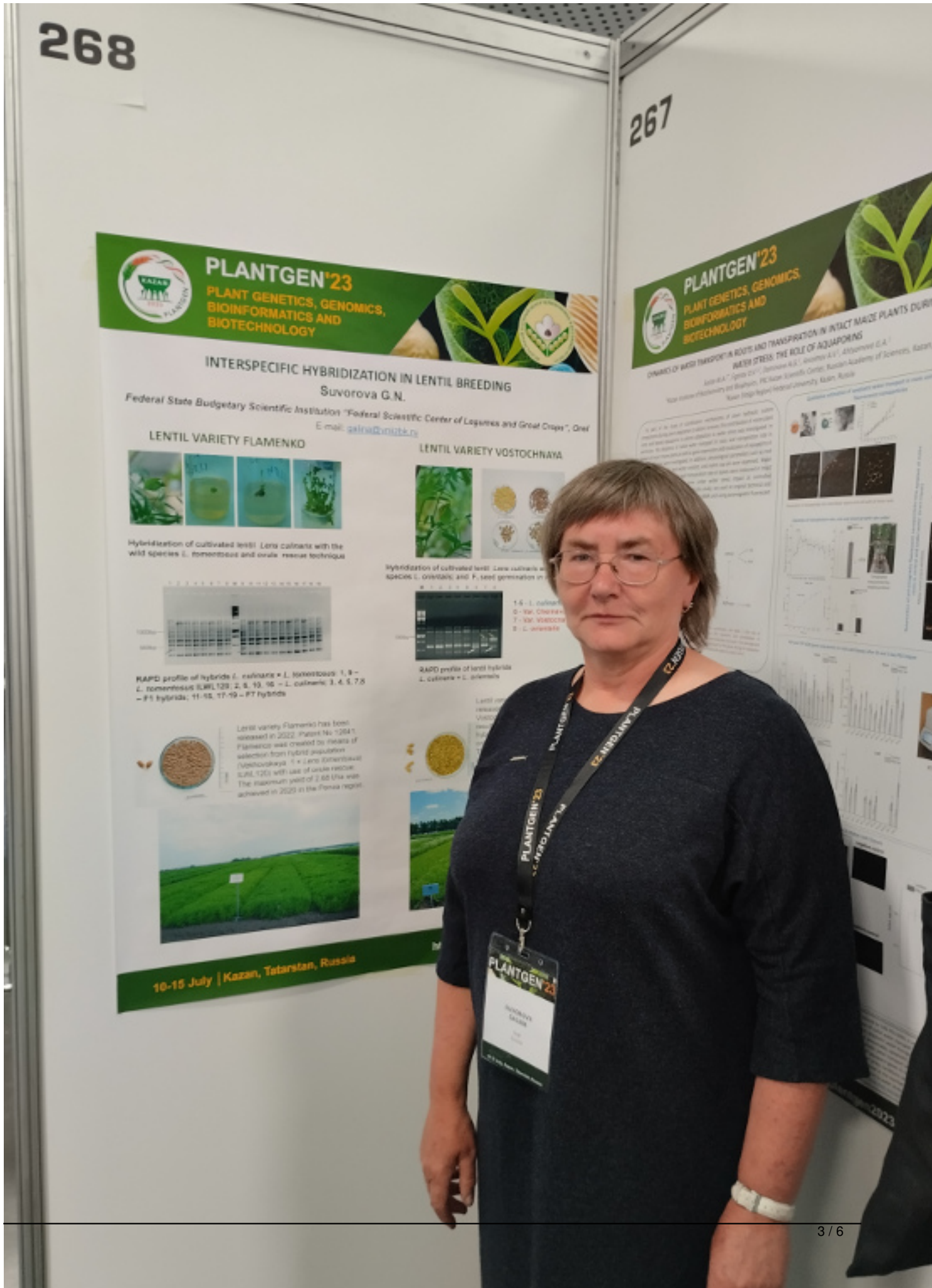


VII

Международная научная конференция «Генетика, Геномика, Биоинформатика и Биотехнология»



С VII Междунардной Научной Конференцией «Генетика, Геномика, Биоинформатика и Биотехнология»



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PLANTGEN'23
PLANT GENETICS, GENOMICS,
BIOINFORMATICS AND
BIOTECHNOLOGY

INTERSPECIFIC HYBRIDIZATION IN LENTIL BREEDING
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LENTIL VARIETY FLAMENKO

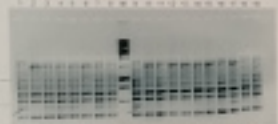


Hybridization of cultivated lentil. Lentil cultivars with the wild species *L. tomentosus* and *ovata* - rescue technique

LENTIL VARIETY VOSTOCHNAYA



Hybridization of cultivated lentil. Lentil cultivars with wild species *L. ovata* and *L. tomentosus* and F₂ seed generation in



RAPD profile of hybrids *L. culinaris* × *L. tomentosus*: 1, 9 - *L. tomentosus* (SWL129); 2, 8, 10, 16 - *L. culinaris*; 3, 4, 5, 7, 6 - F₁ hybrids; 11-15, 17-19 - F₂ hybrids



RAPD profile of lentil hybrids *L. culinaris* × *L. orientalis*

Lentil variety Flamenko has been released in 2022. Patent No. 12841. Flamenko was created by means of selection from hybrid population (*Vostochnaya* × *L. tomentosus* (SWL129)) with use of rescue technique. The maximum yield of 2.66 t/ha was achieved in 2020 in the Fomox region.



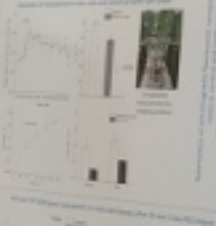
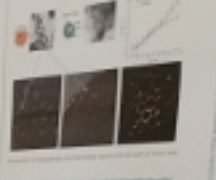
10-15 July | Kazan, Tatarstan, Russia

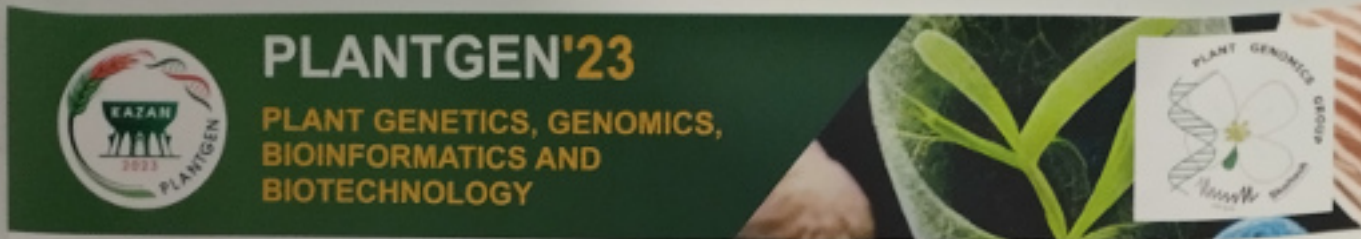
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PLANTGEN'23
PLANT GENETICS, GENOMICS,
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DYNAMICS OF WATER TRANSPORT IN ROOTS AND TRANSPIRATION IN INTACT MAIZE PLANTS DURING WATER STRESS: THE ROLE OF AQUAPORINS
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In all of the types of aquaporins (AQP) in plant cells, water transport is regulated by phosphorylation and dephosphorylation of serine residues. In maize roots, AQP1 is the most abundant AQP. In this study, we investigated the role of AQP1 in water transport in intact maize plants during water stress. We used a mutant maize line with a targeted deletion of the AQP1 gene. The results show that the AQP1 gene is essential for water transport in maize roots. The mutant plants showed a significant reduction in water uptake and transpiration during water stress. The results suggest that AQP1 plays a crucial role in water transport in maize roots and transpiration in intact maize plants during water stress.





Genetic regulation of seed shattering in *Fagopyrum* genus

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Introduction

Seed shattering in buckwheat is almost unstudied, although his knowledge could be very useful for improving buckwheat as a crop. We focused on *F. esculentum* and its wild ancestor *F. esculentum ancestrale*. The previous studies indicate that *F. esculentum* has a single gene responsible for non-shattering phenotype, and it is present in homozygous recessive state in all buckwheat cultivars. We studied the processes which happen in the pedicels during abscission comparing *F. esculentum* with its shattering ancestor and suggested a list of candidate genes which could be responsible for abscission disruption in non-shattering *F. esculentum*.

Approach

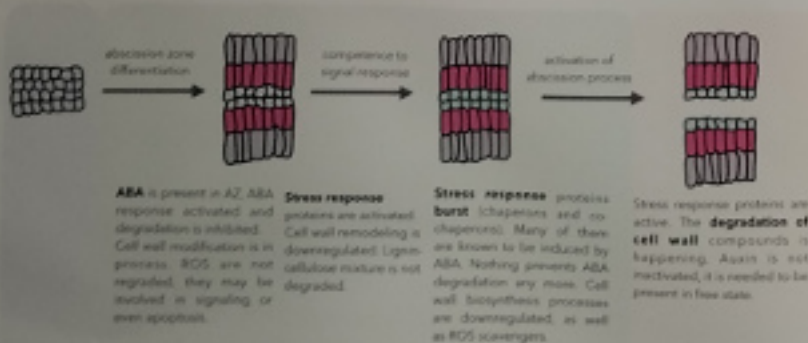
For collecting expression profiles we used the second generation of cross-breeding between *Fagopyrum esculentum* ssp. *ancestrale* and *Fagopyrum esculentum* cultivar Dasha (F₂). For transcriptome analysis, RNA was extracted directly from the pedicels.

To list the candidate genes we used the previously discovered region, which includes the gene of interest. We used the data from buckwheat expression map (Penin et al., 2021), to filter out the genes, which are not expressed in the inflorescence. Then we performed manual of those genes to choose the most plausible candidates.

Candidate genes

The most plausible candidate is **JOINTLESS**. J is a Mads-box protein which regulates the fate of floral meristem in tomato. *Jointless* tomato mutant displays a non-shattering phenotype, because it lacks the AZ. Apart from that, *jointless* disrupts determinate growth of floral meristem, which results in a 'leafy' phenotype. We do not observe a total breakdown of floral meristem; common buckwheat lacks the AZ, but the inflorescence develops normally.

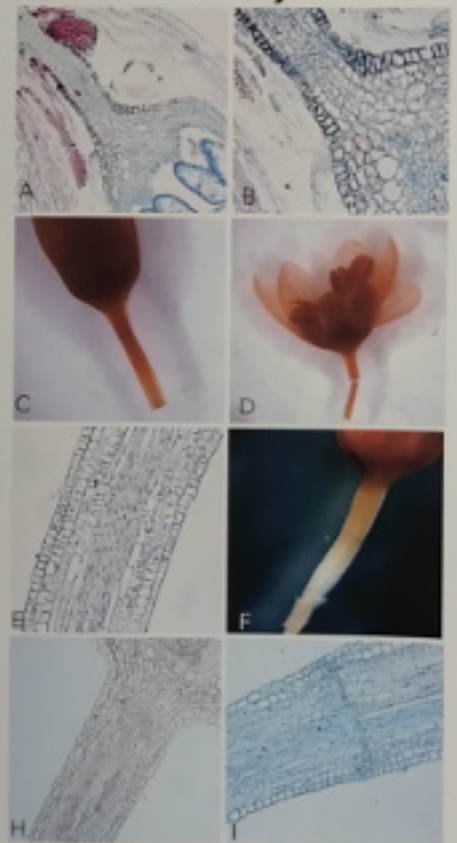
Transcriptome analysis



Aims

- Study the processes which happen in the pedicels during abscission from anatomical and genetical point of view
- Find the gene that switches off seed shattering in *F. esculentum*

Anatomical survey



F. esculentum *ancestrale* AZ anatomy. A, B - microscopic image of a pedicel in flower bud stage; C, D - lignin visualization in flower bud (C) and mature flower (D). *F. esculentum* Dasha AZ anatomy. E - microscopic image of a pedicel in flower bud stage; F - phloroglucinol - quality reaction demonstrates the absence of lignin. Mature flowers of shattering and non-shattering *Fagopyrum esculentum*. H - *F. esculentum* Dasha, AZ is absent; I - *F. esculentum* *ancestrale*, AZ is present.

Conclusions. The AZ anatomy in buckwheat includes several layers of small dense cells and a layer of lignified cells, which is located on a distal part of AZ. AZ starts its development in the very stages. Non-shattering phenotype in common buckwheat is determined by the absence of functional abscission zone. *Jointless* is the most plausible candidate to be a regulator of fruit abscission.

