# Supplementary information

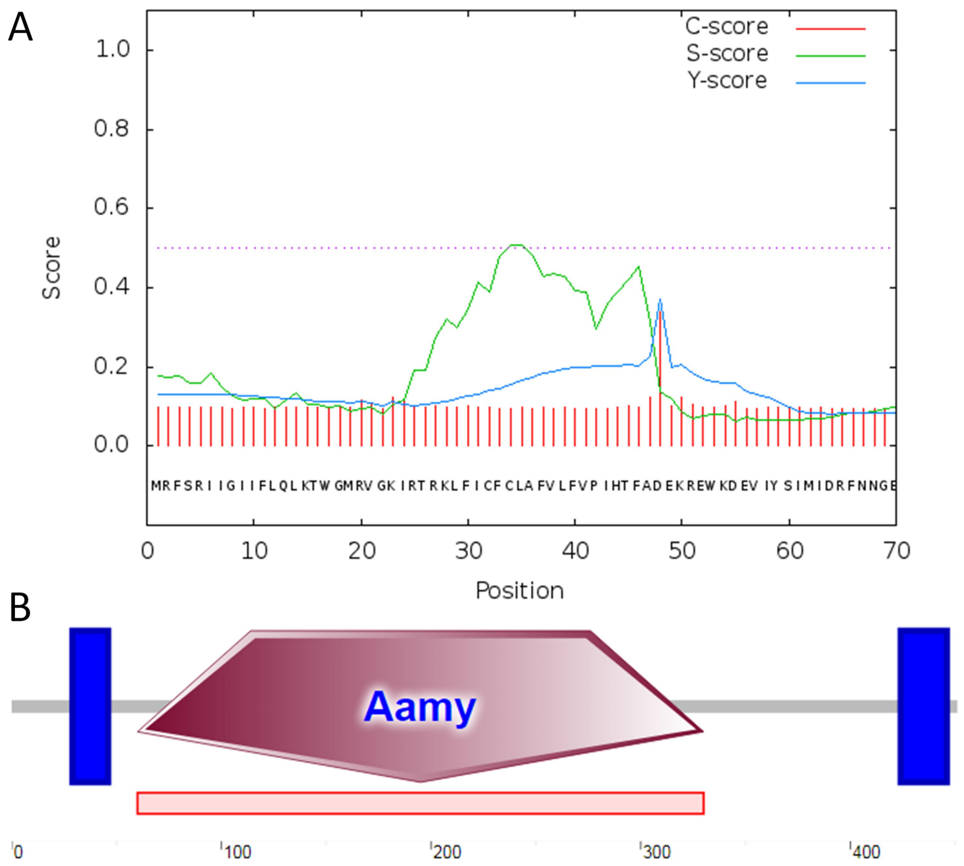

**Fig. S1:** Analysis the *amyC* gene (FRY47_05825) signal peptide and smart domain (A) Analysis the AmyC protein signal peptide through SignalP 4.1. S-score: Each amino acid corresponds to 1 S value, with a high S value in the signal peptide region. C-score: Each amino acid will have a C value, with the highest C value at the shear site. Y-score: Y value is a parameter considering S value and C value, which is accurate than C value alone, because there may be more than one higher C value in a series, but only one shear site; the shear site is with steep S value and high C value. (B) Analysis the AmyC protein smart domain through SMART software. The 60-330 position is catalytic activity, and there are two transmembrane areas at each end of the active area.

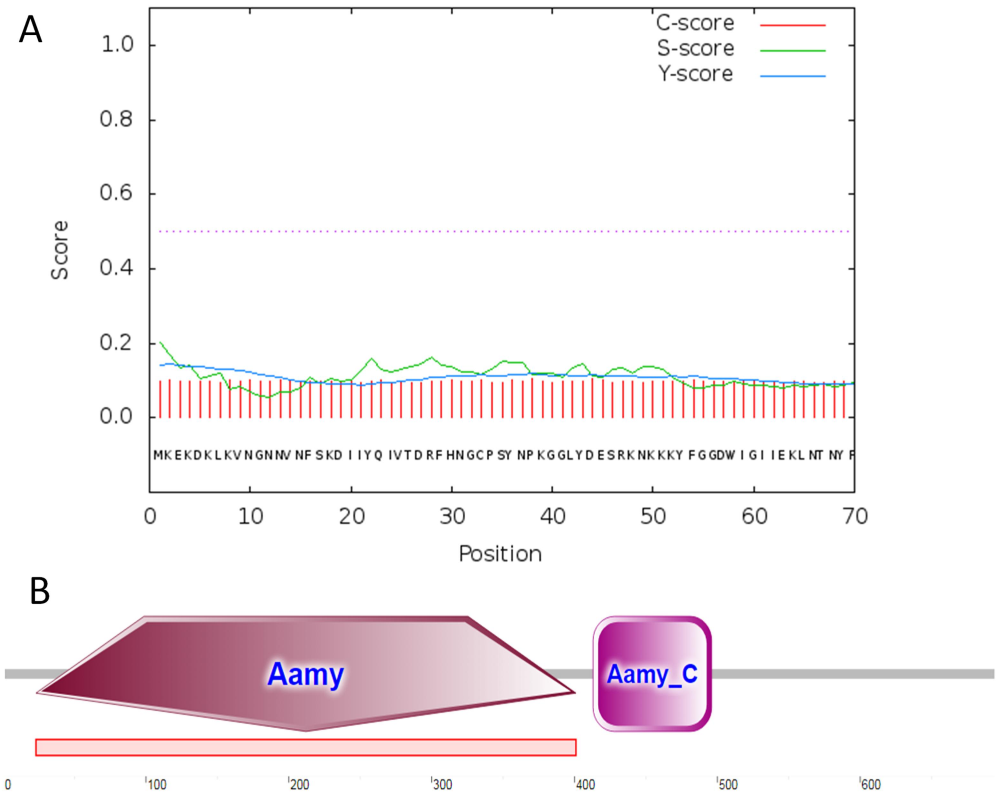

**Fig. S2:** Analysis the *amyP* gene (FRY47_27030) signal peptide and smart domain. (A) Analysis the AmyP protein signal peptide through SignalP 4.1. S-score: Each amino acid corresponds to 1 S value, with a high S value in the signal peptide region. C-score: Each amino acid will have a C value, with the highest C value at the shear site. Y-score: Y value is a parameter considering S value and C value, which is accurate than C value alone, because there may be more than one higher C value in a series, but only one shear site; the shear site is with steep S value and high C value. (B) Analysis the AmyP protein smart domain through SMART software. The 23 to 401 is the catalytic activity, 413 to 496 is the C domain of Aamy, 501 to 577 is the TIG domain, 585 to 681 is the domain of CBM 20, which has starch binding function.

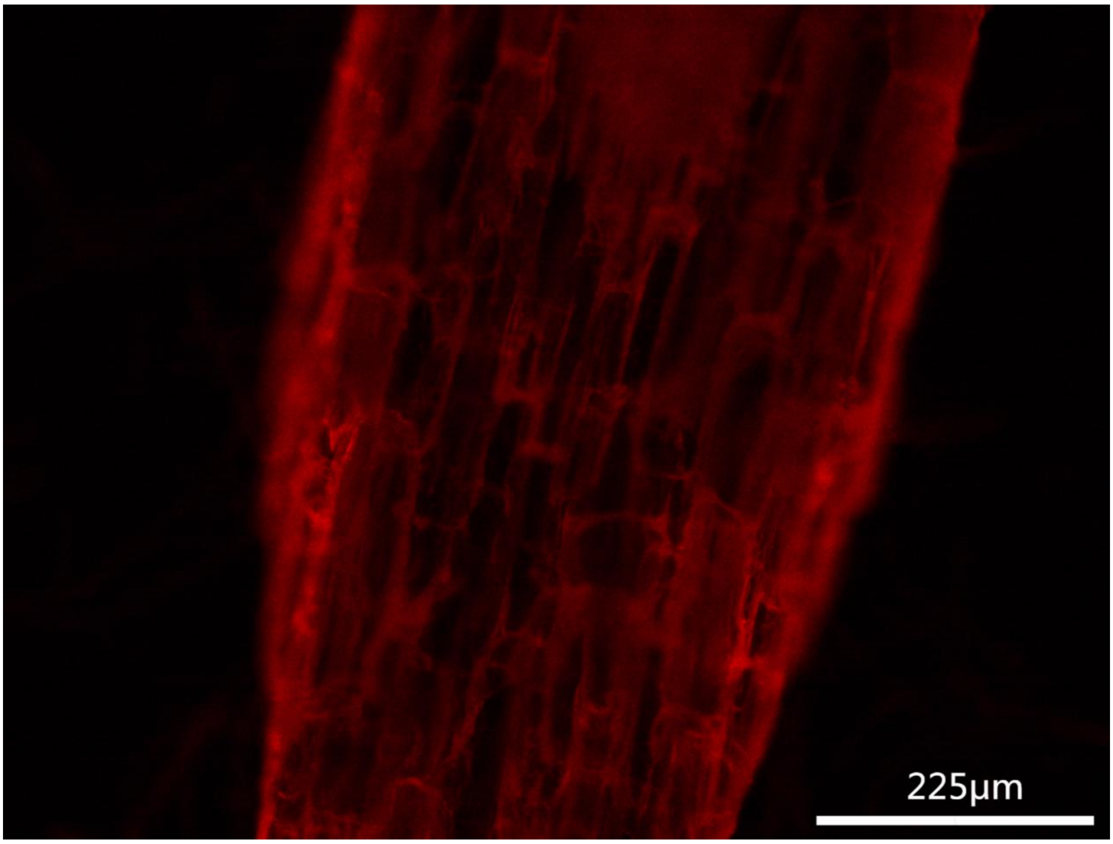

**Fig. S3:** No strains colonization on wheat root (control treatment)

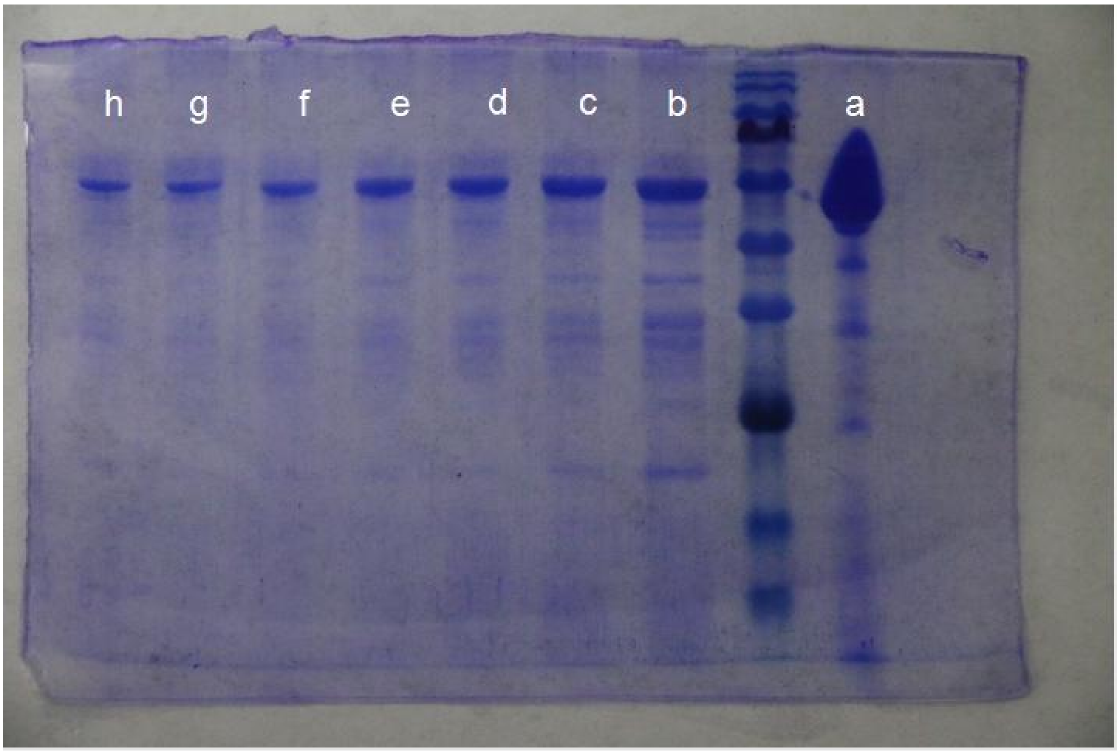

**Fig. S4:** Induced expression of *amyS* gene in *E.coli* BL21(DE3) strain. The strain was cultured to $10^5$ cfu/mL and supplemented with 100 μmol/L IPTG for induction culture at 22°C for 6 h. Then subsequently centrifugated and subjected to ultrasonication. 20 mM imidazole solution was used for a Ni column purification, and obtained the purified protein. (a) represent the commercial α-amylase(Ruibio, Germany); (b) represent unpurified AmyS protein; (c) represent purified AmyS protein; (d) represent the purified protein was diluted twice-fold; (e) represent the purified protein was diluted three-fold; (f) represent the purified protein was diluted four-fold; (g) represent the purified protein was diluted five-fold; (h) represent the purified protein was diluted six-fold.

**Table S1:** The primers used in this study

| Primer name | Alignment (5’→3’) |
|---|---|
| *amyC*-up-*Bam*HI-s | ACACGGATCCTAAATGCAGTTAAAGCTACGT |
| *amyC*-up-*Eco*RI-a | CACAGAATTCTAATTGTAAGAATATTATACCA |
| *amyC*-down-*Eco*RI-s | ACACGAATTCTTTCTAATTGCAGTTAAAAGGA |
| *amyC*-down-*Xho*I-a | CACACTCGAGTATTAATACTTTTTTCATATTC |
| *amyP*-up-*Bam*HI-s | ACACGGATCCTTGTAAAATAGATATATTGATA |
| *amyP*-up-*Eco*RI-a | CACAGAATTCAATTAACGTTGTTCCCATTCAC |
| *amyP*-down-*Eco*RI-s | ACACGAATTCAGTTGTAAAATGGCAAACTGCA |
| *amyP*-down-*Xho*I-a | CACACTCGAGTCAATAAAGTTTCTGCAATATC |
| *amyS*-up-*Bam*HI-s | ACACGGATCCACCATCAATTCCACCATTTACA |
| *amyS*-up-*Hin*DIII-a | CACAAAGCTTGATCAGTTTCCATATATGTTCA |
| *amyS*-down-*Hin*DIII-s | ACACAAGCTTTGTTATTCTTTTAAACATCTG |
| *amyS*-down-*Eco*RI-a | CACAGAATTCTCAGTTAGTTTTACAATAAGAG |
| P*amyS*-*Bam*HI-s | ACACGGATCCCCATTGCGTACATAATGTTAGATA |
| P*amyS*-amyS-a | TATGCTTTACTCCCCTCATACATCTGTACACCATCCCCTTCCAAG |

| | |
|---|---|
| *amyS*-PamyS-s | AAGGGGATGGTGTACAGATGTATGAGGGGAGTAAAGCATATG |
| *amyS*-*Xho*I-a | CACACTCGAGTTATTGTTGAACATATATGGAAACTGATC |
| *amySec*-*Bam*HI-s | ACACGGATCCATGTTTAAAAGAATAACAATAGTC |
| *amyS*-*Xho*I-a | CACACTCGAGTTATTGTTGAACATATATGGAAACTGATC |
| pET28a-*amyS*-*Bam*HI-s | ACACGGATCCATGTATGAGGGGAGTAAAGCATATG |
| *amyS*-*Xho*I-a | CACACTCGAGTTATTGTTGAACATATATGGAAACTGATC |