely sceptic approach about the diagnostic impact of molecular techniques in this field is probably NOT justified. First of all, molecular techniques may help recognize as melanoma an undifferentiated malignancy with a 'null' immunophenotype [10]. Furthermore, and even more important, some subgroups of melanocytic tumors, irrespective of the degree of histopathological atypia, can be identified on a molecular basis. As underlined above, Spitzoid neoplasms can be typified by kinase fusions [5], BAP1 biallelic inactivating mutations [6], or HRAS gains/mutations [7]; along with 83% of uveal melanomas [11] activating mutations of GNAQ (9p21) and GNA11 (19p13) are a hallmark for dermal dendritic melanocytic tumors (blue nevus and related lesions) [12]. Both in Spitzoid and

Technique	Expected results in melanoma
(Array) Comparative Genomic Hybridization	Gains at 1q, 6p, 7p, 7q, 8q, 17q, 20q, 4q, 8q, and 11q. Losses at 6q, 9p, 10p, 10q, 11q, and 21q
Fluorescence in situ hybridization	RREB1 gain >29%; RREB1 gain relative to Cep6 > 55%; CCND1 gain >38%; MYB loss relative to CEP6 >31%; MYC gain >29%; CDKN2A biallelic loss relative to Cep9 >29%; kinase fusions of ROS1, NTRK1, ALK, BRAF, and RET in Spitzoid melanoma (39%)
Gene expression profiling	Compared with nevi, different expression of a set of genes including PRAME, S100A7, S100A8, S100A9, S100A12, PI3, CCL5, CD38, CXCL9, CXCL10, IRF1, LCP2, PTPRC, SELL
DNA sequencing	In familial melanoma: mutations of CDKN2A (40%), MITF (20%), CDK4, BAP1, TERT, POT1 In sporadic melanoma: mutations of BRAF (53-66%), NRAS (9-29%), NF1 (12-14%), KIT (36% of acral melanomas; 88% of oral melanomas), GNAQ/GNA11 (50% of uveal melanomas)
DNA methylation profiling	Methylation of promoters of CDKN2A, PTEN, RASSF-1A, RASSF10, RAR-beta2
Micro-ribonucleic acid (MiRNA) profiling	Upregulation of miRNA192; down regulation of miRNA132
Mass spectrometry	Actin, Vimentin, and three unknown peptides differently expressed in Spitz nevi and Spitzoid melanoma

Table 1: Molecular investigations for melanoma diagnosis.

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in dendritic cell melanocytic tumors, BRAF or NRAS mutation are very rare [12,13]; thus, if a BRAF or NRAS mutation is detected in a seemingly 'Spitzoid' or 'dendritic cell' morphologic context, a careful histopathological re-evaluation is warranted in order to exclude a conventional melanocytic malignancy. Figure 1 illustrates a case of melanocytic tumor of the arm in a 7-year-old boy. The lesion was initially diagnosed as an atypical Spitz tumor, mainly because of the age of the patient, the epidermal hyperplasia, and the epithelioid cell morphology. Unfortunately however, four years after wide excision of the primary tumor, the patient developed a cutaneous satellitosis, along with nodal and distant metastases. Both the primary and the metastatic tumor tissue were found to harbor the BRAF^{V600E} mutation, a finding which was obviously much more in keeping with a conventional melanoma rather than with an atypical Spitz tumor.

In conclusion, the main goal which can be achieved with molecular techniques in the diagnosis of melanocytic skin lesions is the identification of a given "subgroup" of tumors ("conventional" vs "Spitzoid" vs "dendritic cell"). A 'red flag' must be raised for a melanocytic tumor in which molecular data are conflicting with the apparent clinicopathological context.

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