

Supplemental data Fig. 1. Amino acid sequence of CBHI from *P. decumbens*.

The putative N-linked glycosylation sites are underlined, and the amino acid sequences of the four CBHI glycoforms acquired using MALDI-TOF are marked in red. N-linked glycosylation occurs at the asparagines (N) in the consensus sequence motif of N-X-S/T in the catalytic domain. Potential N-glycosylation sites are underlined. CBHI-A, CBHI-B, CBHI-C, and CBHI-D were identified using MALDI-TOF. Three identified peptides were acquired from MS/MS results and are marked in red.

Supplemental data Fig.2. MALDI-TOF mass spectra and PMF of the four purified CBHI glycoforms (CBHI-A, CBHI-B, CBHI-C, and CBHI-D).

The image shows the PMF of the four glycoforms of CBHI. The main peaks in the PMF of the four CBHIs were nearly the same. The list of the peptide masses of the proteins purified from *P. decumbens* JU-A10 were analyzed using the peptide mass tool from ExPASy. Some peptide masses from the mass spectrum were more than the theoretical unmodified tryptic peptides of CBHI. Then, the peptide masses were taken into account and compared with the potential N-glycosylation site. The potential N-glycan structures were speculated according to the molecular weights of the glycans.

Fig.1

MKGSISYQIYKGALLLSLLASVSAQGAGTLTAESHPLTWQKCSAGGSCTPVSGSVVIDANWRWVHDKNGKNC
YTGNTWDATLCPDDKTCAANCAVDGASYASTYGVTTSGNSLRINFVTQASQKNIGSR**LYLLEN****NDTTYQK**FNLLNQ
EFTFDVDVSNLPCGLNGALYFVDMADGGMAKYPTNKAGAK**YGTGYCDSQCPR**DLKFINGIANVEGWTPSSND
PNSGVGGHGTCCAEMDIWEANSISEALTPHPCDTPGQTMCEGNACGGTYSNDRYAGTCDPDGCDNFYRQGV
TNFYGPGMTVDTKSPFTVVTQFLTDDGTSTGTLSEIKR**FYVQNGK**VIGQPQSTVAGVSGNSITDSFCKAQKAAFG
DTDDFTKHGALAGMGAAFEEMVLVMSLWDDHNSNMLWLDSTYPTTASSTTLGAKRGSCDISSGAPNDVESQN
ANSYVVFVSNKAGPIGSTFNSGSTGGG**NGS**GSTTTTKGSTTTTKAPTTTTTTTTSKATTTTAASGGNGGGAAHWAQ
CGGVGYTGPTTCASPYTCTKQNEYYSQCL

Fig .2





