

P073

The complete chloroplast genome sequence of *Avena sterilis* L. using Illumina sequencing

Sebastin Raveendar^{1)*}, Gi-An Lee¹⁾, Kyung Jun Lee¹⁾, Myoung-Jae Shin¹⁾, Yang-Hee Cho¹⁾,
Kyung-Ho Ma¹⁾, Jong-Wook Chung²⁾ and Jung-Ro Lee¹⁾

¹⁾ National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, 370 Nonsaengmyeong-Ro, Wansan-Gu, Jeonju-Si, Jeollabuk-Do, 54874, Republic of Korea

²⁾ Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju, Chungbuk 28644, Republic of Korea.

Abstract

The complete chloroplast genome sequence of *Avena sterilis* L., a dominant wild oat species in the family Poaceae, is first reported in this study. The complete cp genome sequence of *A. sterilis* is 135,887 bp in length with 38.5% overall GC content and exhibits a typical quadripartite structure comprising one pair of inverted repeats (21, 603 bp) separated by a small single-copy region (12,575 bp) and a large single-copy region (80,106). The *A. sterilis* cp genome encodes 111 unique genes, 76 of which are protein-coding genes, 4 rRNA genes, 30 tRNA genes and 18 duplicated genes in the inverted repeat region. Nine genes contain one or two introns. Pair-wise alignments of cp genome were performed for genome-wide comparison. This newly determined cp genome sequence of *A. sterilis* will provide valuable information for the future breeding programs of valuable cereal crops in the family Poaceae.

Keywords: *Avena sterilis*, Chloroplast, Illumina sequencing, wild oat

Corresponding author*

Dr. Sebastin Raveendar

National Agrobiodiversity Center,

National Institute of Agricultural Sciences,

RDA, Jeonju 54874, Republic of Korea.

Tel.: +82-63-238-4863, Fax.: +82-63-238-4829

E-mail: ravibteri@rediffmail.com