A comparative genomic study among various gene families related to the wood degradation biochemistry, using seven Basidiomycete genomes. THE UNIVERSITY OF WARWICK



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Introduction

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Basidiomycete species are a key component in wood degradation and have a great influence in carbon cycling. Two major mechanisms of wood decay have been characterized, termed white rot and brown rot. White rot species effectively degrade lignin, cellulose and hemicellulose while brown rot species degrade mainly the latter two components leaving lignin almost intact (1). The brown rot mechanism has evolved independently in at least six different lineages of Agaricomycotina (2). The genome sequence of the brown rot species Postia placenta revealed that the species has undergone multiple losses in gene families related to wood degradation in comparison to the genome sequence of the white rot species *Phanerochaete* chrysosporium (3). Recently the genome sequence of Serpula lacrymans, which belongs in an independently evolved brown rot lineage in the Boletales, was produced by JGI and along with the increasing sequenced genomes of other white rot species this provides the significant chance to study the evolution of wood degradation mechanism in the level of gene duplications and losses.

Results

767 protein models were included in the reconciliation analysis. 38 reconciled gene trees were generated, two per gene family, corresponding to the two different EWT values set for the analyses. An example of the implied duplications and losses with EWT set to 90 for the Glycoside Hydrolases family 7, mapped on the organismal is presented in Fig. 1. The summarized duplications and losses separately for the 12 CAZY gene families and the 7 gene families involved in oxidoreductative reactions along with the distribution of gene copies per genome on the graphs are summarized in Fig. 2.

Figure 1. Duplications and losses for the Glycoside Hydrolases family 7 mapped on the organismal tree

Gene lineages of cellobiohydrolases Gene lineage of endoglucanases Gene loss along a lineage Speciation event

Conclusions

Laccaria

hizophyllun

Stagonospora

nodorum

60

10

20

30

40

50

80

100

120

ommune

bicolor

•The common ancestor of the 7 Basdiomycete species was estimated to have from 66 to 83 copies of different CAZY gene copies, depending on the EWT settings employed. The brown rot species S. lacrymans and P. placenta and the mycorrhizal species L. bicolor have undergone extensive gene losses in the CAZY gene families in comparison to the common ancestor of the Basidiomycete species and also in comparison to the white rot species or the soil saprotroph (*C. cinerea*) in the dataset. The results suggest convergent evolution in the two independently evolved brown rot lineages while the results for *L. bicolor* are in agreement with the mycorrhizal status of the species, which acquires carbon sources mainly from host-derived photosynthate, not





a) white rot on hardwood caused by *Phanerochaete* sp., b) brown rot on conifer wood, covered with a basidiocarp of Serpula lacrymans, c) brown rot caused by an Antrodia species

Materials and Methods

7 Basidiomycete and 3 Ascomycete genomes were used in the study, using protein sequences published in various studies as queries and performing blastp searches, having as target 19 gene families diversely involved in wood degradation (Table1). The sequences for each gene family were aligned using RAxML analysis was MAFFT. performed for each family, using the appropriate protein evolution model (estimated with ProtTest). The RAxML bootstrapped tree was used as the gene tree along with the species tree shown in Fig. 1 to perform reconciliation analyses using Notung (4). The default costs for duplications (1.5) and losses (1.0) were used. Two different bootstrap values (EWT 90 and 75) were used to define well supported clades on the gene trees in order to perform rearrangements. The calculated duplications and losses after the each for tree rearrangements were eventually mapped on the organismal tree.



Table 1. Gene families used in the study Glycoside Carbohydrate Hydrolases 3 Esterases 1 Glycoside Carbohydrate



Fig.1 History of duplications and losses for the glycoside hydrolases family 7. The three gene copies in the common ancestor of the species have undergone a complicated history of duplications and losses leading to species with multiple gene copies or no copies at all.

Figure 2. Summarized copies numbers, duplications and losses for the 12 CAZY gene families and the 7 gene families with oxidoreductative roles.

12 CAZY gene families



through saprotrophy.

•Regarding gene families with roles in oxidoreductative procedures, S. lacrymans and P. placenta again have a reduced number of gene copies in comparison to the of the Basidiomycetes or the common rest Basidiomycete ancestor (which possessed 27-29 copies of these gene families), but in this case this is more attributed not to extensive gene losses in the brown rot species, but mainly to gene duplications in the rest of the species. The suggested duplication events are prominent in the Class II peroxidases for P. chrysosporium and H. annosum and in the multicopper oxidases for *H. annosum* and *C. cinerea*.

> Fig.2 Species trees with the summarized duplications and losses mapped along the tree and graphs representing the distribution of gene copies along the genomes for the 12 CAZY families (upper tree) and the 7 gene families with genes participating in oxidoreductative procedures (lower tree). The numbers on the internal nodes indicate possible ancestral number of gene copies for the two different EWT settings 90 and 75 respectively. The coupled numbers along the branches indicate duplications/losses leading from one node to the next (numbers on the top for EWT 90, numbers on the bottom for EWT 75). The numbers on the bars indicate the number of gene copies per genome.

Hydrolases 5	Esterases 16
Glycoside	Class II
Hydrolases 6	peroxidases
Glycoside	Multicopper
Hydrolases 7	oxidases
Glycoside Hydrolases 10	Glyoxal oxidases
Glycoside	Cellobiose
Hydrolases 11	dehydrogenases
Glycoside	Quinone
Hydrolases 12	reductases
Glycoside Hydrolases 28	Oxalate oxidases/decarb oxylases
Glycoside	Iron binding
Hydrolases 61	glycopeptides
Glycoside Hydrolases 74	

7 gene families with oxidoreductative roles



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