



S Fig 3: HMMERCTTER Analysis of the Polygalacturonase Superfamily

Numerical analysis in Table 2, details in context. Colors according to HMMERCTTER output, leaves in black could not be clustered. Scale bars indicate 0.1 amino acid substitution per site. (A): C2 clustering; (B): C3 Clustering; (C): C4 Clustering; (D): C7 clustering; (E): Classification based upon C7 with training sequence P15922_1 indicated; (F): C11 Clustering; (G): Classification based upon C11. The C7 clustering and classification is the reference and its numbering is used to guide comparison. 1: Fungal endoPG; 2a Fungal exoPG (PGXA); 2b Fungal exoPG (PGXB); 2c Endo-XyloGalacturonase; 2d; Exo-RhamnoGalacturonase; 3a: Plant PG; 3b: Plant PG; 4 Fungal Endo-RhamnoGalacturonase; 5: Bacterial PG; 6 Fungal exoPG (PGXC); 7 Zygomycete exoPG. H: Detail of poor classification C7_C7; I: Score plot of group C11-C7, note the score drop between group and non group members.