

COMPUTER APPROACHES TO WHEAT HIGH-THROUGHPUT PHENOTYPING

Afonnikov D.^{1,2*}, M. Genaev¹, A. Doroshkov¹, V. Denisyuk², E. Morozova¹, A. Simonov¹, T. Pshenichnikova¹

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

²*Novosibirsk State University, Novosibirsk, Russia*

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

The growing need for rapid and accurate approaches for large-scale assessment of phenotypic characters in plants becomes more and more obvious in the studies looking into relationships between genotype and phenotype. This need is due to the advent of high throughput methods for analysis of genomes. Nowadays, any genetic experiment involves data on thousands and dozens of thousands of plants. Traditional ways of assessing most phenotypic characteristics (those with reliance on the eye, the touch, the ruler) are little effective on samples of such sizes. Modern approaches seek to take advantage of automated phenotyping, which warrants a much more rapid data acquisition, higher accuracy of the assessment of phenotypic features, measurement of new parameters of these features and exclusion of human subjectivity from the process. Additionally, automation allows measurement data to be rapidly loaded into computer databases, which reduces data processing time.

In this work, we present the WheatPGE information system designed to solve the problem of integration of genotypic and phenotypic data and parameters of the environment, as well as to analyze the relationships between the genotype and phenotype in wheat. The system is used to consolidate miscellaneous data on a plant for storing and processing various morphological traits and genotypes of wheat plants as well as data on various environmental factors. The system is available at www.wheatdb.org. Its potential in genetic experiments has been demonstrated in high-throughput phenotyping of wheat leaf pubescence.

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