Statistical Distribution Model of Some Parameters in Second Generation Triticale (x*Triticosecale* Wittm.) crosses

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Classical plant breeding has the main objective to improve the quality and some properties of the crop plants. Because of this, the correct evaluation of the data obtained during the selection process is very important. Statistically significant differentiation of certain breeding groups would be possible only with an accurate statistical analysis. As quantitative parameters in plants are encoded by multiple genes, it is not possible to be given a standard approach for statistical processing of the data. Triticale (x*Triticosecale* Wittm.) as a product of wide hybridization is characterized with its highly complex genome. Often in hybrid populations of the crop some instability in certain parameters is recorded, which results in a distortion of the results and a large deviation from the normal distribution of the data [1]. To establish a model of statistical distribution in triticale for the parameters date of heading and plant height 4,400 plants of 10 segregating hybrid populations of second-generation crosses were studied. As the two parameters are characterized by high stability of their expression in most cereals identical statistical distributions for all crosses are expected [1]. The results obtained for the parameter plant height, exhibit that it has a high stability in all studied populations. The data are distributed close to normal with determined skewness and kurtosis in some crosses. Higly different distribution was observed in regard to the parameter date of heading. Very high deviation from the normal distribution in all studied groups is clearly observed. Regardless of the differences observed in some of the crosses, a model of the statistical distribution for both parameters in second generation triticale crosses is developed.

References

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