ABSTRACT
Cutaneous melanoma is one of the most frequent malignancies of the skin in Caucasian populations. Patients who develop cutaneous melanoma are at increased risk of developing a second primary melanoma. The estimated incidence of multiple primary melanoma (MPM) ranges from 1.2% to 8.2% of cases, with a high preponderance of melanomas occurring metachronously. The aim of this study was to describe dermoscopic, microscopic, clinical, and molecular correlations between first and subsequent melanomas in patients with metachronous MPMs. Twenty-four paired melanomas from 12 MPM patients were evaluated for architectural characteristics based on dermoscopy and confocal microscopy, as well as for mutations in BRAF and NRAS genes by Sanger-based sequencing analysis. Specific scores used for classifying features of dermoscopy (global pattern; 7-point check list; ABCD Stolz score) and confocal microscopy (Segura and Pellacani) were compared with genetic and histological data. Consistency in dermoscopic patterns between the primary and subsequent cutaneous melanomas were observed in about two thirds of cases, whereas concordant features based on confocal microscopy were found in only about two fifths of cases. The majority of patients (7/12; 58%) presented consistent BRAF/NRAS mutation patterns between first and subsequent primary melanomas. A significant association between BRAF mutations and Pellacani score was evident. Similarities between the index melanoma and subsequent cutaneous melanomas were observed with regards to dermoscopic features and, to a much less extent, confocal microscopy findings. Our data further indicate that the Pellacani score may be used to predict BRAF mutations. KEYWORDS: BRAF; NRAS; cancer; confocal microscopy; dermoscopy; melanoma PMID: 29180316 DOI: 10.1684/ejd.2017.3206