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APPLICATION OF CHROMOSOME MAPS TO SOYBEAN IMPROVEMENTS

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Introduction

Biotechnology - the use of the latest tools and techniques to make improvements on life. In the agricultural world, these improvements can be made in quality as well as quantity. Two improvements being explored in soybeans is to lower the saturated fat content of the oil (thus reducing cholesterol levels), and improving the nutritional value of the protein. The creation of molecular maps, an application of Biotechnology itself, will assist in making these improvements. Diers et. al. (1992b) reports an RFLP (Restriction Fragment Length Polymorphism) map for soybeans. This molecular map has assisted researchers in studying such agronomic characteristics as protein, oil, yield, and seed hardedness (Quantitative Traits). Additionally, it is possible to analyze pedigrees and determine the percentage of the chromosomes that were contributed by each parent, the regions of the chromosomes contributed, and finally to begin associating agronomic traits with these regions.
Quantitative Traits

In the future, soybeans may not be grown strictly for their yield potential. Already, standards have been proposed (not passed yet) which would require set minimal levels (%) for protein and/or oil content of seeds. Additionally, specialty soybeans are becoming more popular, such as those targeted for the 'tofu' and 'nato' markets.

Breeding soybeans for specialty markets is difficult due to a lack of knowledge of the underlying genetics that produce the desired phenotype. Breeders can make educated choices about lines to include in their breeding programs, but there is no assurance that these will result in commercially successful varieties. If, on the other hand, chromosomal locations which determine agronomically important characteristics were known, breeders could select lines for their breeding programs that would have a greater probability of bringing desirable characteristics together.

Diers et. al. (1992a) performed a quantitative mapping study to identify regions which affected protein and oil content in an F2 population from the cross A81-356022 (G. max) X PI468916 (G. soja). This study identified two regions which affected both protein and oil content and one region affecting only protein content.

One disadvantage of QTL studies is that they tend to be cross specific, as in a region which is highly significant in one population may have no effect on another. However, through additional studies to gain a greater understanding of these traits, genes can be identified (as opposed to corresponding regions) and breeders will be able to make use of this information in the production of new cultivars.

Chromosomal Contribution

A second application of molecular maps is to trace chromosomal segments as they are passed on through pedigrees. It is possible to look at a "graphical genotype" of a cultivar and its parents, and determine which regions of the chromosomes were derived from each parent. Figure 1 shows how these graphical genotypes are constructed. Banding patterns from a gel are given a numerical score, with a different number for each pattern. This is done for every locus (position) on the map. These numbers are then imported into a software package called Supergene and each number is converted into a different pattern. Now we have gone from a map of a chromosome with a linear order of markers, to map of a chromosome containing different patterns. A graphical representation of chromosome N is depicted in Figure 2. Figure 2 also shows a partial pedigree of the commercial cultivar Frontier 1950. Beginning at the "top": Asgrow 3127 was derived from a cross of Williams X Essex. In looking at the graphical representation of chromosome N, from Asgrow 3127, it is possible to determine that the left half of the chromosome was derived from Williams, while the region corresponding to right end was derived from Essex. In the cultivar Asgrow 2943, the left two-thirds of the chromosome was derived from Asgrow 1564. Finally, in the cross BSR 201 X Asgrow 2943, Frontier 1950 received the region B216a from Asgrow 2943. This information, while
interesting in and of itself, can lend itself to other uses, including the comparison of the theoretical genetic contribution of ancestors to the observed contribution, and the identifying cosegregation of phenotypic traits and molecular markers.

Ancestral Contribution

Using again the partial pedigree of Frontier 1950, Figure 3 shows the percentage of DNA that each parent contributed to the cultivar, as compared to the theoretical value of 50% from each parent. You can see that Asgrow 3127 is composed of 35% Williams and 65% Essex. Asgrow 2943 received 45% of its genetic information from Asgrow 1564, and 55% from Asgrow 3127. Similarly, Frontier 1950 is composed of 53% BSR 201, and 47% Asgrow 2943. Chi-squared analysis indicates that only the cross of Williams X Essex to give Asgrow 3127 differed significantly from the expected, with an $a = 0.01$ (Chi-squared value = 9.0, 1 degree of freedom). It would be expected, due to selection, that these ratios would differ from the theoretical values. However, this does not always appear to be true.

Association of Phenotypic Traits

The creation of molecular maps, and derivation of graphical genotypes from these maps, allows the association of genotype and phenotype to be brought even closer together. For example, resistance to phytophthora root rot is a trait of interest to many soybean breeders. Through the use of near-isogenic lines, Diers et. al. (1992b) was able to place on the molecular map four genes which conferred resistance to phytophthora. Figure 4 shows the location of resistance gene Rps1 in relation to molecular markers A071, K418a, and R022 (Bold Face). Its' location, with respect to the remaining markers, is not known. The cultivar Williams contains the allele rps1 at the Rps1 locus, and is susceptible to phytophthora. Kingwa, on the other hand, is resistant to certain races of phytophthora, and contains resistance allele Rps1-k at the Rps1 Locus. This resistance allele from Kingwa was backcrossed into Williams, producing the resistant cultivar, Williams 82. The locus A-071 is closely linked to the Rps1 locus, and it detects a polymorphism between Williams and Kingwa. In other words, there is a difference between Williams and Kingwa like the one depicted in Figure 1 between marker 1 and marker 2. Thus, by looking at Figure 5, you can see that Williams 82 received the region corresponding to A-071 from Kingwa, as would be expected with Kingwa providing the Rps1-k resistance locus. This brings up the potential that breeders could select for resistance to phytophthora based not on extensive testing, but on the DNA marker it contains, saving time and possibly money in the process.

Conclusions

Biotechnology has provided the tools necessary to create molecular maps of chromosomes. These molecular maps are used by researchers in identifying regions which control such agronomic traits as levels of protein and oil. This, in turn can assist in the manipulation and improvement (in quality and/or quantity) of these characteristics. Chromosomes maps also assist in the understanding of the
'shuffling' of traits during cultivar development. The actual percentage of the chromosomes contributed by a parent can be determined, as well as which portion(s) of the chromosomes were passed along. Finally, Chromosome maps allow the association of traits with molecular markers, and have the potential to assist breeders in making selections, saving time, effort, and potentially money.

References


**Figure 1. Creation of Graphical Genotype.** This ‘flow chart’ shows how a graphical genotype is derived from raw data. First, cultivars are compared for differences. Each of these different 'Gel Patterns' produced by a cultivar is given a different 'score'. Then, each 'score' is converted into an 'Allele Designation', or pattern. A series of these patterns for a particular cultivar is considered to be a "Graphical Genotype."
Figure 2. Chromosomal Contributions. The above pedigree demonstrates the ability to determine what regions of a chromosome were contributed by which parents. For example, Williams (genome designator = black) passed on to Asgrow 3127 the left portion of the chromosome, as shown by the black region (parental contribution line) under its' graphical genotype (Allele Designation). The right portion was derived from Essex.
Figure 3. Theoretical vs. Actual Percentage of Parental Contribution. The above pedigree shows the percentage of genetic information each parent contributed, as compared to the expected 50% from one parent and 50% from the other parent. You can see that Asgrow 3127 is only 35% Williams and 65% Essex. This deviation from the expected is probably due to the selection that takes place in the development of cultivars.
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Figure 4. Linkage Group N. This molecular map shows the location of the Phytophthora resistance gene, Rps1. Its location is known in relation to markers R_022, K_418a, and A-071a.
Figure 5. Cosegregation of Rps Resistance and Locus A-071. The above pedigree demonstrates the ability to associate traits with molecular markers. The above shows that Kingwa, which is resistant to phytophthora, has a 'cross-hatched' allele at the A071 Locus. Williams, which is susceptible to phytophthora, has a 'mesh-patterned' allele at the A071 locus. In the development of Williams82, Kingwa passed its' resistance to phytophthora along with the 'cross-hatched' allele to Williams 82. Thus, if Williams 82 were used to bring phytophthora resistance to another cultivar, this marker could be used to predict presence of resistance in the progeny.