

A novel fungal family of oligopeptide transporters identified by functional metatranscriptomics of soil eukaryotes.

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Figure S1. Phylogenetic relationships (PhyML) between six environmental oligopeptide transporter protein sequences (in red) and 33 reference protein sequences belonging to the FOT clade as defined in Figure 1. Sequence names in black and blue are from Ascomycota and Basidiomycota, respectively. Sequences from species followed by a figure are listed in Supplementary Table S2 and appear in Figure 1. Additional sequences were retrieved from GenBank (*G(lomerella) graminicola*, *N(eosartorya) fischeri*, *T(alaromyces) stipitatus*, *C(occidioides) posadasii*), others from genome projects at the Joint Genome Institute (<http://genome.jgi-psf.org/>) (*M(ycosphaerella) figensis*, *T(hielevia) terrestris*, *T(richoderma) atroviride*, *C(ryphonectria) parasitica*, *C(oniophora) puteana*, *S(erpula) lacrymans*, *S(porobolomyces) roseus*, *R(hodotorula) graminis*, *F(omitopsis) pinicola*, *P(unctularia) strigosozonata*, *S(tereum) hirsutum* and *G(loeophyllum) trabeum*). The *L(entinula) edodes* polypeptide sequence was deduced from the clustering of different EST sequences from GenBank. Bootstrap supports (200 replicates) above 80 are given. For this analysis, the final cured alignment contained 315 positions.

