**Supplemental data**

**Introduction of the *Aspergillus fumigatus* α-1,2-mannosidase MsdSinto *Trichoderma reesei* leads to abnormal polarity and improves the ligno-cellulose degradation**

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**Fig.S1. LC-MS/MS results of the *msdS*-expressing mutant.** Proteins extracted from the *msdS*-expressing mutant Tr-MsdS were separated by 10% SDS-PAGE and stained with Coomassie R-250. Proteins corresponding to 40~60 kDa were cut from polyacrylamide gels After in-gel digestion, peptides were subjected to an EASY-nLC 1000 interfaced via a Nanospray Flex ion source to an Orbitrap Fusion Tribrid mass spectrometer (Thermo Fisher Scientific). The peptides were loaded onto a trap column (C18, 5 μm particles, 100 μm ID, 3 cm length, Dr. Maisch GmbH) and separated using an analytical column (C18, 3 μm particles, 75 μm ID, 15 cm length, Dr. Maisch GmbH) at a flow rate of 400 nL/min with a 60 min LC gradient composed of Solvent A (0.1% formic acid (v/v)) and Solvent B (acetonitrile, 0.1% formic acid (v/v)). The gradient was 3-8% B for 5 min, 8-20% B for 40min, 20-35% B for 10 min, 35-80% B for 3 min, and finally 80% B for 2 min. A data-dependent Top20 method was used with precursor MS1 scan (m/z 350–1550) acquired in the Orbitrap at a resolution setting of 120,000, followed by Orbitrap HCD-MS/MS and ITHCD-MS/MS of the 20 most abundant multiply charged precursors in the MS1 spectrum.MS2 spectra were acquired at a resolution of 30,000. The sequences were identified by SEQUEST with FASTA database of *Aspergillus fumigatus* from NCBI.

Figure-S2.tif

**Fig.S2. Confirmation of expression of MsdS in *T. reesei* with LC-MS/MS.** Proteins extracted from the *msdS*-expressing strain Tr-MsdS were separated by 10% SDS-PAGE and stained with Coomassie R-250. Proteins corresponding to 40~60 kDa were cut from polyacrylamide gels and analyzed using LC-MS/MS. The sequences were identified by SEQUEST with FASTA database of *Aspergillus fumigatus* from NCBI.

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**Fig.S3. Alignment of *A. fumigtus* MsdS and *T. reesei* TRIREDRAFT\_45717.**

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**Fig.S4. Growth kinetics of the wild-type (WT) and Tr-MsdS strain.** Change in colony diameter with different time when same amount of conidia were inoculated and incubated at the designated temperature.

**Table S1. Thickness of the cell wall of parent and Tr-Msds cells.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Temperature** | **WT** | | **Mutant** | |
| Hyphal (µm) | Conidia (µm) | Hyphal (µm) | Conidia (µm) |
| **320C** | 0.06 | 0.06 | 0.14 | 0.07 |
| 0.08 | 0.04 | 0.12 | 0.07 |
| 0.08 | 0.07 | 0.11 | 0.09 |
| **370C** | 0.11 | 0.11 | 0.12 | 0.1 |
| 0.12 | 0.12 | 0.19 | 0.12 |
| 0.15 | 0.13 | 0.14 | 0.12 |

Mycelia and conidial cells were fixed as described in method section. The thickness of cell wall was measured under transmission electron microscopy (TEM) (JEM-1400).

**Table S3. Primer pairs used for RT-PCR.**

|  |  |  |  |
| --- | --- | --- | --- |
| **SN** | **Genes** | **Primer pair sequence (5’-3’)** | |
| 1 | hac1 | FWD | CAGATAAGAAGCCTGCCAAGAA |
| REV | GACGCTGTTCCTTTTCATCTTC |
| 2 | rho3 | FWD | ATACGGCGGGACAGGAGGAATT |
| REV | GTCGTAGGAAATCGTGGGCGGT |
| 3 | sec61 | FWD | ATCCACACCGCCGTCTACATCA |
| REV | TTGGCAGCAATTTCAAAGTAGC |
| 4 | rab5 | FWD | ATTGGAGCGGCTTTCCTCACCC |
| REV | GCTTATCGGGCTGTTCGTTGAC |
| 5 | ftt1 | FWD | CAAACTCCTACCGTCAAAATGG |
| REV | GCCTCGATCTTCTGGCGGTACT |
| 6 | ypt1 | FWD | TTCCGAACCATCACCTCGTCTT |
| REV | GGCGAGCCATGGTCAGGAAAGC |
| **7** | snc1 | FWD | CGCCAGCAGGCACGCTCATTAG |
| REV | GGTGAGGGTTTGGGCGGTATGT |