Fungal Genomics & Biology
ISSN: 2165-8056

Subramaniam, Fungal Genom Biol 2012, 2:2
DOI: 10.4172/2165-8056.1000e108

Editorial Open Access

Next Generation Sequence Technology and Fungal (R)evolution

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It is a pleasure to be invited to be part of the editorial board of Fungal Genomics & Biology. I accept this position during a time, when we are witnessing a major explosion in the applications of next generation sequencing (NGS) technology. To date, draft sequences of more than 50 fungal genomes have been released. Comparative genomics has already provided us with insights into the dynamics of fungal evolution, thus refining our concept of "core" vs "flexible" genomes. The "core" genome is defined by genes that are commonly found in every species and are under strong negative selection. Comparative analysis of bacterial genomes suggests that these evolutionary conserved proteins, termed microbe associated molecular patterns or MAMPs, trigger the innate immunity response, providing a first barrier of defence in the infected hosts. Since MAMP-triggered immunity has the potential of offering durable immunity, the identification and characterization of MAMPs in pathogenic fungi will be an area of intense research in the coming years.

In contrast to the "core" genome, the "flexible" genome will be under strong positive selection to diversify, in order to avoid host recognition. A comparative analysis of bacterial and oomycete genomes have revealed that genes encoded in this segment of the genome undergo more recombination events than the rest of the genome. Analyses indicated that the flexible genome encodes many of the effectors or virulence proteins. The presence of effectors in this high recombination region provides pathogen, the capacity to increase their diversity in an ongoing evolutionary tug of war between pathogen and host. In a recent comparative genomics study of *Fusarium oxysporum*, a segment of chromosome with high recombination events was identified in a pathogenic strain of *Fusarium oxysporum*. When this segment was transferred to a non-pathogenic strain, the strain became pathogenic, suggesting that virulence factors reside in this region. Similar studies in other pathogenic fungi offer unprecedented opportunities to identify virulence factors. Furthermore, periodical monitoring of changes in this high recombination region will give us insight into pathogen diversity and adaptation.

Lastly, NGS technology also allows us to monitor changes that are non-mutational. Increasingly, many phenotypic changes have been attributed to epigenetics. Methylation patterns leading to phenotype differences have been implicated in many organisms. The many cultural practices deployed in agriculture around the world, such as crop rotation and fungicide use, which are in turn influenced by local soil and climatic conditions, can impart enormous selection pressure on fungal population. There is considerable evidence to suggest that adaptation to these pressures can in part be influenced by epigenetics. The whole genome analysis, facilitated by NGS technology will greatly accelerate our understanding of epigenetic influences on fungal population evolution.

It is the "dawn of fungal genomics", and I am looking forward to engaging in research that addresses some of the issues outlined herein.

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Received October 26, 2012; **Accepted** October 28, 2012; **Published** November 04, 2012

Citation: Subramaniam G (2012) Next Generation Sequence Technology and Fungal (R) Evolution. Fungal Genom Biol 2:e108. doi:10.4172/2165-8056.1000e108