

Changing the Landscape of Fungal Genomics: New Trends

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Abstract : Understanding of biological processes encoded in fungi is instrumental in addressing future food, feed, and energy demands of the growing human population. Genomics is a powerful and quickly evolving tool to understand these processes. The Fungal Genomics Program of the US Department of Energy Joint Genome Institute (JGI) partners with researchers around the world to explore fungi in several large scale genomics projects, changing the fungal genomics landscape. The key trends of these changes include: (i) rapidly increasing scale of sequencing and analysis, (ii) developing approaches to go beyond culturable fungi and explore fungal 'dark matter,' or unculturable, and (iii) functional genomics and multi-omics data integration. Power of comparative genomics has been recently demonstrated in several JGI projects targeting mycorrhizae, plant pathogens, wood decay fungi, and sugar fermenting yeasts. The largest JGI project '1000 Fungal Genomes' aims at exploring the diversity across the Fungal Tree of Life in order to better understand fungal evolution and to build a catalogue of genes, enzymes, and pathways for biotechnological applications. At this point, at least 65% of over 700 known families have one or more reference genomes sequenced, enabling metagenomics studies of microbial communities and their interactions with plants. For many of the remaining families no representative species are available from culture collections. To sequence genomes of unculturable fungi two approaches have been developed: (a) sequencing DNA from fruiting bodies of 'macro' and (b) single cell genomics using fungal spores. The latter has been tested using zoospores from the early diverging fungi and resulted in several near-complete genomes from underexplored branches of the Fungal Tree, including the first genomes of Zoopagomycotina. Genome sequence serves as a reference for transcriptomics studies, the first step towards functional genomics. In the JGI fungal mini-ENCODE project transcriptomes of the model fungus *Neurospora crassa* grown on a spectrum of carbon sources have been collected to build regulatory gene networks. Epigenomics is another tool to understand gene regulation and recently introduced single molecule sequencing platforms not only provide better genome assemblies but can also detect DNA modifications. For example, 6mC methylome was surveyed across many diverse fungi and the highest among Eukaryota levels of 6mC methylation has been reported. Finally, data production at such scale requires data integration to enable efficient data analysis. Over 700 fungal genomes and other -omes have been integrated in JGI MycoCosm portal and equipped with comparative genomics tools to enable researchers addressing a broad spectrum of biological questions and applications for bioenergy and biotechnology.

Keywords : fungal genomics, single cell genomics, DNA methylation, comparative genomics

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