

Chloroplast genome analyses of two diploid species *B. Oleracea* and *B. Rapa* and two tetraploid species *B. Napus* and *B. Juncea* of the Cruciferae family (Brassicaceae) by bioinformatics techniques

Talat F.^{1*}, Ghasemi Gh.²

¹ Assistant Professor, Seed and Plant Improvement Research Department, West Azarbaijan Agricultural and Natural Resources Research and Education Center, AREEO, Urmia, Iran

² Researcher, Seed and Plant Improvement Research Department, West Azarbaijan Agricultural and Natural Resources Research and Education Center, AREEO, Urmia, Iran

* (Corresponding author): f.talat@areeo.ac.ir

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Abstract

Nowadays, the popularity of the genus Brassica is increasing due to its nutritional value and medicinal effects. This group includes a large number of vegetable foods such as cabbage, broccoli, cauliflower, mustard, as well as rapeseed oil. In the present study, the complete chloroplast DNA genome of two diploid species of the oleracea family, *B. oleracea* (C, n=9) and *B. rapa* (A, n=10) with two allotetraploid species *B. napus* (AC, n=19) and *B. juncea* (AB, n=18) was studied and evaluated. The results showed that among the selected species, *B. napus* has the shortest nucleotide length with 152860 bp, and two species *B. rapa* and *B. juncea* each have the same length with 153483 bp, and the length of the nucleotide sequence in *B. oleracea* species It is equal to 153364 bp. In the analysis of the coding regions of all four genomes, it was found that the species *B. napus* with 79715 bp in the CDS region has the shortest sequence length in this region, and the two species *B. rapa* and *B. juncea* each with 80463 bp in the CDS region have The length of the game is equal, and in the case of *B. oleracea*, the length of this region is equal to 80559 bp. Intronic non-coding regions in *B. rapa* species with the longest length (30197 bp) which is only two bp different from *B. juncea* (30195 bp). The length of this region in *B. oleracea* is equal to 30178 bp and *B. napus* has the shortest length in the non-coding intronic region with 298660 bp.

Keywords: Bioinformatic, Brassica, Brassicaceae, Chloroplast, DNA.