

eQTL Mapping Identifies *Ptrxbat35* as a Regulator of Adventitious Root Development in *Populus*

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Plant establishment requires the formation and development of extensive root systems whose architecture is modulated by complex genetic networks. Here, we report the identification of the *PtrXBAT35* gene as an eQTL hotspot, mapped using 390 leaf and 444 xylem *Populus trichocarpa* transcriptomes. Among predicted targets of this trans-eQTL were genes involved in plant hormone responses and root development. Overexpression of *PtrXBAT35* in *Populus* led to significant increase in callusing and formation of shoot-borne roots and wound-induced adventitious roots. Omics studies revealed that genes and proteins controlling auxin transport and signaling were involved in *PtrXBAT35*-mediated adventitious root formation. Protein-protein interaction assays indicated that *PtrXBAT35* interacts with components of endosomal sorting complexes required for transport (ESCRT) machinery, implying that *PtrXBAT35* regulated root development may be mediated by regulating endocytosis pathway. Taken together, this work identified a crucial root development regulator and shed lights on the discovery of other plant developmental regulators through combining eQTL mapping and omics approaches.