PROGRESS TOWARD THE DEVELOPMENT OF AN UPLAND NEAR-ISOGENIC INTROGRESSION LINES CARRYING DIFFERENT PIMA CHROMOSOME SEGMENTS

Edward L. Lubbers and Peng W. Chee
Department of Crop and Soil Sciences, University of Georgia, Tifton, GA,

Introduction

Genetic diversity is required for breeding. One cannot select without traits or markers that differ. Continued breeding as well as the initial domestication inherently decreases available genetic diversity. Obviously we need to replace genetic diversity, but we need favorable diversity, not just any type of diversity. Mother Nature has given us a lot of alternate forms of genes but we have had centuries of selection that have eliminated most of them. We are now looking at an apparent yield and fiber quality plateau (W. Meredith, 2006) which some believe is caused by lack of diversity. We are also finding improved fiber quality necessary for the United States producer in the competitive, global cotton market.

To have the required diversity, we need to introduce new germplasm. Germplasm can be described as coming from gene pools depending generally on sexual compatibility and recombination. The primary gene pool for Upland cotton obviously includes the races of *Gossypium hirsutum*. *Gossypium barbadense, G. darwinii, G. mustelinum, and G. tomentosum* are also included here even though there are additional hindrances to introgression. The secondary gene pool includes the Gossypium diploids that can recombine once the sexual incompatibility is overcome and then those diploids that have reduced chromosome homology are in the tertiary gene pool.

The greatest hindrances in introgressing alleles from the related tetraploids are overwhelming allelic deluge and linkage drag. This is likely to be the greatest reason that breeders avoid using exotic germplasm. One method that has been suggested to overcome these problems is the AB-QTL (Advanced Backcross – Quantitative Trait Loci) analysis (Table 1). Using molecular markers to monitor QTLs may be a more effective technique to quickly remove the linkage drag as well as sifting out the desirable alleles despite the background noise caused by the environment.

Our objective is to develop a series of near-isogenic introgression lines (NIILs) by interspecific backcross of *G. barbadense* into Upland cotton using a modified AB-QTL. The intent is to cover the entire *G. barbadense* genome.

Materials and Methods

Our research uses Pima S-6, a *G. barbadense*, as the donor parent in an AB-QTL analysis. It is in the primary gene pool and is an excellent source of additional genetic diversity because it has high quality fiber and many available polymorphic markers. It is

also domesticated, thereby giving some chance that there are fewer undesirable alleles. Direct use is inefficient because of hybrid breakdown, partial sterility, and later maturity than many Upland cultivars, but AB-QTL renders these specific difficulties less relevant.

We are using RFLPs (262 loci from a map with more than 2500 loci (Jiang et al., 2000)) to monitor the introgression of the Pima S-6 donor DNA into Tamcot 2111, the backcross parent. Three backcrosses were performed at which time the individual plants in the BC3F1 were genotyped and the BC3F2 families from those individuals were phenotyped (Fig. 1). Fiber quality phenotypes were measured in the first subset of this series to monitor the effects of the DNA segments (Chee et al., 2005a, b; Draye et al., 2005). QTL analyses via the analyses of variance is a secondary benefit in this research.

Results and Discussion

In the genotyping phase of the NIILs development (Fig. 2), we found three categories of NIILs: *group 1*) 37 lines were already NIILs, *group 2*) 491 lines, the bulk of the lines, are pre-NIILs that required further selfing and monitoring, and *group 3*) 68 lines that were required to be backcrossed again with further selfing and monitoring to provide at least 2 pre-NIILS each (for a total of more than 136 pre-NIILs). This totals to more than 664 NIILs from which we can select to cover the Pima S-6 genome. The NIILs in the field look very much like the recurrent parent, Tamcot 2111.

As we increased seed for the *group 1* NIILs, we took fiber quality data. With this data from three field plots grown in two years, a single factor ANOVA was performed with F-protected LSD mean separation. Micronaire (Mic) (Fig. 3), length as Upper Half Mean in inches (UHM) (Fig. 4), strength in grams/tex (STR) (Fig. 5), and % short fiber content (SFC%) (Fig. 6) all had significant differences between their respective fiber quality means. HVI Uniformity Index and HVI Elongation also followed this pattern (Figures not reported). The distribution of Mic and STR show the backcross parent, Tamcot 2111, in the center as would be expected (Figs. 3 and 5). Tamcot 2111 was found to be towards the shorter side of the distribution of length (Fig. 4) as we might expect since Pima S-6 is known for long staple. Tamcot 2111 was also found skewed toward greater SFC% (Fig. 6). Although this was not expected, it does show that we should easily be able to select for lint with less short fiber.

Our future work will include fine mapping of selected genomic regions that are associated with fiber quality traits as well as determining the performance of the QTLs of the NIILs under different genetic backgrounds along with stacking / pyramiding the QTLs to build better quality fiber.

All of the fiber quality traits showed genetic diversity that is available for introgression from these NIILs into elite cultivars. These NIILs are useful in that 1) they are a source of variation with less penalty of linkage drag, 2) they will have a more discrete segregation of the alleles within the genomic segment, and 3) they will allow fine mapping without the clutter of the original cross.

Acknowledgements

We acknowledge the financial support from the Georgia Agricultural Experiment Station, Cotton Incorporated, and USDA-IFAFS.

References

Chee, P., X. Draye, C-X Jiang, L. Decanini, T.A. Delmonte, R. Bredhauer, C. W. Smith, and A.H. Paterson. 2005a. Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: I. Fiber elongation. Theor. Appl. Genet. 111:757-763.

Chee, P., X. Draye, C-X Jiang, L. Decanini, T.A. Delmonte, R. Bredhauer, C. W. Smith, and A.H. Paterson. 2005b. Molecular dissection of phenotypic variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: III. Fiber length. Theor. Appl. Genet. 111:772-781.

Draye, X., P. Chee, C-X Jiang, L. Decanini, T.A. Delmonte, R. Bredhauer, C. W. Smith, and A.H. Paterson. 2005. Molecular dissection of interspecific variation between *Gossypium hirsutum* and *G. barbadense* (cotton) by a backcross-self approach: II. Fiber fineness. Theor. Appl. Genet. 111: 764-771.

Jiang, C., P. Chee, X. Draye, P. Morrell, C. Smith, and A. Paterson. 2000. Multi-locus interactions restrict gene flow in advanced-generation interspecific populations of polyploid Gossypium (Cotton). Evolution 54:798-814.

Tanksley, S.D. and C.J. Nelson. 1996. Advance backcross QTL analysis: a method for the simultaneous discovery and transfer of valuable QTLs from unadapted germplasm into elite breeding lines. Theor. Appl. Genet. 92:191-203.

Table 1. AB-QTL Analysis Summary (Tanksley & Nelson, 1996)

• Backcross to elite for BC1 and BC2 populations
– Can select at this stage against undesirable donor alleles using markers and/or phenotypes
• Molecular marker characterization at the BC2 or BC3 level.
• Generate BC3 or BC4 families
• Evaluate for agronomic performance and analyze for QTLs.
• Target valuable genomic regions
• Produce NILs with elite genetic background by employing MAS
• Evaluate the agronomic performance of the NILs and elite parent control in replicated environments

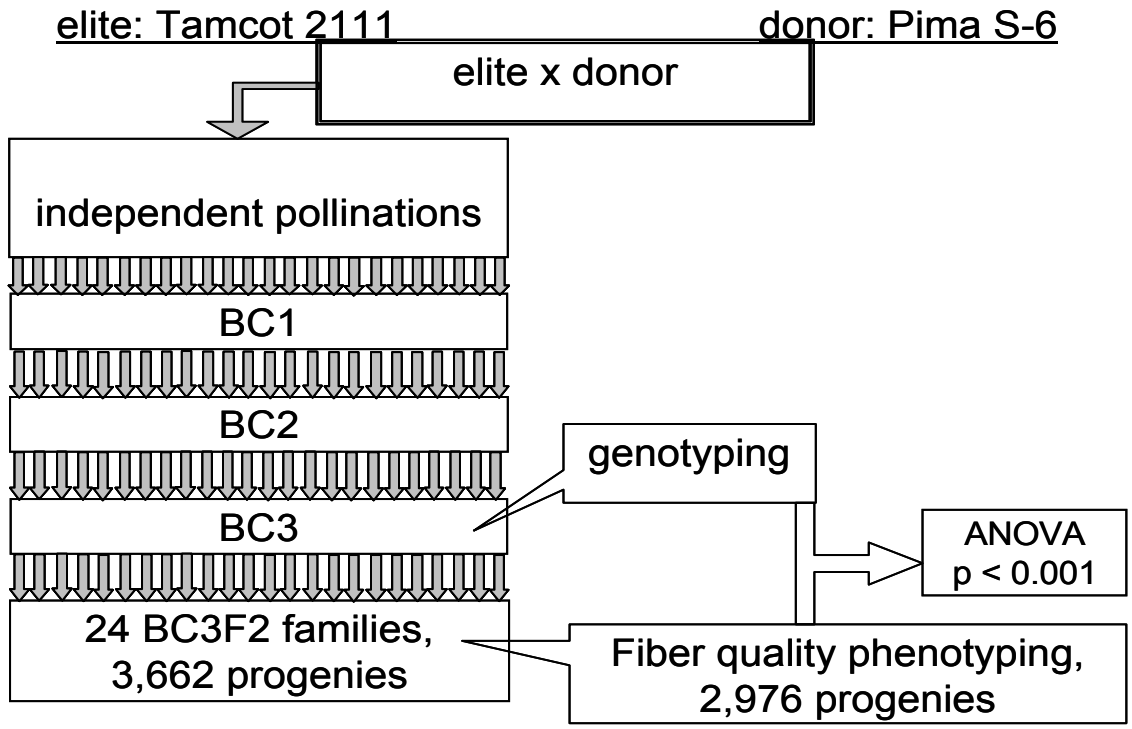

Fig. 1. The Methodology of the QTL Analysis

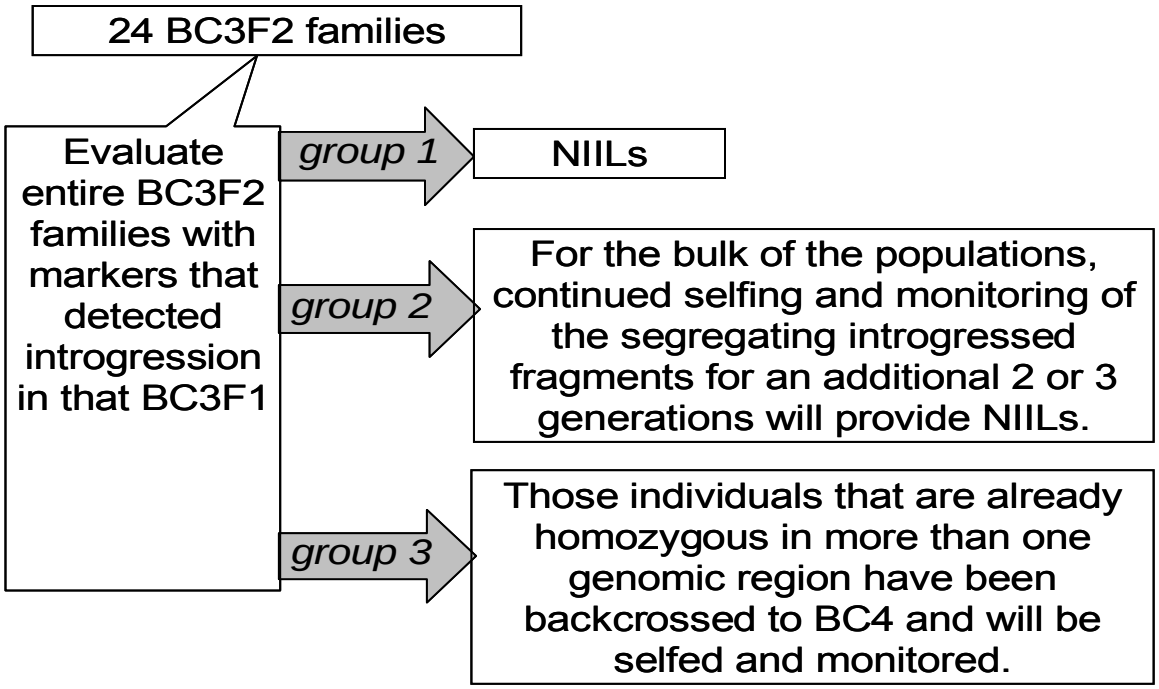

Fig. 2. The Methodology of the NIILs Development

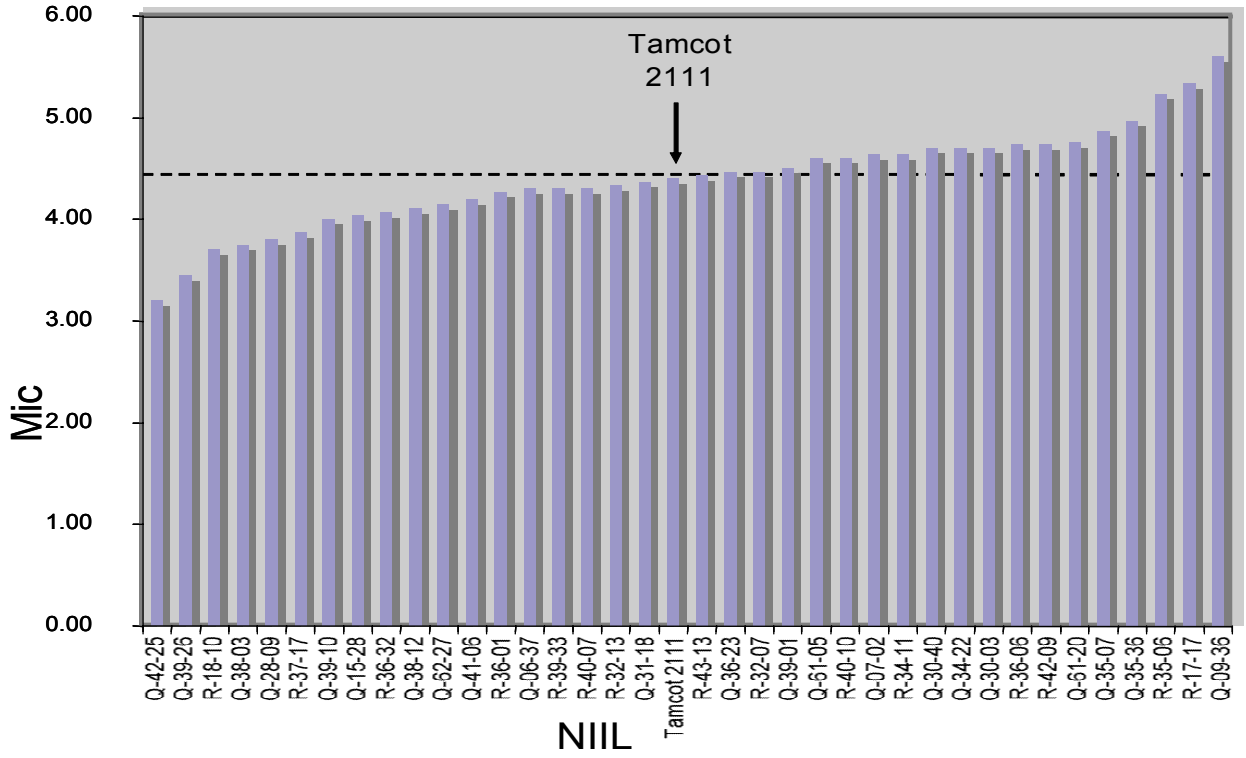

Fig. 3. The distribution of HVI micronaire of the *Group 1* NIILs

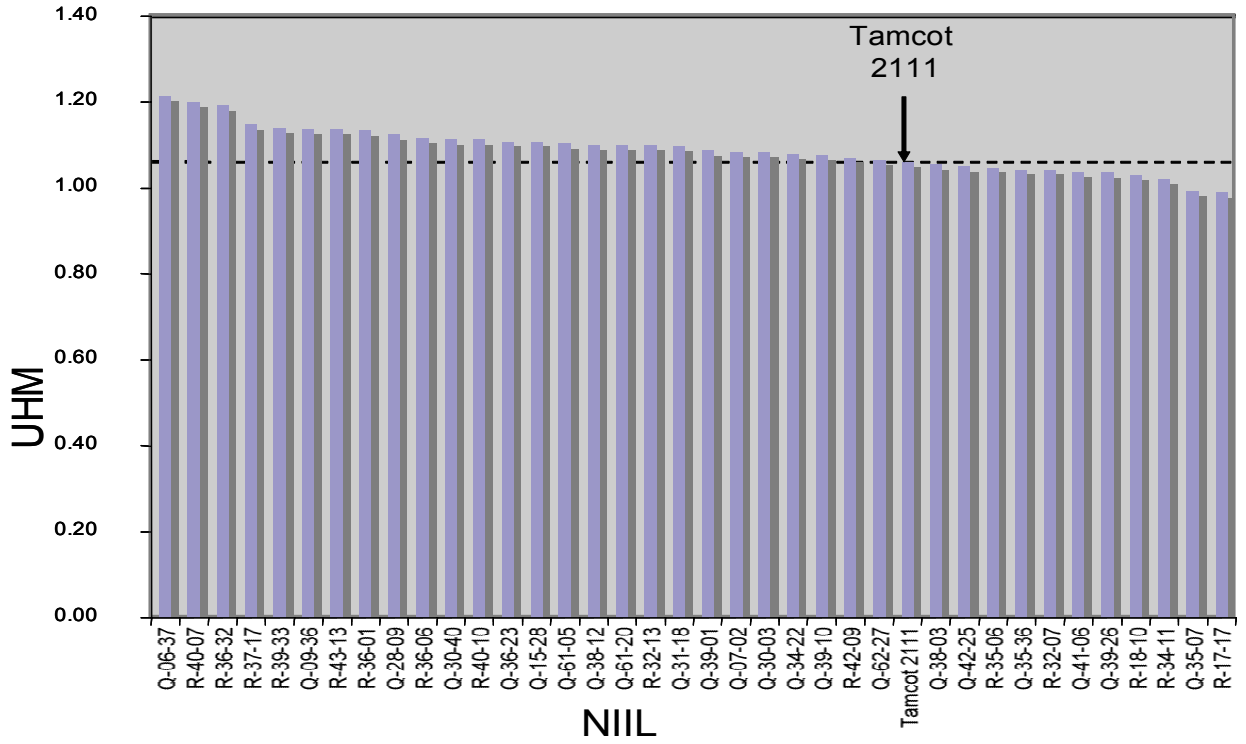

Fig. 4. The distribution of HVI UHM Length of the *Group 1* NIILs

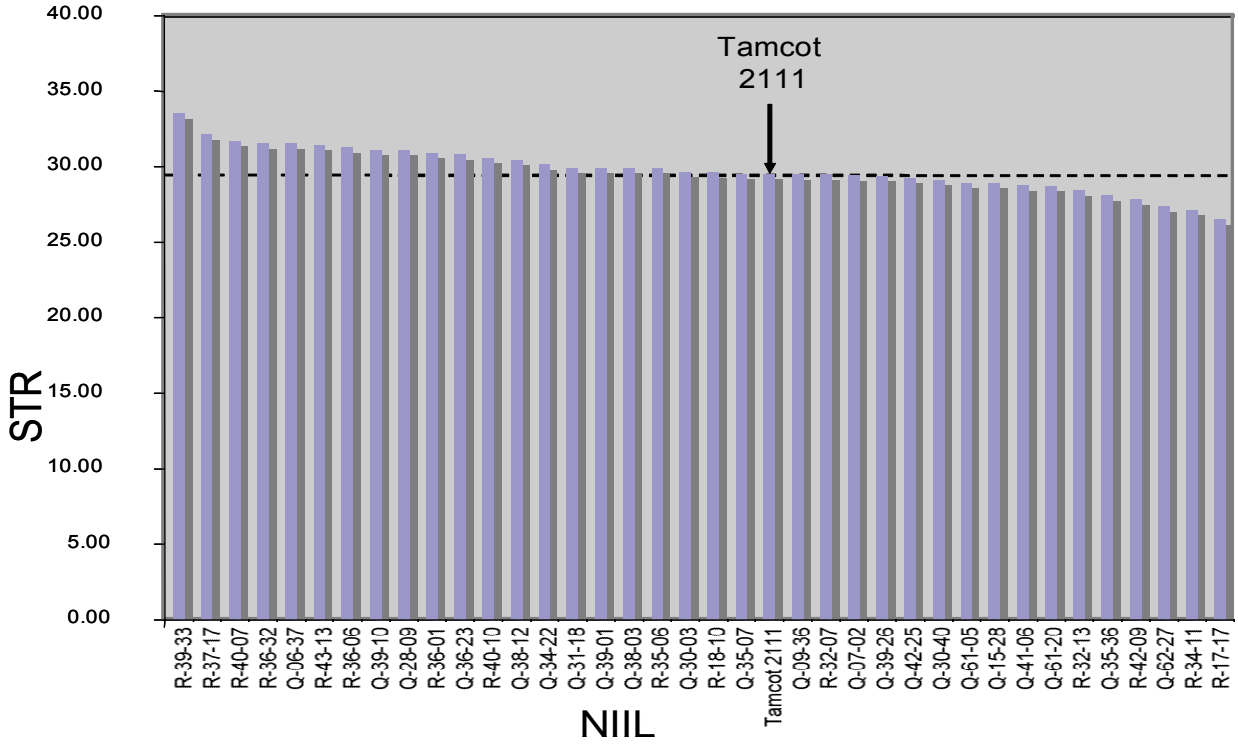

Fig. 5. The dist. of HVI Strength in g/tex of the *Group 1* NIILs

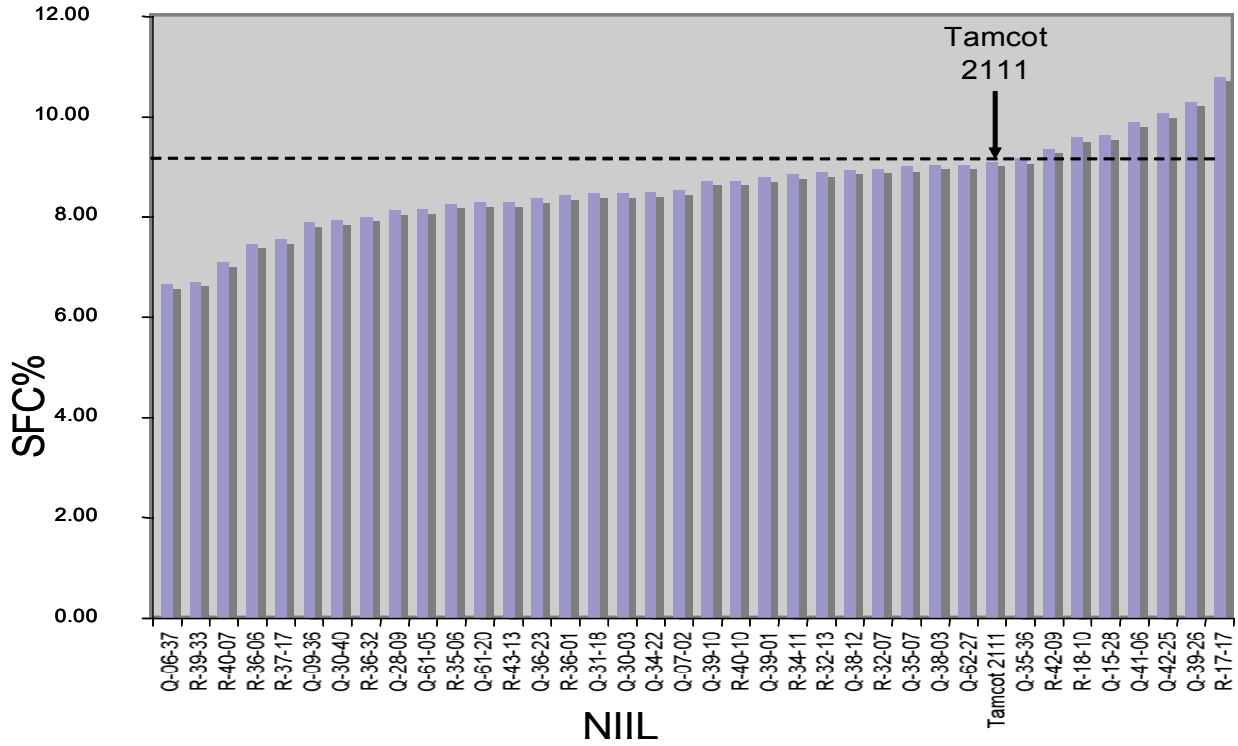

Fig. 6. The dist. of HVI % Short Fiber Content of the *Group 1* NIILs