

Supplementary Method

Identification of XYLP proteins

By running the BLAST build and search (E-value < 10⁻⁷) and using the protein sequences of ZeXYP1, AtXYP1 and AtXYP2, we screened the Pepper^[1], Tomato^[2] and Potato^[3] Genome database to identify CanXYLP, SlyXYLP and StuXYLP proteins respectively. Then putative AG glycomodules and the percentage of amino acid P(Proline)/A(Alanine)/S(Serine)/T(Threonine) of the identified protein sequences were predicted mainly followed the rules described in the previous researches^[4,5]. Next, the protein sequences were submitted to InterProScan^[6], SignalP 5.0^[7], Big-PI Plant Predictor (http://mendel.imp.ac.at/gpi/plant_server.html), and NetNGlyc 1.0 Server (www.cbs.dtu.dk/services/NetNGlyc) to make sure the presence of non-specific lipid transfer protein-like (nsLTP) domain, N-terminal signal peptide, GPI-anchored signal, and N-glycosylation sites. The characteristics of all of the *Solanaceae* XYLP protein sequences were listed in Supplementary Table S1.

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