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Evolutionary Insights from the Giant Genome of *Cuscuta japonica* (≈40 Gb): Unraveling the Genetic Basis of Extreme Genome Expansion in a Parasitic Plant

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Genomes of dodder *(Cuscuta)* are typically highly reduced (≈300 Mb–1 Gb), reflecting extensive gene loss associated with holoparasitism. In striking contrast, *Cuscuta japonica* possesses an exceptionally large genome (≈40 Gb). Here we report a high-contiguity draft assembly of *C. japonica* from Muju, South Korea: 1,835 scaffolds spanning 34.6 Gb with an N50 of 374.6 Mb, providing a foundational reference for a giant-genome member of the genus. This resource enables comparative genomic and evolutionary analyses to investigate the genomic and physiological correlates of extreme genome expansion relative to congeners such as *C. campestris*. By contrasting *C. japonica* with small-genome *Cuscuta* species, our study is designed to elucidate mechanisms underlying genome size inflation and to assess how these changes intersect with features of the parasitic lifestyle that are conserved across the genus. The assembly and comparative framework presented here establish a basis for probing genome-scale innovation in parasitic plants and for refining models of genome size evolution under holoparasitism.