

**Development of immortal introgression populations; genome wide Near Isogenic Lines  
(NILs) for cotton**

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Crop and Soil Sciences Seminar

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Cotton is the world's foremost textile fiber crop and contributes to a multibillion textile industry. Cotton fiber has been the focal point of most research efforts in cotton. The mystery of fiber development by the elongation of a single cell remains unsolved. Therefore, various breeding efforts have been conducted for a long time to develop mapping populations so that dissection of gene networks responsible for the functional genomics behind fiber development can be accomplished. The objective of our research is to develop immortal introgression mapping populations; genome wide Near Isogenic Lines (NILs) for cotton. NILs enable the mapping of QTL with small phenotypic effect and also, reduced background noise. Further NILs provide the platform to study the effect of epistatic interaction on the phenotype. We are aiming to develop two reciprocal set of NILs by introgression between *Acala Maxxa* (*Gossypium hirsutum*) and *Pima S6* (*Gossypium barbadenes*). The ultimate population that will be used for genotyping is BC4. A total of 192 BC4 plants in each set of NILs will contain a single introgressed segment of the donor genome but will collectively 'tile' the genome. A population with a sufficient number of backcross lineages is expected to provide 3x coverage of donor genome (~4500 cM) for high resolution mapping. Development of genome wide NILs will solve three purposes simultaneously; identification of QTL, fine mapping, and incorporation of the QTL in the elite germplasm (Eshed and Zamir, 1995). Furthermore, it provides an opportunity to study species divergence and breeding of these species.

**References**

- Eshed Y, Zamir D. 1995. An introgression line population of *Lycopersicon pennellii* in the cultivated tomato enables the identification and fine mapping of yield-associated QTL. *Genetics* **141**:1147-62
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- Keurentjes JJB, Bentsink L, Alonso-Blanco C, Hanhart CJ, Vries HBD, Effgen S, Vreugdenhil D, Koornneef M. 2007. Development of a near-isogenic line population of *Arabidopsis thaliana* and comparison of mapping power with a recombinant inbred line population. *Genetics* **175**:891-905