

Addressing the Limitations of Peanut Resistance Due to Narrow Genetic Diversity

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Most food crops have undergone domestication and selection, resulting in a substantial reduction of genetic diversity. Peanut is an extreme case since it has a recent origin (about 8000 years ago) and it is sexually incompatible with its wild relatives, that possess high levels of genetic diversity and a range of adaptive traits that are of agricultural relevance (resistance to pests and diseases, tolerance to abiotic stresses, broader range of environment adaptation). Like many other crops, peanut is most important away from its origin and its wild relatives, South America; for breeding, these wild species should be available in different areas of the planet. Because of restrictions of germplasm exchange due to various international convention of Biological Diversity and Nagoya protocol, make the use of wild species for peanut breeding has been very limited. In the Wild Peanut Lab at UGA we have created a pipeline to characterize wild species, render them into a tetraploid, peanut-compatible form, introgress and genetically characterize the segments that confer resistance to the crop. These tetraploid lines (induced allotetraploids) are being deposited in the USDA/NPGR gene banks, so they are preserved and available to breeders in the USA and worldwide. We envisage this will be a major legacy for the peanut community for decades to come, enabling the production of a more sustainable and affordable crop.