Background

Mucosal melanoma is a rare malignancy, notoriously resistant to conventional chemotherapy, with few treatment options. Because of their origin, they do not receive screening and, hence, are detected in advanced stages where prognosis and curative rates are poor. The purpose of this study is to identify novel, potential targets and therapeutic options for this disease, utilizing a multiplex approach.

Methods

In total, 93 mucosal melanoma specimens were tested via a multiplex profiling service (Caris Life Sciences, Phoenix, AZ) consisting of gene sequencing (Sanger or next generation sequencing [NGS]), protein expression (immunohistochemistry [IHC] and/or gene amplification [CISH or FISH]). Conjunctival melanoma was excluded.

Results

Conclusions

• Multiplex tumor profiling can identify multiple potentially actionable targets for therapy in mucosal melanomas.
• The tumor heterogeneity of mucosal melanomas imports a potential benefit of using multiplex tumor profiling.
• NRAS mutation rates where highest in sinonasal melanomas and 477 mutations were highest in vulvovaginal and anorectal mucosal melanomas. In a sub-analysis of the head and neck melanoma specimens, most mutations were found in vulvovaginal melanomas (21.2%).
• Future studies involving BRAF, KIT, and NRAS should verify the variable mutation rates based on the anatomic location of the primary tumor. Such information could potentially be used for diagnostic and therapeutic purposes.
• The high rate of PD-1 and PD-L1 co-expression in advanced mucosal melanoma warrants further exploration in clinical trials testing novel immunotherapeutics (e.g. pembrolizumab, nivolumab, MPDL3280A).

References
