

**COMPARISONS OF QTL MAPPING PROPERTIES
FOR TWO METHODS OF RI DEVELOPMENT**

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Abstract

Recombinant inbred (RI) populations offer several advantages for QTL mapping over more commonly used F_2 or backcross populations. First, RI lines can be evaluated in many different environments or by different researchers. Second, a more accurate assessment of the genetic component of variance or QTL mapping precision can be made in studying quantitative traits. To obtain more precise mapping results, a quite large population is required. However, breeders may have some difficulties employing the traditional single seed descent (SSD) method to develop a large number of RI lines because the maintenance of the family size can be hard to manage from F_2 . Therefore, it is useful to find other convenient ways to develop a large RI population. In our previous work, we have applied bulk-selfing technique to develop 190 RI lines from 96 F_2 individuals of upland cotton cross MARCABUCAG8US-1-88/HS 46. Before using them, we need to know the QTL mapping properties of RI lines derived by this technique. In this study we compared the properties of QTL mapping between a bulk-selfing RIL population and a SSD RIL population through Monte Carlo simulations. The simulation results indicated that the mapping properties were similar for both kinds of populations. It also indicated that these RI lines developed in our lab can be further used for linkage constructing and QTL mapping. Some statistical properties for several agronomic traits among these upland cotton RI lines were provided from the location at Mississippi State. The results indicated that these traits were normally distributed. Our future work will be to construct linkage groups based on SSR and AFLP techniques and map the QTLs for agronomic traits (including developmental traits) and fiber properties using different mapping methods.