

The Genome Sequence of Peanut

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We report the genome sequence of cultivated peanut (*Arachis hypogaea* cv. Tifrunner). As expected, it harbors essentially complete sets of chromosomes from the two ancestral species (*A. duranensis* and *A. ipaënsis*). However, we show that after its origin, the genome has evolved through mobile element activity, deletions and homeologous recombination; the flow of genetic information between corresponding chromosomes derived from the different ancestors. Uniformity of some of the patterns of recombination favors a single origin for cultivated peanut and its wild counterpart *A. monticola*. However, through much of the genome, homeologous recombination has created diversity. Using a new polyploid hybrid made from the ancestral species, we demonstrate how this can generate phenotypic change: a spontaneous change of flower color. This flow of genetic information is strongly influenced by chromosome structure and is asymmetrical: chromosomes derived from *A. duranensis* are more modified over time than the other. Homeologous recombination is ongoing and is orders of magnitude more frequent than mutation. It seems likely that this mechanism, which creates genetic diversity, helped favor the domestication of *A. hypogaea* over other diploid *Arachis* species cultivated by man.