Supplementary Fig. 1: Whole self-organizing map (SOM) clusters and gene ontology (GO) terms for parasitism and grafting between *P. japonicum* and *Arabidopsis*. **a** SOM clusters with similar patterns in parasitism (top) and grafting (bottom) are shown. GO terms commonly found in the parasitism and grafting were listed among clusters. BP, CC and MF stand for GO-subcategory of biological process, cellular components and molecular function, respectively. 20 GOs with a *P* value of 0.05 or less were selected in each category. **b** Tissue sections of the graft junction are shown. Fluorescence images of the graft junction are also shown where *P. japonicum* was grafted to *Arabidopsis RPS5a::LTI6b-tdTomato*. Green indicates the cell wall, magenta indicates tdTomato fluorescence. Scale bars, 100 μm.
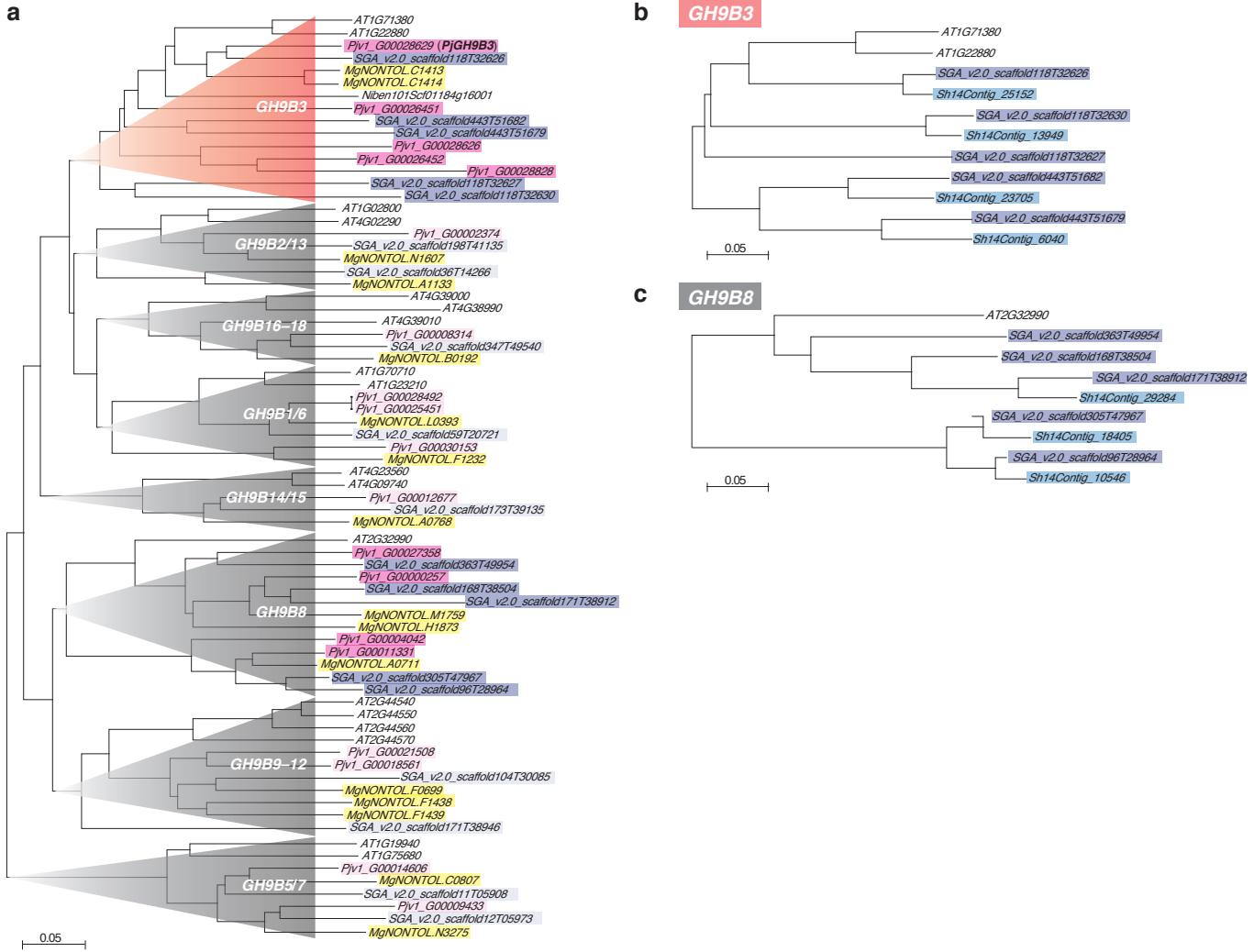
Supplementary Fig. 2: Phylogenetic trees of the *GH9B* gene family for *Arabidopsis*, *P. japonicum*, *S. asiatica*, *E. guttata*, and *S. hermonthica.* **a** Phylogeny of *Glycosyl hydrolase 9B* genes of *E. guttata* (yellow), *P. japonicum* (red), *S. asiatica* (indigo), and *Arabidopsis* reconstructed using deduced amino acid sequences. Genes with less than three genes contained in each clade were given light backgrounds. **b**, **c** Phylogeny of *GH9B3* (b) and *GH9B8* (c) clades of *S. hermonthica* (blue), *S. asiatica* (indigo), and *Arabidopsis*.
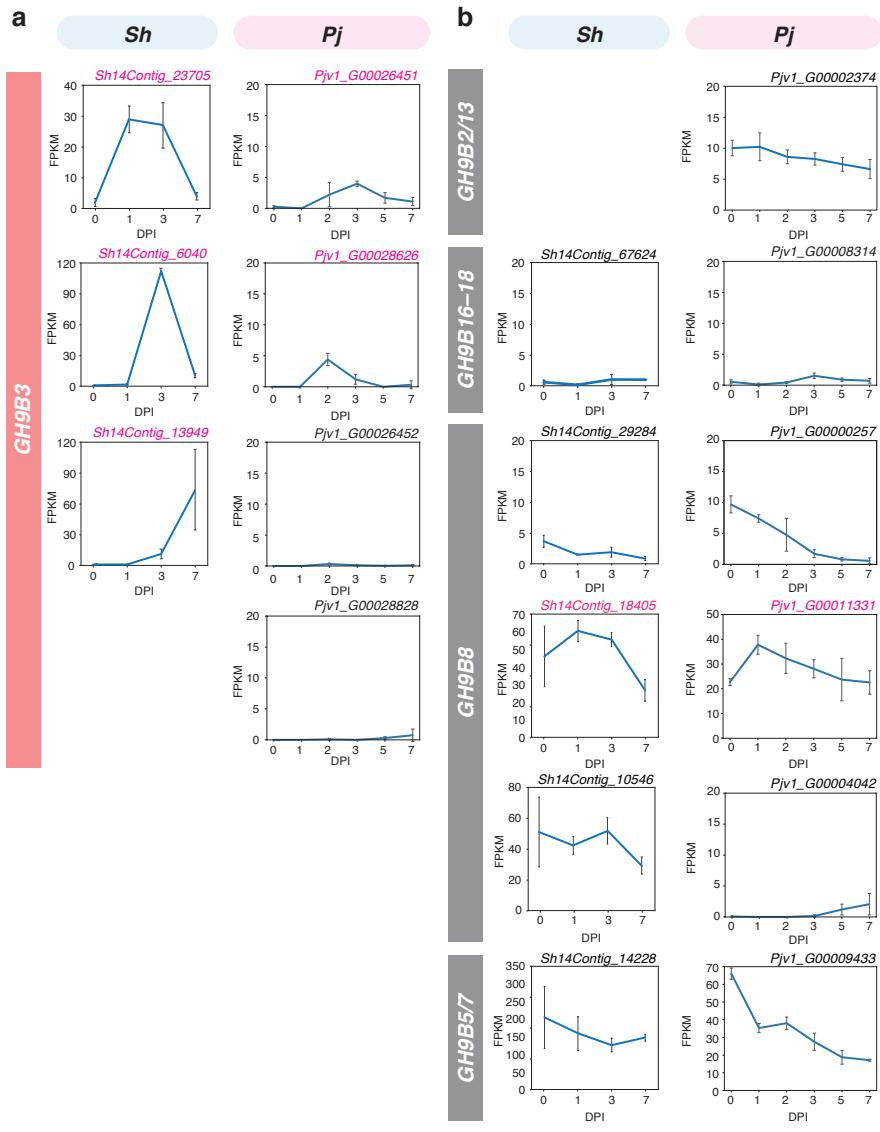
Supplementary Fig. 3: Expression levels of other genes for *Glycosyl hydrolase 9B* family in Orobanchaceae. **a** Expression patterns of other genes of *S. hermonthica* belonging to the GH9B3 clade. **b** Expression patterns of other GH9B genes belonging to clades other than GH9B3 in *S. hermonthica* and *P. japonicum*. *Sh*, *S. hermonthica*; *Pj*, *P. japonicum*.

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Pjv1_G00026452    1  -----MAFL-NGSQYFLSILLFCLLTFKNSGGDAHDYKDALAKSILFFEGQRSGKLPSMQRMDWRGDSALSDG--AKAGV
Pjv1_G00028828    1  -------------------------------------------------------------------------MLQV
Pjv1_G00028626    1  -----MAFLKNGSQYYLFILLFCLP-FIIRGGDEYNYKEALTKSILFFEGQRSGELPPNQRLNWRADSALYDG--NEAGV
AT1G22880         1  ----------MASPFFFVFLLSALS-LENTY-ASPNYREALSKSLLFFQGQRSGRLPSDQQLSWRSSSGLSDG--SSAHV
AT1G71380         1  ----------MTSLFFFVLLFSSLL-ISNGD-ANPNYKEALSKSLLFFQGQRSGPLPRGQQISWRASSGLSDG--SAAHV
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Pjv1_G00026451    1  MAFLNG-----STSFLILFSFTFLCNLRNVQSADHNYKEALTKSITFLQGQRSGKLPSTQQITWRGDSALSDGEKAGAGV


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AT1G22880        67  DLTGGYYDAGDNVKFNFPMAFTTTMLSWSSLEYGKKMGP--ELQNSRVAIRWATDYLLKCARATPG--KLYVGVGDPNGD
AT1G71380        67  DLTGGYYDAGDNVKFNLPMAFTTTMLSWSALEYGKRMGP--ELENARVNIRWATDYLLKCARATPG--KLYVGVGDPNVD
Pjv1_G00028629   77  DLTGGYYDAGDNVKFNFPMAYTTTMLSWGAIEYGKRLGP--QLQSTRAAIRWGTDYLLKCARATPG--KLYVGVGDPNRD
Pjv1_G00026451   76  NLTGGYYDAGDNVKFNFPMAYTTTMLSWGVIEYGKRLGA--ELQHAREAIRWGTDYLLKCALETPG--KLYVGVANPNLD


Pjv1_G00026452  153  HNCWERPEDMDTDRSVYSVTA---GSDVAGETAAALAAASIVFRKANSSYSKLLRNTANDVMQFAINNKGAYSDQLGGNV
Pjv1_G00028828   85  HQCWERLEDMDTDRSVFSVTA---GSDMAGETAAALAAASIDFKRAELTYSKLLRKTADVVMRFAINNKWAYSDQLRNNV
Pjv1_G00028626  152  HSCWERPEDMDTPRTVYRVTA---GSDLAGEIAAALAAASIVFRKANHRYSEQLRNTAEVVMQFATNNQVSY-----GSV
AT1G22880       143  HKCWERPEDMDTPRTVYSVSPSNPGSDVAAETAAALAASSMVFRKVDPKYSRLLLATAKKVMQFAIQYRGAYSNSLSSSV
AT1G71380       143  HKCWERPEDMDTPRTVYSVSASNPGSDVAAETAAALAAASMVFRKVDSKYSRLLLATAKDVMQFAIQYQGAYSDSLSSSV
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Pjv1_G00026452  230  CPFYCSYSGFKDELLWGAAWLYKATGSPVYRNYITSYGENDDVDIFSWDNKFAGANVLLAKEYLVGNNRTFQKFNEKAET
Pjv1_G00028828  162  CPFYCSCLEFKDELLWGEVGLYKATRLPFYRNYITSYGDNDDADILSLDSKFAGANVLLAREYLVGKDRTFEKFSGRAET
Pjv1_G00028626  224  DGFYQSYSGFEDELLWGAAWLYKATNKTSYRNYITSYGCTDDVDTFGWDSKFPGAYVVLAREYLVGKDENFEKFKEKAET
AT1G22880       223  CPFYCSYSGYKDELLWGASWLLRATNNPYYANFIKSLGGGDQPDIFSWDNKYAGAYVLLSRRALLNKDSNFEQYKQAAEN
AT1G71380       223  CPFYCSYSGYKDELMWGASWLLRATNNPYYANFIKSLGGGDQPDIFSWDNKYAGAYVLLSRRALLNKDSNFEQYKQAAEN
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Pjv1_G00026451  232  CPFYCSYSGYKDELFWGAAWLFRATNSVYYDFIRTLGANDDANIFSWDNKFAGARVLLSR----------QFSQQAEN


Pjv1_G00026452  310  FMCKILRG--SPSLSIQYTQGGLIH--RLHDSTLQYTTSMTFLITVYAKYLANRNAPKHSFNCNGRGFNSTNLRVQAKAQ
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Pjv1_G00028626  304  FMCKILRD--SPSLSIQFTGGGMMYNKNLPDSPLQYVTSLSFLITTYAKYLANRHSPTHKIDCEGHAFNPKKLRNQAKAQ
AT1G22880       303  FMCKILPN--SPSSSTKYTKGGLMY--KLPQSNLQYVTSITFLLTTYAKYMK---STKQTFNCGNSLIVPNALINLSKRQ
AT1G71380       303  FICKILPD--SPSSSTQYTQGGLMY--KLPQSNLQYVTSITFLLTTYAKYMK---ATKHTFNCGSSVIVPNALISLSKRQ
Pjv1_G00028629  313  FMCRILPNSYSRSSSTQYTPGGLMY--KMDASNLQYVTSITFLMTTYSKYMA---TTKHTFNCGNLPITSNILRTLAKKQ
Pjv1_G00026451  301  FMCKVLPNS-PYLSDTQYTKGGLMY--KLDGSNLQYVTAITFLFTTYAKYLANRNSPKHSFTCGGQIYTASYLRVVAKSQ


Pjv1_G00026452  386  VDYILGTNRMKMSYMVGYGPKYPMRVHHRGASLP----LGKKISCGDGF-TYLHTPNPNPNILTGAIVGGPDENDFYKDN
Pjv1_G00028828  307  -------------------PTYS-----------------------------------------------------
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AT1G22880       376  VDYVLGVNPMKMSYMVGFSSNFPKRIHHRGSSLPSRAVRSNSLGCNGGF-QSFRTQNPNPNILTGAIVGGPNQNDEYPDQ
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Pjv1_G00028629  388  VDYILGDNPMKMSYMVGYGQSFPKRIHHRGSSLPSRNVSPQSFGCDGGK-QFFYSPNPNPNTLTGAIVGGPNHNDFFADE
Pjv1_G00026451  378  VDYILGDNPMKMSYMVDYTKNFPKRIHHRGSSVPSIIDHPKKITCGEGF-SYLQTSSANPNILTGAIVGGPDRNDRYADD


Pjv1_G00026452  461  RDEYSQSEPATYINAPLVGTLAYFAAKQK-
Pjv1_G00028828       ------------------------------
Pjv1_G00028626  462  RSSYSQSEPATYINAPLVGILAYFAGKKQ-
AT1G22880       455  RDDYTRSEPATYINAAFVGPLAYFAASRSP
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Pjv1_G00026451  457  RNNFGQSEPTTYINAAIVGPLAYLAAKQ-
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Supplementary Fig. 4: Alignment analysis of amino acid sequences for genes of the GH9B3 clade in *Arabidopsis* and *P. japonicum*. Amino acid sequence alignments were performed on genes of *Arabidopsis* and *P. japonicum* GH9B3 clade using clustal2.1 software. The amino acid residues highlighted in tangerine and magenta indicate a catalytic domain and *O*-glycosylation sites, respectively. Red line indicates the secretory signal peptides.
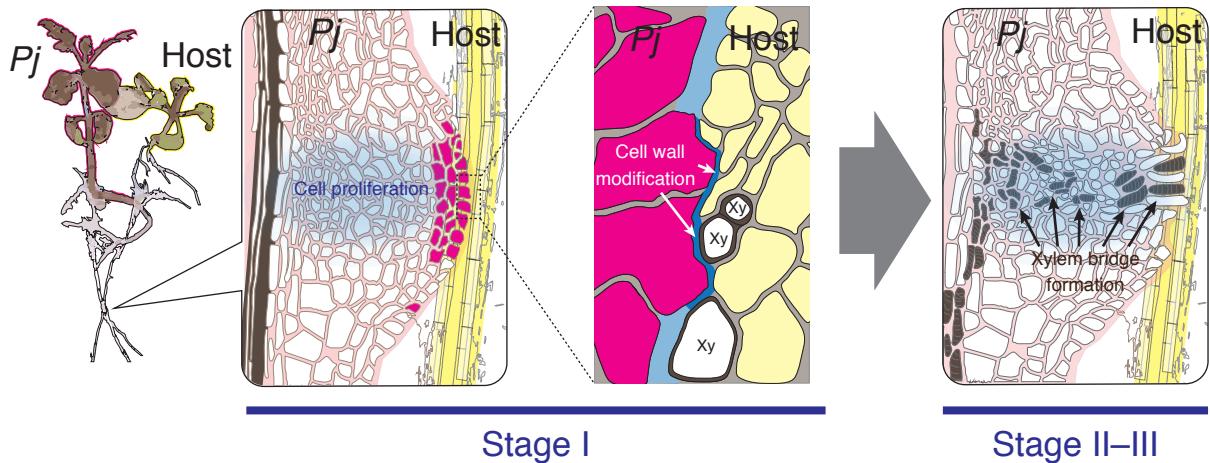
Supplementary Fig. 5: Model of parasitism by *P. japonicum*. Upon detection of host plant roots, *P. japonicum* generates haustoria where cells are proliferated through cell division (colored in blue shade). *PjGH9B3* is induced at the periphery of the haustorium (colored in magenta) to facilitate tissue adhesion when in contact with the host plant root (stage I). In magnified illustration, the interface between cells of *P. japonicum* and host plant is marked in blue and especially thin cell wall region through cell wall modification is marked in dark blue. Subsequently, a xylem bridge (colored in brown) is formed between *P. japonicum* and the host plant root (stages II–III). Arrows indicate decreased cell wall thickness at the interface between parasitic and host tissues. *Pj*, *P. japonicum*. Xy, Xylem.