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GUEST EDITORIAL

Placing enabling technologies at the forefront of translational research

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A recent paradigm shift in translational research has placed the role of cutting-edge technologies that enable innovative solutions at the forefront of efforts to improve patient care. The tremendous power of the methods available in basic labs — whole-genome and targeted sequencing, high-resolution microscopy, mass spectroscopy, cell-based assays — are only just beginning to have impact on clinical experimentation, in large part because the venues for collaborative, interdisciplinary, cross-institutional interactions that sustain intellectual exploration of translational challenges are scarce. Many of these methodological advances have been attributed to the Human Genome Project. Standardization of these technologies has begun, so that they can reliably be applied in clinical practice and regulatory decision-making[2,3]. The advances of "omics" technologies have created a framework for our understanding of diseases and in developing integrative computational resources that can decipher the enormous amounts of data derived from these technologies. "Omics" technologies fall into several categories that include genomics, transcriptomics, proteomics and metabolomics. These technologies have the potential to revolutionize current approaches to diagnosis and prediction of diseases and the development of novel therapeutics. Obviously, the backbone of these advances depend on the interaction of cross-disciplinary and cross-institutional translational researchers "from the bench to the bedside/clinic" and vice versa.

Current and esoteric "omics" technologies can provide a "system's biology" approach by which translational researchers can achieve a better understanding of normal cellular function and dysfunction by simultaneously monitoring thousands of molecular components. The data generated can be used to enhance our ability to understand mechanisms underlying biological processes in a variety of diseases and in doing so; it can elucidate potential therapeutic interventions. The strategies circling around "omic" technologies can provide meaningful insight leading to the identification of biomarkers and/or panels that can be used in diagnosis, patient stratification and disease monitoring. In a recent publication by Jinnin, et al.[1], they have discovered a mechanism for the rapid growth seen in infantile hemangiomas, the most common childhood tumor, through the use of an enabling technology, the PamGene "kinase chip". The "kinase chip" contains 144 peptides derived from full length kinases of 10-15 pathways, has helped confirm the hypothesis of VEGFR2 signaling in infantile hemangiomas. The data suggest that any therapy that is directed against vascular endothelial growth factor— anti-VEGF therapy—is the rational therapy to use in these tumors.

Adapting these powerful technologies to provide actionable clinical data will require systematic effort from a team of professionals who understand real-world constraints on the availability and quality of clinical samples, turnaround time for clinical experiments, and the ways in which inter-patient variability may impact experimental robustness. Basic scientists currently can offer little help to solve these problems, since there is no systematic mechanism for communicating the problems inherent in clinical work to basic researchers; even the subset of basic researchers who are already interested in the problem of applying their work clinically do not have access to appropriate clinical samples. Given the technological resources available today, it is an ideal opportunity to combine the effort of "omics" technologies, technologists, clinical investigators, applied and basic research scientists and the market place (patient derived specimens with annotated clinical outcome information) to solve pressing unmet dental/medical needs and ultimately to change the standard of practice in treating these patients.

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2- Kuo WP, Liu F, Trimarchi J, Punzo C, Lombardi M, Sarang J, et al. A sequence-oriented comparison of gene expression measurements across different hybridization-based technologies.Nat Biotechnol. 2006;24(7):832-40.

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