

Report 44: Biomarker Development Using Omic & Systems Biology Approaches for Use in Disease & Injury

Convener: Rick Paules

Brief History: There was a consensus for a need for better biomarkers and a better approach for the development of biomarkers for use in human studies. In particular there was a general agreement for the need of a systems approach with an integration of platforms in biomarker development. In the past there has been a lack of integration of platforms, lack of quantitation, lack of comparisons across species for utility of biomarkers, as well as a lack of informatics resources supporting the development of biomarkers. As a result, biomarkers have not lived up to their initial promise. In addition, biomarkers need to go beyond association derived from population studies to testing in individuals.

Discussion Highlights: There was uniform passion about the power of exploiting a systems biology approach to biomarker development. We need to understand mechanisms of injury or disease for prevention, early detection, treatment and health promotion. Biomarkers need to provide insight into mechanisms. There needs to be an integrative approach using model systems (e.g. mouse), individuals, populations, communities, integrated using systems biology. We need mouse/cell based models to tease out complex effects, to validate effects in humans. Cross species comparisons can reveal important differences in pathways and systems that will inform better biomarker development.

Recommendations:

- Need working group to define approach for platform integration in biomarker development.
- Need new clinic models for identifying risk and rapidly testing potential biomarkers (too many potential biomarkers to test in very large epi cohorts).
- Need mechanistic based biomarkers, not just associations.
- There is a need for bioinformatics support of biomarker development.
- There is need for cross platform validation, quantification, standardization, and integration. Also, there must be transparency within the research community and general public of data collection and results in all stages of biomarker development and data must be place in the public domain.
- There needs to be an integrative approach using model systems (e.g. mouse), individuals, populations, communities, integrated using systems biology.
- Need precise, quantitative exposure information instead of retrospective recall studies.
- There is a need for Private/NIEHS partnerships to leverage resources and advance development.

Discussion Participants: Rick Paules, Victoria Seewaldt, Bill Suk, John Groopman, Mike Holsapple, Chris Kemp, Richard Miller, Frank Mirer, Jonathan Pollock, Robert Rickard, Jim Swenberg, Jack Taylor, Rick Woychik (partial) and Linda Birnbaum (partial)s