

The parasitic plant dodder (*Cuscuta pentagona*) establishes a continuous vascular system through which water and nutrients are drawn. To discover the route of mRNA transportation, *insitu* RT-PCR technique was used to locally amplify host transcript within parasitic tissue. The stability of host mRNA molecules was also checked by monitoring specific transcripts along the growing dodder thread. Four mRNAs, B and C subunits of *PPI-DEPENDENT PHOSPHOFRUCTOKINASE* (*LePFP*), the small subunit of Ribulose-1,5-bisphosphate carboxylase/oxygenase (RubisCO), and *GIBBERELLIC ACID INSENSITIVE* (*LeGAI*), were found to move from host to dodder. *LePFP* mRNA was localized to the dodder parenchyma cells and to the phloem. *LePFP* transcripts were found in the growing dodder stem up to 30 cm from the tomato-dodder connection. Long distance RNA movement from host plants into parasites presents an opportunity to control parasitic plants by transforming the host with RNA interference (RNAi) vectors that target the parasite's essential genes. RNAi plants against *Striga* and dodder respectively have been developed using *KNOX* [*KNOTTEDI-like homeobox*] genes required for meristem maintenance and proper leaf patterning as targets for RNAi. Transgenic tobacco plants (*Nicotiana tabacum*) were exposed to dodder 4 weeks after transplanting to pots. Two transgenic lines showed irregular infection appearance. Dodder formed haustoria in a single spot along the plant stem, and grew from that spot extensively without forming haustoria in other spots. In addition, six weeks old *Nicotiana benthamiana* plants were infiltrated with *Agrobacterium* harboring dodder *KNOX* RNAi construct. As a control, *N. benthamiana* plants were infiltrated with *Agrobacterium* harboring the GREEN FLUORESCENT PROTEIN (GFP) reporter gene construct. After 3 days, when the GFP plants showed expression in leaves, the plants were exposed to dodder. Dodder infection was evaluated after about 3 weeks. Plants that were infiltrated with *Agrobacterium* harboring dodder *KNOX* RNAi construct showed partial resistance to dodder with a phenotype similar to the one observed on the stably transformed lines while GFP plants showed normal infection. Although genetic engineering offers the prospects of improving the maize germplasm for resistance against *Striga*, maize is recalcitrant to transformation and time consuming. A protocol to rapidly establish transformed hairy roots in maize using *Agrobacterium rhizogenes* is described. Two tropical maize lines (CML 216 and Katumani) and one temperate line (A188) were used in the generation of transformed maize roots. Using a pTF102 binary and pMDC plasmid containing the *GUS* and *GFP* reporter genes respectively, transformation frequencies could be estimated. Transformation frequencies were found to be maize genotype specific. Transformation frequencies of 88% were obtained from maize lines- CML 216, 57% and 47 % from A188 and Katumani respectively using the *A. rhizogenes* strain K599. The transformed roots exhibited a hairy root phenotype that is the hallmark of *A. rhizogenes* mediated transformation. Multiplex PCR analyses on roots that showed GUS activity confirmed that all transformed roots were positive for the expected *GUS* fragment. The methodology developed is suitable for application to functional genomic projects for genes whose phenotypes manifest in the roots representing a significant advantage over existing transformation protocols which rely on expensive and time consuming methods.