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## LIST OF SELECTED PUBLICATIONS (Last five years)

1. Khassanova G., Kurishbayev A., Jatayev S., Zhubatkanov A., Zhumalin A., Turbekova A., Amantaev B., Lopato S., Schramm C., Jenkins C., Soole K., Langridge P., Shavrukov Y. (2019). Intracellular vesicle trafficking genes, *RabC-GTP*, are highly expressed under salinity and rapid dehydration but down-regulated by drought in leaves of chickpea (*Cicer arietinum* L.). ***Frontiers in Genetics*** 10, Article 40. DOI: 10.3389/fgene.2019.00040. **IF = 4.151.**
2. Zotova L., Kurishbayev A., Jatayev S., Goncharov N.P., Shamambayeva N., Kashapov A., Nuralov A., Otemissova A., Sereda S., Shvidchenko V., Lopato S., Schramm C., Jenkins C., Soole K., Langridge P., Shavrukov Y. (2019). The General transcription repressor *TaDr1* is co-expressed with *TaVrn1* and *TaFT1* in bread wheat under drought. ***Frontiers in Genetics*** 10, Article 63. DOI: 10.3389/fgene.2019.00063. **IF = 4.151.**
3. Borisjuk N., Kishchenko O., Eliby S., Schramm C., Anderson P., Jatayev S., Kurishbaev A., Shavrukov Y. (2019). Wheat genetic modification for functional gains: from transgenesis to genome editing. ***BioMed Research International*** 2019, Article: 6216304. **IF = 2.583.**
4. Bulatova K., Mazkirat S., Didorenko S., Babissekova D., Kudaibergenov M., Alchinbayeva P., Khalbayeva S., Shavrukov Y. (2019). Trypsin inhibitor assessment with biochemical and molecular markers in a soybean germplasm collection and

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5. Schramm C., Shavrukov Y., Anderson P., Kurishbaev A., Jatayev S. (2019). Development of Single nucleotide polymorphism (SNP) markers for cereal breeding and crop research: current methods and future prospects. In: *Ordon F., Friedt W. (Eds). Advances in Breeding Techniques for Cereal Crops*. Cambridge: BD Publishing, (In press).
  6. Bi H., Shi J., Kovalchuk N., Luang S., Bazanova N., Chirkova L., Zhang D., Shavrukov Y., Stepanenko A., Tricker P., Langridge P., Hrmova M., Lopato S., Borisjuk N. (2018). Overexpression of the *TaSHN1* transcription factor in bread wheat leads to leaf surface modifications, improved drought tolerance and no yield penalty under controlled growth conditions. ***Plant, Cell and Environment*** 41 (11), 2549–2566. DOI: 10.1111/pce.13339. **IF = 5.415.**
  7. Ismagul A., Yang N., Maltseva E., Iskakova G., Mazonka I., Skiba Y., Bi H., Eliby S., Jatayev S., Shavrukov Y., Borisjuk N., Langridge P. (2018). A biolistic method for high-throughput production of transgenic wheat plants with single gene insertions. ***BMC Plant Biology*** 18, Article 135. DOI: 10.1186/s12870-018-1326-1. **IF = 3.93.**
  8. Zotova L., Kurishbayev A., Jatayev S., Khassanova G., Zhubatkanov A., Serikbay D., Sereda S., Sereda T., Shvidchenko V., Lopato S., Jenkins C., Soole K., Langridge P., Shavrukov Y. (2018). Genes encoding transcription factors TaDREB5 and TaNFYC-A7 are differentially expressed in leaves of bread wheat in response to drought, dehydration and ABA. ***Frontiers in Plant Science*** 9, Article 1441. DOI: 10.3389/fpls.2018.01441. **IF = 3.678.**
  9. Wanniarachchi V.R., Dametto L., Sweetman C., Shavrukov Y., Day D.A., Jenkins C.L.D., Soole K.L. (2018). Alternative respiratory pathway component genes (*AOX* and *ND*) in rice and barley and their response to stress. ***International Journal of Molecular Sciences*** 19, Article 915. DOI: 10.3390/ijms19030915. **IF = 3.226.**
  10. Absattar T., Absattarova A., Fillipova N., Otemissova A., Shavrukov Y. (2018). Diversity array technology (DArT) 56K analysis, confirmed by SNP markers, distinguishes one crested wheatgrass *Agropyron* species from two others found in

- Kazakhstan. *Molecular Breeding* 38, Article 37. DOI: 10.1007/s11032-018-0792-3. **IF = 2.465.**
11. Yerzhebayeva R., Abekova A., Konysbekov K., Bastaubayeva S., Kabdrakhmanova A., Absattarova A., Shavrukov Y. (2018). Two sugar beet chitinase genes, *BvSP2* and *BvSE2*, analysed with SNP Amplifluor-like markers, are highly expressed after *Fusarium* root rot inoculations and field susceptibility trial. *PeerJ* 6, Article e5127. DOI: 10.7717/peerj.5127. **IF = 2.20.**
  12. Jatayev S., Kurishbaev A., Zotova L., Khasanova G., Serikbay D., Zhubatkanov A., Botayeva M., Zhumalin A., Turbekova A., Soole K., Langridge P., Shavrukov Y. (2017). Advantages of Amplifluor-like SNP markers over KASP in plant genotyping. *BMC Plant Biology* 17 (S2), Article 254. DOI: 10.1186/s12870-017-1197-x. **IF = 3.93.**
  13. Shamaya N.J., Shavrukov Y., Langridge P., Roy S.J., Tester M. (2017). Genetics of Na<sup>+</sup> exclusion and salinity tolerance in Afghani durum wheat landraces. *BMC Plant Biology* 17 (1), Article 209. DOI: 10.1186/s12870-017-1164-6. **IF = 3.93.**
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  15. Kovalchuk N., Chew W., Sornaraj P., Borisjuk N., Yang N., Singh R., Bazanova N., Shavrukov Y., Guendel A., Munz E., Borisjuk L., Langridge P., Hrmova M., Lopato S. (2016). The homeodomain transcription factor TaHDZipl-2 from wheat regulates frost tolerance, flowering time and spike development in transgenic barley. *New Phytologist* 211 (2), 671–687. DOI: 10.1111/nph.13919. **IF = 7.433.**
  16. Shavrukov Y., Baho M., Lopato S., Langridge P. (2016). The *TaDREB3* transgene transferred by conventional crossings to different genetic backgrounds of bread wheat improves drought tolerance. *Plant Biotechnology Journal* 14 (1), 313-322. DOI: 10.1111/pbi.12385. **IF = 6.305.**
  17. Shavrukov Y., Hirai Y. (2016). Good and bad protons: Genetic aspects of acidity stress responses in plants. *Journal of Experimental Botany* 67 (1), 15-30. DOI: 10.1093/jxb/erv437. **IF = 5.354.**

18. Shavrukov Y. (2016). Comparison of SNP and CAPS markers application in genetic research in wheat and barley. ***BMC Plant Biology*** 16 (S1), Article 11. DOI: 10.1186/s12870-015-0689-9. **IF = 3.93.**
19. Shavrukov Y., Zhumalin A., Serikbay D., Botayeva M., Otemisova A., Absattarova A., Sereda G., Sereda S., Shvidchenko V., Turbekova A., Jatayev S., Lopato S., Soole K., Langridge P. (2016). Expression level of the *DREB2*-type gene, identified with Amplifluor SNP markers, correlates with performance and tolerance to dehydration in bread wheat cultivars from Northern Kazakhstan. ***Frontiers in Plant Science*** 7, Article 1736. DOI: 10.3389/fpls.2016.01736. **IF = 3.678.**
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21. Yadav D., Shavrukov Y., Bazanova N., Chirkova L., Borisjuk N., Kovalchuk N., Ismagul A., Parent B., Langridge P., Hrmova M., Lopato S. (2015). Constitutive overexpression of the *TaNF-YB4* gene in transgenic wheat significantly improves grain yield. ***Journal of Experimental Botany*** 66 (21), 6635-6650. DOI: 10.1093/jxb/erv370. **IF = 5.354.**
22. Shavrukov Y., Sokolov V. (2015). Maize-gamagrass interspecific hybrid, *Zea mays* x *Tripsacum dactyloides*, shows better salinity tolerance and higher Na<sup>+</sup> exclusion than maize and sorghum. ***International Journal of Latest Research in Science and Technology***, 4 (1), 128-133. **IF = 1.267.**
23. Schilling R.K., Marschner P., Shavrukov Y., Berger B., Tester M., Roy S.J., Plett D. C. (2014). Expression of the *Arabidopsis* vacuolar H<sup>+</sup>-pyrophosphatase gene (*AVP1*) improves the shoot biomass of transgenic barley and increases grain yield in a saline field. ***Plant Biotechnology Journal*** 12 (3), 378-386. DOI: 10.1111/pbi.12145. **IF = 6.305.**
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  27. Shavrukov Y. (2014). Vacuolar H<sup>+</sup>-PPase (*HVP*) genes in barley: Chromosome location, sequence and gene expression relating to Na<sup>+</sup> exclusion and salinity tolerance. In: *Hasunuma K. (Ed.) Barley: Physical Properties, Genetic Factors and Environmental Impacts on Growth*. NOVA Science Publisher, NY, pp. 125-142. Available at: [https://www.novapublishers.com/catalog/product\\_info.php?products\\_id=48834](https://www.novapublishers.com/catalog/product_info.php?products_id=48834).
  28. Kovalchuk N., Jia W., Eini O., Morran S., Pyvovarenko T., Fletcher S., Bazanova N., Harris J., Beck-Oldach K., Shavrukov Y., Langridge P., Lopato S. (2013) Optimization of *TaDREB3* gene expression in transgenic barley using cold-inducible promoters. ***Plant Biotechnology Journal*** 11 (6), 659-670. DOI: 10.1111/pbi.12056. **IF = 6.305.**
  29. Shavrukov Y. (2013) Salt stress or salt shock: Which genes are we studying? ***Journal of Experimental Botany*** 64 (1): 119-127. DOI: 10.1093/jxb/ers316. **IF = 5.354.**
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