The Potential for Cellulose Deconstruction in Fungal Genomes

Subjects: Virology

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Fungal cellulolytic enzymes are carbohydrate active enzymes (CAzymes) essential for the deconstruction of the plant cell wall. Cellulolytic activity is described in some glycoside hydrolases (GH-cellulases) and in auxiliary activities (AA-cellulases) families. Across environments, these enzymes are mostly produced by some fungi and some bacteria. Cellulolytic fungi secrete these enzymes to deconstruct polysaccharides into simple and easy to metabolize oligo- and mono-saccharides. The fungal ability to degrade cellulose result from their repertoire of CAZymes-encoding genes targeting many substrates (e.g., xylan, arabinose). Over the past decade, the increased number of sequenced fungal genomes allowed the sequence-based identification of many new CAZyme-encoding genes. Together, the predicted cellulolytic enzymes constitute the fungal potential for cellulose deconstruction. As not all fungi have the same genetic makeup, identifying the potential for cellulose deconstruction across different lineages can help identify the various fungal strategies to access and degrade cellulose (conserved vs. variable genomic features) and highlight the evolution of cellulase-encoding genes. Here, the potential for cellulose deconstruction identified across publicly accessible, and published, fungal genomes is discussed.

Keywords: fungi ; cellulose ; cellulase ; glycoside hydrolase ; LPMO ; MycoCosm ; CAZy

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Cellulose, composed of β-1,4-linked β-D-glucose units and constituting ~30% of the carbon in the biosphere, is the single most abundant source of organic carbon on Earth. Its synthesis (mostly by plants) and deconstruction by fungi and bacteria are some of the main drivers of global carbon cycling [1]. However, not all microbes are made equal and only some are equipped with the necessary genes encoding the cellulolytic enzymes required for cellulose deconstruction [2][3][4]. As complete deconstruction of the cellulose produces glucose, cellulolytic organisms and their enzymes have been the primary focus of intensive research and many biotechnological applications (e.g., biofuels production, [5][6][7]). In recent years, high throughput DNA sequencing and the development of bioinformatics algorithms for gene prediction and functional annotation have allowed for the gaining of insight into the diversity of cellulolytic enzymes and microbes [8][9][10][11]. The large number of sequences generated is deposited in general purpose databases (e.g., GenBank [12], Ensembl Genomes [13]) and in dedicated databases. Specifically, the MycoCosm database is a repository for sequenced fungal genomes sequenced at the Joint Genome Institute [11].

Many cellulase genes and proteins have been biochemically characterized [14]. Beside enzymes involved in the catabolism of cellulose, some characterized cellulases support other processes (e.g., plant–fungi interaction [15], cellulose production [2][16]). However, the systematic identification of cellulase genes and proteins in known cellulolytic organisms support their central function in cellulose degradation. Beside biochemically characterized genes and enzymes, the vast majority of known genes encoding cellulolytic enzymes have been identified and characterized using bioinformatic tools only [17]. Hence, the genes encoding potential cellulolytic enzymes in a given genome, in the absence of biochemical characterization, constitute the “functional potential for cellulose deconstruction” [2][18]. Describing the functional potential for cellulose deconstruction across genomes highlight (i) the conserved evolutionary patterns in groups of organisms (i.e., phylogenetic conservatism), (ii) the adaptation to specific ecological niches (e.g., degraders vs. opportunists), and can help identify new enzymes [2][4][8][9].

Across environments, beside supporting the catabolism of cellulose from live and dead plant material, cellulases produced by fungi are required to infest and cause disease in plants and to establish symbiotic relation with plants [3][7][15][19]. Here, the potential for cellulose deconstruction across publicly accessible, and published, fungal genomes from the MycoCosm portal is discussed.

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