Using a clinicopathologic and gene expression model to predict sentinel lymph node metastasis in primary cutaneous melanoma could reduce the rate of sentinel lymph node biopsies with >70% in thin melanoma: a multicentre Danish cohort study

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Background: Sentinel lymph node biopsy (SLNB) is used to staging and guide subsequent management of melanoma. However, proper patient selection for SLNB is challenging; approx. 80% of all SLNB are negative, with even higher negative rates when looking only at thin melanoma (T1) which account for the vast majority of cases. The clinicopathological and gene expression profile model (CP-GEP) was developed to identify low risk melanoma patients who may safely forgo SLNB. The CP-GEP combines Breslow thickness and patient age with the expression of eight genes to classify patients as high or low-risk for nodal metastasis. This study presents data from an independent validation of the CP-GEP in a multicentre Danish cohort.

Material and Method: Archived formalin-fixed paraffin-embedded primary cutaneous melanoma tissue from 537 T1-T3 melanoma patients was collected and analysed with CP-GEP. The patients had undergone SLNB between 2010 and 2015 at either of two university clinics in Denmark. The CP-GEP result was compared with the SLNB result, calculating the diagnostic value of CP-GEP for SLNB metastasis.

Results: Median age at diagnosis was 58 years (IQR 44-70) and median Breslow thickness was 1.3 mm (IQR 0.95-1.82). The distribution of T1, T2 and T3 melanoma was 32.8%, 46.9% and 20.3%, respectively. The SLNB positivity rate was 18.1%. The CP-GEP model identified 219 (40.8%) patients as having a low risk for nodal metastasis with a negative predictive value (NPV) of 91.3%. When analysing the T1 subgroup (n=176) the CP-GEP low risk rate was 72.7% with a NPV of 94.5%.
Conclusion: The CP-GEP identifies most patients at low risk for SN metastasis, especially in patients with T1 melanoma. Results are in line with previous retrospective validation studies on European and US cohorts. This study, however, contains the largest T1 subgroup validation with a potentially very high SLNB reduction rate.