**An Integrated Framework for Linkage Map Construction Across Selfing Generations: Application to Common Bean**

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Increasing the genetic resolution of QTL mapping enhances the ability to pinpoint narrow genomic regions of interest. One promising strategy is the joint analysis of multiple interconnected mapping populations, which improves the robustness and resolution of linkage and QTL mapping. This study presents a framework and software for constructing integrated linkage maps across selfing generations, using F₂ and RIL populations from the same cross. To validate the method, we used both simulated and empirical datasets. The simulation involved 5,000 replicates per generation under successive selfing from F₂ to F₁₃, considering one chromosome with 1,000 markers and a single seed descent scheme. Recombination fractions were estimated and compared to true genetic distances to assess accuracy. The real dataset included F₂ (n = 333) and F₆ (n = 342) populations derived from a cross between a moderately resistant and a susceptible common bean genotype (IAC-Tybatã × Branquinho) in response to root-knot nematode (RKN). Genotypic data from both populations were integrated using a Hidden Markov Model with population-specific transition probabilities, leveraging shared SNPs to anchor the joint map. Our results show that integrating generations leads to better haplotype block estimation, higher resolution, and improved map accuracy. The larger effective sample size enhances recombination estimation and reduces noise in marker ordering, particularly in low-recombination regions. This approach yields higher marker saturation and more informative coverage for downstream QTL analyses. As a next step, we will apply this framework to fine-map QTLs for RKN resistance in common bean.