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Melanoma types by in vivo reflectance confocal microscopy correlated with protein and molecular-genetic alterations: a pilot study.

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#### Abstract

Cutaneous melanoma (CM) is one of the most prevalent skin cancers, which lacks both a prognostic marker and a specific and lasting treatment, due to the complexity of the disease and heterogeneity of patients. Reflectance confocal microscopy (RCM) in vivo analysis is a versatile approach offering immediate morphological information, enabling the identification of four primary cutaneous RCM CM types. Whether RCM CM types are associated with a specific protein and molecular-genetic profiles at the tissue level, remains unclear. The current pilot study was designed to identify potential correlations between RCM CM types and specific biological characteristics, combining immunohistochemistry (IHC) and molecular analyses. Eighty primary CM evaluated at patient bedside with RCM (type 1 (19, 24\%), type $2(12,15 \%)$, type $3(7,9 \%)$ and type $4(42,52 \%)$ were retrospectively evaluated by IHC stains (CD271, CD20, CD31, cyclin D1), fluorescence in-situ hybridization FISH for MYC gain and CDKN2A loss and molecular analysis for somatic mutations (BRAF, NRAS and KIT). RCM CM types correlated with markers of stemness property, density of intratumoral lymphocytic B infiltrate and cyclin D1 expression, while no significant association was found with blood vessel density, nor molecular findings. RCM CM types show a different marker profile expression, suggestive of a progression and an increase in aggressiveness, according to RCM morphologies. This article is protected by copyright. All rights reserved. This article is protected by copyright. All rights reserved. PMID: 30636079 DOI: 10.1111/exd. 13877


