

Mitochondrial genome variation in *Helianthus*

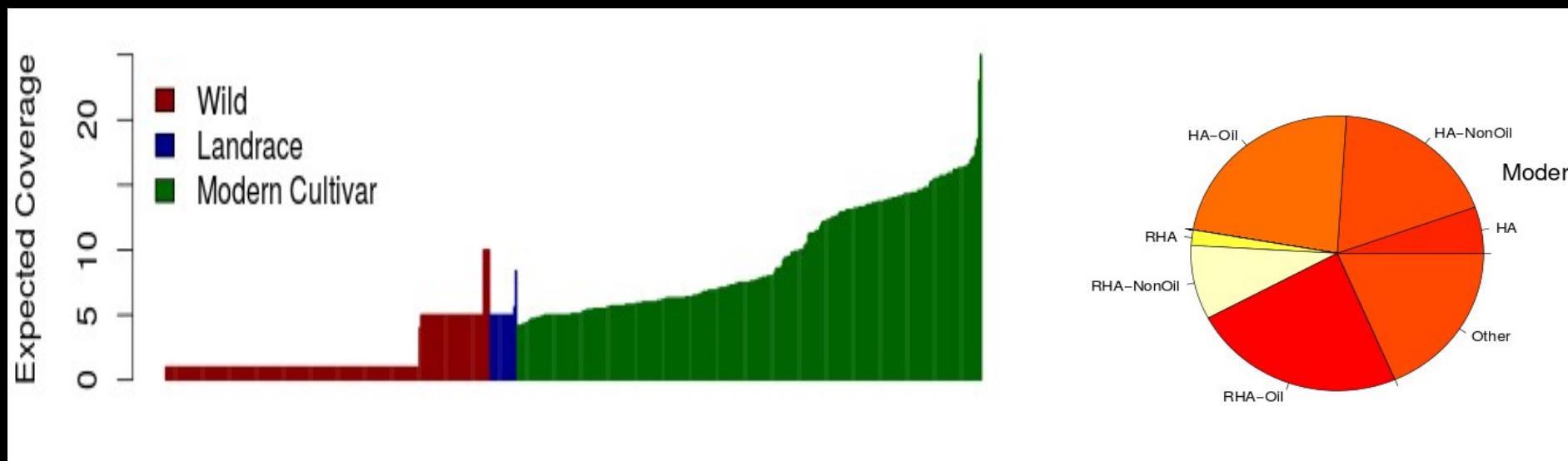


Sariel Hübner

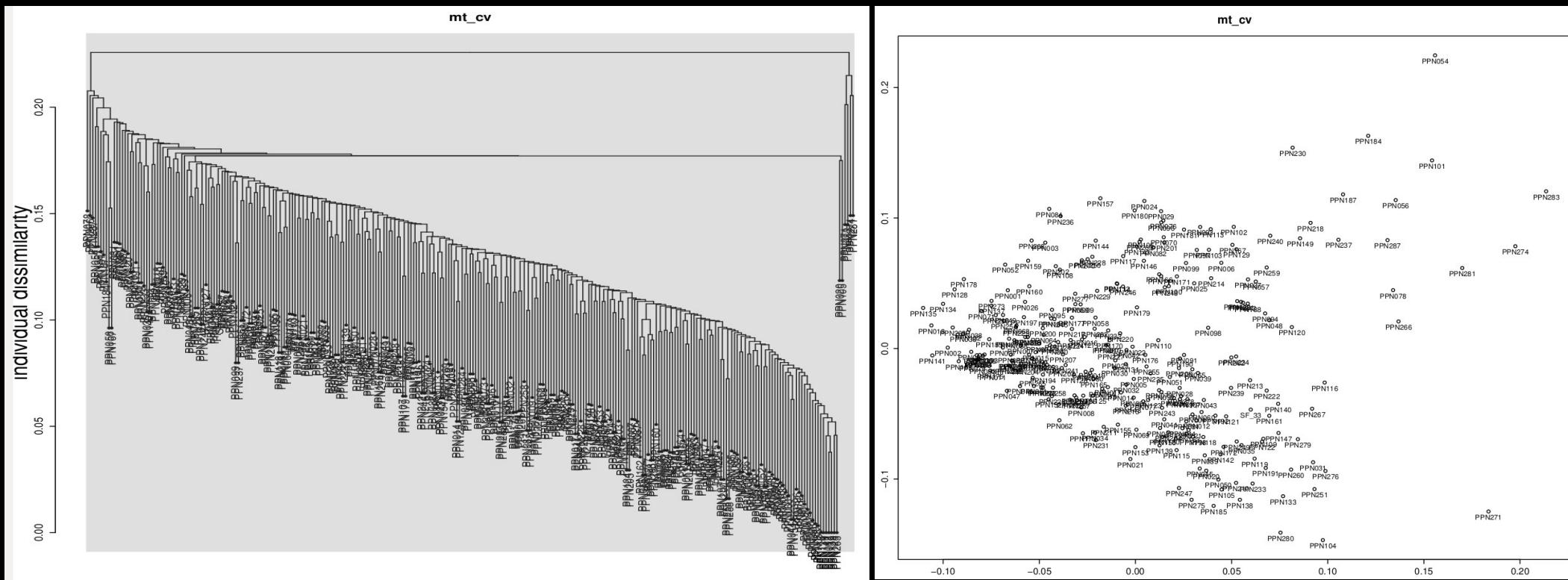
PAG - 2016

The cultivated sunflower genepool

- The SAM population: 288 accessions representing most of the variation in cultivated sunflower
- WGSS of 5-25X

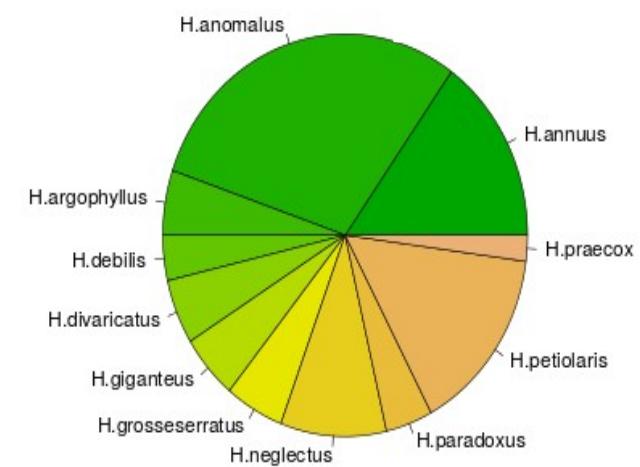
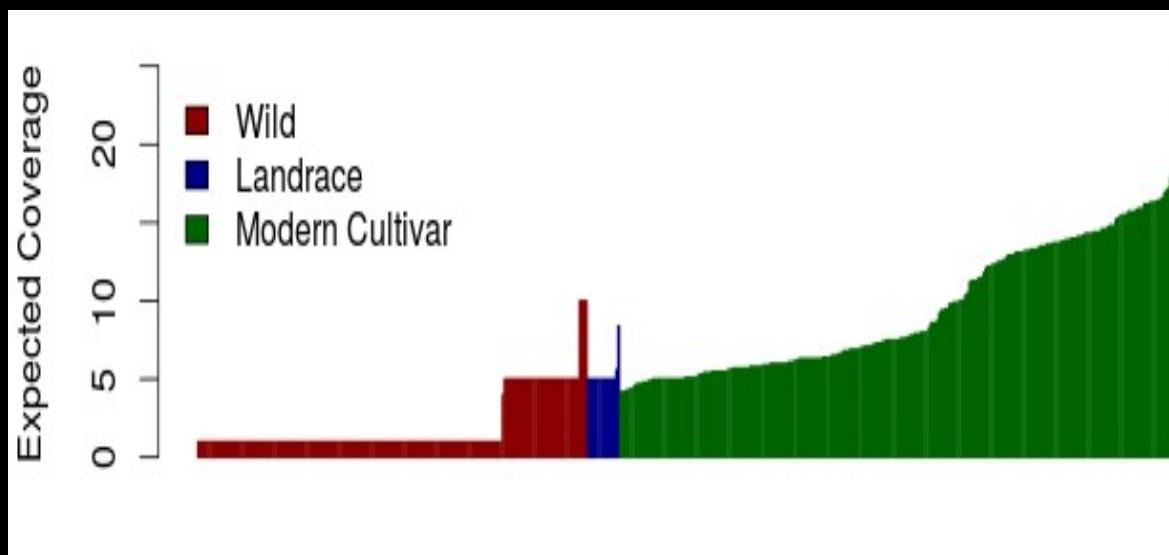


The cultivated mitochondria

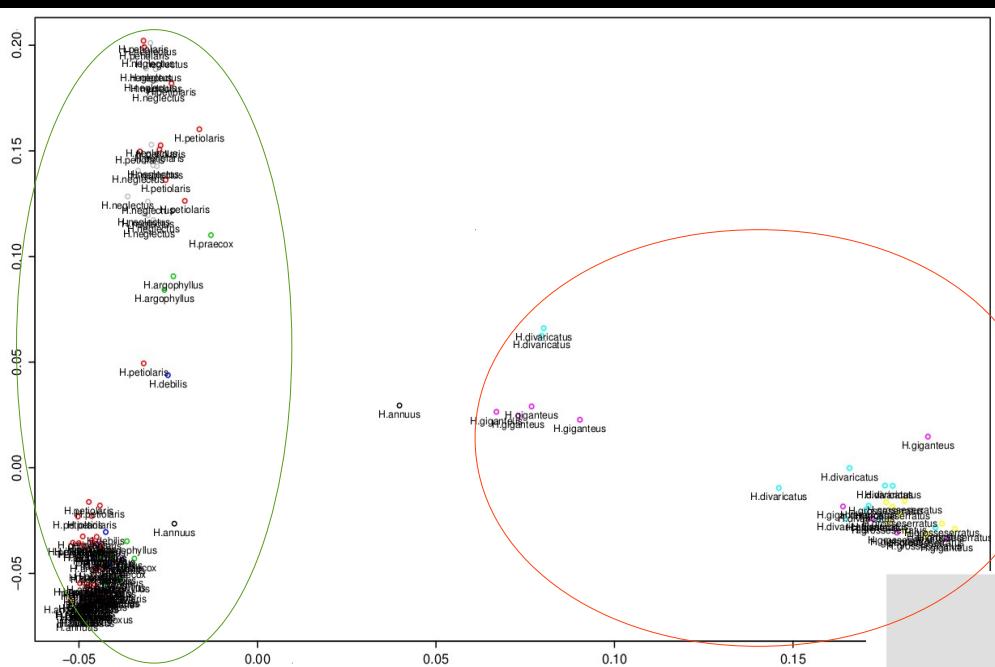


The wild genepool

- Sunflower wild relatives: 193 accessions representing 11 species.
- WGSS of 1-5X

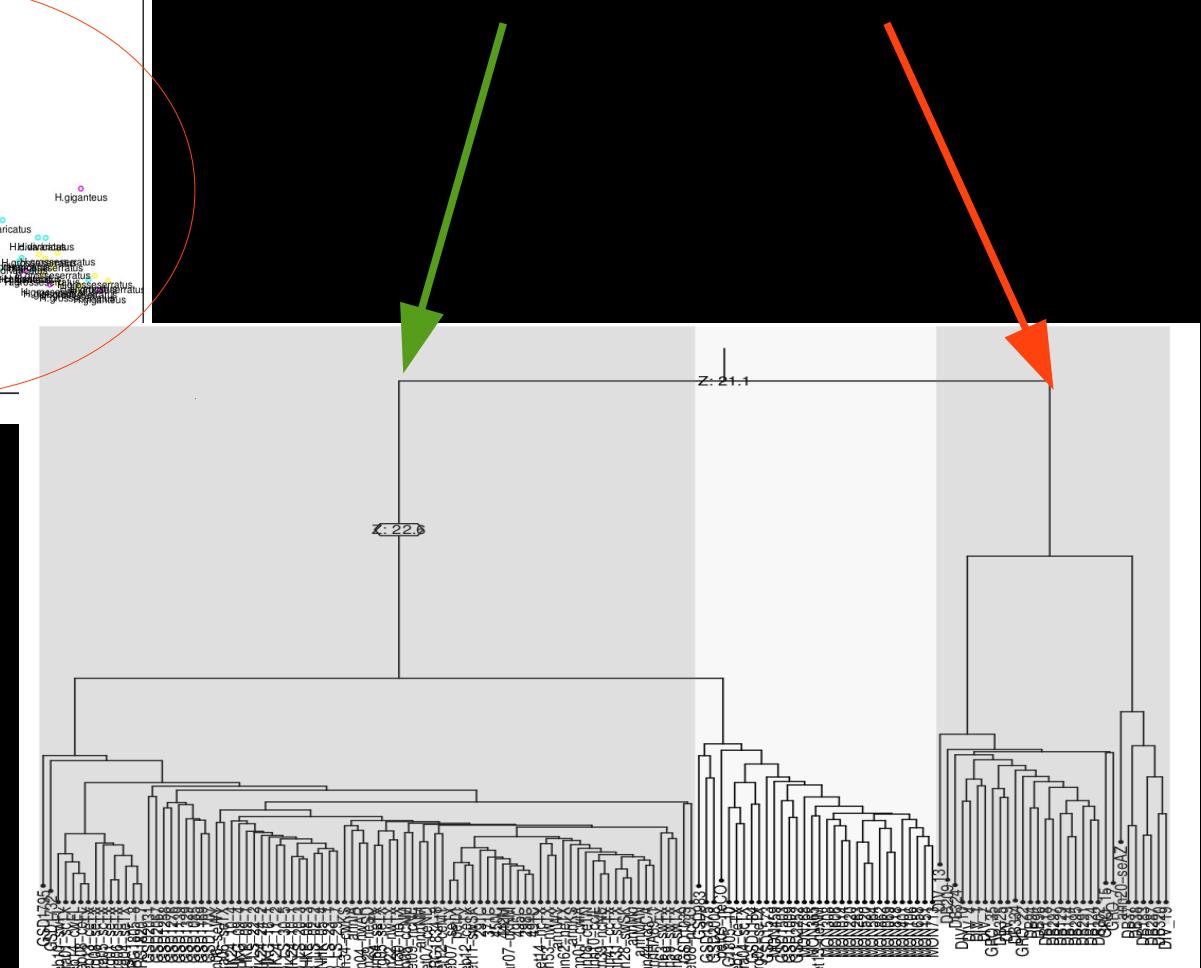


The wild mitochondria



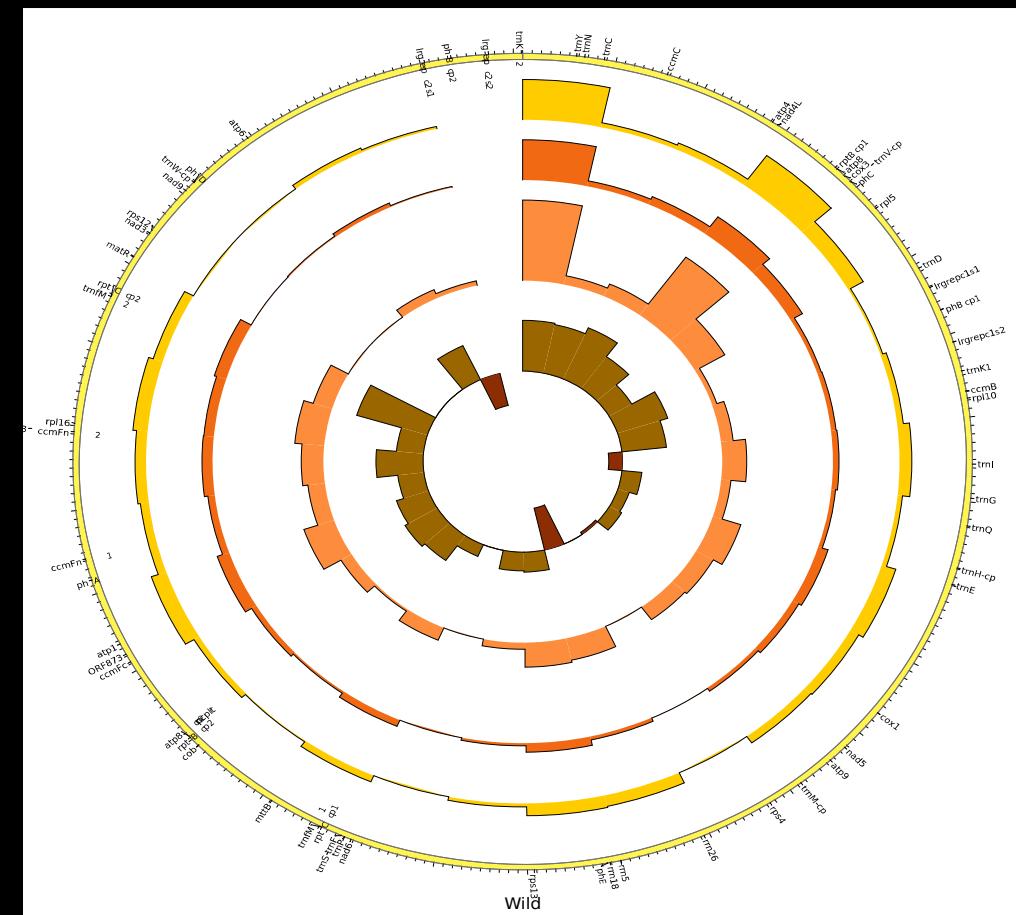
Long branches

Mitochondria variation clusters
into
annuals/perennials

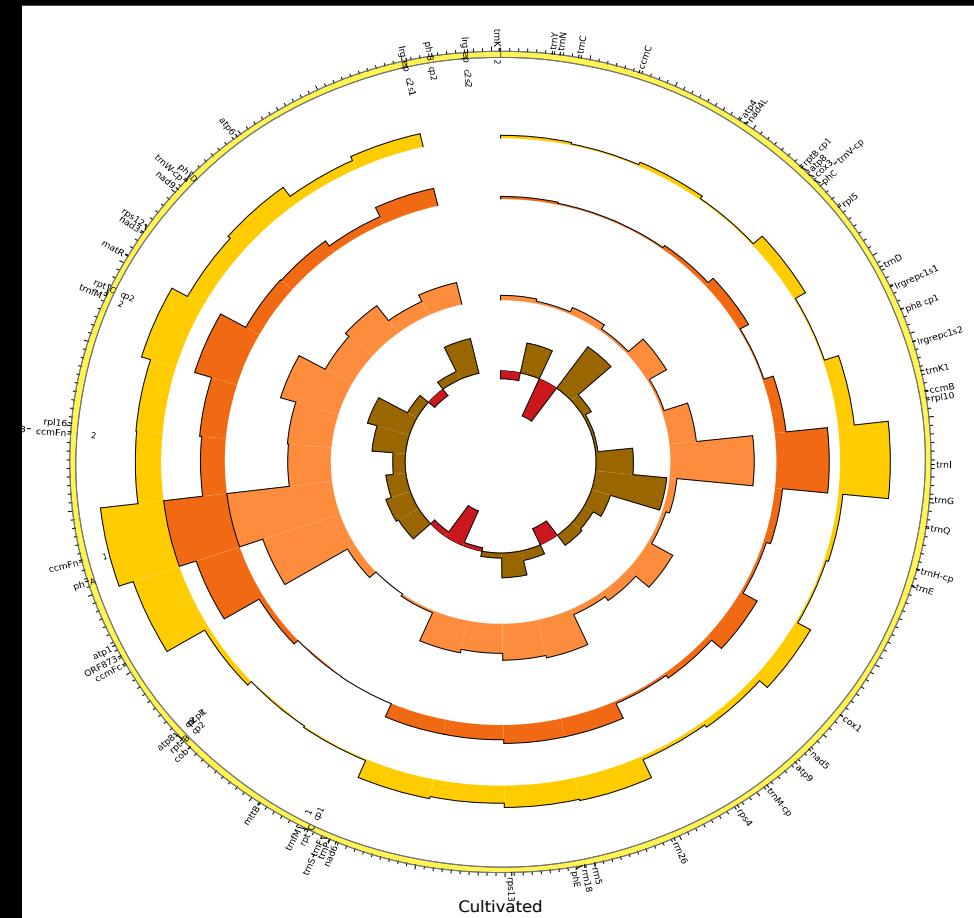


The *Helianthus* collection

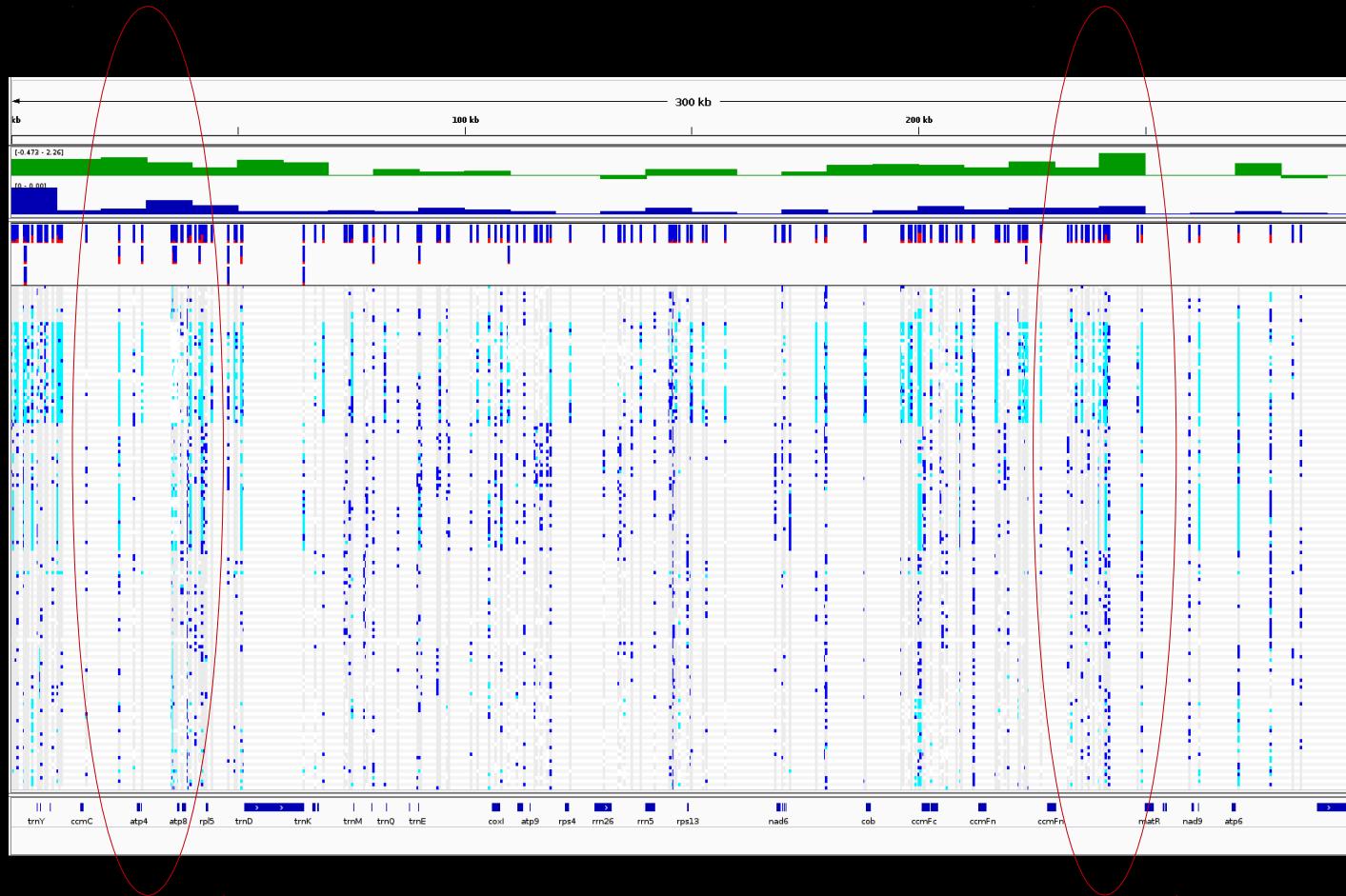
wild



cultivated



Variation among wild mitochondria



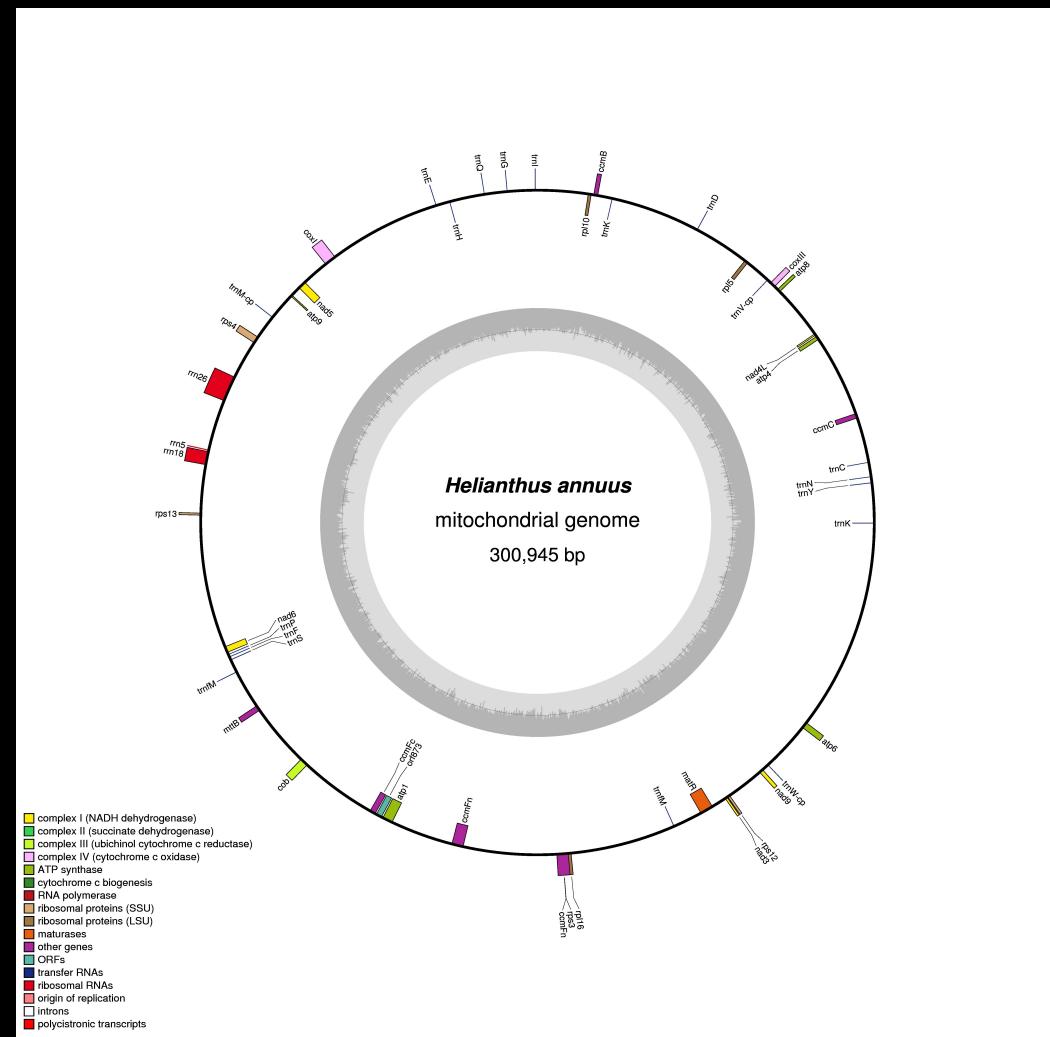
The sunflower mitochondrial genome



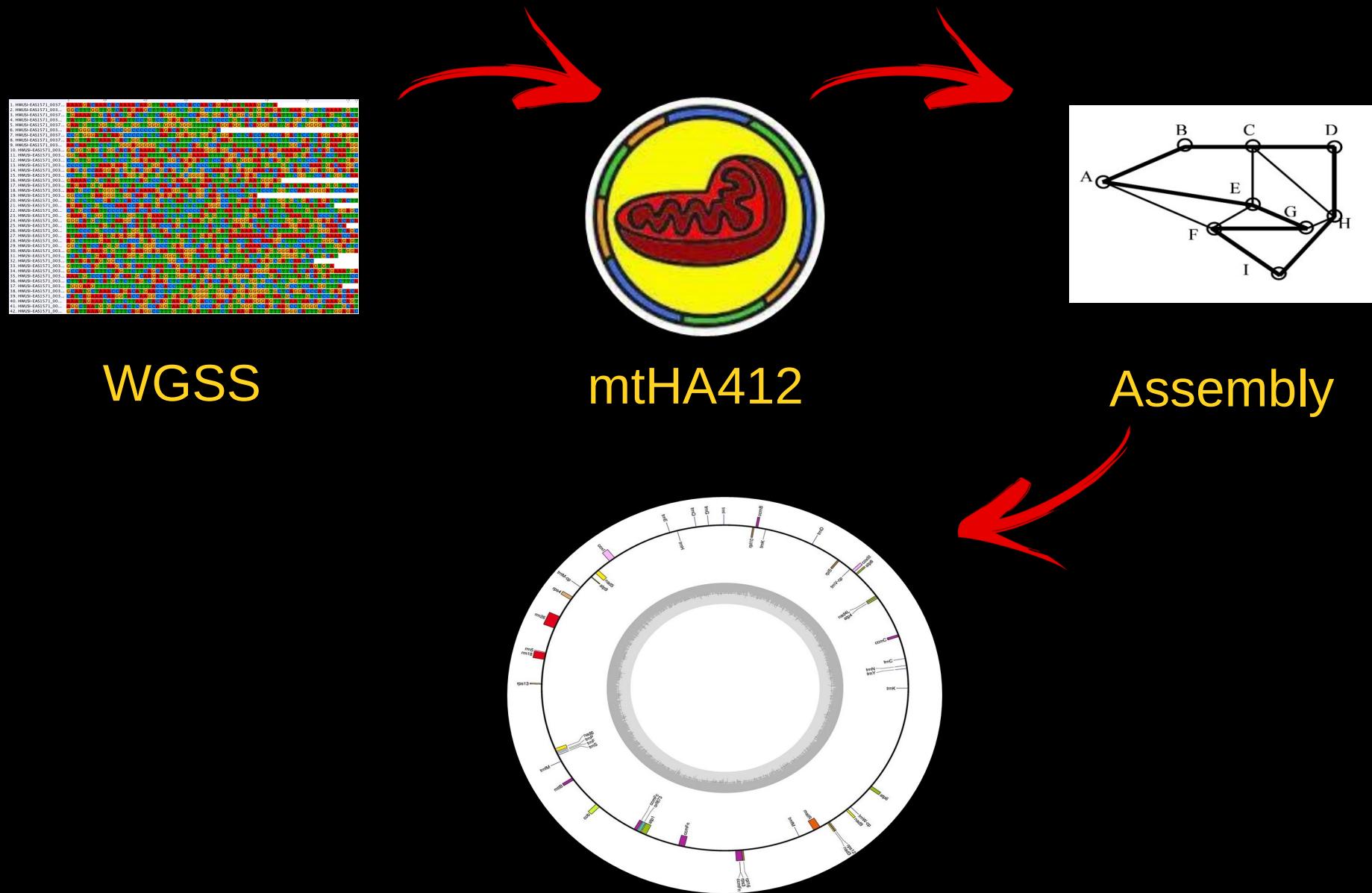
Kai Blumberg



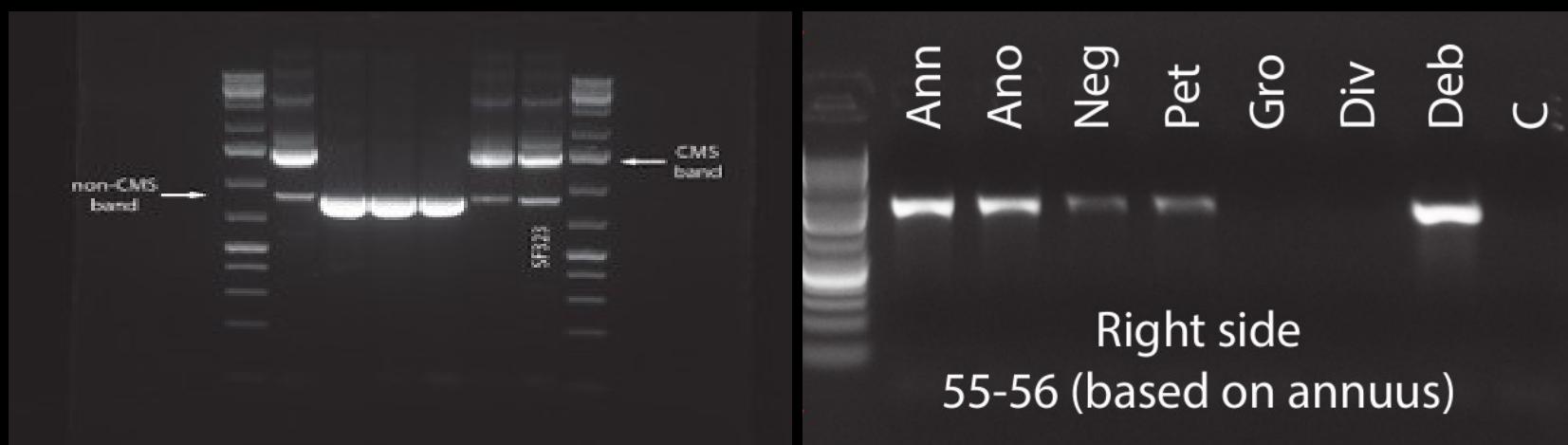
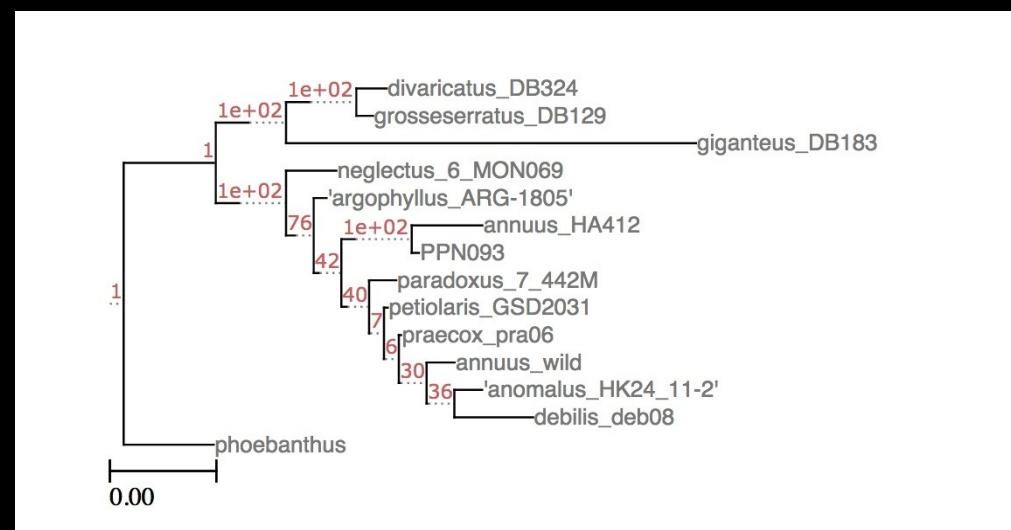
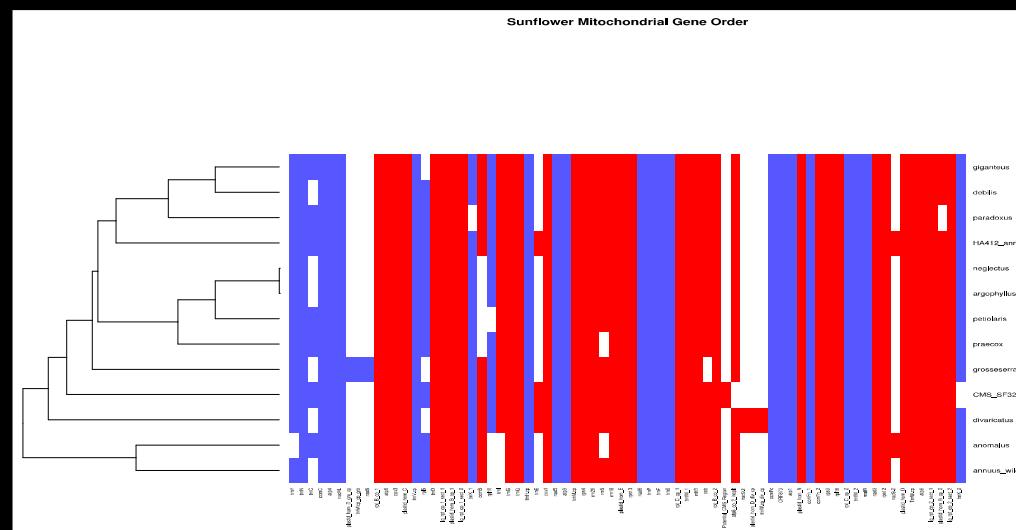
Tal Shalev



Mitochondrial genome assembly from WGS



Mitochondria assemblies





Thanks!

Loren Rieseberg

Kai Blumberg

Tal Shalev

Marco Todesco

Chris Grassa