Rosaceae Gene naming committee meeting held on the 20 March 2014

Present: Sook, Carole, Lee, Doug, Robert

Appologies: Janet, Michela

*Gene naming:*

For the species it is now agreed that the 3 letter naming convention will be followed. 1 for the genus and 2 for the species. The commercial species will be put into a table in the paper.

*Paper progress:*

The paper is a good start, there needs to be some cleaning up but on the whole OK. We went through the paper section by section addressing issues

Section 1 species:

OK Doug to add table and numbers selected.

Section 2 Gene naming convention

This is Standard across most organisms and is not contentious

Section 3

The actual genes... It was discussed that we should not use Like in the name because once called this name then if it is the actual gene then the name will not change. Therefore we will put in a sentence about uncertaintanty. Due to most of the genes being selected on homology, there is an uncertainty to gene function. We encourage authors to look for the best match in the genome to call the gene after a known gene in another species. The naming from model species will be the most widely used methodology.

The possibility of requiring a threshold was discussed and dropped as it is too variable.

We will go with first right. Those that register the genes first will have naming righs.

We decided not to persue the 1 and 101 suggestion as each is a unique gene, and therefore should get a unique number. For polypolody it is harder. But it was suggested that genes should be named from the diploid model species, then homeologous genes within the polyploidy could be identified.

We aim to get the Paper first draft by the middle of April

Google doc location (advisable to open in something other than Microsoft IE): <https://docs.google.com/document/d/1BA0JOIAAaj1nRa_IQ_MnpxGrTjMmtGyNLIbVJMQoro8/edit?usp=sharing>

The GDR web pages

Sook presented two key web pages.

1. Gene families. Based on the Arabidopsis gene family website, it was proposed to have a gene family group, and go to person for that group. Sook requested volunteers for some gene families
   1. Carole Dehydrins
   2. Lee ??
   3. Robert Glycosyl hydrolase families
   4. Doug MADS box genes
2. Spreadsheet of individual names
   1. It was decided that there should be one table per species as it gets too complicated to combine.
   2. Gene name, gene model, and importantly level of confidence for that gene model. Starting at the gold standard single molecule sequencing, through transcriptomic assemblies, (manually annotated from genome), to computer model predition

Carole to get better definitions for the 3 (4)

1. Single molecule cDNA sequence;
2. Compilation of RNA-seq;
3. Computational evidence

* 1. A separate column for previous naming conflicts were also suggested

Sook to set up a web page for us to test in the next month

Other business:

There was a suggestion for a poster presentation in RGC7 which was supported Sook and Robert to write abstract.

8.15 am (NST) meeting closes