

Whole genome analysis of fungi

Abstract

Fungi represent a ubiquitous but highly-diverse biology group of life on the earth. They are crucial players for human, ecosystems, and environments in many matters such as chemotherapy, bioremediation, pest control, food supply, biofuel production, carbon sequestration, or climate management. Current analyses of fungal genomes have significantly enhanced our understanding about fungal diversity, genome structure, genetic/proteomic functionality et cetera and improved our utilizations of these amazing organisms. This mini review is aimed to summarize some recent sequencing projects done for fungal whole genomes and briefly elucidate information been explored from these fungal genomic analyses.

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Kingdom fungi

Under the Eukaryota domain, kingdom fungi includes a group of organisms which are either unicellular (e.g., molds or yeasts) or multicellular (e.g., mushrooms). Uniquely, these organisms have chitin-containing cell walls making them different from other kingdoms (i.e., bacteria, plants, or animals). From anthropological point of views, some fungi are valuable but some are harmful with certain impacts for ecosystems as well as environments on the earth. While some fungi are pathogenic for human, many of others may have different functions such as biotrophic, symbiotic, saprotrophic, or entomopathogenic etc; thus, are essential players for human's uses in matters of chemotherapy, bioremediation, pest control, food providing, biofuel production, carbon sequestration, or climate management.

Up to now, overall fungal types have been estimated to be around 1.5-5million species; but currently, only some of them have been well identified and further classified into 7 phyla under the kingdom fungi (including *Ascomycota*, *Basidiomycota*, *Blastocladiomyceta*, *Chytridiomycota*, *Glomeromycota*, *Microsporidia*, and

Neocallimastigomycota). In this taxonomical system, two other previously-defined phyla of Anamorphic and Zygomycota had lately been eliminated but still have been kept using by some mycology researchers. Fundamental research works for evaluating fungal diversity, genome structure, genetic/proteomic functionality et cetera are still essential developing subjects to be explored continually. Recent technique improvements of metagenomic sequencing approach have made it feasible to analyze whole genome of fungi which has truly opened another innovative door to enhancing our understanding and exploitation of fungi.

Whole genomes of fungi

During the past decade, several fungal whole genomes had been completed (Table 1). For instance, some entomopathogenic fungi such as *Beauveria bassiana*,¹ *Cordyceps militaris*,² *Metarhizium anisopliae*³ had been comparatively analyzed for their genomes (~30-40Mbps) and found a complex set of secreted proteins has evolved in entomopathogenicity.³ This finding may help humankind to control some agricultural insect pests or some insect-borne human diseases.

Table 1 Some examples of fungal whole genomes

Phylum	Species	Features	Size (Mbps)	References
Ascomycota	<i>Beauveria bassiana</i>	entomopathogenic	~33.7	Xiao et al. ¹
	<i>Botrytis cinerea</i>	necrotrophic	~39.5	Amselem et al. ⁴
	<i>Cordyceps militaris</i>	entomopathogenic	~32.2	Zheng et al. ²
	<i>Daldinia eschscholzii</i>	lignocellulosic	~35.5	Ng et al. ⁷
	<i>Metarhizium anisopliae</i>	entomopathogenic	~38.5	Staats et al. ³
	<i>Neurospora crassa</i>	Saprotrophic	~38.6	Galagan et al. ⁶
	<i>Sclerotinia sclerotiorum</i>	necrotrophic	~38.3	Amselem et al. ⁴
	<i>Trichoderma reesei</i>	lignocellulosic	~33.9	Martinez et al. ⁸
Basidiomycota	<i>Laccaria bicolor</i>	ectomycorrhizal	~65.0	Martin et al. ⁵
	<i>Phanerochaete chrysosporium</i>	lignocellulosic	~29.9	Martinez et al. ¹¹
	<i>Paxillus rubicundulus</i>	mycorrhizal	~53.0	Kohler et al. ⁹

Besides, genome sequences of two necrotrophic fungi (i.e., *Botrytis cinerea* and *Sclerotinia sclerotiorum*) were determined to examine genomic features that may distinguish them from saprotrophic and

other pathogenic fungi⁴ but, no unique feature in their genomes was found to distinguish *B. cinerea* and *S. sclerotiorum* from other pathogenic and non-pathogenic fungi.⁴

Additionally, some fungi capable of secreting lignocellulosic enzymes (e.g., *Trichoderma reesei*, *Neurospora crassa*, and *Daldinia eschscholzii*) had also been analyzed for their genome sequences.⁵⁻⁷ These analyses explored some unexpected aspects. For example, *T. reesei* genome encodes fewer celluloses and hemicellulases than any other sequenced fungus able to hydrolyze plant cell wall polysaccharides.⁸

N. crassa genome includes some genes potentially associated with red light photobiology, some genes implicated in secondary metabolism and some genes involved unique calcium ion signaling.⁶ Moreover, genomes of mycorrhizal symbiotic fungi such as *Laccaria bicolor* and *Paxillus rubicundulus* also had been reported.^{8,9} In *L. bicolor* genome, some ectomycorrhizae-specific small secreted proteins (SSPs) were found which probably have a decisive role in the establishment of the symbiosis; but, no carbohydrate-active enzymes involved in degradation of plant cell walls were found.⁵ The genomic information allows deeper understanding for symbionts interactions between the mycorrhizal fungi and plants regarding carbon and nitrogen cycles.

1000 fungal genome (1kfg) project

Recently, a 5-year international collaboration project, so called 1000 fungal genome (1KFG) project, has been conducted by the Joint Genome Institute (JGI) of the US Department of Energy in attempt to sequence 1000 fungal genomes from across the kingdom fungi (at least 2 reference genomes from each of more than 500 recognized families of fungi).¹⁰ Up to early 2016, at least 70 fungal whole genomes had been completed; and, further analyses on genome comparison had also been done to better understand genomic structures, genetic components, similarities, differences, etc.³ For instance, genomes of 13 ectomycorrhizae (EMC) fungal species had been comparatively analyzed and came out with a finding of a unique array of plant cell wall-degrading enzymes (PCWDEs) suggesting these EMC fungi possess diverse abilities to decompose lignocelluloses.³ Consequences of the 1KFG project would provide further information about fungal genome, diversity, functionality.¹¹

Future perception

Despite of several bioinformatics challenges regarding sequence assembly, gene annotation, and genome comparison still need to be conquered for better manipulation of metagenomic sequencing results, better understanding fungal genomes has truly opened another inventive door to improving our utilization and reservation for fungi.

Recent outcomes of fungal whole genomes have approved impacts of such analyses on humankind. It is essential to continually explore fungal whole genomes to full-fill some of our knowledge gaps on fungi.

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Conflict of interest

The author declares no conflict of interest.

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