

UNDERSTANDING GENOMIC EVOLUTION AND SEGREGATION DISTORTION IN SOLANACEAE: A COSII LINKAGE MAP IN *NICOTIANA*

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ABSTRACT

Genetic linkage maps are excellent tools to investigate genomic evolution, genomic structure and quantitative trait loci. In our study, we created comparative linkage maps in a reciprocal cross between *Nicotiana longiflora* and *N. plumbaginifolia*. We used genetic markers derived from the Conserved Ortholog Set II (COSII) to investigate synteny between *N. longiflora* and *N. plumbaginifolia* (n = 10) and other Solanaceae species (n = 12), such as tomato, pepper and eggplant. We produced two linkage maps; one in a maternal *N. longiflora* background (43 markers covering 808.1 cM) and a reciprocal map in the maternal *N. plumbaginifolia* background (54 markers covering 1110.4 cM). Segregation distortion was evident in both backgrounds, especially for the dominant ISSR markers, and was more prevalent in the maternal *N. longiflora* cross. In both backgrounds, there was a significant preference for the self-fertilizing *N. plumbaginifolia* allele for distorted markers. Finally, using the COSII markers, we infer many chromosomal rearrangements have occurred since the divergence of *Nicotiana* and tomato (*Solanum lycopersicum*) from a common ancestor.