**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.