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Genetic analysis of the naked trait in panicles of hexaploid oat

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Abstract – *The aim of this study was to estimate the number of genes that control the naked (hull-less) trait and the mode of expression of this characteristic in panicles of hexaploid white oat. Parents and the segregating population (in the F_2 and F_3 generations) were evaluated in regard to the presence and distribution of naked grains in panicles of individual oat plants. For each plant, a drawing of the main panicle was developed. From the drawings obtained in the progenies of the F_2 population, six distinct phenotypic classes were produced. The expected phenotypic proportion of 3:9:4 (naked:segregating:hulled) was that which best fit by the Chi-square test. In the F_3 generation, the results showed agreement with the hypothesis observed in the F_2 generation. The naked trait in oat is passed on by two genes and the greatest expression of this trait occurs in the upper third of the panicles. Expression of this trait in oats is not complete, even in homozygous genotypes.*

Key words: Avena sativa*, multiple floret spikelets, oat grains.*

INTRODUCTION

Oat is one of the most important cereal crops in the world and the genus *Avena* L. includes wild and domesticated species with different levels of ploidy and, consequently, with extensive genetic diversity among and within species.

Hexaploid white oat (*Avena sativa* L.) has differentiated nutritional and functional characteristics in relation to grains of other cereals and is an important source of proteins and soluble fibers, such as beta-glucans (Wood 2007). Nevertheless, the hull that surrounds the oat grain is often undesirable because, in general, it is waxy, fiber-laden and indigestible by monogastric organisms, and it must be eliminated by dehulling, which impedes processing of the grains in industrial use. Naked oat, originating in China (Valentine 1995), which is a subspecies of *Avena sativa* L., denominated *Avena sativa* L. *ssp. nudisativa* (Rodionova et al. 1994), has the ability to form grains that separate from the hull during the threshing process, which makes the production process in industrial use more rapid and efficient. In addition, it allows inclusion of naked oat in the formulation of poultry, pig, cattle and horse diets, substituting cereals such as corn and barley (MacLean et al. 1993, Lopez et al. 1998, Peltonen-Sainio et al. 2004, Flis et al. 2007).

Growing of naked oat is still not of great importance; it currently has expressive crop area only in China (Wan et al. 2009). In Brazil, cultivars are not yet available on the market. This fact is mainly due to incomplete expression of the naked (hull-less) trait in the oat panicles, even in genotypes which are homozygous for the trait. In the genotypes with greater expression, it is possible to obtain 95% of the grains without hulls, but there is still a residue of 5% of grains with hulls. The cause of incomplete expression is unknown, but has already been attributed to environmental effects such as temperature, cold, and hours of light. More recently, in rice, the naked trait was observed due to the activity of microRNAs which are highly affected by the environment (Zhu et al. 2009). Among the panicles of the same genotype, expression of the naked characteristic is greater in the upper and middle thirds of the panicles.

Most genetic studies suggest that this characteristic in oat is controlled by a single gene (Norton 1907, Zinn and Surfaice 1917, Clamot 1969, Kibite and Taylor 1994); however, other studies report the existence of up to four genes controlling this trait (Moule 1972, Jenkins and Hanson 1976). Knowledge regarding the number of genes of the trait under study and the distribution of the naked grains in the panicles in Brazilian germplasm will allow development of more efficient selection strategies to bring about oat cultivars with this characteristic.

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The aim of this study was to estimate the number of genes that control the naked trait and determine the mode of expression of this characteristic in panicles of Brazilian germplasm.

MATERIAL AND METHODS

The experiments were conducted at the Estação Experimental Agronômica (EEA) (Agronomic Experimental Station) of the Universidade Federal do Rio Grande do Sul (UFRGS) in the municipality of Eldorado do Sul, RS, Brazil. Soil in the region according to Brazilian soil classification is an Argissolo Vermelho Distrófico típico (Embrapa 1999) (Acrisol). Climate at the Station is the Cfa type, according to the Köeppen classification, i.e., humid subtropical with a hot summer. Mean annual rainfall is 1445 mm, with June, July and August being the rainiest months (Bergamaschi et al. 2013).

The F_2 and F_3 segregating generations were used, and derived from crosses between the parents UFRGS 006131 (naked) and UFRGS 01B7114-1 (hulled). In 2010, the parental genotypes plus the F_2 generation were sown in the field. The plants were arranged every 30 cm in 3 m length rows which were 0.40 m apart. The quantity of 20 seeds of each parental genotype and 100 seeds of the F_2 generation were sown per replications, with a total of 4 replications.

The plants were monitored during vegetative development and the main panicle of each plant was marked in the flowering period by means of adhesive tape. Each panicle was harvested individually and, for analysis, was divided into thirds: upper third (A), middle third (B) and lower third (C). This division into three was performed to allow evaluation of the presence of multiple and non-multiple floret spikelets, and their segregation in the panicle. In addition, each spikelet of the panicle was threshed and individually analyzed in regard to the presence and distribution of the grains with and without hulls. Multiple floret spikelets are modified spikelets that have an extension of rachis, allowing the presence of a large number of flowers, normally six flowers or more, in contrast with the two flowers commonly observed in hulled oats. This phenotype, which is easily recognized in the field, is associated with the presence of naked type grains. Nevertheless, not all the grains present in a multiple floret spikelet have the naked trait; they may also have grains with hulls.

For each panicle, a drawing was made. All the branches present in the main panicle and all the types of spikelets present were marked on the drawing according to the following classification: 100% naked grains, when they exhibited only grains without hulls; 100% hulled grains, when they exhibited only grains with a hull attached to the caryopsis; and mixed, when they showed grains with a hull and without a hull in the same spikelet. As of the drawings obtained of each panicle, a new classification was made based on the distribution of spikelets in the panicle, giving rise to six distinct classes, which are shown in Figure 1. The F_2 seeds of each panicle were stored in a cold chamber, and in 2011 were used in the progeny test.

Each F_2 panicle harvested (2010) was planted in the form of a paired F_3 row (2011). The plants were monitored during vegetative development and were marked in the flowering period, and all the main panicles of the same row were harvested together. The same analyses as performed on the F_2 panicles were carried out in the laboratory. Nevertheless, due to the size of the population in that year, priority was given to analyzing all the panicles derived from those that in F_2 were classified in Class I (100% naked), and a sample of those that were classified in Classes II, III, IV and V. Evaluation was not performed on those belonging to Class VI.

Observing the distribution pattern of the segregating plants in the F_2 generation, a genetic hypothesis that explains the genetic control of the naked trait in oat panicles was created and tested. The possibility of distinction in phenotypic classes and the proportion of individuals in each class (100% naked (I), segregating (II to V) and 100% hulled (VI))

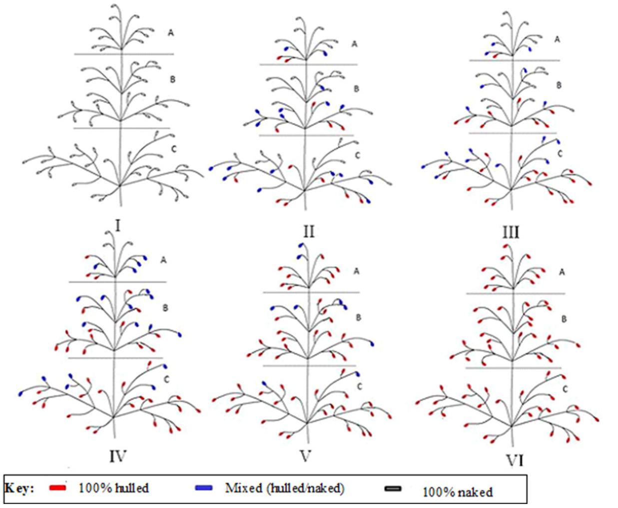

Figure 1. Representation of the classes found in the F_2 generation. EEA – Eldorado do Sul, RS, 2010 and 2011. I) Panicles that formed spikelets containing 100% of grains without hulls, and absence of spikelets with complete expression of grains with hulls; II) Panicles containing 100% naked spikelets and some 100% hulled in all the third parts; III) Panicles containing 100% naked spikelets only in the upper two thirds; IV) Panicles containing 100% naked spikelets only in the upper third; V) Panicles without spikelets with 100% naked grains, few mixed, most of the grains hulled; VI) Panicles that formed only spikelets containing 100% hulled grains. A = upper third; B = middle third; C = base third.

served as the basis for formulation of the genetic hypothesis.

Based on the data obtained in the F_2 generations, the Chi-square test (χ^2) was performed to test adherence of the genetic models to the phenotypic proportions expected, in accordance with Steel and Torrie (1980).

In the F_3 generation, the Chi-square test was performed only for the progenies which in F_2 belonged to Class I. Thus, the Chi-square test, with correction from Yates, called continuity correction, was used, which consists of subtraction of 0.5 of the difference between each value observed and its expected value.

RESULTS AND DISCUSSION

In the parent UFRGS 01B7114-1 (hulled), mixed spikelets or multiple floret spikelets were not observed, nor grains without a hull in any of the panicles evaluated, in 2010 and in 2011. This shows that hulled grain expression is stable, regardless of the growing environment.

As for the parent UFRGS 006131 (naked), it exhibited variation in regard to the presence of mixed spikelets, and grains with and without hulls, in the two years of evaluation (Table 1). As already reported by Cabral et al. (2000), 100% of naked grains was not observed even in the genotype UFRGS 006131 after 20 generations of self-pollination. Expression of the naked trait varied with the years of evaluation, such that, in 2010, the number of spikelets with 100% naked grains was above that observed in 2011 in all the third parts of the panicles (Table 1). Nevertheless, within the year of evaluation itself, there were variations in expression of the trait within the same oat panicle, and the greatest expression occurred in the upper third of the panicle. In the year of less variation of expression of the trait (2010), the formation of spikelets with 100% of the grains with hulls was not observed in any of the thirds of the panicles of the genotypes that have the naked trait. In years of greater variation, like 2011, there was the formation of spikelets with 100% hulled grains in the middle and base third of the panicle.

Incomplete expression of the gene(s) for the naked trait, even in homozygous genotypes, makes genetic analysis and its interpretation difficult. The presence of grains with hulls in the genotypes with the naked trait has been documented in the literature and may be related to different factors, such as variations in temperature, light, nutrients, and soil (Lawes and Boland 1974), or may even be due to the activity of

Table 1. Number of naked, mixed and hulled spikelets, and number of grains with hull and without hull in each third part of the panicles from the naked parent UFRGS 006131. EEA/UFRGS, Eldorado do Sul, RS, Brazil, 2010 and 2011

"A" Third (Upper)					
	Type of Spikelet			Type of Grain	
Year	NS	HS	MS	NG	HG
2010	203	0	7	711	9
2011	927	0	351	3504	387
	%			%	
2010	96.7	0	3.3	98.7	1.3
2011	72.5	0	26.5	90.1	9.9
"B" Third (Middle)					
	Type of Spikelet			Type of Grain	
Year	NS	HS	MS	NG	HG
2010	426	0	48	1213	63
2011	1940	46	948	6698	1122
	%			%	
2010	89.9	0	10.1	95.1	4.9
2011	66.1	1.6	32.3	85.7	14.3
"C" Third (Base)					
	Type of Spikelet			Type of Grain	
Year	NS	HS	MS	NG	HG
2010	380	0	66	979	98
2011	1209	25	414	3189	483
	%			%	
2010	85.2	0	14.8	90.9	9.1
2011	73.4	1.5	25.1	86.8	13.2

NS = Spikelet with 100% naked grains; HS = Spikelet with 100% hulled grains; MS = Mixed spikelets, containing grains with and without hulls; NG = Naked grains; HG = Hulled grains.

microRNAs, which are quite affected by the environment (Zhu et al. 2009).

The F_2 population showed a high segregation pattern and, consequently, a broad variation of types of spikelets in the panicles in regard to expression of the naked trait. In spite of 400 F_2 seeds having been sown, only 132 plants survived, which were individually evaluated, observing the main panicles of each one of them. In Class I, which is the class which draws closest to the naked parent, 25 panicles were classified, 17 panicles in Class II, 17 panicles in Class III, 15 in Class IV, 14 in Class V and 44 in Class VI, which is the class that is phenotypically similar to the hulled parent. Lower germination of the seeds was widely reported and constitutes one of the problems in the development of genotypes with this trait. Nevertheless, previous results show that there is no variation in segregation of the naked trait when seeds derived from panicles that contain hulled and naked grains are used.

The panicles classified in Class I, in large part, had 100% naked spikelets and some mixed spikelets and did not exhibit 100% hulled spikelets (Table 2), like that observed for the naked parent in 2010 (Table 1). In this class, the naked grains represented more than 90% of the grains distributed in any third part of the panicles (Table 2). Thus, Class I is characterized in large part by having spikelets with expression of the complete naked trait and total absence of spikelets with expression of hulled grains in any third part of the panicle.

A total of 17 panicles were classified in Class II, which exhibited most of the spikelets as 100% naked in the upper third part while, in the middle and lower third, most of the spikelets were of the mixed type (Table 2). In addition, in the upper third part, a low frequency (3.0%) of 100% hulled spikelets was observed, which increased greatly in frequency in the middle (9.7%) and lower (16.3%) thirds (Table 2). In Class II, the proportion of naked grains varied according to the position of the grains in the panicle. The proportion of grains with the naked trait decreased from 81.9% in the upper third to 62.4% in the middle third and to 52.3% in the lower third (Table 2). Thus, Class II is characterized by panicles that exhibit spikelets with 100% naked grains and some spikelets with 100% hulled grains in all the thirds of the panicle.

In Class III, 17 panicles were classified. The presence of 100% naked spikelets is less than 50% in the upper third and decreases to 9.3 % in the middle third and was not observed in the lower third of the panicles (Table 2). The frequency of spikelets with only hulled grains increased from 22.3 % in the upper third to 48.7 % in the middle third, and to 77.9 % in the lower third (Table 2). In addition, the proportion of grains with a naked trait decreased from 65.6% in the upper third to 29.1% in the middle third and 13.8% in the lower third (Table 2). Class III is characterized by the presence of spikelets with all grain types (naked, mixed and hulled) in the upper and middle third, and mixed spikelets or spikelets with hulled grains in the lower third, without any spikelet with 100% naked grains (Table 2).

The 15 panicles classified in Class IV did not show 100% naked spikelets in the middle and lower third, exhibiting this type of spikelet only in the upper third (26%), which also showed the greatest proportion of naked grains (51.2%). The middle and base third, for their part, showed greater magnitude of spikelets with 100% hulled grains and, consequently, more than 90% of grains with hulls (Table 2). Class IV is characterized by the presence of spikelets with 100% naked grains only in the upper third, and absence of this type of spikelet in the middle and lower third.

Class V is differentiated from the others by the absence of spikelets with 100% naked grains in any third part of the panicles (Table 2). The upper and middle third of the panicles analyzed showed spikelets with the same pattern, i.e., spikelets with 100% hulled grains and mixed spikelets. In the lower third, only spikelets with hulled grains were observed. In addition, the proportion of hulled grains was greater than that of naked grains in the three thirds of the panicles (Table 2).

In Class VI, 44 panicles were observed, which showed 100% hulled grains in all the thirds of the spikelets and did not show any spikelet of the mixed type or 100% naked type (Table 2).

Based on the distribution of the panicles in the classes, a genetic hypothesis was proposed. The proportions tested were 3 (Class I): 9 (Class II to V): 4 (Class VI). In this model, two genes govern the naked trait, and, for that, the presence of locus 1 in the homozygous condition (N_1N_1) and at least one of the alleles of locus 2 in the dominant $N_2_$condition would be necessary.

When only one dominant allele is present in the first gene, the resulting phenotype would be mixed, and the alleles present in the second gene would determine the proportions of grains with and without hulls in the panicles. The combinations that would express the mixed classes (mosaic) would be: $N_1N_1n_2n_2$, $N_1n_1N_2N_2$, $N_1n_1N_2n_2$, $N_1n_1n_2n_2$ (Table 3). The presence of two recessive alleles in the first gene would necessarily result in hulled phenotypes, regardless of the alleles present in the second gene ($n_1n_1N_2N_2$, $n_1n_1N_2n_2$, $n_1n_1n_2n_2$). The model proposed was tested by the Chi-square test (5.08) and it was accepted with a probability of P = 0.28.

The lower number of panicles in segregating Classes II to V may be associated with better germination of the hulled grains when compared to the naked/hull-less grains (which could be present in the other classes).

The genetic model proposed in the present study was of two genes (Table 3). Nevertheless, most of the pioneering studies on inheritance of the naked trait in oats indicated

Table 2. Number of naked, mixed and hulled spikelets and number of grains with and without hulls in each third part of the panicles of the F_2 generation. EEA/UFRGS, Eldorado do Sul – RS/2010

“A” Third (Upper)					
Class	NS	HS	MS	NG	HG
I	228	0	31	777	40
II	100	5	59	402	89
III	86	46	74	401	211
IV	47	64	70	230	219
V	0	79	92	137	317
VI	0	526	0	0	1125
Class	%			%	
I	88.0	0.0	12.0	95.1	4.9
II	61	3	36	81.9	18.1
III	41.7	22.3	35.9	65.5	34.5
IV	26	35.4	38.7	51.2	48.8
V	0	46.2	53.8	30.2	69.8
VI	0	100	0	0	100
“B” Third (Middle)					
Class	NS	HS	MS	NG	HG
I	559	0	85	1519	120
II	141	40	231	666	402
III	49	203	213	389	950
IV	0	344	84	92	888
V	0	334	45	65	765
VI	0	1084	0	0	2197
Class	%			%	
I	86.8	0.0	13.2	92.7	7.3
II	34.2	9.7	56.1	62.4	37.6
III	9.3	48.7	51.3	29.1	70.9
IV	0	80.4	19.6	9.4	90.6
V	0	88.1	11.9	7.8	92.2
VI	0	100	0	0	100
“C” Third (Base)					
Class	NS	HS	MS	NG	HG
I	481	0	61	1043	89
II	107	60	200	424	387
III	0	373	147	160	1003
IV	0	333	27	29	716
V	0	315	25	26	621
VI	0	1060	0	0	2097
Class	%			%	
I	88.7	0	11.3	92.1	7.9
II	29.2	16.3	54.5	52.3	47.7
III	0	77.9	30.7	13.8	86.2
IV	0	92.5	7.5	3.9	96.1
V	0	92.6	7.4	4	96
VI	0	100	0	0	100

NS = Spikelet with 100% naked grains; HS = Spikelet with 100% hulled grains; MS = Mixed spikelets, containing grains with and without hulls; NG = Naked grains; HG = Hulled grains.

that this characteristic is conditioned on a single gene with partial dominance (Caporn 1918 and Jensen 1966). Nevertheless, Hoekstra et al. (2003), upon reexamining inheritance of the naked trait previously studied by other researchers, concluded that the phenotypic indices studied (naked:mosaic:hulled) do not fit in a consistent way for the model of a single locus governing the naked trait. It is fitting to highlight that most of the genetic studies of the naked trait used the proportion of the number of hulled and hull-less grains regardless of their location in the panicles as a model of analysis; the studies show a large variation of methods and of results (Jenkins and Hanson 1976, Cabral et al. 2000, Hoekstra et al. 2003). Thus, it is possible that the choice of the method of analysis and the source of germplasm has influenced genetic analysis of the trait and has resulted in the different genetic models proposed in other studies to explain inheritance of the naked trait in oats.

In the progeny test in the F_3 generation to confirm the proposed two-gene model, one third of the families coming from Class I with 100% naked characteristic was expected, and two-thirds should segregate. Although the hypothesis was accepted, the values observed in the progenies were distant from that expected (Table 4). Nevertheless, the lower frequency of segregating families in this class may be associated with the small population size used in the progenies. The expectation was that in the progenies of the segregating type ($N_1N_1N_2n_2$) only ¼ (25%) ($N_1N_1n_2n_2$) would present spikelets different from the 100% naked. For each F_2 plant, eleven progenies would be necessary so that all the genotypes had the chance of being represented with the probability of error of 5%. Nevertheless, it was not possible to obtain this number of plants due to low germination of the seeds.

For the progenies belonging to Classes II, III, IV and V, it was expected that all the F_3 families would segregate to the naked trait; however, four families showed non-standard behavior (data not shown). This fact may be associated with the number of panicles evaluated and/or erroneous classification of the panicles in the F_2 generation. The same occurred in studies carried out by Gaines (1917) and Love and McRostie (1919), which also showed non-standard behavior in the F_3 generation, thus affirming that the panicles of the F_2 generation had been wrongly classified, i.e., that hulled grains could have been dehulled during threshing, or that other factors affected the expression of naked grains. In spite of the small number of panicles evaluated in this study, the data of the F_3 generation show agreement (Table 4) with the hypothesis proposed in the F_2 generation (Table 3).

Considering the two-gene genetic model proposed, the existence of stable, completely naked genotypes for the grains without hulls (naked) trait would be expected since the selection of genotypes $N_1N_1N_2N_2$ in breeding programs would not be difficult. According to Ougham et al. (1996), the N_1 allele has an effect on lignin deposition

Table 3. Frequencies observed and expected for the naked trait in the different classes of panicles of oats in the F_2 generation. EEA/UFRGS, Eldorado do Sul, RS, Brazil, 2010

F_2 Generation Phenotype	F_2 Generation Genotype	Panicle Class	FO	FE	χ²	P
Naked	$N_1N_1N_2N_2$ $N_1N_1N_2n_2$	I	25	24.75	0.0025	
Segregating	$N_1n_1N_2N_2$	II	17	16.50	0.0151	
	$N_1n_1N_2n_2$ e $N_1N_1n_2n_2$	III and IV	33	41.25	1.6500	
	$N_1n_1n_2n_2$	V	14	16.50	0.3787	
Hulled	$n_1n_1N_2N_2$ $n_1n_1N_2n_2$ $n_1n_1n_2n_2$	Class VI	43	33.00	3.0303	
Total			132		5.08	0.28

FO = Frequency observed; FE = Frequency expected; χ² = Chi-square; P = Proportion.

Table 4. Frequencies observed and expected in the F_3 generation, considering only progenies coming from oat panicles belonging to Class I in the F_2 generation. EEA/UFRGS, Eldorado do Sul, RS, Brazil, 2011

F_2 Generation Phenotype	F_2 Generation Genotype	F_3 Expected Proportion	F_3 Total of Families	FO	FE	χ²	P
Naked	$N_1N_1N_2N_2$	1/3	25	13	8		
	$N_1N_1N_2n_2$	2/3		12	17	**3.13**	**0.08**

FO = Frequency observed; FE = Frequency expected; χ² = Chi-square (Yates Correction); P = Probability.

in the development of spikelets. This phenomenon may be responsible for the difference in the lignification pattern in naked species. Thus, understanding of the role of the N_1 locus in lignin deposition may lead to breeding strategies to overcome incomplete expression of the naked trait in white oat panicles.

The presence of hulled grains in homozygous genotypes ($N_1N_1N_2N_2$) may also be associated with incomplete penetrance and/or variable expressiveness of the genes; i.e., the genotype has the gene which exhibits the naked characteristic; nevertheless, the frequency of expression of the phenotype is less than 100%, as was observed in the naked parental genotype and in other studies of this trait in oats (Valentine 1995, Cabral et al. 2000). In this sense, alteration in the expected segregations may be attributed to differences in the penetrance and expressiveness of the genes as a result of the environmental effect (Arantes et al. 2008).

Incomplete penetrance and variable expressiveness make analysis difficult because, at first, it may appear that traits with more complex genetic control are being dealt with when, in fact, it is a trait in which one allele has varied expressions. For that reason, the possibility of the naked trait having monogenic inheritance is not discarded. That is in agreement with Cabral et al. (2000), who affirm that the naked trait in oats is controlled by one gene with dominance and incomplete expressiveness, and that, in addition, the gene may be associated with some physiological factor of the plant, or associated with other genes responsible for the degree of lignin deposition in the grains. One of the hypotheses that may explain the expression of the naked trait being different in the three thirds of the panicles observed (upper, middle and base), as well as the emergence of grains with and without hulls in the same spikelet, is due to modifier genes, corroborating the hypothesis of Moule (1972). Modifier genes and/or action of microRNA (Zhu et al. 2009) may interrupt transcription and thus disconnect the gene responsible for forming grains without hulls (N_1) interrupting gene expression.

The expression of naked grains, as well as multiple floret spikelets, decreases in the middle and base thirds of the panicle. Although the naked grain characteristic seems to be easily transferred, high pressure of selection for expressiveness of this trait must be used. Since it is a qualitative characteristic, that is, governed by few genes and with easily distinguished phenotypic classes, selection based on the type and location of the spikelet (multiple floret) allows it to be performed in the initial generations, namely, as of the F_2 generation. In addition, selection based on panicles that exhibit multiple floret spikelets in the base third is an indication that the panicle is probably 100% naked, and this becomes important in the selection process in search of homozygous lines for the naked characteristic in white oats.

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Análise genética do caráter nuda em panículas de aveia hexaplóide

Resumo – *O objetivo deste trabalho foi estimar o número de genes que controlam o caráter nuda e o modo de expressão desta característica em panículas de aveia branca hexaplóide. Genitores e população segregante (nas gerações F_2 e F_3) foram avaliadas quanto à presença e distribuição de grãos nudas em panículas de plantas individuais de aveia. Para cada planta, um desenho da panícula principal foi desenvolvido. A partir dos desenhos obtidos nas progênies da população F_2, seis classes fenotípicas distintas foram produzidas. A proporção fenotípica esperada de 3:9:4 (nuda:segregante:com casca) foi a que melhor se ajustou pelo teste do Qui-quadrado. Na geração F_3, os resultados demonstraram concordância com a hipótese observada na geração F_2. O caráter nuda em aveia é herdado por dois genes e a maior expressão deste caráter ocorre no terço superior das panículas. A expressão deste caráter em aveia não é completa, mesmo em genótipos homozigotos.*

Palavras-chave: Avena sativa*, espiguetas multiflora, grãos de aveia.*

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