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GENETIC AND STATISTICAL PARAMETERS OF THE HEIGHT OF WINTER RYE PLANTS WITH THE PHENOTYPIC MANIFESTATION OF EL AND WC GENES IN THE HOMOZYGOUS STATE

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Aim. To create a genetic change in the architecture of winter rye with the phenotypic manifestation of el and wc genes in the homozygous state of carriers of both individual valuable traits and their combinations. **Methods**. Field, laboratory, and analytical. Field research was carried out under the conditions of monitoring surveys under field research methods, carrying out qualification examination of plant varieties, and examination of plant varieties of the cereal group with the basics of statistical processing of research results. **Results.** The genetic and statistical parameters of the height of winter rye plants with the phenotypic expression of el and *wc* genes in the homozygous state were determined in F1 hybrids. The average arithmetic height of winter rye plants of the P1 population, which was heterozygous for the phenotypic expression of the erectness gene (*Elel*) and the absence of a wax coating (*Wcwc*), was significantly (P<0.001) higher than the average arithmetic height of the populations homozygous for the recessive *elel* P2 or *elelwcwc* P3 genes. Populations P2 and P3 in the 2nd generation were formed by the phenotypic expression of *elel* or *elelwcwc* genes in the homozygous state. The parameters of the inheritance coefficient in the broad sense and the nature of the relationships of quantitative traits in hybrids from the crossing of morphologically different winter rye samples were determined. **Conclusions.** The height of short-stemmed plants showed low phenotypic and genotypic variation; populations with a recessive manifestation of erectoidity and the absence of a wax coating (P2 and P3), in contrast to a similar heterozygous population for these genes (P1), had high inverse genetic additive correlations of plant height with productive bushiness, grain weight per ear and weight of 100 grains. Genetic improvement of plant height in subsequent generations of grain populations, regardless of the phenotypic manifestation of leaf plate erectoidity (*elel*) separately and together with the absence of a wax coating (*elelwcwc*), can be carried out by direct selection. The inverted genetic cluster of plant height with productive bushiness, grain mass per ear, plant, and 100-grain mass creates prospects for genetic change in rye architecture.

Key words: *hybrids, quantitative traits, phenotypic and genotypic variation, population, inheritance coefficient, genetic cluster.*

Plant height is geographically and phenotypically is a variable feature of each rye population winter [1, 2]. In the studies of plants for height is distributed on short stature or undersized – <120 cm; medium height – 120-150 cm; tall – >150 cm. Samples own collection and varieties obtained from others institutions differed significantly in terms of growth lin [3 – 5]. Yes, in our growing conditions except for the Dwarf variety, were short varieties Kobza (114 cm), Zabava (114.5 cm) and No. 1514 (110.1 cm). Medium-sized – standard variety Pamyat Khudoyerka (130 cm), varieties Hasto (130.8 cm), Hamarka (129.2 cm), Harvest (132.3 cm), No. 14413 (138.2 cm), Khair (141.5 cm), Stoir (138 cm), Iryna (131.2 cm), No. 14713 (122.1 cm), Witwitske (139.9 cm), Severske (137.6 cm), Intensive 95 (138.9 cm), Intensive 99 (142.2 cm), No. 1414 (143.8 cm), No. 1714 (144.1 cm), No. 2514 (139.7 cm). Tall there were varieties of Giants (164.1 cm) and No. 1614 (153.8 cm). In breeding populations, a group of plants was selected and isolated with erectoid leaf type, deviation from the stem by 5-7o [6-8]. Erectoidism has the symbol of the genes of the trait is *elel* (erectum leafe). During the crossing of sources from the alternative genes *elel* with normal samples with a hanging leaf plate prothere is recessive inheritance in the 1st generational and Mendelian splitting in F2 (ratio 3:1).

In breeding populations, certain mi plants with phenotypic manifestation of the trait "absence of a wax coating on the stems and leaves" – genes *wcwc* (waxy cover). By crossing varieties with a wax coating in F1 the specified feature disappears, in F2 the manifestation poured again at a ratio of 3 to wax up to 1 waxless plant. No sign the presence of a wax coating is inherited one recessive gene in the homozygous condition [9].

Hereditary diversity of populations in the hidden state, recessive by them alleles in heterozygous plants. Most often, hidden diversity happens is for inbreeding. Direct analysis heterozygosity from self-pollination of rye of mine in populations is ineffective due to the high what degree of self-incompatibility. Therefore, the population in the 2nd generation, formed according to the phenotypic manifestation of elel or *elelwcwc* genes in homozygous state, showed that the mean squared neither the deviation (S) nor the variance (S2) of the feature are of exceptional interest for selection. According to these parameters, the coefficient is determined inheritance in the broadest sense.

The purpose of research is to create a genetic a change in the architecture of winter rye from the phenotypic full manifestation of el and *wc* genes in homozygous the state of the bearers as separate valuable features, and their combinations.

Research materials and methods. Field experiments and structural analysis of the breeding material was carried out on the basis of the department in the field of selection and seed production of grain crops (NSC "Institute of Agriculture of the National Academy of Sciences"). The material was donors of winter rye, created earlier and used in hybrid dizations as their own selection material [1, 5, 10]. During field research traces were applied corresponding general adopted methods [Dospyekhov B.O., 1985; 11]. During the growing season, rye mine recorded the phases of plant development, collected samples were evaluated for winter bone, resistance to diseases, lying down, proconducted other assessments and analyzes in accordance with appropriate methodical recommendations [12; V. D. Kobylianskyi, 1982; 13]. Methods creation of new breeding material: parallel convergence of hybrid populations regarding the height of plants, productive bushiness, length and density of the ear, masses of grain from a plant, an ear of corn, 100 grains from plants, quality of grain and green mass. Also took into account the peculiarities of the development of photosynthetic apparatus, the number of germ cells roots using a suppressor gene *HlHl* with dominant inheritance features who Highly productive populations are created on the basis of dominant short-stemmed for using a series of backcrosses; homozygosity hybrid populations from saturating ones of crossings is controlled by analysts crossings, concentration of desired genes breeding, self-pollination, cloning. Inbreeding with alternation of self-pollination and pollination sibs makes it possible to conduct more directed van selection of lines for various characteristics and significantly reduces the volume of plant insulation.

Individual selection of plants is carried out were in the phase of full ripeness of the grain, lot – individually by plants per lot MKK-2 thresher. Structural analysis to determine the elements of the seed productivity (plant height, product bushiness, spike length, quantity flowers and grains in an ear, masses of grain from a plant and from an ear of corn, mass of 100 grains from a plant) prodrove with the use of measuring and advanced methods. Granularity and density of colwere calculated by the calculation method.

Research results. Characteristics average values of genetic parameters arithmetic (X), mean squareth deviation (S), coefficient of variation (V), amplitudes of variability (lim), inherited in the broad (H2) and narrow (h2) sense are of interest against a phenotypic background expression of the genes of quality traits *el* and *wc*, which distribution of phenotypic or genotyping values for quantitative characteristics. Parameters corresponding distributions and the results obtained from them larvae have a genetic component (Table 1).

Arithmetic mean plant height winter rye of the P-1 population, which is heterozygous on the phenotypic manifestation of the erectoid gene bearing (*Elel*) and lack of wax coating (*Wcwc*) is significantly ($P<0.001$) higher than the population these, homozygous for recessive genes *elel* P-2 or *elelwcwc* P-3. Population P-2 and P-3 in the 2nd generation was formed according to the atypical manifestation of *elel* or *elelwcwc* genes in the homozygous state.

Height of plants with expression of the *elel* P-2 gene turned out to be significantly lower than the height of the group plants selected by phenotypic proexpression of genes *elelwcwc* P-3 ($P<0.01$). General phenotypic variation of plant height by generally significantly higher than genotypic in all of them populations

Mean square deviations (S) or variance (S2) features are exclusively interest for selection. According to these parameters, the inheritance coefficient was determined in a broad sense (H2=S2 G/S2 P). Inheritance coefficients in a wide range of assumptions are defined for H2 P – 1= 0.77, H2 P – 2 = = 0,71 i H2П – 3 = 0,68. Such values of plant height inheritance coefficients in the broadest sense were noted as high.

The distribution of plant height of 3 short-stemmed populations is shown, which differ in the manifestation of erectoidity of the leaf blade (P-2) and the absence of a wax coating on the stem and leaf (P-3) in comparison with the population (P-1), caused by the heterozygous manifestation of both mark (Fig. 1). In the heterozygous population (P-1) according to the expression of *ElelWcwc* genes, plant height variability was observed – 68-118 cm, and despite the wide range, it is close to a normal distribution. The F3 population, homozygous for the erectoid gene (*elel*), had less variability in plant height, their minimum height was 83 cm with a deviation from the average (X=95.32 cm). The F3 *lglgtgtg*/(F2 *Elel*/*wcwc*) population showed significantly the greatest variability in plant height – 68–118 cm, and despite some heterogeneity, the distribution curve was normal. Elongation of the top of the distribution curve indicates the heterogeneity of plant height in the population with no wax coating (Fig. 1).

The component determined by genetic factors has a greater influence on the phenotypic variation of plant height in all experimental populations. Inheritance indicators in the narrow sense were calculated in populations by the doubled coefficient of genetic additive correlation between the height of parent plants and the average height of a generation of direct descendants. In the F3 *lglgtgtg*/(*Elel*/ *Wcwc*) (P-1) population, the genetic additive correlation between the height of parent plants in F2 and the average height of families in F3 was rA = 0.29. The coefficient of inheritance in the narrow sense was defined as the doubled correlation coefficient between the trait of the parents and the average trait of the offspring – h2P – O = 0.58. At the bottom, the symbol P O means parents, offspring. The general genetic variability of plant height is determined by the heritability coefficient in the broad sense H2=0.77, and the genetic variation caused by the additive effect is heritability in the narrow sense – h2 = 0.58. From the value that depends on general genetic and additive factors, it is possible to determine the component determined by non-additive factors – H2 – h2 = = 0.77 – 0.58 = 0.19. The last value shows the total contribution of dominant and epistatic (non-additive) factors to the genetic variability of plant height (P-1). The effect of the influence of non-additive factors in the next generation is usually not manifested, because as a result of crossing over, dominant and epistatic associations of genes in the vast majority disintegrate, therefore the effect of heterosis cannot be fixed by selection. Differentiation of the influence of genetic variation on additive and non-additive components is important for selective improvement of the height of rye plants (P-1).

Inheritance of plant height in the broad and narrow sense for the large-grain population F3 *lglgtgtg*/(F2 *elel*/*Wcwc*) (П-2) is determined as H2=0.71 and h2=0.66. The main contribution to the genetic variation in the height of plants of the erect orientation of the leaf plate (EOLP) depends on genes with an additive effect. At this stage of population research with EOLP, effective selection can be carried out by direct selection by plant height. The largest number of additive genes was also found in the large-grain population F3 `*lglgtgtg*/ (F2 *elelwcwc*) (P-3) – as H2 = 0.68 and h2 = 0.49. When carrying out selection for the height of plants in the next generations (P-3), one should take into account the corresponding error of a possible decrease in the effectiveness of the selection, due to the low influence of non-additive factors.

Based on the results of the analysis of phenotypic and genotypic correlation coefficients, ranks were established: with an absolute value greater than 0.7 high, 0.5–0.69 medium, within 0.3–0.49 low. A positive correlation shows a direct relationship between the signs: as one increases, the other increases. With a negative (negative) correlation, the relationship between the characteristics is reversed – an increase in one characteristic is correspondingly associated with a decrease in the other.

The analysis of plant height relationships in related grain populations with the manifestation of phenotypic traits determined by the Erer and *Wcwc* genes in the heterozygous (P-1) and erer (P-2) and *ererwcwc* (P-3) homozygous states revealed low direct phenotypic correlations with grain mass from the ear (rP=0.33 – 0.49) and productive bushiness (rP = 0.22 – 0.38). The variation in the height of plants (4-48%) is due to the phenotypic variability of the mass of grain from an ear with productive bushiness. Genetic additive correlation coefficients of the height of parent plants with the productive bushiness of direct descendants depending on the homoor heterozygosity of 2 alternative quality genes showed inadequacy in direction (±) and magnitude. In the population (P-1) F3 *lglgtgtg*/(F2 *Elel*/*Wcwc*), the correlation between the height of the parents and the productive bushiness of the offspring was directly high (rA = 0.72). In populations where the recessive genes elel (П-2) and *elelwcwc* (П-3) are in a homozygous state, the genetic additive correlations between these traits were also high, but reversed: rA is -0.74 and -0.78, in accordance. With a decrease in the height of homozygotes parental *elel* (P-2) and *elelwcwc* (P-3) genes plants in F2 by 55 – 61% genetically increased the productive bushiness of the F3 offspring was low.

Genetic additive correlation in population with the homozygous gene *elel* (P-2) established novelty rA = – 0.44, homozygous genes *elelwcwc* (П-3) – rA = – 0.48. In a similar population with heterozygous expression of genes *ElelWcwc* (P-

1) correlations of productive kuthe purity of the parents with the height of the offspring plants not established.

So, between height and productivity bushiness in populations with homozygous prothe manifestation of erectoid genes and the absence of wax negative genetic tic correlation – rG = – 0.54 (according to Hazel). The presence of el and wc genes in a homozygous state in combination with coarse-grained (*lglgtgtg*) in selectures on short stemness (*HlHl*) contributes to the improvement the cultivation of productive bushiness. Selective program with the use of appropriate norms of the specified signs should be provided netic optimization of shortness levels with productive bushiness.

Conclusions

It was established that the height of plants in of rhizome populations of winter rye shows low phenotypic and genotypic variation Populations with recessive prothe phenomenon of erectoidity and the absence of wax cover (P-2 and P-3), in contrast to analog of the logical heterozygous population according to these genes (P-1), show high reverse nor genetic additive correlations of height plants with productive bushiness, mass of grain from an ear and mass of 100 grains. Genetic improvement of plant height in subsequent generations of large-grain populations regardless of the phenotypic manifestation leaf blade erectness (*elel*) separately and together with the absence of wax cover (*elelwcwc*) can be carried out directly by our choice Reverse genetic classter height of plants with a productive cupurity, mass of grain from an ear, plant and with a mass of 100 grains creates prospects for the genetic change of rye architecture.

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