A Non-Invasive Gene Expression Assay for Cutaneous Basal Cell and Squamous Cell Carcinoma

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Introduction

We recently validated a non-invasive dermatology gene expression platform using adhesive patches to collect epidermal skin samples. LINC (Long Intergenic Non-Coding RNA 518) and/or PRAME (Preferentially Expressed Antigen in Melanoma) gene expression signatures differentiated primary melanomas from atypical nevi and other pigmented lesions with a Negative Predictive Value of over 99%, a sensitivity of 91% and a specificity of 69% to help clinicians with the management of difficult to assess pigmented lesions. Board certified dermatologists who use this non-invasive test, surgically biopsied about half as often while missing fewer melanomas. [1-3]

Patient and clinician demand for a similar test to non-invasively differentiate non-melanoma skin cancers (generally excised) from benign or precursor lesions (generally treated via non-surgical modalities such as cryotherapy or chemical and immunological destruction) has been growing.

Materials and Methods

We embarked on developing such a qRT-PCR gene expression test based on targets identified through microarray screening of human transcriptomes from adhesive patch skin biopsy samples and literature searches. The identified target candidates were evaluated in prospectively collected basal (BCC) and squamous cell carcinoma (SCC) as well as actinic keratosis (AK) and other control samples also obtained via non-invasive adhesive patches. Cycle threshold (Ct) values from qRT-PCR analyses were used to demonstrate changes in target gene expression. Algorithms were developed, trained and subjected to primary validation in histopathologically confirmed samples (n=160 cases).

Results

With a robust qRT-PCR strategy and a novel 13-target gene panel, we successfully differentiated BCC and SCC cases from AK and other non-cancerous skin lesions of similar appearance with a sensitivity of 91% (95% CI 86% - 95%) and a specificity of 87% (95% CI 80% - 92%) based on 160 non-invasively collected adhesive patch skin samples ($p<0.001$) when employing the best performing Random Forest (rf) model.

Figure 1 depicts the comparison of various algorithmic models evaluated.

Figure 2 shows AUC data for the rf analysis model where an AUC value of 0.95 was observed.

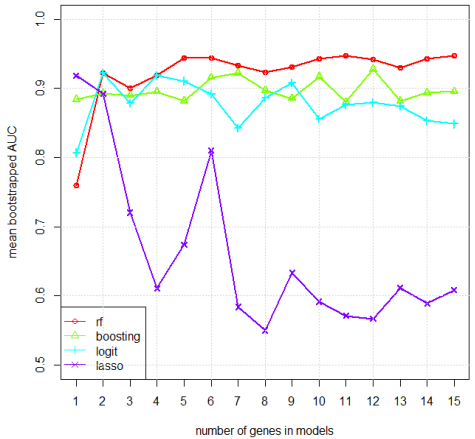

Figure 1. Comparison of algorithmic models. Ct values of a 13-target gene panel from 160 BCC, SCC and AK and other control cases were analyzed with different statistical models.

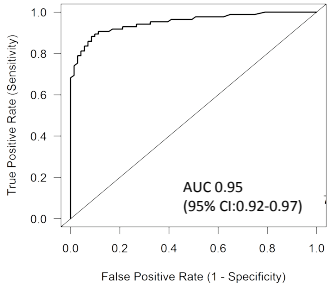

Figure 2. Assay AUC from the Random Forest (rf) analysis model.

Conclusion

Non-invasive gene expression testing differentiates primary cutaneous BCC and SCC cases from benign and precursor lesions such as AK with high sensitivity and specificity. Such a test, once fully validated in an ongoing large prospective study, has the potential to reduce the number of avoidable surgical procedures while missing fewer cases of non-melanoma skin cancer.

References

1. Gerami et al. Development and validation of a non-invasive 2-gene molecular assay for cutaneous melanoma. Journal of the American Academy of Dermatology 2017; 76(1)114-120.e2.
2. Ferris et al. Utility of a non-invasive 2-gene molecular assay for cutaneous melanoma and effect on the decision to biopsy. JAMA Dermatology 2017; 153(7):675-680.
3. Yao et al. An adhesive patch-based skin biopsy device for molecular diagnostics and skin microbiome studies. Journal of Drugs in Dermatology 2017; 16(10):611-618.

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