Secondary meristem initiation is central to post-embryonic plant development. Both vegetative and reproductive development depend on this process, as secondary meristem initiation is the first step in branching and inflorescence formation. Vegetative secondary meristem initiation is regulated by a set of boundary genes. In this work, the role of boundary genes in inflorescence development was studied in tomato. Furthermore, characterization of the regulator of secondary meristem initiation *Uniflora* (*Uf*) was approached in an evolutionary context.

To identify targets of the branching regulator *Blind* (*Bl*), transcriptome profiling was performed on pre-meristematic tissue by RNA-Sequencing. 56 genes were found to be at least two-fold differentially expressed between wt and *bl-2* ($p \leq 0.05$). Six of these *Bl* target candidates were further analyzed by RNA *in-situ* hybridization. It was confirmed that expression of *AP1 complex subunit μ* (*AP1μ1*) and *Self-Pruning* (*SP)* are positively regulated by *Bl*. Both *AP1μ1* and *SP* are specifically expressed in axils of leaf primordia of wt, but not *bl-2* mutant plants. Upon emergence of the AM, *SP* expression is confined to cells surrounding the expression domain of the meristematic marker *Tomato knotted 2 (Tkn2).* However, *SP* cannot be the main mediator of *Bl* function, because *sp* mutants are not impaired in branching of the primary shoot. Besides, expression of several *Bl* target candidates was found in leaflet boundaries, which underlines that AM initiation and leaf dissection are regulated by similar mechanisms.

In reproductive secondary meristem initiation, *Bl* and *Lateral Suppressor* (*Ls*) act in concert with *Uf*. In this work it was confirmed that *Uf* is the only tomato ortholog of the bHLH transcription factors *LAX1*, *Ba1* and *ROX*. 1500 bp upstream and 700 bp downstream sequence was shown to encompass sufficient parts of the endogenous *Uf* promoter to cause a partial complementation of the *uf-1* inflorescence phenotype. Phenotyping and expression analysis revealed that *Bl*, *Ls* and *Uf* have both shared and distinct functions in inflorescence development. Loss of *uf* had a negative effect on *Ls* expression. However, a direct interaction of the regulators could not be shown. During vegetative development, the severity of defects in AM initiation and in organ separation coincide; *ls-1* has the strongest defects in side-shoot formation and organ separation, in *bl-2* both phenotypes are at an intermediate level and in *uf-1,* neither were observed. This distinguishes *Uf* from other branching regulators, and emphasizes that its function is restricted to inflorescence meristem initiation.

Loss of *Compound Inflorescence (S)* and *Uf* have opposing effects on inflorescence architecture. Therefore, it was tested whether the suppressor of inflorescence branching *S* antagonizes *Uf* function. Expression analysis revealed that both transcription factors do not determine each other's expression. Furthermore, expression analysis did not clearly show opposing effects of both transcription factors on expression of their potential regulatory target *Jointless* (*J)*. Findings rather suggest that *S* and *Uf* act in independent pathways, controlling meristem maturation and initiation, respectively.

In contrast to tomato, some other nightshades form single flowered inflorescence. In these species, *Uf* may be altered or lost. In this work, *Uf* orthologs were characterized in pepper (*Capsicum annuum* and *chinense*) and tobacco (*Nicotiana benthamiana* and *tabacum*). *Capsicum annuum* and *Nicotiana benthamiana* are single flowered, and also *Capsicum chinense* has no cymose inflorescence. Two *Uf* orthologs in *N. benthamiana* and single orthologous genes in the other three species were identified by phylogenetic analysis. Expression studies revealed specific expression of the *Uf* orthologs in *Nicotiana benthamiana* and *tabacum* in apices. *Uf* in *N. benthamiana* was not only detected in reproductive, but also vegetative apices, like for example its ortholog in Arabidopsis. In *Capsicum annuum* and *chinense*, expression of *Uf* orthologs could not be detected by qRT-PCR in any tissue analyzed. In both species, loss of the primary START codons causes severe truncations of the predicted proteins and changes in protein sequence are even found within the functional domain. Furthermore, comparison of both genes in different pepper varieties revealed elevated sequence variation. These results strongly suggest a loss of *Uf* function in *Capsicum annuum* and *chinense*. Thus, *Uf* qualifies as a central component in evolution of single flowered pepper.