PERSPECTIVES IN GENOMICS

Cytopostgenomics: What is it and how does it work?

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In 2018, a special hot-topic issue of *Current Genomics* covering numerous important aspects of molecular cytogenetics and cytogenomics in the postgenomic era was published (*Current Genomics*, Volume 12, Issue/Number 3, Pages: 157-246) [1]. As a result, the theoretical basis for a new emerging field of cytogenomic research tentatively termed as "cyto(post)genomics" was provided. Tragically, the passing away of my co-editor and closest colleague, Professor Yuri B. Yurov [2], hindered immediate attempts to delineate the area of "cytopostgenomics". Accordingly, I take the opportunity to contribute a *Perspectives in Genomics* article to re-introduce cytopostgenomics in remembrance of Professor Yuri B. Yurov, the brilliant researcher of chromosomes and cellular genomes.

More than a decade ago, cytogenomics (molecular cytogenomics) was introduced to define a body of research in human genomics (genetics) focused on genomic variations and architecture at microscopic/submicroscopic level and at molecular resolutions [3]. Later, it expanded to include a wide spectrum of applications of whole-genome Copy Number Variation (CNV) analysis (cytogenomic analysis or analysis of cytogenomic variations) in diagnostic research [4, 5].

Currently, cytogenomics (in its widest sense) seems to encompass almost all areas of chromosome biology addressed in the genomic context [1, 3-5]. Using postgenomic approaches to chromosomal variations and instability, a number of discoveries in chromosome biology and re-evaluations of current concepts in genomics have been made [6]. In addition to analysis of submicroscopic genomic variations for the association with specific phenotypes [3-5], cytogenomics has shed light on genome behavior (*i.e.* genome instability) throughout ontogeny [7] including more specific genomic changes (accumulation of somatic genomic variations) associated with normal and abnormal aging [8, 9]. Moreover, genome-environment interactions highlighting normal and pathogenic responses of cellular genomes to environmental stimuli, which partially underlie somatic mutagenesis, have been highlighted [10]. The variable effects of the genomic variations have resulted in the interpretational problem of cytogenomic data [3-6, 11]. Fortunately, postgenomic research has provided numerous bioinformatic opportunities to solve the problem by proposing a variety of algorithms for processing molecular cytogenetic and (cyto)genomic data [11, 12]. As a result, actual cytogenomic research cannot be appropriately performed without corresponding postgenomic analysis (*i.e.* systems biology approaches and pathway-based classification) [12]. Furthermore, genome analysis for specific medical tasks (*e.g.* pediatric research) has already benefited from the application of postgenomic approaches to processing genomic data [13]. More precisely, pathway-based views on human diseases have heavily influenced our understanding of the disease etiology [14]. Finally, postgenomic approaches to processing cytogenomic data are able to deliver effective therapeutic interventions in individual cases of chromosomal imbalances, which are generally considered to be incurable conditions [15]. In total, one can conclude that, with the development of postgenomic technologies for assessing molecular and cellular effects of the genomic variations, cytogenomics has evolved in a kind of a new emerging field of bioscience. To define the result of this evolution, the term "cytopostgenomics" may be introduced to cover a new emerging field focused on causes and consequences of genome variations (specific architecture) at chromosomal level unveiled by postgenomic analyses.

Big medical data sets require us to reach an unprecedentedly high level of basic and diagnostic research for the interpretation in therapeutic purposes [16]. Cytopostgenomic studies, which include not only the detection of genomic variations, but also the definition of their functional consequences and impacts on the phenotype may solve the problem of interpreting big genomic data in chromosomal diseases/imbalances. Once solved, our understanding of chromosome/genome variations will be significantly advanced in order to deliver successful therapeutic interventions in previously incurable chromosomal and genomic diseases. The cyto(post)genomic research in the author's labs is partially supported by RFBR and CITMA according to the research project No. 18-515-34005.

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