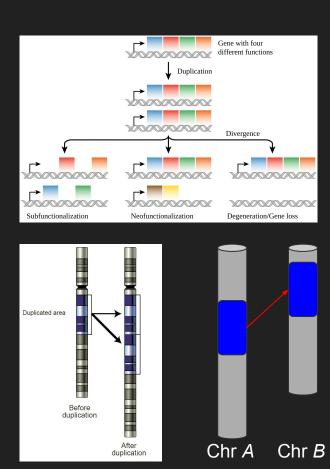
# Evolution after duplication The fate of gene function studied in eight Brassicaceae

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#### Introduction

- Gene duplication is a major mechanism through which new genetic material is generated during molecular evolution.
- A duplicate can mutate and change its gene function without reducing fitness through loss of function.
- No large scale comparison of tandem and trans duplication done.

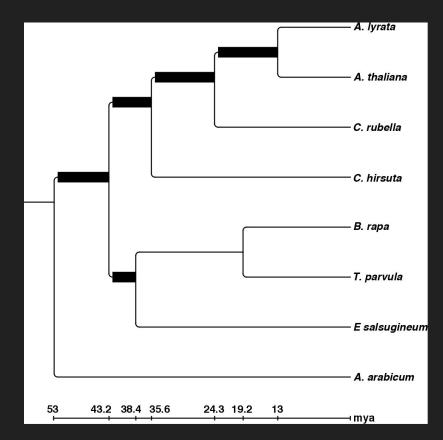


#### Material

- Eight Brassicaceaen genomes
- Coding Sequences

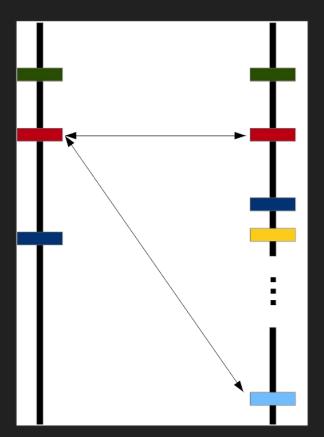
Gan, X. et al. The Cardamine hirsuta genome offers insight into the evolution of morphological diversity.

Nature Plants 2, 16167 (2016).



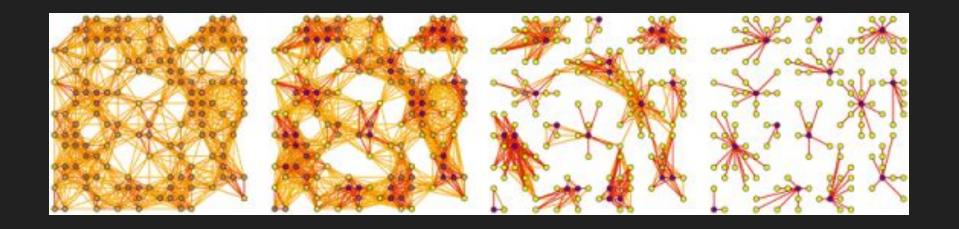
#### Methods: Ortholog and Tandem detection

- Reciprocal highest local pairwise sequence similarity
- Synteny: Gene neighborhood



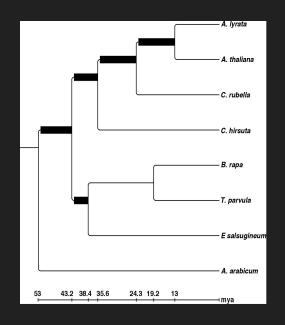
#### Methods: Gene family reconstruction

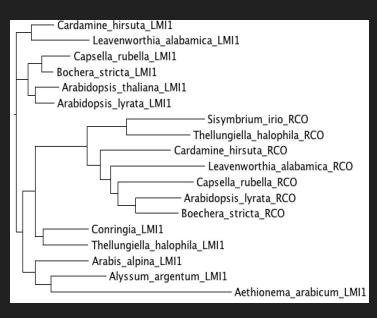
 Markov clustering on local pairwise sequence similarity (Blast)



#### Methods: Expansion / Contraction of gene families

- Ultrametric gene tree (UST)
  - Concatonated
     MSA of approx.
     10,000 ortholog
     clusters
  - A prioriknowledge drivenscaling
- Fit gene birth/death
   rate to UST
- Compare per species gene number with simulated trees





UST Gene Family Tree

#### Methods: trans duplicate identification

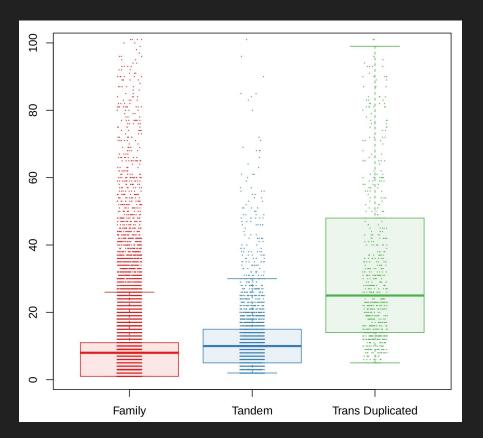
- Member of significantly expanded gene family
- By exclusion
  - Non-Ortholog
  - Non-Tandem



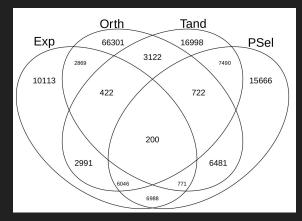
Poor guy - I mean: Gene

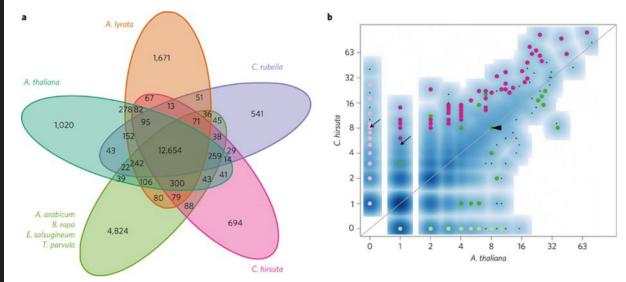
#### Results: Some numbers

- 10,111 groups of orthologous genes
- 16,910 non singleton gene families
- 758 families were significantly expanded or contracted
- 3,266 tandemly duplicated gene clusters



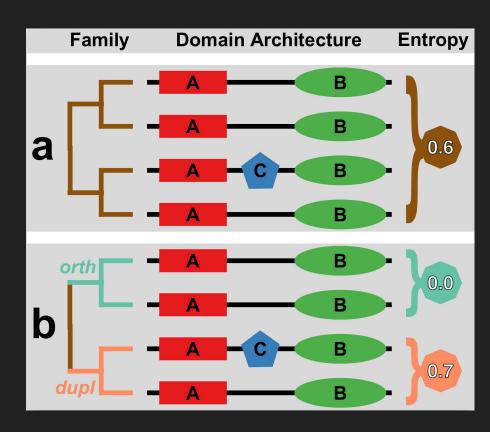
#### Results: Gene Families



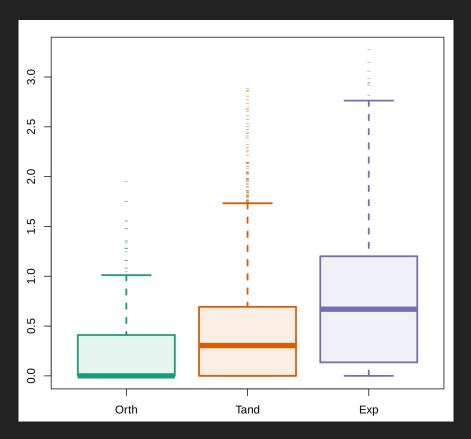


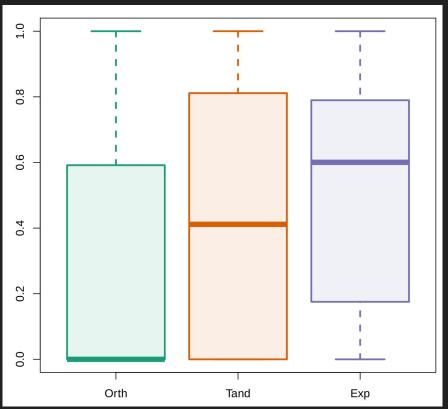
#### Methods: Protein domain architecture

- InterProScan identified conserved protein domains
- Each protein has a unique domain architecture
- Groups of genes (families, ortholog clusters, tandem clusters) have diversity of domain architecture
  - Shannon Entropy

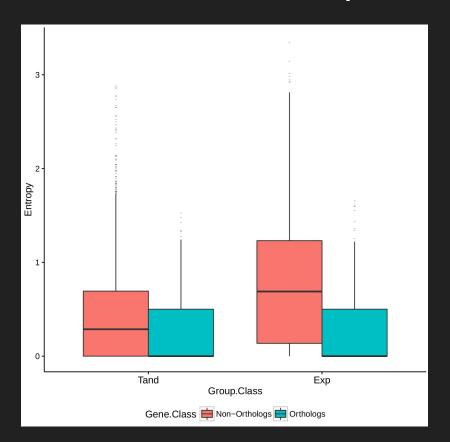


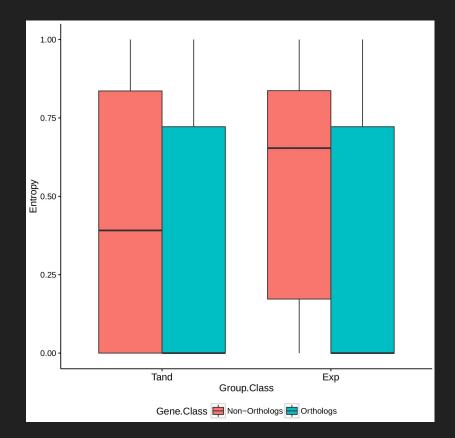
## Results: Domain Architecture Diversity





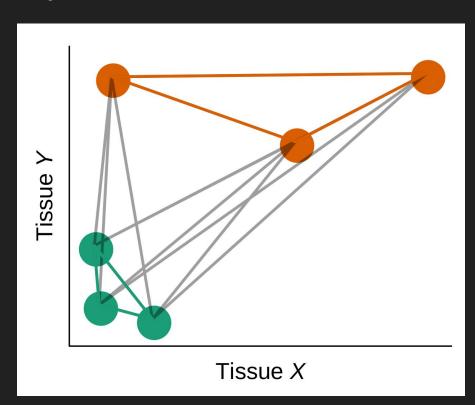
#### Results: Intra-Group domain architecture diversity



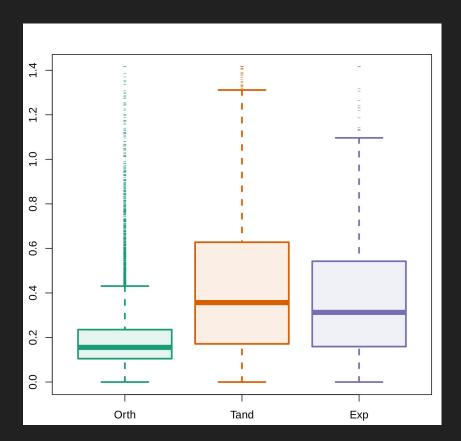


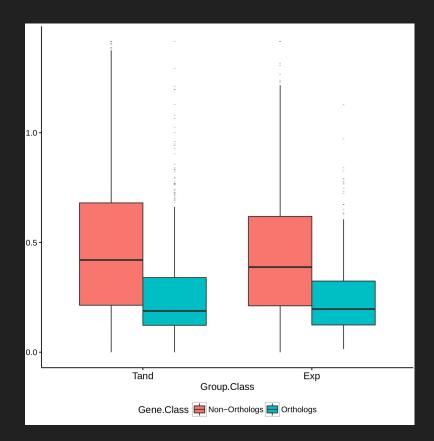
#### Methods: Expression Diversity

- RNA-Seq for five tissues:
  - Two species <u>only</u>:
    - A. thaliana
    - C. hirsuta
  - Seedling
  - Cotyledon
  - Developing Leaf
  - Flower stage 9
  - Flower stage 16
- Expression vector space on RPKM values
  - Relative for euclidean distance measures
  - Median of in-group pairwise euclidean distances



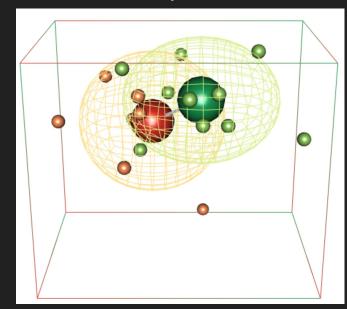
# Results: median Expression Distances

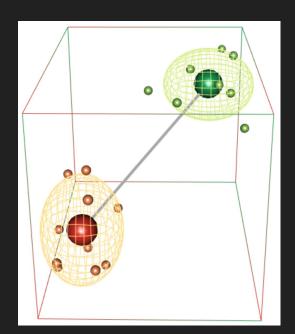




#### Methods: Significant diversification of expression

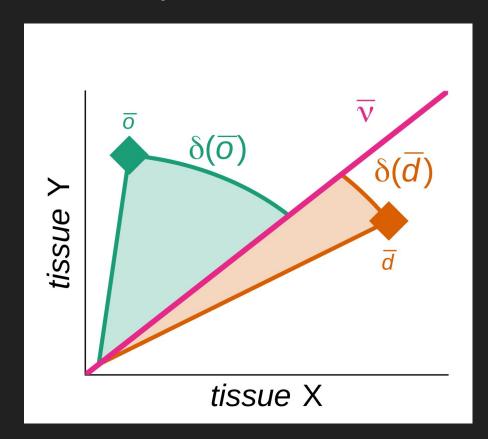
- Group-wise mean expression: Orthologs vs Duplicated
- Standard deviation space
- Separation or overlap?



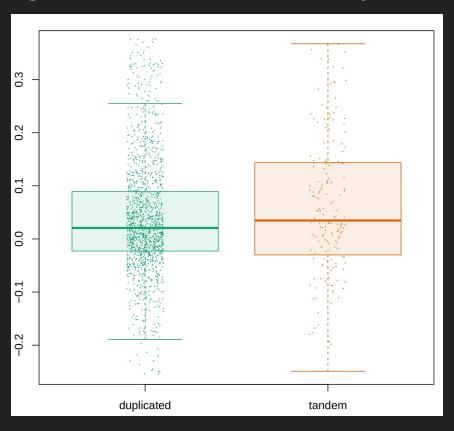


#### Methods: Change in tissue versatility

- Groups with significant separation of expression
- Gain or loss in number of tissues?

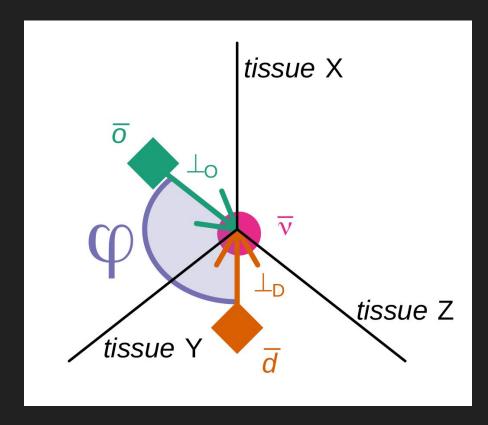


## Results: Change in tissue versatility

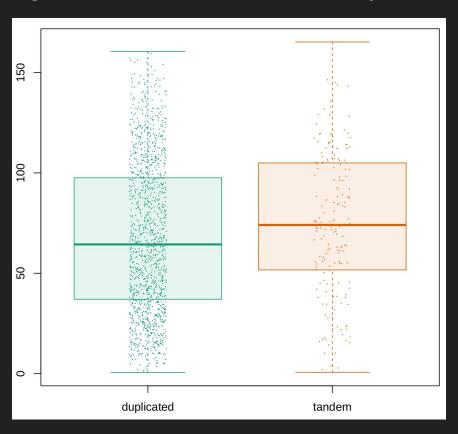


#### Methods: Change in tissue specificity

- Groups with significant separation of expression
- Switch to other tissues?



# Results: Change in tissue specificity



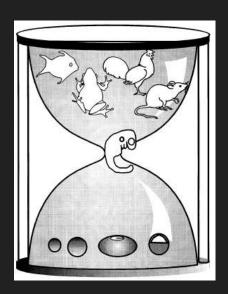
#### Conclusion

After gene duplication

- Tandem Duplicates tend to expressional diversification
- Trans Duplicates tend to molecular diversification

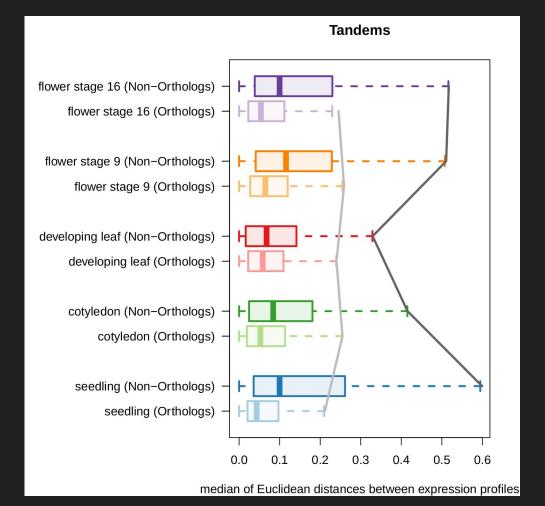
#### Side story: The developmental hourglass

- Expression diversity is highest in early and late developmental stages of embryos
- Conserved in animals and plants
- What kind of genes contribute to this effect?
- Plants develop through their whole life-span



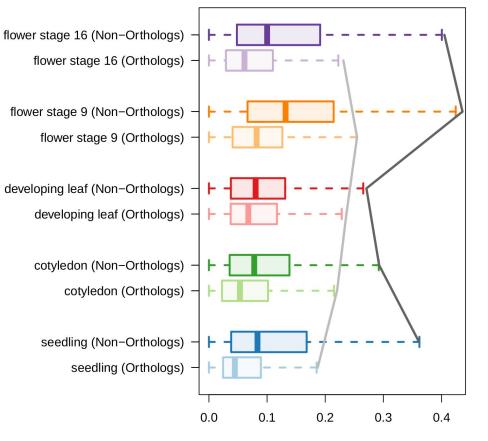


# Results: Tandems - Tissue specific expression diversity



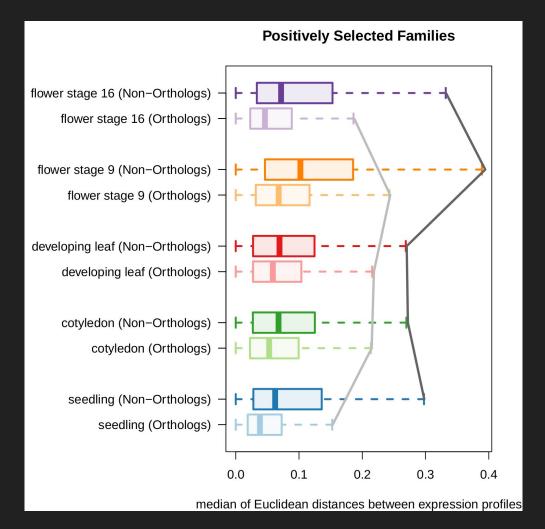
# Results: trans duplicates -Tissue specific expression diversity

#### **Expanded Families**



median of Euclidean distances between expression profiles

# Results: Pos. selected genes Tissue specific expression diversity



#### Side Story Conclusion

- Indication for a developmental hourglass throughout the plant's life-span?
- Tandem duplicates, trans duplicates, and positively selected genes appear to underpin this expression diversity.
- Gene duplication and diversification of expression leads to differential morphogenesis?
- Evidence might be too weak.

# Thank you very much



Yokozuna Harumafuji gives you all a big big hug