|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| *Hyper-GFP* (*hgf*) mutant | Name | AGI number | Predicted function in splicing | No. of alleles | Effect on GFP pre-mRNA splicing | Effect of mutation on development | Reference |
| *hgf1* | **coilin** | **At1g13030** | **a protein marker protein for Cajal bodies, which are facilitate snRNP maturation** | **121** | **AT-AC↑** | **no** | **Kanno et al., 2016** |
| *hgf2* | **CWC16a** | **At1g25682** | **step I factor** | **31** | **AT-AC↑** | **no** | **Kanno et al., 2017a** |
| *hgf3* | **SMU1** | **At1g73720** | **Recruited prior to B\*; may recognize spliceosomal targets for ubiquitination** | **1** | **AT-AC↑** | **no** | **Kanno et al., 2017a** |
| *hgf4* | **SMFA** | **At4g30220** | **a small nuclear ribonucleoprotein present in snRNPs** | **1** | **No change** | **no** | **Kanno et al., 2017a** |
| *hgf5* | **PRP39A** | **At1g04080** | **U1 snRNP component** | **51** | **AT-AC↑** | **no** | **Kanno et al., 2017b** |

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| *GFP-weak* (*gfw)* mutant | Name | AGI number | Predicted function in splicing | No. of alleles | Effect on GFP pre-mRNA splicing | Effect of mutation on development | Reference |
| *gfw1* | **AtRTF2** | **At5g58020** | **may contribute to ubiquitin-based regulation of the spliceosome** | **2** | **AT-AC↓, unspliced↑** | **embryo lethal** | **Sasaki et al., 2015;****Kanno et al., 2017a** |
| *gfw2* | **PRP8A** | **At1g80070** | **a U5 snRNP component that acts at the catalytic core of the spliceosome** | **3** | **AT-AC↓, unspliced↑** | **embryo lethal** | **Sasaki et al., 2015;****Kanno et al., 2017a** |
| *gfw3* | **RBM25** | **At1g60200** | **U1 snRNP component** | **2** | **AT-AC↓, unspliced↑** | **low seed set** | **Kanno et al., 2017b** |
| *gfw4* | **PRP18A** | **At1g03140** | **step II factor** | **1** | **AT-AC↓,** **GT-AG↑** | **short roots, small siliques** | **Kanno et al., 2018** |
| *gfw5* | **PRP4KA** | **A3g25840** | **Recruited prior to B\*; Protein kinase needed for catalytic activation of spliceosome2** | **5** | **AT-AC↓, unspliced↑** | **flat rosettes, late flowering, tall stature** | **this study** |
| *gfw6* | **SAC3A** | **At2g39340** | **Putative mRNA export factor** | **5** | **AT-AC↓, unspliced↑** | **no** | **this study** |

**Table S2**: **Mutants identified so far in forward genetic screen**

The mutants retrieved to date in a forward genetic screen based on an alternatively-spliced *GFP* reporter gene in Arabidopsis (**Figure 1**) include a predicted core spliceosomal protein (SMFa); putative components of the U1 (PRP39a, RBM25) and U5 (PRP8) snRNPs; putative step I and step II factors transiently associated with the spliceosome (CWC16a and PRP18a, respectively); putative splicing regulatory proteins (RTF2, SMU1 and PRP4ka); one structural protein presumed to be important for snRNP maturation (coilin), and a putative mRNA export factor (SAC3a). So far we have only observed developmental phenotypes in five identified *gfw* mutations, two of which are embryo-lethal. The biological significance of these findings is not yet clear.

1Further screening of the M2 population after publication of the first alleles of coilin, *PRP39a* and *CWC16a* has identified three new alleles of coilin (R9H; first intron, 3’ splice site; second intron, 5’ splice site), one new *prp39a* allele (R226\*) and two new *cwc16a* alleles (W18\*; fifth intron, 3’ splice site). These unpublished alleles are counted in the number of alleles shown here.