Genetic Inheritance of Aluminum Tolerance in Oat

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ABSTRACT

Aluminum toxicity is an important factor that limits crop productivity in acid soils. Understanding the inheritance of this trait may help breeding programs to develop aluminum-tolerant cereal crops. The objectives of this work were to study this trait in oat (*Avena sativa* L.) genotypes not yet investigated and to determine the allelic relationships between aluminum tolerant genotypes. Three tolerant (UFRGS 17, UFRGS 93605 and UFRGS 15), two sensitive genotypes (UFRGS 911715 and UFRGS 93598), and their respective F_2 populations were evaluated for root regrowth in the presence of 20 ppm of aluminum. One dominant gene for tolerance was identified in crosses involving UFRGS17 and UFRGS93605 and two genes with epistasis in crosses with UFRGS 15, indicating that the tolerant genotypes included in this study have different genetic constitution.

KEY WORDS: Nutrient solution, Root regrowth, Dominance, Epistasis.

INTRODUCTION

Aluminum is one of the most abundant earth metals and is found in large amounts in tropical soils. The Brazilian tropical and subtropical areas are formed by acid soils, where the toxicity of this metal is one of the most important environmental stresses affecting cereal development (Delhaize *et al.*, 1993; Camargo, *et al.*, 1992). Associated to this fact, the action of the lime application is limited to the zone of incorporation, and it certainly will not penetrate deeper than the plowing levels. Its application in sub superficial levels represents great cost to the farmer. Thus, the existence of cultivars with tolerance to toxic aluminum is of great importance for oat breeding programs.

Roots affected by Al^{+++} present a peculiar development at their tips. The meristematic region of the main and lateral roots, in the presence of Al^{+++}, gets darker, smaller and thicker, with fewer ramifications (Foy, 1974), resulting in low nutritional efficiency and water supply for the plant (Carver *et al.*, 1988; Foy and Fleming, 1978). Such phenomenon allows the identification of genotypes that are sensitive to this cation.

According to Camargo (1984), Dornelles (1994) and Sànchez-Chacòn (1998), tolerance to Al^{+++} is easy to detect in tests under controlled conditions (in greenhouse or laboratories) and nutritive solution. This is, therefore, an easy method to identify plants that are tolerant to aluminum, saving space and time.

Several studies have investigated aluminum toxicity tolerance in cereals. However, few were carried out with oats. In an seminal study, Sànchez-Chacòn (1998) characterized the germoplasm from the UFRGS oat breeding program and identified one dominant gene for aluminum tolerance in nine populations from crosses between tolerant and sensitive genotypes. However, the presence of different sources of genes for aluminum tolerance among oat genotypes from the UFRGS that can be combined in a breeding program is unknown. The present work has been developed to study the inheritance of Al^{+++} tolerance in other source genotypes and to investigate the allelic relations between genes present in different oat genotypes.

MATERIALS AND METHODS

The assessment of the tolerance to aluminum toxicity was done with the method described by Camargo and Oliveira (1981) and adapted to oats by Sánchez-Chacón (1998). Seedlings from P_1, P_2 and F_2 generations derived from the cross between the tolerant (UFRGS 15, UFRGS 17 and UFRGS 93605) and sensitive parents (UFRGS 911715 and UFRGS 93598) (Table 1) were evaluated for their response to Al^{+++} toxicity through the regrowth of the primary root. The F_2 segregating populations with their respective parents were submitted to nutritional solution in pots with 20 ppm of cation arranged in a completely randomized experimental design, considering that each pot constituted a population.

The seedlings assessed were divided in sensitive and tolerant in relation to their response to toxicity to Al^{+++}, having the class separation limit at 0.8 mm for all populations. The same class limit separation was used in the work done with oats by Sànchez-Chacòn (1998). A genetic hypothesis in relation to the number of segregating genes was proposed for each population, based on the frequency distribution obtained in the F_2 generation, and tested using the chi-square analysis (Steel and Torrie, 1960).

Crosses among genotypes within each tolerant and sensitive class were also performed. The F_2 populations evaluated for these crosses were UFRGS 17 x UFRGS 15 (number of individuals n = 76), UFRGS 17 x UFRGS 93605 (n= 58), UFRGS 93605 x UFRGS 15 (n=19), and UFRGS 911715 x UFRGS 93598 (n=70).

RESULTS AND DISCUSSION

We began testing the genetic hypothesis of just one gene segregating in crosses from populations between tolerant x sensitive genotypes since, according to several studies, one to two genes for tolerance explain most of the variation for this character in cereal crops (Kerridge *et al.*, 1971; Camargo, 1984; Lagos *et al.*, 1991; Camargo *et al.*, 1992; Riede and Anderson, 1996; Johnson *et al.*, 1997; Sànchez-Chacòn, 1998). This genetic hypothesis was confirmed for the populations from the crosses UFRGS 17 x UFRGS 911715, UFRGS 17 x UFRGS 93598 and UFRGS 93605 x UFRGS 911715 (Table 2) and is in agreement with that reported by Sànchez-Chacòn (1998).

Table 1 - Genealogy, type of response to aluminum toxicity and mean± standard deviation (sd) of primary root regrowth (cm) of the oat genotypes included in this study. Janeiro, 1998.

Genotypes UFRGS	Genealogy	Aluminium response	Mean±sd[1/]
17	COR^2/CTZ^3/PENDEK/ME1563//76-29/76-23/75-28/CI833	Tolerant	2.32±1.0
93605	UFRGS 15/UFRGS 881920	Tolerant	1.57±0.7
15	COR^2/CTZ^3/PENDEK/ME 1563/c16crcpx/c7512/srcpx/74c8014	Tolerant	1.79±0.6
911715	UFRGS 86A 1194-2/UFRGS8	Sensitive	1.12±0.4
93598	UFRGS 15/UFRGS 881920	Sensitive	0.49±0.08

[1/] Mean±sd of each genotype grown in all pots of the experiment.

A segregation ratio of 9 tolerant to 7 sensitive genotypes was observed for the F_2 populations derived from crosses involving the tolerant genotype UFRGS 15. This indicates that there are two genes segregating in those populations and their interaction is shown through epistasis (Table 2).

Crosses between the tolerant UFRGS 17 x UFRGS 93605 and UFRGS 17 x UFRGS 15 showed continuous segregation and since the parental genotypes were both tolerant and overlapped for their response to Al^{+++}, it was not possible to classify the progeny accurately in two distinct phenotypic classes only (Wagner, 1999). The fact that crosses of sensitive genotypes with UFRGS 15 segregate as two instead of one gene, indicates that this source of tolerance to aluminum toxicity differs from those of UFRGS 17 and UFRGS 93605. It is possible, however, that one of these loci is common to all tolerant sources studied here. Unfortunately, due to the variation in the measurement of primary root regrowth from environmental effects and to the size of the F_2 populations examined, this hypothesis could not be accurately tested in this work. Thus, further studies using larger populations and genetic designs to control environmental effects may help to determine these allelic relationships.

Crosses between the sensitive genotypes UFRGS 911715 and UFRGS 93598 did not show discontinuous segregation and most F_2 progeny had from 0.3 to 0.8 mm of primary root regrowth, indicating that these sources have similar genetic constitution. Nevertheless, UFRGS 93598 is the most sensitive genotype that has been identified in our studies and is more affected by Al^{+++} than UFRGS 911715 as can be seen from the means and standard deviations of primary root regrowth of both genotypes in Table 1.

Variation within the fixed genotypes P_1 and P_2 for primary root regrowth and some overlapping of tolerant and sensitive classes were observed, indicating the influence of environmental effects on the expression of this trait. This result shows that, although the methodology used in this work was widely utilized in tolerance assessments in different species (Camargo, 1984; Ferreira *et al.*, 1997; Sànchez-Chacòn, 1998), it still needs improvement in assessing oats. On the other hand, it is important to point out that the variation observed in this work was not bigger than that observed by Sànchez-Chacòn (1998). It was possible to distinguish genotypes that were tolerant and sensitive to aluminum. The parents from this study behaved like those described by Sànchez-Chacòn (1998).

Table 2 - Segregation of the F_2 generation from crosses between three tolerant and two sensitive oat genotypes to aluminum toxicity and the Chi-square test for each genetic hypothesis. Agosto, 1998.

Populations UFRGS	Number of Seedlings[1/]		Expected ratio (T:S)	χ^2	P - value
	T	S			
17 x 911715	39	6	3:1	3.27	0.07
17 x 93598	22	3	3:1	2.25	0.13
93605 x 911715	46	18	3:1	0.33	0.56
15 x 911715	21	19	9:7	0.23	0.63
15 x 93598	36	33	9:7	0.46	0.49

[1/] S = Sensitive; T = tolerant.

CONCLUSIONS

Tolerance to aluminum toxicity is governed by either one dominant or two epistatic genes in the oat genotypes of different genetic constitution evaluated in this study.

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RESUMO

Herança Genética da Tolerância ao Alumínio em Aveia

A toxicidade do alumínio é um importante fator na limitação dos cultivos em solos ácidos. A melhor compreensão da genética dessa característica auxiliará os programas de melhoramento no desenvolvimento de genótipos tolerantes a esse metal. O presente trabalho foi desenvolvido para estudar a herança da tolerância ao alumínio e estabelecer as relações alélicas entre genes presentes em diferentes genótipos de aveia. Foram avaliados através do recrescimento das raízes primárias submetidas a 20 ppm de alumínio três genótipos tolerantes (UFRGS 15, UFRGS 17 e UFRGS 93605), dois sensíveis (UFRGS 911715 e UFRGS 93598) e as populações segregantes na geração F_2, proveniente do cruzamento entre esses genótipos. Foram identificados um a dois genes segregando para essa característica e as fontes de tolerância existentes possuem constituição genética distinta.

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