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Can legume synteny be useful in guiding the introgression of wild genes into cultivated peanut?

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Most agriculturally important legumes fall within two sub-clades of the Papilionoids. The phaseoloids clade is an essentially tropical group that includes bean, cowpea, soya and pigeon pea. The galegoids, are mostly temperate, and include clover, pea, lentil, field bean, chickpea, and *Medicago* and *Lotus*. However, peanut (*Arachis hypogaea* L.) falls in the more basal, mostly tropical, Dalbergioid clade. Cultivated peanut is an allotetraploid of recent origin, with genome type AABB. A severe genetic bottle-neck was imposed at the species origin, via hybridisation of two wild diploid species followed by a spontaneous chromosome duplication. This led to a low genetic diversity which, coupled with the complexity of tetraploid genetics, has constrained the advances in genetics necessary for modern breeding. Under the framework of the Generation Challenge Program we have worked to overcome these limitations. Firstly, we dissected the tetraploid genetics of peanut by constructing two diploid maps: one for the AA (Moretzsohn *et al.*, 2005), and one for the BB genome. Secondly we are constructing tetraploid maps, using synthetic amphidiploids. For markers, we used microsatellites, because they are codominant and polymorphic, have good transferability between species, and are ideal for breeders. We have used the same markers for all maps, thus generating a framework for map comparison and the mapping of QTLs in different genetic backgrounds. Clearly, the utility of the reference map, based on the AA-genome map, would be greatly enhanced if it could be used to access the near-complete genome sequences of *Lotus* and *Medicago*, in a way that would enhance our understanding of the *Arachis* genome. With this aim, we placed more than 80 legume anchor markers (Fredslund *et al.*, 2006) on the AA-genome map and analyzed the synteny between *Arachis* and the model legumes. The main affinities of nine of the ten *Arachis* linkage groups and model legume chromosomes were identified. Some substantial regions of marker co-linearity are evident. The data indicates that the last whole genome duplication seems to have predated the divergence of *Arachis* from the Galegoids and Phaseoloids. The inclusion of *Arachis* within a single genetic system for the legumes appears to be feasible. This should help in the characterization of the *Arachis* genome, and the implementation of molecular breeding for this crop.

References

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