Determining the role of *Petunia hybrida NH16* in Petal Fusion using Virus-Induced Gene Silencing

Abstract:

In *Petunia hybrida PhNH16* is in the NAC family of genes. In this study we determined if *PhNH16* was directly involved in petal fusion by using a method called Virus-induced gene silencing (VIGS). We infiltrated *Petunia hybrida* seedlings with TRV-1 and TRV-2 vectors containing *PhNH16*. Over the course of about 6 weeks the seedlings grew with the target gene in them. We also extracted RNA from wild-type *Petunia hybrida* in different tissues to obtain results showing expression levels of *PhNH16* using the qPCR method. We expect to find that *Ph-NH16* indeed does have a role in petal fusion in *Petunia hybrida*. This can be confirmed by the presence of mutant phenotypes in flowers of *Petunia* infected with the VIGS construct. In VIGS plants after about the fourth or fifth flower the mutant phenotypes start to show up. The mutant phenotypes can have variation within them.

Further Section:

Further research in the NAM family of genes will determine the role of each gene in petal fusion in *Petunia hybrida*.

- where exactly is PhNH16 in NAM gene tree.. is it closely related to CUP because then it could have a role in lateral organ formation and a defect in SAM initiation (Weir et al. 2003)
- The *No Apical Meristem* (*NAM*) gene is required for pattern formation in flowers and is expressed at meristem and primordial boundaries (Sour et al. 1996). NAM is thought to have an evolutionary role in petal fusion. In Petunia petal fusion results from lateral expansion of the five initially separate petal primordia, forming a ring-like primordium that determines further development (Vandenbussche et al. 2009).