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Title: Leveraging genomic data and tools from botanical models in peanut improvement

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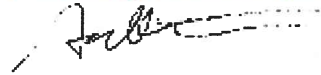
While peanut still lacks a genome sequence, several other legumes and botanical models have now been sequenced, and we are near completion of the first ‘physical map’ for peanut, a framework for assembling the peanut genetic blueprint in the near future. ***The greatest challenge now facing the peanut community is no longer genome sequencing per se but the conversion of sequence to actionable knowledge.*** While a growing number of investigations show parallels in gene arrangements among well-studied legume genomes and those of botanical models, data for investigating these important parallels in peanut are just beginning to achieve critical mass. Using methods that we pioneered, our objective is to utilize emerging peanut data to begin to ‘align’ the chromosomes of peanut to those of sequenced legumes and botanical models, providing the means to begin to locate key peanut genes and deduce their functions based on knowledge from better-studied plants. We have conducted initial alignments of the current peanut physical map to the genome sequences of other available legumes and botanical models, identifying numerous areas in which the physical map is in need of additional and/or improved information. Lab work has begun to develop this additional information.

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Objectives and approach. While peanut still lacks a genome sequence, several other legumes and botanical models have now been sequenced, and we are near completion of the first ‘physical map’ for peanut, a framework for assembling the peanut genetic blueprint in the near future. **The greatest challenge now facing the peanut community is no longer genome sequencing per se but the conversion of sequence to actionable knowledge.** For example, completion of the *Arabidopsis thaliana* sequence was quickly followed by inception of the NSF 2010 project, which has greatly increased knowledge about functions of *Arabidopsis* genes but at a cost near US\$200 million. Using this information, the functions of perhaps half of the estimated 30,000 peanut genes might be quickly deduced by analogy to those of *Arabidopsis* and other botanical models such as *Medicago truncatula*, *once we understand the gene-by-gene relationships among these genomes.*

While a growing number of investigations show parallels of chromosome ‘macrostructure’ among well-studied legume genomes, as well as between these genomes and those of botanical models, data for investigating these potentially important parallels in peanut are just beginning to achieve critical mass. The required data for peanut are now emerging from several sources including (a) sequencing of carefully-chosen segments of the peanut genome that contain particular genes of interest (disease resistance genes, allergen-encoding genes, nodulation-related genes), (b) physical mapping including end-sequencing of large-insert BAC clones of peanut DNA and hybridization of sequence-tagged site DNA markers to the same BACs, and (c) enriched genetic mapping.

Using methods that we pioneered (Tang et al., 2008), our objective is to utilize these emerging peanut data to begin to ‘align’ the chromosomes of peanut to those of sequenced legumes and botanical models, providing the means to begin to locate key peanut genes and deduce their functions based on knowledge from better-studied plants. The PI was among those who participated in formulating national and international peanut genomics and biotechnology goals – this proposal contributes to goals 1, 3, 4, and 5, as well as to improvement (breeding) for quality, disease, and stress resistance/tolerance and other traits.

Progress to date. We have conducted initial alignments of the current peanut physical map to the genome sequences of other available legumes and botanical models, identifying numerous areas in which the physical map is in need of additional and/or improved information. Lab work has begun to develop this additional information.

In addition, we have completed sequencing of carefully-chosen segments of the peanut genome that contain allergen-encoding genes, and are presently analyzing correspondence of these regions to the genome of other legumes.

Expected Results. The resulting capabilities will accelerate progress toward a wide range of goals in peanut improvement. Researchers will be able to quickly deduce the locations in peanut of genes that have been implicated in other plants in mitigation of disease, drought, seed quality

and composition, and many other important improvement targets. This activity need not wait for the peanut genome sequence to be completed ... a physical map of the peanut genome, made in the lab of the proposer based on resources and approaches that have been described in the past several years (Burow et al., 2001; Yuksel et al., 2005; Yuksel and Paterson, 2005) that have been validated in other crop genomes (Bowers et al., 2005), now includes a sufficient number of sequence-tagged-site markers to provide alignments for the gene-rich portions of the genome. Such alignments will permit scientists to begin now to reap many benefits that will be further accelerated by the eventual genome sequence. Indeed, better understanding of the relationship of the peanut chromosomes to those of other plants will be an important tool to assess the accuracy of the eventual genome sequence.

Data dissemination will be via the *Plant Genome Duplication Database* (PGDD: <http://chibba.agtec.uga.edu/duplication>), devoted to facilitating comparisons of multiple angiosperm genomes toward 'translational genomics' that permits study of large and complex genomes such as those of many crops to benefit from knowledge and resources available for one another and for botanical models. We recently obtained competitive support from the National Science Foundation to maintain and further improve PGDD functionalities, benefiting the peanut community at no cost.