DermTech Smart Stickers can non-invasively detect RNAs that are associated with non-melanoma skin cancer

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INTRODUCTION

Background

- Non-melanoma skin cancers (NMSC) are the most common types of skin cancer and include both basal cell carcinoma (BCC) and squamous cell carcinoma (SCC)¹.
- NMSCs primarily form on sun exposed skin areas and are expected to cause approximately 15,000 deaths in a year².
- Current diagnosis of NMSC relies on medical history and visual assessment of suspicious lesions.
 In some instances, it is difficult to distinguish and differentiate NMSC from actinic keratoses and other malignant and benign skin tumors from non-skin cancers, so skin biopsies are collected for further histopathologic review. This is problematic in cosmetically sensitive areas.
 We investigated whether non-invasive collection of skin tissue and subsequent genomic analysis could properly classify NMSC.

METHODS

- Subjects \geq 18 years of age with visually suspected NMSC were enrolled in this study from >20 Clinical sites. All subjects provided written informed consent prior to enrollment.
- Skin samples were collected non-invasively from enrolled subjects using the DermTech Smart Sticker[™]. Skin biopsies were also collected from all subjects for histopathological confirmation.
- The breakdown of histopathologically confirmed subjects for the Training Set and Test





Set is provided in the table below:

Sample Set	Basal Cell Carcinoma	Squamous Cell Carcinoma	Other*/AK
Training Set	94	87	173
Test Set	108	89	169
*Subjects were classified as "other" if histopathology confirmed their diagnosis as a non-cancerous skin disease including but not limited to seborrheic keratosis, actinic keratosis, verruca vulgaris, and plaque psoriasis			

- RNA was extracted from the Smart Stickers using the DermTech's custom bead-based extraction method on the KingFisher Flex instrument (Thermo Fisher Scientific).
- Whole transcriptomic data was collected for the Training Sample Set using RNA sequencing.
- Targeted RNA AmpliSeq data was collected for the Test Sample Set.
- Random Forest machine-learning was used to analyze sequencing data

NOVEL GENE IDENTIFICATION FOR NMSC

HETEROGENEITY OF NMSC

- Principal Component Analysis (PCA) was conducted with RNA-sequencing data to evaluate the natural distribution of genes expression among all sample types
- PCA did not reveal any distinct patterns or signatures for NMSC compared to Non-Cancer Skin Disease (NCSD)
- Applying a Random Forest algorithm to the RNA-sequencing data led to the identification of 161 candidate genes with the potential to differentiate between NMSC and NCSD

•AmpliSeq Panel generated with initial 161 genes as well as 145 genes identified from literature and disease pathogenesis

•Targeted RNA AmpliSeq data was collected using the AmpliSeq Panel of 306 genes on the Test Sample Set.

•Random Forest machine-learning was used to analyze the targeted RNA AmpliSeq data

•30 genes were significantly (fold change >2; multiple-testing adjusted P<0.05) increased in NMSC compared to NCSD

•16 genes were lower in NMSC (fold change >2; multiple-testing adjusted P<0.05)



BCC+SCC vs Ak+Othe









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- ~40% of subjects enrolled in this study had discordant pathology results from the clinical assessment and diagnosis of BCC or SCC, suggesting the importance of additional objective assessments in ruling out non-melanoma skin cancers prior to a surgical biopsy.
- Non-invasively collected skin samples (Smart Sticker[™]) enabled the identification of RNAs that are differentially expressed between NMSC and NCSD.
- This non-invasive platform technology creates the opportunity for a multi-gene machinelearning algorithm to rule out NMSC without the need for surgical biopsy.
- Additional studies will provide further characterization of BCC and/or SCC lesions to aid in the diagnosis of NMSC.