# Plastid genome evolution in the genus Allium

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# Plastid genes are highly conservative and used in plant systematics

## May they evolve not only neutrally?

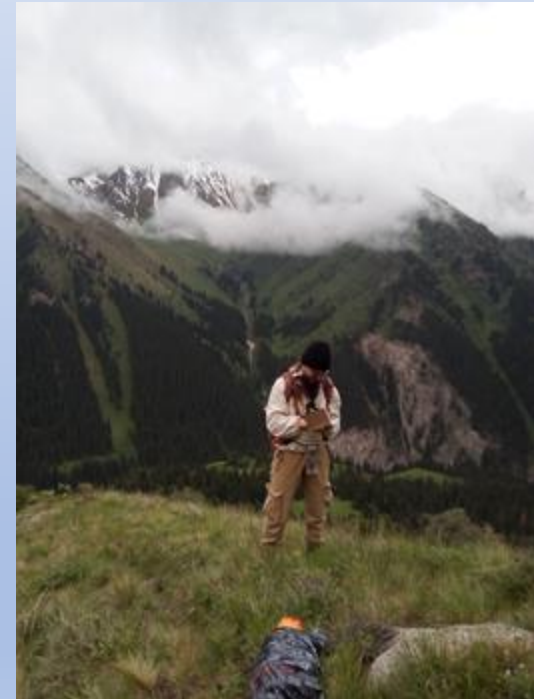Looks possible, plants from genus Allium occupy habitats with very different general insolation, UV radiation, temperature and humidity



Allium platyspatum



Allium semenovi



Habitat of A.semenovi in Kyrgyzstan, 3100m above sea level

- We sequenced and assembled de novo plastomes of the following species: A. fistulosum L., A. macleanii Baker, A. moly L., A. nutans L., A. obliquum L., A. platyspathum Schrenk, A. pskemense B.Fedtsch., A. schoenoprasum L., Allium semenovii Regel, Allium tuberosum Rottl. ex Spreng., A. victorialis L., Allium zebdanense Boiss. & Noë

- cpDNA was extracted from living specimen with standard CTAB protocol. DNA samples were sequenced using the Illumina MiSeq high-throughput sequencing platform. The TruSeq protocol (NEBNext® DNA Library Prep Master Mix Set for Illumina, E6040, NEB reagents) was used for preparing the genomic libraries according to manufacturer's recommendation. PE sequences (2x250bp or 2x300bp) using MiSeq.

- After the quality trimming with Trimmomatic sequencing reads were filtered using chloroplast genome sequences of A. cepa and A. sativum by Bowtie mapper. Dual Organellar GenoMe Annotator (DOGMA) and GeSeq were used for gene annotation

- Alignments for evolution rate analysis of each region of chloroplast genome were built using MUSCLE. FUBAR was used for selection seeking. Phylogenetic trees were made with iqtree, using nucleotide alignment. With iqtree Partition finder were determined 3 partitions and evolution rates were calculated independently for each partition.

- The general structure and gene order across all species show high similarity and absence of rearrangements, with A. paradoxum, being the only exception

- This species has a major inversion described in our previous work  We have not found any large inversions in any other studied species of Allium



Allium paradoxum has big inversion in chloroplast genome and inverted leaf morphology . Central leaf vein protrudes on top side of the leaf, in all other Allium species it protrudes on bottom side. A.paradoxum inhabits shadow places, with low UV radiation. Similar habitats occupy A.ursinum

- Several regions under selection within Allium plastomes were identified. The major region is located from ycf1 (the last gene of the IRa) to ycf2 (the first gene of IRb) and covers the whole SSC region (except only trnL).

- Partitions evolve with quite different speed from 0.16 (genes clpP rpl2 rps7 rps12 rpl2) to 1.43 (genes psbM psbL ndhD ndhE ndhI ndhA).

- Alium plastomes are highly conservative. Alignment has 13 sequences with 45030 columns, 614 distinct patterns,  879 parsimony-informative and  1410 singleton sites.

- The highest rates of evolution in our study have genes, involved in light phase of photosynthesis. It might be associated with adaptation to environments with high general insolation and UV radiation. We need more data,  especially expression data from controlled green house experiments

# Thank you for your attention

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