

## The GAME genes as a target for *de novo* domestication of wild potato

S.V. Gerasimova<sup>1\*</sup>, K.A. Ivanova<sup>1</sup>, E.K. Khlestkina<sup>1, 2</sup>

<sup>1</sup>*Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*

<sup>2</sup>*N.I. Vavilov All-Russian Research Institute of Plant Genetic Resources (VIR), Saint-Petersburg, Russia*

\* e-mail: gerson@bionet.nsc.ru

**Key words:** domestication, potato, Solanaceae, steroidal glycoalkaloids, GAME genes, genome editing

Genome, transcriptome, and metabolome analysis of wild and domestic plants reveals so-called domestication genes associated with different traits of crop plants. *De novo* domestication via targeted modification of these genes is a new approach to accelerate domestication of wild plants, create new donors of valuable traits and increase a diversity of existing domestic forms. In the domestication process, humans have selected plants with desired traits. One of the main directions in domestication of edible Solanaceae species was selection against bitterness and toxicity. Wild potato species have bitter tubers and wild tomato has bitter fruits due to high steroidal glycoalkaloid (SGA) content. Recent study of genome changes associated with domestication of Solanaceae sp. revealed signatures of selection in genes controlling SGA biosynthesis and regulation (glycoalkaloid metabolism, GAME genes). In both potato and tomato genomes the GAME9 gene was found to be associated with domestication process [1, 2]. This gene encodes AP2/ERF transcription factor, shown to be the key transcriptional regulator of other GAME genes encoding enzymes in the SGA-specific pathway. Strong domestication signatures were observed in squalene synthase (SQS) gene of potato [1]. This gene controls early steps of SGA synthesis. For tomato genome, it was shown that selection of five major loci reduced the accumulation of SGA in fruits [2]. These loci contained few known GAME genes and a co-expression gene cluster potentially involved in SGA biosynthesis. This data allows us to consider the GAME genes as domestication genes for Solanaceae sp. The SGA biosynthesis is realized via the cytosolic mevalonate pathway and consists of three stages. The first two stages are required for the synthesis of primary metabolites, and lead to cycloartanol and cholesterol, respectively. At the third stage (the synthesis of glycoalkaloids from cholesterol), about 20 enzymes participate. In the potato genome, 14 corresponding genes were identified [3]. The reduction of SGA content in wild potato species via targeted modification of different GAME genes will create a new experimental model of domestication and provide a donor material for potato breeding. The both modeling of existing domestication events and induction of alternative changes in the GAME genes may provide essential information about regulation of SGA metabolism and genetic background of Solanaceae domestication.

*Acknowledgements:* The study is supported by the RFBR (18-316-00068).

### References

1. Hardigan M.A. et al. (2017) Genome diversity of tuber-bearing *Solanum* uncovers complex evolutionary history and targets of domestication in the cultivated potato. *Proc. Natl. Acad. Sci.* 201714380.
2. Zhu G. et al. (2018) Rewiring of the Fruit Metabolome in Tomato Breeding. *Cell.* 172:249-255.e12.
3. Ivanova K.A. et al. (2018) The biosynthesis regulation of potato steroidal glycoalkaloids. *Vavilovskii Zhurnal Genetiki i Selekcii = Vavilov Journal of Genetics and Breeding.* 22(1):25-34 (in Russian).