MELANOMA AND MELANOCYTIC NAEVI

GENETIC PROFILE OF ACRAL LENTIGINOUS MELANOMA AND NEVI IN A CHILEAN POPULATION

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Introduction: Acral lentiginous melanoma (ALM) represents 2-8% of melanomas and has reduced overall survival and disease-free survival. ALM shows chromosomic aberrations in CCDN1, TERT and KIT. There are few studies comparing the genetic profile or protein expression between ALM and Acral Nevus (AN).

Objetive: To compare the genetic profile between ALM and AN in Chilean population using protein expression of selected genes using immunohistochemistry.

Material and Methods: A case-control observational study to evaluate immunohistochemical expression of CCND1, TERT, BRAF and KIT in ALM and AN was performed.

Results: There was a significantly higher expression of CCND1 in AN compared with ALM (91% and 69% respectively p = 0.007); and higher expression of TERT in AN compared with ALM (63% and 19% respectively, p= 0.000). Whereas most AN were negative for KIT expression (23% vs 44% respectively, p= 0.044). There were no significant differences in BRAF expression between AN and ALM. When evaluating ALM, there was a significantly higher expression of CCND1 in in situ ALM (isALM) compared to invasive ALM (91% and 57% respectively; p=0.005). For invasive ALM, BRAF positivity was significantly correlated with higher Breslow thickness (2.7 vs. 1.2 mm; p= 0.03); and invasive ALM with BRAF expression showed significantly higher lymphovascular invasion.

Discussion: In our cohort ALM and AN had different protein expression. ALM showed significantly higher CKIT expression, but negative CCND1 and TERT expression. CCND1 positivity was significantly higher for isALM compared with invasive ALM. BRAF positivity was associated with worse prognostic markers.