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Peter the Great
St. Petersburg Polytechnic
University

Structural Variation in the Flax *Linum Usitatissimum* L. Genome

Maria Duk ^{1,2}

¹Centre for Computational Biology, Peter the Great St. Petersburg Polytechnic University,
St. Petersburg, 195251, Russia

²The Ioffe Institute, St. Petersburg, 194021 Russia

Flax dataset

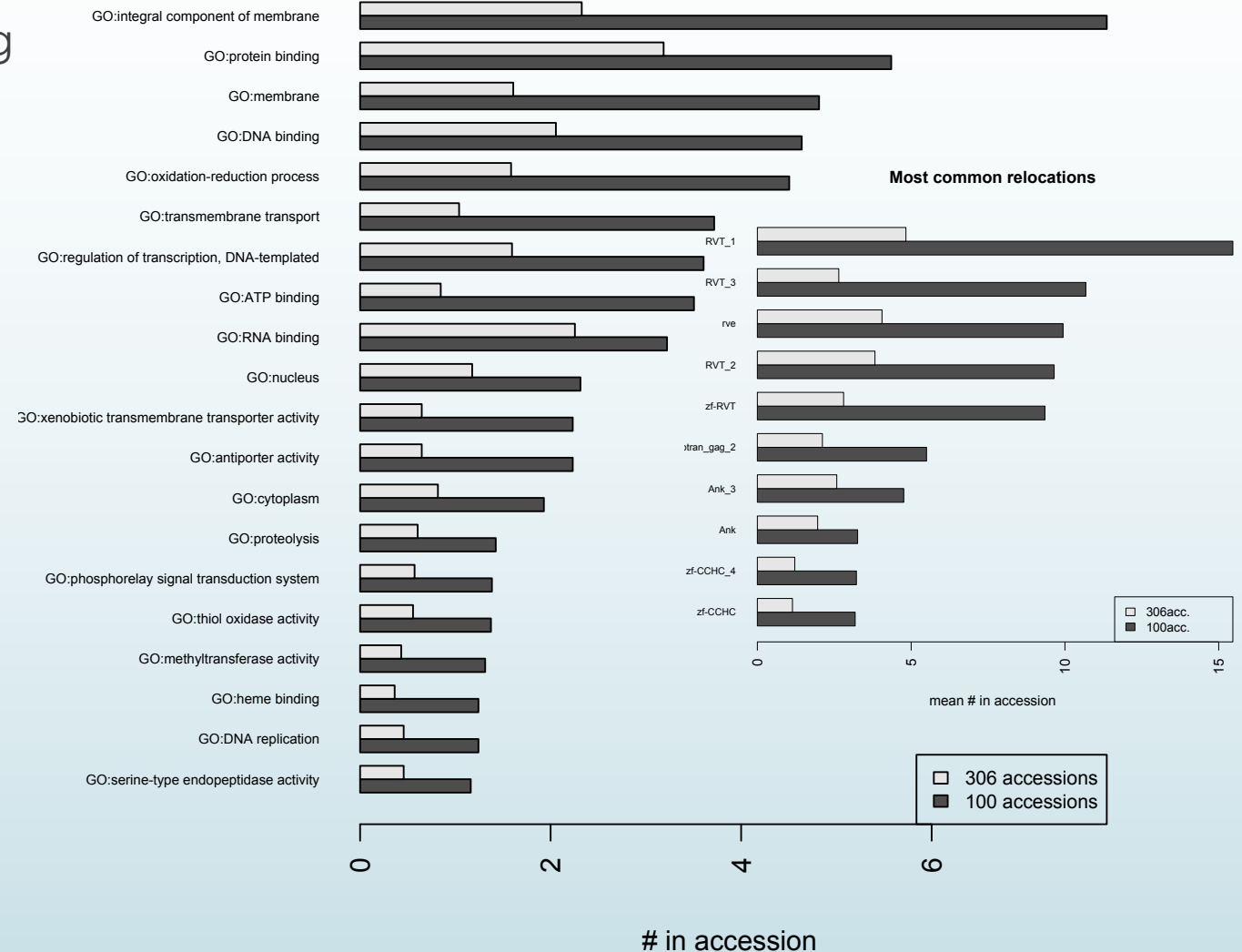
- ▶ Flax is a significant agricultural crop cultivated for fiber and oil
- ▶ Characterization of genetic diversity is important for successful breeding programs
- ▶ Two datasets: 100 accessions (coverage 20.6x), 306 accessions (coverage 9.3x)
- ▶ grown in the experimental fields of Federal Research Center for Bast Fiber Crops, Torzhok, Russia
- ▶ Two types of structural variation:
 - Presense-absense variation (PAV)
 - Copy number variation (CNV)



New insertions & relocations

- Coverage in sequencing is important
- Insertions were enriched in genes involved in membrane processes, DNA&RNA binding, energy and oxygen exchange and gene regulation.
- Relocations of genome regions were mostly enriched in genes with retrotransposon activity.

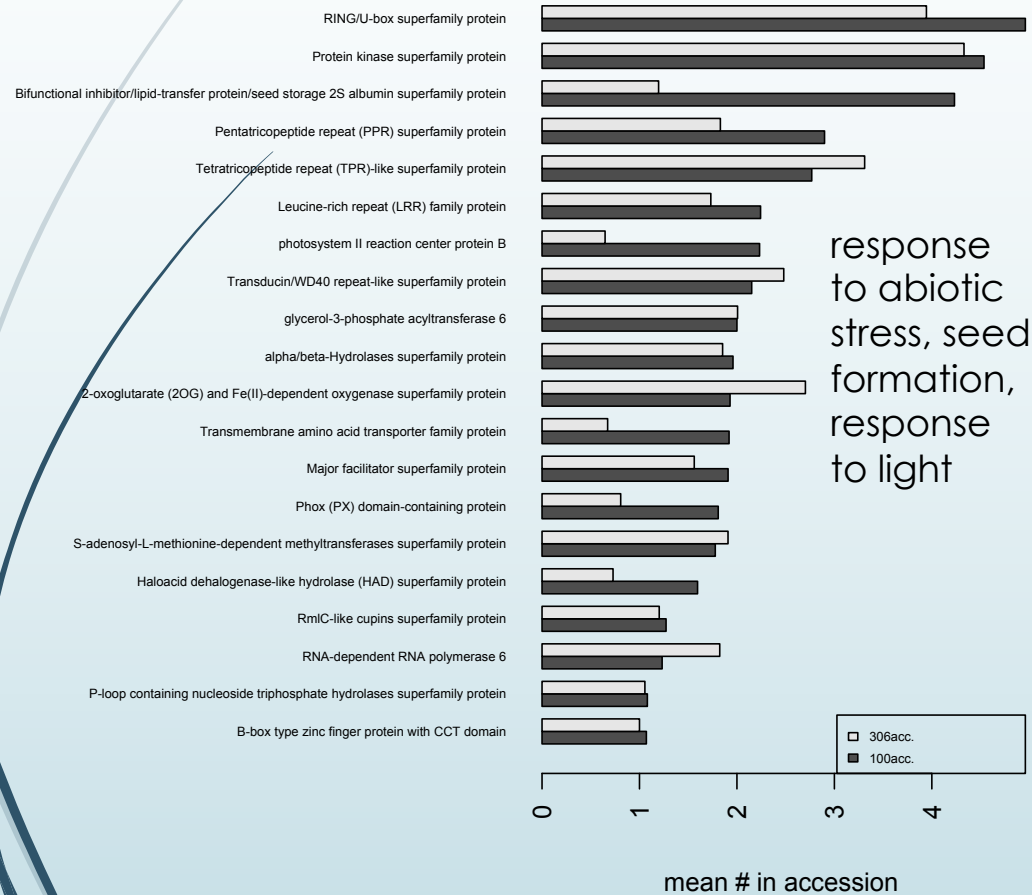
Most common domains annotated in GO



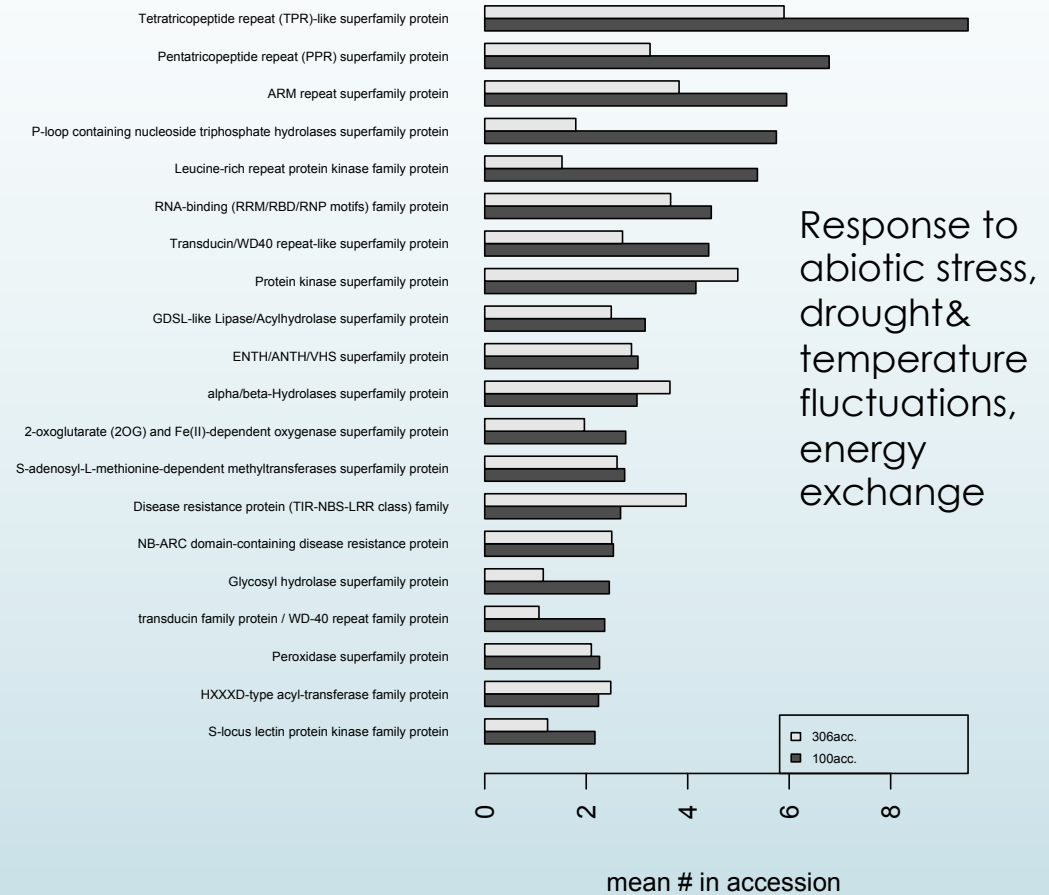
Deletions & amplifications

➤ Many important domains are deleted in one accessions and duplicated another (TPR, PPR, WD40, LRR), this shapes genetic flax landscape and bestows unique features to each cultivar

The most common functions in amplifications



The most common functions in deletions





Conclusions

- ▶ We analysed two types of structural variation: gene presence/absence variation (PAV) and copy number variation (CNV).
- ▶ In individual genomes we observed (1) deletions of DNA sequences, (2) insertions of new sequences, (3) copy number amplification.
- ▶ The functional annotation of the corresponding regions in the reference genome and new sequences showed that they encode proteins involved in the plant response to biotic and abiotic stresses, in energy metabolism, viral and transposon activity, and in the formation of cell membranes.
- ▶ Flax adapts to regional growing conditions by means of structural variation.
- ▶ Our results provide a valuable resource for future pangenomic studies.

Aknowledgements



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<http://compbio.spbstu.ru/lab>