

## Commentary on Biology and Biomarkers

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### COMMENTARY

Medical practitioners have invariably relied on surrogate markers of inaccessible biological processes to form their designation, whether or not it absolutely was the achromatic of shock, the flush of inflammation, or the jaundice of liver failure. Obviously, the present implementation of biomarkers for malady is much additional refined, relying on extremely reproducible, quantitative measurements of molecules that are usually mechanistically related to the malady in question, as in glycated Hb for the designation of polygenic disease or the presence of cardiac troponins within the blood for confirmation of myocardial infarcts. In cancer, wherever the initial symptoms are usually delicate and also the consequences of delayed diagnosis usually forceful for malady management, the impetus to find without delay accessible, reliable, and accurate biomarkers for early detection is compelling. Nevertheless despite years of intense activity, the stable of clinically valid, efficient biomarkers for early detection of cancer is pitifully tiny and still dominated by a few markers (CA-125, CEA, and PSA) 1st discovered decades ago. It is time, one might argue, for a recent approach to the invention and validation of malady biomarkers, one that takes full advantage of the revolution in genomic technologies and within the development of computational tools for the analysis of enormous complicated datasets.

This issue of Markers is devoted to at least one such new approach loosely termed the 'Systems Biology of Biomarkers'. What sets the Systems Biology approach excluding alternative, additional ancient approaches, is each the categories of information used, and also the tools used for knowledge analysis – and each mirror the revolution in high outturn analytical ways and high outturn computing that has characterised the beginning of the twenty 1st century. The primary article during this series, 'Systems Biology and also the Discovery of Diagnostic Biomarkers, provides associate degree silver-tongued description of the thought of 'systems biomedicine', and the way this new approach is wont to support a prognosticative and customized approach to practice that will revolutionize health care.

The ability of this approach is incontestable in associate degree analysis of particle malady's exploitation mouse models and

dynamic measurements of organic phenomenon changes over the course of the disease. Vital changes in factor expression, mapping to biologically relevant pathways, are detected long before the onset of clinical symptoms, providing support for the thought that diagnosis designation through biomarkers is feasible. In their discussion of 'Systems Biology Approach Eds to malady Marker Discovery', gives an outline of the foremost current methodologies presently in use for biomarker discovery, together with macromolecule microarrays, high through place sequencing technologies for RNA and deoxyribonucleic acid, and mass-spectrometry-based genetic science.

Exploitation high density macromolecule microarrays, the Snyder cluster have had vital success distinctive biomarkers for SARS coronavirus infection and gonad cancer by production macromolecule microarrays that target the host immune response to infection or on co-proteins. 'Reverse part macromolecule Microarrays: Applications in biomarker discovery/validation, malady understanding, and high outturn clinical screening describes a unique technology that virtually stands macromolecule arrays on their head, by printing high density microarrays of the target (tumor biopsies, cell lysates, etc) and inquiring these arrays during a multiplex fashion for phosphor-proteins indicative of activated signal transduction pathways. As delineate by the authors, the ensuing profiles give specific data regarding the disruption of important sign networks in malady, so facilitating the identification and characterization of promising targets for molecular medicine.

The process of distinctive biomarkers for cancer and alternative diseases is likened to the method of threat detection within the national Defense arena. There are several parallels – the requirement to spot susceptibilities, the requirement to reply adaptively because the threat changes over time, the matter of distinctive signal from noise in highly complicated datasets. The defence community has responded by adopting 'composite signatures of threat that use multidimensional datasets during which every dimension could be a completely different mensuration or technique. Maybe it's time for medical specialty scientists to adopt constant strategy – and Systems Biology provides the suitable tools for building, testing, and collateral a composite signature of malady.

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Received: October 11, 2021; Accepted: October 22, 2021; Published: October 29, 2021

Citation: Phelia J (2021) Commentary on Biology and Biomarkers. Bio Med 13: 453.

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