EDITORIAL

Systems Genomics in the Age of Next Generation Sequencing (Part I)

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With the advent of next-generation sequencing (NGS) technologies, there arose a need to identify candidate mutations for causality. A challenge often faced in identifying and inferring the causal SNPs from sequence data is that different methods need to be preferentially used to predict the effect of mutations for determining *bona fidelity*. This thematic issue received very encouraging submissions in the areas of various facets of genomics, but not limited to exploring non-coding RNAs and genome-wide studies. While the articles focused on a wide array of highly sensitive, if not less stringent methods that the NGS has delivered in the recent past using genomic integration systems, a summary of them is provided herewith.

Sakshi Singh *et al*., [1] in their article titled "Identification of Differentially Expressed Hematopoiesis-associated Genes in Term Low Birth Weight Newborns by Systems Genomics Approach," exploited the role of high-risk infection, morbidity, and mortality in low birth weight-normal birth weight infants. In their analyses, they identified differentially expressed genes (DEGs) associated with hematopoiesis, which are further validated by good statistical significance. A distinct set of genes was upregulated which led them demonstrate their role in cell proliferation and differentiation, thereby concluding that the DEGs are associated with inherent pathways besides their role in building the weak immune defense against life-threatening infections.

Aier and Varadwaj [2], in their work titled "Understanding the Mechanism of Cell Death in Gemcitabine Resistant Pancreatic Ductal Adenocarcinoma: A Systems Biology Approach" predicted the driving factors behind pancreatic ductal adenocarcinoma to understand the disease paradigm and its contribution to cell growth and proliferation. They found prominent dysregulated elements and pathways regulating the effect on gemcitabine-induced hypoxia.

Monga and Banerjee [3], in their work titled "Computational Identification of piRNAs Using Features Based on RNA Sequence, Structure, Thermodynamic and Physicochemical Properties", identified novel PIWI-interacting RNAs (piRNAs), a class of small non-coding RNAs (ncRNAs) with roles in gene expression regulation, transposon silencing and viral infection inhibition. The predictions were made by employing hybrid features and stochastics of various sequence-structure based features with good machine learning heuristics and training efficiency. They believed that their discovery of piRNAs could help understand novel functions associated with this class of non-coding RNAs.

Aparna Banerjee *et al*. [4], in their pangenomic study titled "Molecular and Genomic Characterization of PFAB2: A Non-virulent *Bacillus anthracis* Strain Isolated from an Indian Hot Spring", aimed to characterize thermophilic and environmental isolates of *B. anthracis* strain PFAB2. The phenotype they obtained could serve as an interesting model strain for deciphering the pathogenesis.

One most common thing in the aforementioned papers is to perform characterization through robust methods and statistical inference, which is the need of the hour.

REFERENCES

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