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THE COMPLETE CHLOROPLAST GENOME OF *ALLIUM PSKEMENSE* (AMARYLLIDACEAE, ALLIOIDEAE)

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Allium pskemense is an uncommon wild onion species found in parts of Central Asia, specifically in Uzbekistan, Kyrgyzstan, and southern regions of Kazakhstan. In this study, complete chloroplast genomes of A. pskemense were sequenced and analyzed, revealing conserved structure and gene content typical of Allium species. Phylogenetic analysis placed A. vavilovii in a well-supported clade with A. cepa, confirming their close evolutionary relationship. Crossability data further demonstrated high hybrid fertility between the two species. These results support the potential of A. vavilovii as a valuable genetic resource for onion breeding and studies on domestication.

Key words: *Allium pskemense, Allium cepa, chloroplast genome, phylogeny, onion breeding, plastome evolution, domestication.*

Allium vavilovii – редкий вид дикого лука, встречающийся в Центральной Азии. В рамках исследования был секвенирован и проанализирован полный хлоропластный геном этого вида; выявлена консервативная структура, типичная для представителей рода Allium. Филогенетический анализ показал, что A. vavilovii образует единую устойчивую кладу с A. cepa, подтверждая их тесную эволюционную связь. Результаты скрещивания продемонстрировали высокую фертильность гибридов между этими двумя видами. Полученные данные подтверждают потенциал A. Vavilovii как ценного генетического ресурса для селекции и программ одомашнивания лука.

Ключевые слова: *Allium vavilovii, Allium cepa, хлоропластный геном, филогения, селекция лука, эволюция пластома, одомашнивание*.

Allium species (Amaryllidaceae), particularly those within the subgenus *Allium*, comprise some of the most economically significant cultivated crops worldwide, such as onion (*A. cepa*), garlic (*A. sativum*), leek (*A. ampeloprasum*) and *A. fistulosum* (bunching onion). These crops form a critical backbone of global horticulture (Khassanov, 2018, Yusupov et al. 2021). Within this context, *Allium pskemense* is an uncommon wild onion species found in parts of Central Asia, specifically in Uzbekistan, Kyrgyzstan, and southern regions of Kazakhstan (Friesen et al., 2006; van Raamsdonk et al., 2003, Yusupov et al. 2021).

In this study, the complete chloroplast (cp) genomes of *A. pskemense* were assembled and annotated to better understand their evolutionary relationship with other species in section *Cepa*. The sequencing lemployed Illumina HiSeq technology with paired-end 150 bp reads, followed by de novo assembly using NovoPlasty v3.8.3 (Dierckxsens et al., 2017) and annotation with Geneious v10.2 (Kearse et al., 2012). The physical map of the genomes arrangement of the plastome’s major structural components were created utilizingusing the online sofware package Organellar Genome DRAW (OGDraw) version 1.3.1 (Lohse et al. 2013) (Fig. 1). These genomes displayed the typical quadripartite structure found in angiosperms, with a total length of 153,670 (PQ585581) and 153,672 (PQ586983) base pairs. The cp genomes consist of a large single-copy (LSC) region (82,697 and 82,697), a small single-copy (SSC) region (17,936 and 17,938 bp), and two inverted repeats (IRs) of 26,475 bp each. The GC content was 34.6% in the LSC, 29.7% in the SSC, and 42.7% in the IR regions—values that are consistent with other species in the section *Cepa* (Yusupov et al. 2021). The genomes contain 114 unique genes, including 80 protein-coding genes, 30 transfer RNA (tRNA) genes, and 4 ribosomal RNA (rRNA) genes. These structural and genic features indicate a high level of conservation across *Allium* plastomes, but also reveal subtle differences that aid in phylogenetic resolution.

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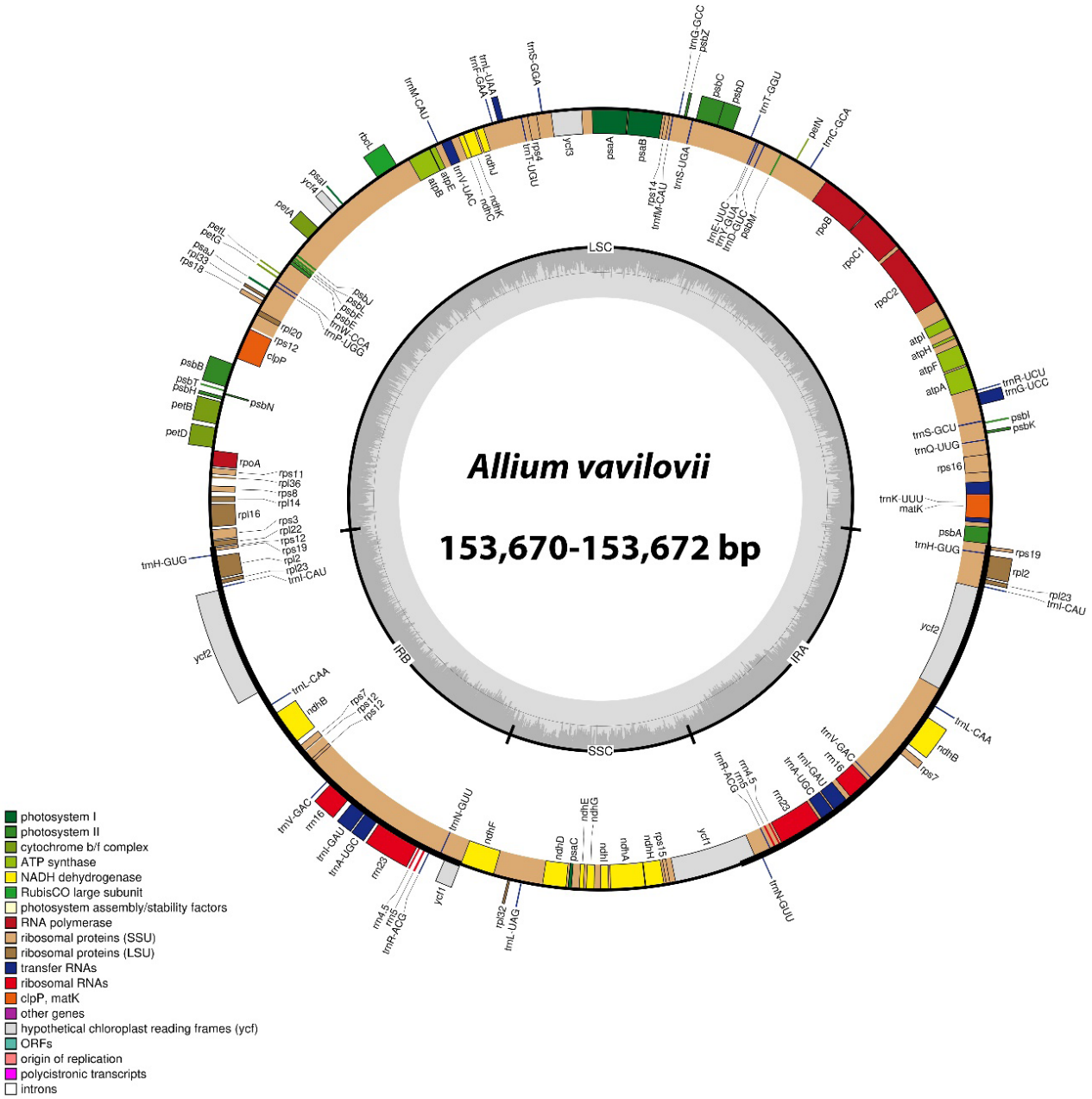


Figure 1. Map of the newly sequenced chloroplast genome of two *A. vavilovii* species. Genes inside the circle are transcribed clockwise, gene outside are transcribed counterclockwise. The dark grey inner circle indicates the GC content and the light represents AT content.

A maximum likelihood (ML) phylogenetic tree was generated using RAxML-HPC v8.1.24 (Stamatakis, 2006) based on 80 protein-coding genes from 16 plastomes, with *A. sativum* included as an outgroup. In this tree, *A. vavilovii* forms a strongly supported clade with multiple accessions of *A. cepa*, reinforcing its close genetic affinity. This high-resolution plastid-based phylogeny substantiates earlier nuclear DNA studies that placed *A. vavilovii* in close relation to *A. cepa* (Friesen et al., 2006; Li et al., 2010). These findings suggest either recent divergence or ongoing gene flow, and confirm the monophyly of the cultivated onion complex within section *Cepa*.

Complementing the phylogenetic data, a crossability diagram derived from van Raamsdonk et al. (2003) illustrates reproductive compatibility among *Allium* species. The diagram (Fig. 2) shows that *A. vavilovii* and *A. cepa* share high levels of hybrid fer-

tility, with more than 25 F_1 plants per 100 flowers, and with viable seed and ovary development following interspecific pollination. Such compatibility is critical for breeding programs aiming to introduce traits like stress resistance or disease tolerance from wild relatives into cultivated onions (Kik et al., 1997). The combination of plastome similarity and hybrid fertility underscores the potential of *A. vavilovii* as a resource for onion pre-breeding and evolutionary study.

The availability of these complete chloroplast genome sequences greatly enhances our understanding of species relationships within *Allium* sect. *Cepa*. Not only do these plastomes provide markers for resolving phylogenetic relationships, but they also inform cytoplasmic inheritance and may aid in the development of cytoplasmic male sterility (CMS) systems used in hybrid breeding. As more plastome data become available for wild and cultivated *Allium* species, a clearer picture of domestication pathways and plastome evolution will emerge. In this context, the inclusion of *A. vavilovii* genomes provides a crucial piece of the puzzle, bridging the gap between wild genetic resources and cultivated forms.

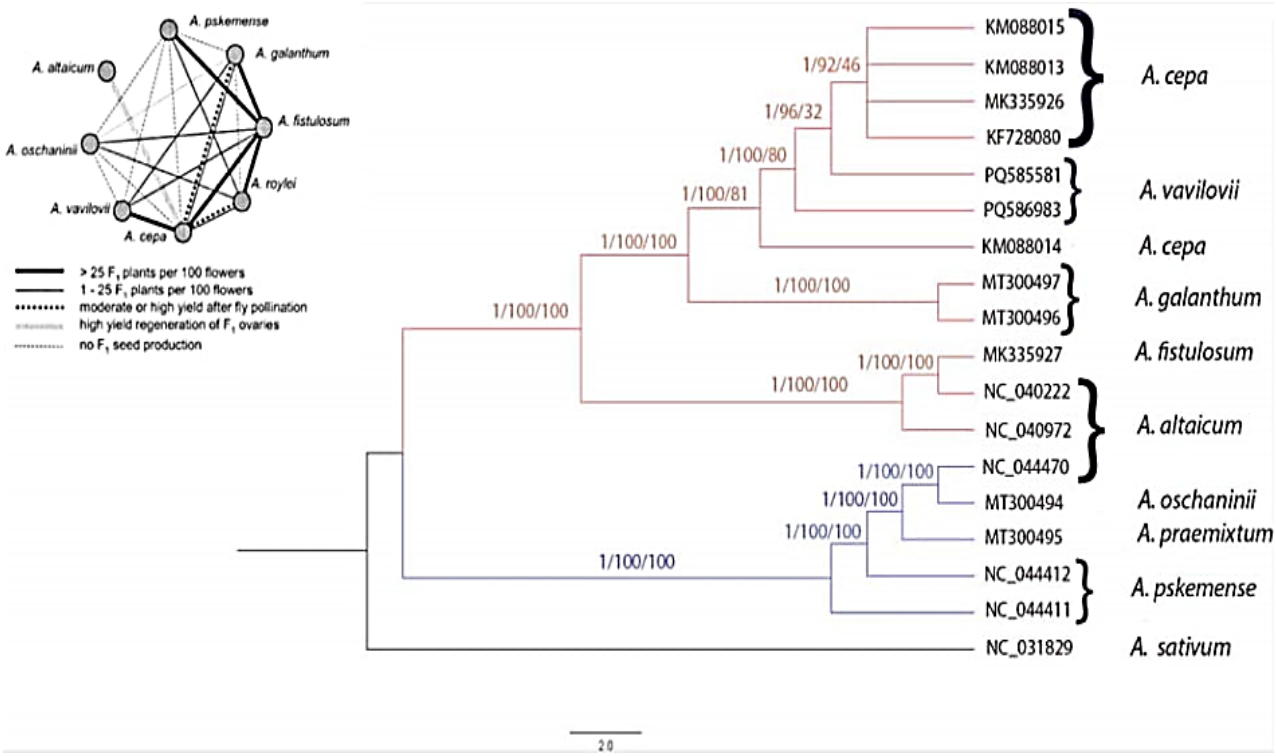


Figure 2. Phylogenetic tree based on 80 protein-coding genes of 16 plastomes of *Allium* sect. *Cepa* plus an outgroup plastome (*A. sativum*), and sect. *Cepa* crossability diagram (extracted from van Raamsdonk et al., 2003).

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Kalit so‘zlar: *Allium vavilovii*, *Allium cepa*, *xloroplast genom, filogeniya, piyoz seleksiyasi, plastoma evolyutsiyasi, madaniylashtirish.*

Allium turkumi (Amaryllidaceae oilasi) dunyo miqyosida muhim bo‘lgan qishloq xo‘jaligi ekinlarini o‘z ichiga oladi. Xususan, piyoz (*Allium cepa*), sarimsoq (*A. sativum*), A. ampeloprasum va A. fistulosum global oziq-ovqat tizimida muhim rol o‘ynaydi. Ular sabzavotchilikda katta iqtisodiy ahamiyatga ega. Shunga qaramay, ushbu guruhga kiruvchi ba’zi yovvoyi turlar hali to‘liq o‘rganilmagan. Ulardan biri A. pskemense O‘zbekiston, Qirg‘iziston va Qozog‘istonning janubiy hududlarida tarqalgan, kam uchraydigan yovvoyi piyoz turi hisoblanadi. Ushbu tadqiqotda A. pskemense turining xloroplast (plastid) genomlari to‘liq yig‘ildi va annotatsiya qilindi. Tadqiqotning asosiy maqsadi A. pskemense turining boshqa Allium turlari, ayniqsa, Cepa bo‘limiga kiruvchi madaniy turlar bilan evolyutsion aloqalarini aniqlashdan iborat. Ushbu ma’lumotlar kelajakdagi seleksiya ishlari va filogenetik tadqiqotlar uchun muhim asos bo‘lib xizmat qiladi. Xloroplast genomlari Illumina HiSeq texnologiyasi yordamida sekvenslandi. Bu jarayonda 150 bp uzunlikdagi paired-end o‘qishlar qo‘llanildi. Genomlarni yig‘ish uchun NovoPlasty dasturining 3.8.3 versiyasi, genlarni aniqlash (annotatsiya) uchun esa Geneious dasturining 10.2 versiyasi ishlatildi. Plastid genomining fizik xaritasi OGDraw dasturi orqali yaratildi. Ushbu usullar natijasida A. pskemense turiga tegishli xloroplast genomining to‘liq tuzilmasi aniqlandi. Olingan genomlar odatdagi angiosperm o‘simliklarga xos bo‘lgan to‘rt bo‘limli (kvadripartit) tuzilishga ega bo‘lib, umumiy uzunliklari 153,670 va 153,672 juft nukleotid (bp)ni tashkil etdi. Genomlar quyidagi qismlardan iborat: katta yakka nusxadagi (LSC) hudud — 82,697 bp; kichik yakka nusxadagi (SSC) hudud – 17,936–17,938 bp; ikkita 26,475 bp uzunlikdagi inversiya takrorlari (IR). Har bir hududdagi GC foizi mos ravishda 34,6%, 29,7% va 42,7% bo‘ldi. Genomlar jami 114 ta noyob genni o‘z ichiga oldi: 80 ta oqsil-kodlovchi, 30 ta tRNA va 4 ta rRNA geni. Bu tuzilmaviy xususiyatlar Allium turkumidagi boshqa turlar plastid genomlari bilan yuqori

darajada o‘xshashlikni ko‘rsatadi. 80 ta oqsil-kodlovchi gen asosida maksimal ehtimollik usulida tuzilgan filogenetik daraxtda A. vavilovii turi A. cepa bilan bir klasterda joylashdi. Bu ularning genetik jihatdan juda yaqin ekanini ko‘rsatadi. Ushbu natijalar avvalgi yadro DNK asosidagi tadqiqotlar bilan mos keladi va A. cepa bilan A. vavilovii orasidagi qarindoshlikni tasdiqlaydi. Bu yaqinlik ularning evolyutsion jihatdan yaqinda ajralganini yoki hali ham gen almashinuvi bo‘layotganini ko‘rsatadi.

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