

Morphogenesis and differentiation genes were identified from a published dataset (Ichihashi *et al.*, 2014). The full lists are included in Supplemental dataset 3.

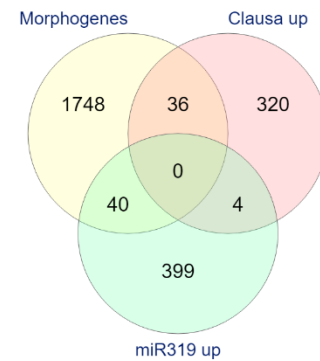
1824 genes fit the condition of m+P3 exp> P4 exp> P5 exp> P6 exp and are considered "Morphogenetic" genes.

1451 genes fit the condition of m+P3 exp< P4 exp< P5 exp< P6 exp and are considered "differentiative" genes.

"Morphogenetic" genes, as a group, are significantly enriched in the upregulated group in *clausa*, *pFIL>>miR319*, and *pFIL>>TKN2*, and in the downregulated group in *La2/+* and *pFIL>>TKN2-SRDX*. They are also significantly depleted in the downregulated group in *clausa* and *pFIL>>TKN2*, and in the upregulated group in *La2/+*.

Genotype	Representation factor of "morphogenetic" genes
<i>clausa</i> up	Significantly over-represented Representation factor: 1.5 $p < 0.014$
<i>clausa</i> down	Significantly under-represented Representation factor: 0.4 $p < 0.008$
<i>La2/+</i> up	Significantly under-represented Representation factor: 0.6 $p < 0.016$
<i>La2/+</i> down	Significantly over-represented Representation factor: 1.4 $p < 0.011$
<i>pFIL>>miR319</i> up	Significantly over-represented Representation factor: 1.3 $p < 0.044$
<i>pFIL>>miR319</i> down	Not significant Representation factor: 1.2 $p < 0.205$
<i>pFIL>>TKN2</i> up	Significantly over-represented Representation factor: 2.2 $p < 3.954e-28$
<i>pFIL>>TKN2</i> down	Significantly under-represented Representation factor: 0.3 $p < 1.710e-16$
<i>pFIL>>TKN2-SRDX</i> up	Not significant Representation factor: 1.1 $p < 0.251$
<i>pFIL>>TKN2-SRDX</i> down	Significantly over-represented Representation factor: 1.6 $p < 9.486e-06$

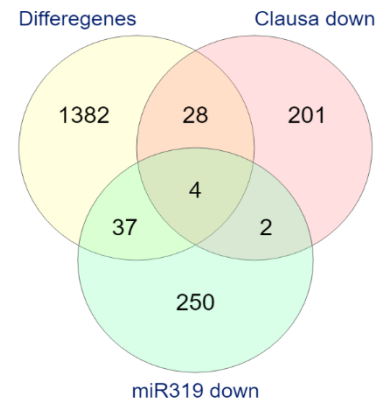
Interestingly, we see that the genes upregulated in *clausa* and *pFIL>>miR319* are different genes, supporting the notion that CLAU and LA operate in parallel pathways.



"Differentiative" genes, as a group, are significantly enriched in the upregulated group in *La2/+*, and in the downregulated group in *pFIL>>TKN2*, *clausa* and *pFIL>>miR319*. They are also significantly depleted in the downregulated group in *La2/+* and in the upregulated group in *pFIL>>miR319*, *pFIL>>TKN2*, and, interestingly, *pFIL>>TKN2-SRDX*.

Genotype	Representation factor of "differentiative" genes
<i>clausa</i> up	Not significant Representation factor: 1.4 $p < 0.057$
<i>clausa</i> down	Significantly over-represented Representation factor: 2.5 $p < 1.657e-06$
<i>La2/+</i> up	Significantly over-represented Representation factor: 4.0 $p < 2.309e-24$
<i>La2/+</i> down	Significantly under-represented Representation factor: 0.3 $p < 1.772e-04$
<i>pFIL>>miR319</i> up	Significantly under-represented Representation factor: 0.7 $p < 0.049$
<i>pFIL>>miR319</i> down	Significantly over-represented Representation factor: 2.6 $p < 2.808e-08$
<i>pFIL>>TKN2</i> up	Significantly under-represented Representation factor: 0.4 $p < 1.772e-09$
<i>pFIL>>TKN2</i> down	Significantly over-represented Representation factor: 2.7 $p < 9.404e-33$
<i>pFIL>>TKN2-SRDX</i> up	Significantly under-represented Representation factor: 0.7 $p < 0.027$
<i>pFIL>>TKN2-SRDX</i> down	Not significant Representation factor: 1.2 $p < 0.150$

Once again, looking at the specific differentiation genes downregulated in *clausa* and *pFIL>>miR319*, we see very little overlap.



Ichihashi Y, Aguilar-Martinez JA, Farhi M, Chitwood DH, Kumar R, Millon L V, Peng J, Maloof JN, Sinha NR. 2014. Evolutionary developmental transcriptomics reveals a gene network module regulating interspecific diversity in plant leaf shape. *Proc Natl Acad Sci U S A* **111**: E2616-21.