

MITOGENOME ANNOUNCEMENT

**The complete chloroplast genome sequence of the wild cucumber
Cucumis hystrix Chakr. (*Cucumis*, cucurbitaceae)**Zhiming Wu^{1*}, Li Jia^{1*}, Jia Shen¹, Biao Jiang², Chuntao Qian¹, Qunfeng Lou¹, Ji Li¹, and Jinfeng Chen¹¹College of Horticulture, Nanjing Agricultural University, Nanjing, P.R. China and ²Vegetable Research Institute, Guangdong Academy of Agriculture Sciences, Guangzhou, P.R. China**Abstract**

The complete nucleotide sequence of the wild cucumber (*C. hystrix* Chakr.) chloroplast genome has been determined in this study. The genome was composed of 155,031 bp containing a pair of inverted repeats (IRs) of 25,150 bp, which was separated by a large single-copy region of 86,564 bp and a small single-copy region of 18,166 bp. The chloroplast genome contained 130 known genes, including 89 protein-coding genes, 8 ribosomal RNA genes (4 rRNA species) and 37 tRNA genes (30 tRNA species), with 18 of them located in the IR region. In these genes, 16 contained 1 intron, and 2 genes and one *ycf* contained 2 introns.

KeywordsChloroplast genome, *C. hystrix*, wild cucumber**History**

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Plastids are organelles present in almost every plant cell that are usually inherited maternally (Havey et al., 2002). They contained the major protein complex necessary for photosynthesis. They have their own genomic DNA (cpDNA) of about 150 kb and is present in many copies. cpDNAs are believed to be among the best-known parts of the plant genomes. For over 30 years, it has been believed that the basic form of cpDNA is a circular molecule (Kolodner & Tewari, 1979), which was similar to typical animal mitochondrial genomes (Chen et al., 2013; Li et al., 2013).

The Cucurbitaceae family is an important group of cultivated species, mostly known as popular vegetables. The cultivated cucumber (*Cucumis sativus*) belongs to the genus *Cucumis* of the family Cucurbitaceae, it is an economically important vegetable crop in the world. *C. hystrix* is a wild *cucumis* species which is a reservoir of valuable genes for improving elite cucumber cultivar. Recently, a further confirming findings showed that *C. sativus* is sister to *C. hystrix* using DNA sequences from plastid and nuclear markers for some 100 *Cucumis* accessions from Africa, Australia and Asia (Zhuang & Chen, 2003). Thus, *C. hystrix* was believed to be the direct ancestor of cultivated cucumber.

The cultivated cucumber chloroplast genome was reported previously (Kim et al., 2006). In this study, we sequenced the complete chloroplast genome of the wild cucumber. The chloroplast genome of *C. hystrix* was double-stranded circular DNA with 155,031 bp in length (GenBank accession no. KF957866; Figure 1). Its structure was consistent with most of the described chloroplast genomes from the higher plants (Shinozaki et al., 1986; Wang et al., 2013) composing of two inverted repeated regions (IRa and IRb) of 25,150 bp, which was divided by a large single-copy (SSC) region of 86,564 bp and a small single-copy (LSC) region of 18,166 bp. The GC content was 37.4% which was typical of AT-rich and similar to those reported for most of the chloroplast genomes of other vascular plant species (e.g. 37.8% in *N. tabacum*; Shinozaki et al., 1986). The chloroplast genome of *C. hystrix* contained 130 genes, in which 18 were in the IR regions. Most genes occurred in a single copy, while all the rRNA genes and some of the tRNA and protein-coding genes in the IR occurred as double copies. Among the genes identified, 19 contained one or two introns. The chloroplast genome contained 30 different tRNA genes, and seven were present in the IR, giving a total of 37 tRNA genes per genome. Both number and types of the tRNA are identical to

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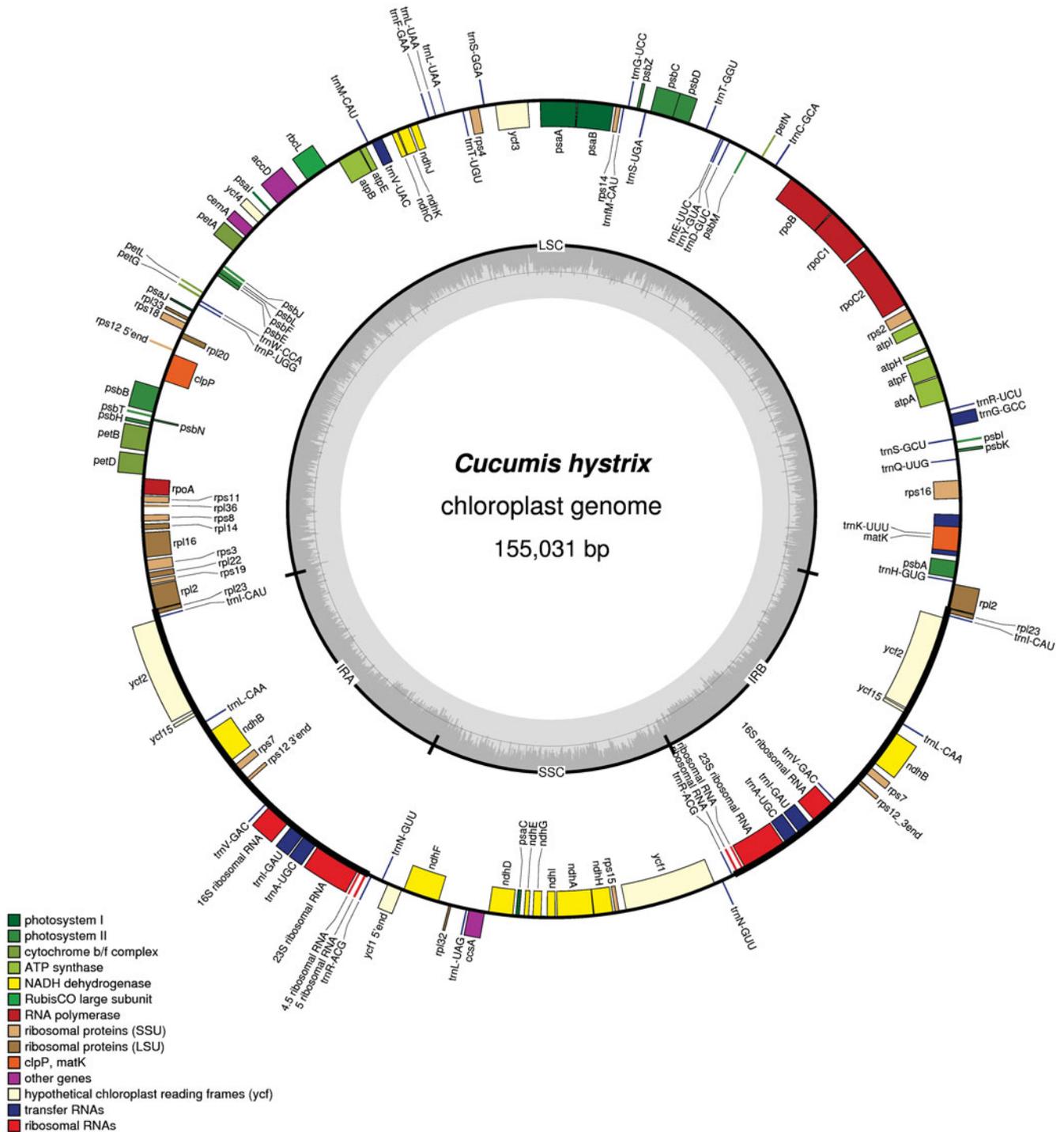


Figure 1. Genome map of the wild cucumber *C. hystrix*.

those presented in other species of vascular plants (Shinozaki et al., 1986; Wang et al., 2013).

Declaration of interest

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The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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