Arachis genetic resources: evaluation of peanut smut resistance in wild species

Recursos genéticos de *Arachis*: evaluación de resistencia al carbón de maní en especies silvestres

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Abstract

Genetic resources are essential for crop improvement. Particularly, wild species related to peanuts are an important source of resistance to various factors. *Thecaphora frezii*, a pathogen causing peanut smut, leads to yield losses in Argentina's peanut sector up to 35%. This study evaluated the response of 11 diploid species with A, B, F and K genomes, *A. monticola* (AABB), and diploid interspecific hybrids (BB), to *T. frezii* over two cropping seasons. Plants were grown in 20L pots (three replicates each) under field conditions and inoculated with teliospores of the pathogen (20,000 tel./g of soil). The disease was quantified through incidence (% of diseased pods) and severity (scale from 0 to 4). Among A genome species, *A. duranensis* exhibited the highest incidence at 15.27%; for K genome species, *A. batizocoi* reached 13.18%. Resistance to *T. frezii* was observed in the wild species *A. diogoi* and *A. stenosperma* (A genome), *A. williamsii* (B genome), A. *trinitensis* (F genome), *A. cruziana* (K genome), and the intragenomic hybrids, constituting new records. Our findings expand the peanut gene pool information for breeders and identify resistant genotypes, supporting the need to preserve wild peanut germplasm to ensure its availability.

Keywords
Thecaphora frezii • *Arachis hypogaea* • wild peanut • resistance • genomes

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Resumen

Los recursos genéticos son fundamentales para el mejoramiento de los cultivos. Particularmente, las especies silvestres afines al maní cultivado constituyen una valiosa fuente de resistencias. *Thecaphora frezii* Carranza & Lindquist ocasiona pérdidas en el sector manisero argentino de aproximadamente el 35% del rendimiento. Se evaluó, durante dos campañas, el comportamiento frente a *T. frezii* de 11 especies diploides con genomas AA, BB, FF y KK; *A. monticola* AABB, y un híbrido interespecífico diploide BB. Los materiales se sembraron en macetas de 20L (tres repeticiones por c/u), en condiciones de campo, inoculándose con teliosporas del patógeno (20000 tel./g de suelo). Se cuantificó la enfermedad mediante la incidencia (% de vainas enfermas) y la severidad (escala de 0 a 4). Entre las especies con genoma A, *A. duranensis* presentó la mayor incidencia, 15,27%; y en las de genoma K, *A. batizocoi*, 13,18%. La resistencia a *T. frezii* hallada en las especies silvestres *A. diogoi* y *A. stenosperma* (genoma A), *A. williamsii* (genoma B), *A. trinitensis* (genoma F), *A. cruziana* (genoma K) y en el híbrido intragenómico BB constituyen nuevos registros. Nuestros resultados permiten ampliar el acervo genético del maní y generar genotipos resistentes; ratificando que el germoplasma de maní silvestre debe preservarse cuidadosamente para asegurar su disponibilidad.

Palabras clave
Thecaphora frezii • *Arachis hypogaea* • maníes silvestres • resistencia • genomas

Introduction

Peanut (*A. hypogaea* L.) is an allotetraploid species (2n=4x=40, AABB) originated in South America. It is cultivated in warm regions worldwide, with an annual production of 45.5 million tons (32). Given the small intern market, Argentina exports approximately 80% of its production. Córdoba province accounts for nearly 90% of Argentina's peanut industry (28).

The fungus *Thecaphora frezii* Carranza & Lindquist causes peanut smut, an endemic disease in Argentina (23) first detected in commercial crops in north-central Córdoba (18). Symptoms include pod malformation and replacement of seeds by dark-brown teliospores (figure 1, page 211). Literature reports almost 50% incidence (21) and yield losses up to 35% (20, 23).

Current management practices, such as tillage, crop rotation, cultivar selection, fungicide and fertilizer applications or soil amendments, have had limited success in reducing yield losses (1, 11, 22). However, the development of recombinant inbred lines (RILs) has enabled breeding strategies, generating resistant genotypes (8). These RILs originated from crosses involving one synthetic amphidiploid parent, obtained from a triple cross among wild species [(*A. correntina* x *A. cardenasii*) x *A. batizocoi*)]^{4x}, and an experimental line of *A. hypogaea*. These findings highlight the importance of wild species as biotic resistance sources in breeding strategies, targeting novel genetic resources with stable resistance to peanut smut.

Wild *Arachis* diploid species with A, B, D, F y K genomes (24, 25, 29, 30), are phylogenetically close to cultivated peanuts, constituting the genetic secondary pool PG-2 (14), defined as those species that can be crossed with local cultivars/elite germplasm, to produce fertile F1. Some of these species have been previously evaluated for smut resistance (3). Most of them are preserved in the "Banco de Germoplasma BGCTES" (IBONE, FCA-UNNE) germplasm bank. Although these genetic resources constitute fundamental breeding resources (31), they have not yet been fully exploited.

This study evaluated wild *Arachis* species with A, B, F y K genomes (24, 25) and intragenomic reciprocal hybrids (10), conserved in the BGCTES germplasm bank, aiming to identify wild sources of resistance against peanut smut.

Materials and Methods

Eleven diploid species with AA, BB, FF, and KK genomes, a tetraploid *A. monticola* AABB, and two intragenomic diploid hybrids (table 1) were evaluated over two cropping seasons (2019/2020 and 2020/2021), under field conditions at Criadero El Carmen in General Cabrera, Córdoba, Argentina (32°49'39.49" S - 63°51'55.57" O). The species were sown in 20L pots during the first week of December and maintained under field conditions in a completely randomized design with three replicates. Susceptible *A. hypogaea* var. Granoleico was included as a control treatment. Teliospores obtained from infected pods were used to inoculate the pots at a concentration of 20000tel/g soil. During harvest in April, pods were manually opened to quantify disease incidence (percentage of infected pods) and severity, following the 0 to 4 scale proposed by Astiz Gassó *et al*. (2008), where 0=healthy pod, 1 = normal pod with initial seed infection, 2 = normal pod with 50% seed infection, 3 = normal pod with 75% seed infection, and 4 = deformed pod with 100% seed infection. Severity was calculated using equation 1.

$$\textbf{Severity} = (0.x_0 + 1.x_1 + 2.x_2 + 3.x_3 + 4.x_4) \,/\, \textbf{total fruit number} \quad (1)$$

where
(x_0-x_4) = the number of fruits in each classification
(0-4) = the classification number.

Data were analyzed using ANAVA and Duncan´s test ($p \leq 0.05$) with InfoStat software 2020 (9).

Table 1. Analyzed material (species/hybrids, collection data and genome) and disease evaluation results.
Tabla 1. Material analizado (especies/híbridos, datos de colección y genoma) y resultados obtenidos de la evaluación de la enfermedad.

Species	Collection data*	Genome	Inc.		Sev.	
A. cardenasii	K 36021. Bolivia, Santa Cruz, Prov. Chiquitos	**AA**	0	a	0	a
A. cardenasii	K 36015. Bolivia, Santa Cruz, Prov. Chiquitos	**AA**	0	a	0	a
A. diogoi	G 10602. Paraguay, Alto Paraná, Pto. Casado	**AA**	0	a	0	a
A. duranensis	V 14167. Argentina, Salta, Capital	**AA**	6.31	a	0.24	ab
A. duranensis	K 7988. Argentina, Salta, Campo Durán	**AA**	15.27	b	0.57	c
A. kuhlmannii	K 30017. Brasil, MS, Aquidauana	**AA**	0	a	0	a
A. kuhlmannii	V 7639. Brasil, MS, Miranda	**AA**	0.78	a	0.01	a
A. stenosperma	V 10309. Brasil, MG, Rondonopolis	**AA**	0	a	0	a
A. ipaënsis	K 30076. Bolivia, Tarija, Gran Chaco, Ipa	**BB**	0	a	0	a
A. magna	K 30097. Bolivia, Sta. Cruz, Velazco, San Ignacio	**BB**	0	a	0	a
A. williamsii	W 1118. Bolivia, Beni, Trinidad	**BB**	0	a	0	a
[A. williamsii x A. ipaënsis]^{x2}	W 1118 x K 30076. Argentina, Corrientes, IBONE	**BB**	0	a	0	a
[A. ipaënsis x A. williamsii]^{x2}	K 30076 x W 1118. Argentina, Corrientes, IBONE	**BB**	0	a	0	a
A. trinitensis	W 1117. Bolivia, Beni, Trinidad	**FF**	0	a	0	a
A. batizocoi	K 9484. Bolivia, Sta. Cruz, Parapetí	**KK**	13.18	b	0.41	bc
A. cruziana	K 36024. Bolivia, Sta. Cruz, Chiquitos	**KK**	0	a	0	a
A. monticola	K 30061. Argentina, Jujuy, Lozano	**AABB**	0	a	0	a
A. monticola	K 30062. Argentina, Jujuy, Yala	**AABB**	0	a	0	a
A. hypogaea variedad Granoleico	Argentina, Córdoba, Gral. Cabrera	**AABB**	50.65	c	1.45	d

Except for the control, the analyzed materials are stored at the BGCTES (Corrientes, Argentina).

* G, W.C. Gregory; K, A. Krapovickas; V, J.F.M Valls; W, D.E. Williams; Inc. incidence (%), Sev. Severity (0-4). Different letters in each column indicate statistically significant differences ($p \leq 0.05$).

Los materiales analizados se mantienen en el BGCTES (Corrientes, Argentina), excepto el control.

* G, W.C. Gregory; K, A. Krapovickas; V, J.F.M Valls; W, D.E. Williams. ; V, J.F.M Valls; W, D.E. Williams. Inc. Incidencia (%), Sev. Severidad (0-4). Letras diferentes indican diferencias estadísticamente significativas ($p \leq 0,05$).

Results

Only species with AA and KK genomes exhibited symptoms of fungal infection. Among AA species, both entries of *A. duranensis* and one of *A. kuhlmannii* showed affected pods, with *A. duranensis* K 7988 presenting the highest average incidence of 15.27% (figure 1). Among KK genome species, *A. batizocoi* showed an average incidence of 13.18%, while *A. cruziana* showed no affected pods. Conversely, no affected pods were observed in species with BB and FF genomes, in the tetraploid *A. monticola* AABB, or BB hybrids [*A. ipaënsis* x *A. williamsii*]^{2x} and its reciprocal cross. The control, *A. hypogaea* var. Granoleico, displayed an average incidence of 50.65%. This value, along with those obtained for the wild species *A. duranensis* and *A. batizocoi*, showed statistically significant differences with the other wild species and the interspecific hybrid results (table 1, page 210).

Powder inside the pods evidences *Thecaphora frezii* teliospores. Scale bar = 1 cm.

El polvillo que se observa en el interior son las teliosporas de *Thecaphora frezii*. Escala de barra = 1 cm.

Figure 1. *Arachis duranensis* pods (K 7988) with smut (Severity Scale: 4).
Figura 1. Vainas de *A. duranensis* (K 7988) afectadas con carbón (Grado de Severidad: 4).

Regarding severity analysis in wild species, *A. duranensis* K 7988 achieved the highest value at 0.57, followed by *A. batizocoi*, with an average of 0.41. The control species, *A. hypogaea* var. Granoleico, had an incidence value of 1.45. Statistical analysis revealed significant differences ($p \leq 0.05$) between these values and those obtained for the rest of the species evaluated.

Discussion

The *Arachis* genus includes nine infrageneric sections according to cross-compatibility and exomorphic traits (17). Among these, the Arachis section is notable for comprising the largest number of wild species (32 spp.), and for its economic importance, as it includes the cultivated peanut *A. hypogaea.* In this section, 15 species possess A genome, six have B genome, K and G genomes are represented by three species each, F genome is represented by 2 species and only one has D genome (24, 25, 26, 29, 30). According to Harlan and Wet (1971), all 32 species integrate *A. hypogaea* secondary gene pool (PG-2).

Wild diploid *Arachis* species constitute valuable gene-transfer resources for cultivated peanuts, providing resistance to biotic and abiotic factors. Several techniques and methodologies have been developed for gene introgression from wild to cultivated genotypes (7, 31). In Argentina, the introgression of resistance to peanut smut from wild species has allowed important breeding advancements, such as the development of EC - 191 RC (AO) and EC - 394 RC (AO); (19).

Our results revealed a close relation between genome types and resistance to *T. frezii.* Accessions with A genome responded as previously observed by De Blas *et al.* (2019), except *A. duranensis*. Previous evaluations indicated susceptibility in *A. duranensis* (3), which aligns with our results, thus constituting the first susceptible A genome species identified. In our tests involving K genome species, *A. cruziana* was non-susceptible, while *A. batizocoi* exhibited susceptibility, which contrasts with prior results (8). Despite that, values were not markedly higher than those reported in this work. Species with B genome, alongside with [*A. ipaënsis* x *A. williamsii*]^{x2} and the reciprocal hybrid, showed non-infected pods, suggesting that B genome would be resistant to *T. frezii*, as previously reported (8).

Resistance to *Thecaphora frezii* in the wild species *A. diogoi*, *A. stenosperma* (A genome), *A. williamsii* (B genome), *A. trinitensis* (F genome), *A. cruziana* (K genome), and the diploid intragenomic hybrids constitute new records for *Arachis* genus.

The identification of resistant resources offers new breeding opportunities for peanut improvement. The literature documents successful incorporations of wild *Arachis* species in breeding programs. For instance, the A genome species *A. cardenasii* and *A. stenosperma*, which exhibit resistance to *T. frezii,* have also shown resistance to nematodes, rust and leaf spots (31). NemaTAM, a nematode-resistant genotype, was developed from wild *A. cardenasii* (27). Additionally, resistance to *Meloidogyne arenaria* was successfully transferred from *A. stenosperma* to tetraploid peanut (4).

Considering tetraploids, *A. hypogaea* is a segmentary allotetraploid with 2n=40 chromosomes (6, 13, 15, 16). The AABB cultigen arose through interspecific hybridization of two diploid AA and BB species (*A. duranensis* and *A. ipaënsis*, respectively), followed by chromosomal duplication (5, 6, 12). This event originated the wild tetraploid ancestor *A. monticola,* which subsequently underwent domestication, resulting in the cultigen *A. hypogaea.* In this study, our control species *A. hypogaea* exhibited the highest value of disease incidence and severity, whereas *A. monticola* showed no susceptibility. Given the susceptibility of *A. duranensis* to *T. frezii*, we hypothesize that *A. monticola´s* resistance may be derived from the B genome in *A. ipaënsis,* a hypothesis that could be further explored.

Conclusions

Our results provide valuable insights into wild *Arachis* species as sources of resistance to peanut smut disease, enabling breeders to expand peanut genetic pool and develop resistant genotypes. This underscores the importance of carefully preserving wild peanut germplasm collections to ensure their availability for future breeding efforts.

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