***HAWAIIAN SKIRT*, and F- box gene from Arabidopsis, is a new player in the microRNA pathway**

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F-box proteins belong to a multi-protein E3 ubiquitin ligase complex (SCF) that target proteins for degradation via the proteasome. We demonstrated that *HAWAIIAN SKIRT* (*HWS*), an Arabidopsis ubiquitin protein ligase (SCF^{HWS}), regulates organ growth, flower development and timing of abscission. Mutants of this gene (*hws-1*) are pleiotropic and the most obvious phenotype is the fusion of its floral organs, a phenotype shared with the *cuc1/cuc2* double mutants and over-expressing lines of *MIR164B*. To understand the molecular mechanisms of *HWS* during plant development, an ethylmethylsulphonate mutagenized population of *hws-1* seeds was generated and screened for mutations suppressing the *hws-1* sepal fusion. We isolated *shs-1/hws-1*, *shs-2/hws-1*, and *shs-3/hws-1*, (suppressor of *hws-1*) mutants. Mapping analyses shown that *shs1* is mutated in the *miRNA164* binding site of *CUP-SHAPED COTYLEDON1* (*CUC1*) mRNA; while *shs-2* and *shs-3* are novel alleles of the plant homolog of Exporting-5 *HASTY* (*HST*), known to be important in miRNA biogenesis, function and transport. Consequently, we renamed them *cuc1-1D, hst23* and *hst24,* respectively. We demonstrated that transcript levels of *CUC1* and *CUP-SHAPED COTYLEDON 2* (*CUC2*), and MIR164 change in *cuc1-1D* and in *hws-1* mutants; analyses revealed a role for *HWS* in cell proliferation and control of floral organ number. Additional genetic crosses between *hws-1* and mutant lines for genes in the miRNA pathway were performed and double mutants obtained shown restoration of the *hws-1* sepal fusion phenotype. Our data propose *HWS* as a new regulator in miRNA pathway and reveal a role for *HWS* to control floral organ number and cell proliferation.