

Phenotype characters statistical analysis for selection perspectives

T.V. Erst^{1*}, V.K. Khlestkin^{1,2}

¹*Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia*

²*Novosibirsk State University, Novosibirsk, Russia*

* e-mail: erst@bionet.nsc.ru

Key words: potato, starch, granule, morphology

Motivation and Aim: Potato is one of the most important crop plants. In addition to the traditional use for food purposes, potato is a renewable resource of such technical material as potato starch. Potato starch properties depend on its composite polysaccharides ratio and structure – linear amylose and branched amylopectin – and are regulated by starch biosynthesis genes. Despite starch biosynthesis genes are sequenced and studied, effects of allelic variations on polysaccharides molecular structures and, consequently, starch physicochemical properties, are not known. We carry out chemical phenotyping of potato starch varieties for developing scientific approaches to the most rational production and use of new varieties producing the optimal starch for a particular application. Contemporaneously, potato varieties genotyping and further “genome – starch property” correlation determination is carried out.

Methods and Algorithms: Microscopy of starch granules and study of their morphology is one of the way to phenotyping starch and to selection of the contrast forms. It is known, that amylopectin chains branching, size [1] and irregular granule shape [2] are affected by genes *SBE I, II* (starch branching enzyme). Tuber starch content and irregular granule shape [2] likely to be affected by genes *SSI-SSIV* (starch synthase). Microscopy images processing using ImageJ software [3] allow quickly get the data on the granules’ area projection in the frame, Feret’s diameter, circularity, roundness, aspect ratio simultaneously for hundreds and thousands granules. The morphology data obtained can be processed by mathematical statistics methods and treated as biological traits. We clustered our varieties in the Past software using the Word’s method.

Results: We have treated 57 varieties of the 2017 year. Using the average values of listed morphological parameters, preparative yield and information on ripeness we performed clustering of the data and obtained four clusters. Using principal component analysis we obtained a varieties distribution which shows that there are significantly different varieties in our selection. Based on the obtained varieties distribution it can be concluded there is some heterogeneity in our selection, which gives us opportunities in further selection. Thus, for new varieties creations with altered values of interesting features when crossing, it is necessary to use a selection of varieties with different values of the features of interest.

Acknowledgements: Supported by the RFBR (17-29-08006).

References

1. Hofvander P., Andersson M., Larsson C.-T., Larsson H. (2004) Field performance and starch characteristics of high amylose potatoes obtained by antisense gene targeting of two branching enzymes. *Plant Biotechnol. J.* 2:311-320.
2. Schwall G.P., Safford R., Westcott R.J., Jeffcoat R., Tayal A., Shi Y.-Ch., Gidley M.J., Jobling S.A. (2000) Production of very-high-amylose potatostarch by inhibition of SBE A and B. *Nat. Biotechnol.* 18:551-554.
3. Khlestkin V.K., Erst T.V. (2017) A practical guide to the starch granules’ morphology study by microscopy. *Vavilov Journal of Genetics and Breeding.* 21(6):728-734 (in Russian).