

A Detective Tale: The Worldwide Influence of the Wild Species *Arachis cardenasii* on the Peanut Crop Revealed through the Lens of Genome Analyses

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Wild crop relatives have been used to introduce genetic diversity into elite cultivars worldwide. For peanuts, one of the pioneering works was done in the 60's and 70's at NCSU, where lines were created from a cross of peanut with *Arachis cardenasii*. The resulting sterile tetraploid hybrids were colchicine-treated, and, after multiple generations of selection and chromosome reduction, stable tetraploid improved lines were obtained. At the time, free germplasm exchange was possible, and exchange was done on the basis of individual agreements. These lines were then shared with colleagues at ICRISAT, India in the early 80's. As in all germplasm banks, names were changed but the pedigrees were not recorded. These lines had various resistances to foliar diseases and therefore, a large impact in breeding worldwide: they were distributed to breeders in several countries, like Australia, Mali and Brazil, and extensively used to create cultivars. By broadening the genetic basis of peanut, the lines also enabled the first works on marker-trait association and marker assisted selection on (then thought as) "pure" peanut. The catch is: for decades the various researchers and breeders didn't even know they were dealing with lines derived from a wild species. Here, we genotyped DNAs from different breeding lines and cultivars, looked at pedigrees, exchanged data, and a myriad of scientific articles and reports. With all this information, we pieced together the history of the amazing impact that these lines, anonymously, had on peanut breeding and genetics worldwide. This presentation will show a clear application of the genome sequence, addressing current issues such as germplasm exchange and breeders' rights.