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The complete chloroplast genome sequence of *Capsicum tovarii*-A Peruvian wild pepper**Myoung-Jae Shin, Gi-An Lee, Jung-Ro Lee, Yang-Hee Cho, Kyung-Ho Ma and Sebastin Raveendar**

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Capsicum tovarii is a very rare wild species native to the Rio Mantaro basin in south-central Peru. Availability of complete chloroplast genomes of Solanaceous species, *Capsicum* have been used as model systems in comparative and evolutionary genomics. Similarly, molecular markers derived from the complete chloroplast genome can provide effective tools for species identification and phylogenetic resolution. However, so far, only partial taxonomic and phylogenetic analyses have been carried out for the genus. Thus, the complete chloroplast genome sequence of a rare Peruvian wild pepper (*C. tovarii*) has been reported here for the first time. The total length of the chloroplast genome is 156,816 bp, with 37.7% overall GC content. A pair of IRs (inverted repeats) of 25,792 bp was separated by a small single copy (SSC) region of 17,853 bp and a large single copy (LSC) region of 87,379 bp. The chloroplast genome harbors 111 known genes, including 87 protein-coding genes, 8 ribosomal RNA genes, and 37 tRNA genes. A total of seven of these genes are duplicated in the inverted repeat regions, nine genes and six tRNA genes contain one intron, while two genes and *ycf* have two introns. Analysis revealed 144 simple sequence repeat (SSR) loci and 96 variants, mostly located in the intergenic regions. The types and abundances of repeat units in *Capsicum* species were relatively conserved and these loci will be useful for developing *C. tovarii* cp genome vectors.

Biography

Myoung-Jae Shin has started working at National Agrobiodiversity Center (NAC, RDA, Republic of Korea) from 2016 as a Researcher and has been In Charge of the distribution of plant genetic resources.

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