Microsphere Affinity Proteomics in Dermatology

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Daniel de la Rosa Carrillo, dermatologist at the Oslo University Hospital, recently defended his doctoral thesis "Microsphere affinity proteomics – a new tool for skin proteome research" at the University of Oslo with Fridtjof Lund-Johansen as his main supervisor. Opponents were Professors Mike Taussig, Cambridge, UK, and Jochen Schwenk, Solna, Sweden.

Skin proteomics has the potential to unravel mechanisms involved in skin disease, and thereby facilitate the discovery of proteins that can be targeted by new therapies. Studies on the skin proteome are, however, scarce, as proteomics is still an expensive and complex technology. Antibody-based assays have higher throughput than mass spectrometry and are simpler to use, but current techniques are to a large extent limited to detecting one or a few proteins at a time. Array-based platforms may greatly enhance throughput, but the use of this technology has been hampered by concerns about specificity.

The main objective of the thesis was to develop better methods for large-scale analysis of human keratinocyte proteins. Specifically, we aimed at developing a low-cost array platform that can be used with commercially available antibodies and that provides high multiplexing capacity and high throughput. We also intended to implement protein separation in antibody array analysis to obtain an internal reference of specificity. The next objective was to provide an overview of the current methods for subcellular fractionation, prior to application of antibody array analysis to study proteins and protein complexes in human primary keratinocytes. The final objectives were to apply antibody array analysis to study the subcellular localization of proteins and protein complexes, and determine the feasibility of the platform for large-scale protein analysis in standard punch biopsies from human skin.

The most important novel aspect of our studies is the concept of combining antibody array analysis with protein separation. With this approach, proteins capable of binding to the same antibody are detected independently. The fractionation methods that were used have the additional advantage of providing information about the subcellular localization and context of proteins. This provides a unique platform for proteomic studies of skin diseases, where protein components of pathophysiologic pathways can be studied simultaneously. Our studies have established the basis for large-scale antibody-based protein analysis of the skin, opening a wide range of possibilities for future research on the skin proteome in health and disease.

From left to right: Jon Anders Halvorsen (acting dean), Mike Taussig (1st opponent), Inger Nina Farstad (member of the evaluating committee), Jochen Schwenk (2nd opponent), Daniel de la Rosa Carrillo and Fridtjof Lund-Johansen (main supervisor).