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Broadening the genetic base of peanut: Introgression of wild *Arachis* resistance genes using the Tetraploid Route with the aid of molecular and cytogenetic markers

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Peanut diseases are the most important reducers of crop yield. Wild species harbor resistances against pests and diseases, but are agronomically unadapted, therefore little used in breeding. In addition, they are almost all diploid, while *A. hypogaea* is an allotetraploid. Here, we report the introgression of wild resistance genes into cultivated peanut by the creation of synthetic tetraploid donors. The initial interaction between the diploid *A. stenosperma* and late leaf spot, rust and nematodes were characterized by electron and light microscopy. Fungi were suppressed at early stages of germination, and nematode infection was also prevented at pre-penetration step. Gene expression analyses identified genes responsive to these biotic challenges. Late leaf spot resistance QTLs were identified close to RGAs on an *A. duranensis* x *A. stenosperma* cross. *Arachis stenosperma* was identified as a very promising source of disease resistance for peanut. In order to enable the introgression of wild genes into breeding populations, synthetics were obtained from *A. batizocoi* x *A. stenosperma*, *A. gregoryi* x *A. stenosperma*, *A. batizocoi* x *A. duranensis* and *A. ipaënsis* x *A. villosa* crosses. Synthetics derived from *A. batizocoi* as B-genome donor and their hybrids with cultivated had surprisingly high viability and fertility rates. Synthetics also presented high levels of resistance to rust. Hybridizations of the 74 synthetics produced here with cultivated varieties are underway. The introgression of genome regions is being monitored cytogenetically using DAPI-banding and genomic *in situ* hybridization (GISH) and by using molecular markers.

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