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Introduction

"Hot technologies" for clinical immunology research

Techniques developed by basic and clinical immunologists have catalyzed advances in biomedical research, not just in the field of immunology, but also in every other discipline of biology. For example, monoclonal antibodies are widely used in every field or research, and have risen to the fore as highly successful targeted therapeutics for autoimmunity, transplantation biology, and cardiovascular medicine. Another technology, fluorescence-activated cell sorting (FACS), has enabled the discovery and characterization of pluripotent stem cells, cancer cells, regulatory lymphocytes, and more recently the identification of signaling pathways within cells [1]. FACS is now a mainstay of clinical laboratory diagnosis in the fields of oncology and clinical immunology, with the results serving to guide therapeutic decision-making in the clinic. Interested readers are referred to a recent *Clinical Immunology* Special Issue, *Analysis of Immune Function Using Flow Cytometry*, (Clin. Immunol. 110, 197–284), devoted entirely to FACS technologies.

At the 2002 Federation of Clinical Immunology Societies (FOCIS) meeting in San Francisco, a Satellite Symposium was organized to showcase "Hot Technologies" that were emerging as exciting and useful tools for researchers. While a subset of the technologies was developed by immunologists specifically for clinical immunology applications, others were spawned from fields such as genomics, cancer biology, and mechanical engineering. I have commissioned the speakers from this meeting to update their presentations from the FOCIS meeting and to provide clear examples of how these cutting-edge techniques can be applied to answer clinical immunology questions that have previously been "unapproachable." Several other exciting technologies that were not presented at the meeting will also be briefly described [1–6].

The reports in this Special Issue of *Clinical Immunology* are organized from the "outside of the cell to the inside of the cell"—in other words to first discuss techniques such as FACS (Thiel et al.) that were initially developed and employed for the analysis of cell surface markers and to follow the signals generated by ligation of cell surface receptors (Chan-Hui et al.) as they culminate in changes in signaling pathways (Chan-Hui et al.), the transcriptome (van der Pouw Kraan et al.), and ultimately the proteome (multiple papers in this issue). Novel technologies for imaging of whole organisms and analyzing cell trafficking are also described (Hildebrandt and Gambhir). A schematic of where in these pathways each technology can be utilized for experimentation is shown in Fig. 1. Several other prominent technologies that are also applicable to clinical immunology research, but which are not discussed in this Special Issue, are illustrated for completeness. Readers interested in a more comprehensive overview of emerging proteomics technologies are referred to Ref. [7].

One of the take-home messages from this Special Issue of *Clinical Immunology* is that multiplexed technologies designed to simultaneously interrogate thousands of biomolecules already exist and will be further developed in the future. Multiplexed assays will provide insights into disease pathogenesis, will define precise mechanisms by which poorly characterized therapeutics work (or fail), and will be used to design tailored, patient-specific therapeutics. We are entering one of the most exciting periods in the history of clinical immunology research. All of the technologies described herein will contribute to this excitement and may usher in an entirely new era of discovery.

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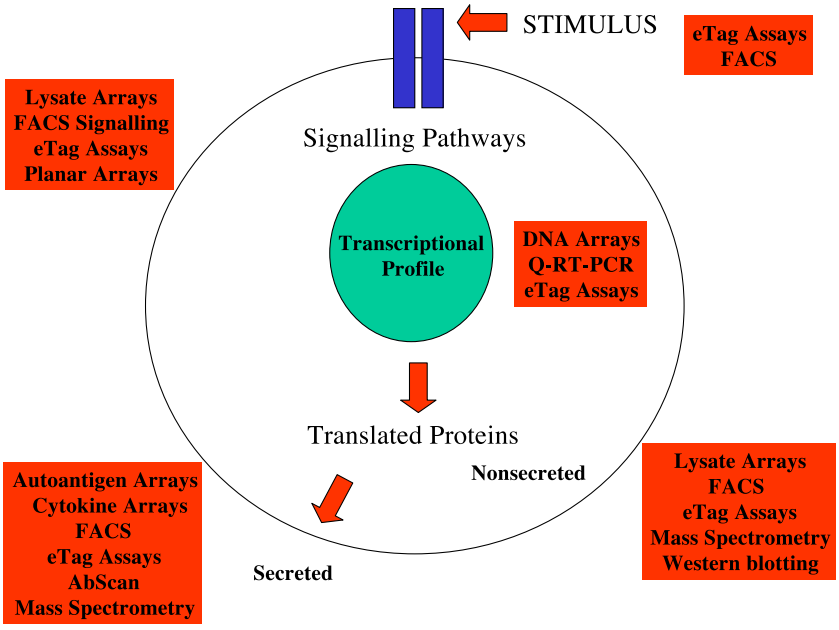

Fig. 1. "Hot Technologies" for the analysis of immune cells and their products. Depicted is a hypothetical cell of the immune system and the assays that can be employed to dissect events that (i) are initiated at the cell surface (stimulus, e.g., engagement of a cell surface receptor); (ii) generate intracellular signals mediated by kinases and other signaling molecules; (iii) alter the genetic program of the cell; and (iv) ultimately alter the cellular proteome, including the intracellular proteome (nonsecreted proteins) and the extracellular proteome (secreted proteins). This figure is by no means complete but focuses on emerging technologies described in this Special Issue and in a recent review by the author [7]. Many other competing technologies have been described that can also be used for similar studies. FACS, fluorescent-activated cell sorting; Q-RT-PCR, quantitative reverse transcription polymerase chain reaction; AbScan, antibody-mediated systematic characterization of antigens. Not shown are methods designed to study how cells interact with one another in an intact organism, for example, the work described in Hildebrandt and Gambhir in this issue.

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