Analysing Labskin using different 'Omic' technologies

LabSkin
SKIN SCIENCE

Objective:

To highlight the diversity in the different 'Omic' approaches including genomic, proteomic, lipidomic and metabolomic analysis, which can be applied to Labskin.

Each approach provides a comprehensive and potentially global assessment of multiple molecules simultaneously in a high throughput manner.

Method:

Genomic Analysis: Microarray analysis was used to assess genomic changes in Labskin inoculated with *S. epidermidis* and *S. aureus* (Figure 1).

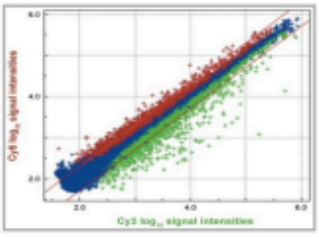
Proteomic and metabolomic analysis: Mass Spectrometry (MS) and MS imaging (MSI) analysis was used to characterise and quantify xenobiotic metabolising enzymes in Labskin (Figure 2).

Lipidomic analysis: MSI analysis with Labskin was performed to identify biomarkers associated with the wound healing process (Figure 3).

Results:

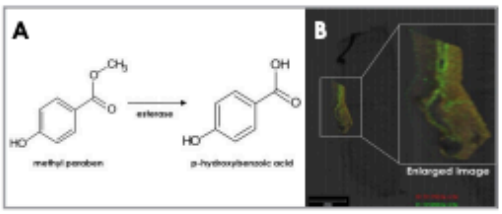
Genomic analysis

Figure 1 - Labskin gene expression response to *S. epidermidis* & *S. aureus* using a whole human genome oligo microarray (red = up regulation, blue = unchanged and green = drown regulation in gene expression).



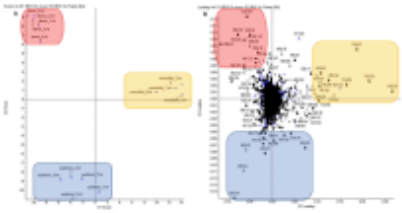
Proteomic and metabolomic analysis

Figure 2 - (A) Diagram showing metabolism reaction of SB-MSI probe methyl paraben with esterase to form p-hydroxybenzoic acid. (B) MSI image of Labskin treated with methyl paraben highlighting esterase activity (red = methyl paraben and green = p-hydroxybenzoic acid).



Lipidomic analysis

Figure 3 - Principal component analysis-discriminant analysis of a (A) scores plot and (B) loadings plot from MSI data representing all three regions of interest (red (dermis), yellow (wound site), blue (epidermis)) in wounded Labskin.



Summary:

Labskin combined with different 'Omic' technologies generates a vast amount of information in a high throughput manner. These techniques allow each stage of the central dogma of molecular biology to be assessed to obtain a greater understanding of changes to the skin environment.

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