

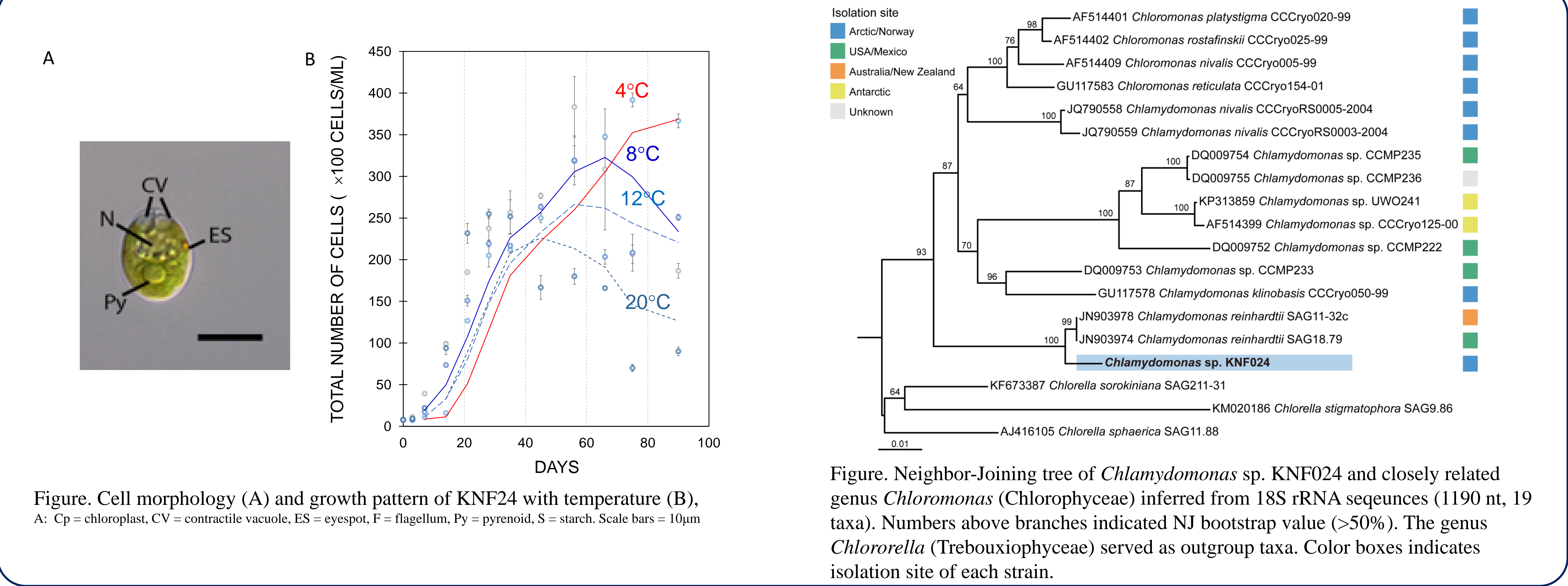
Temperature-dependent Transcriptome Analysis of the Arctic *Chlamydomonas* sp.

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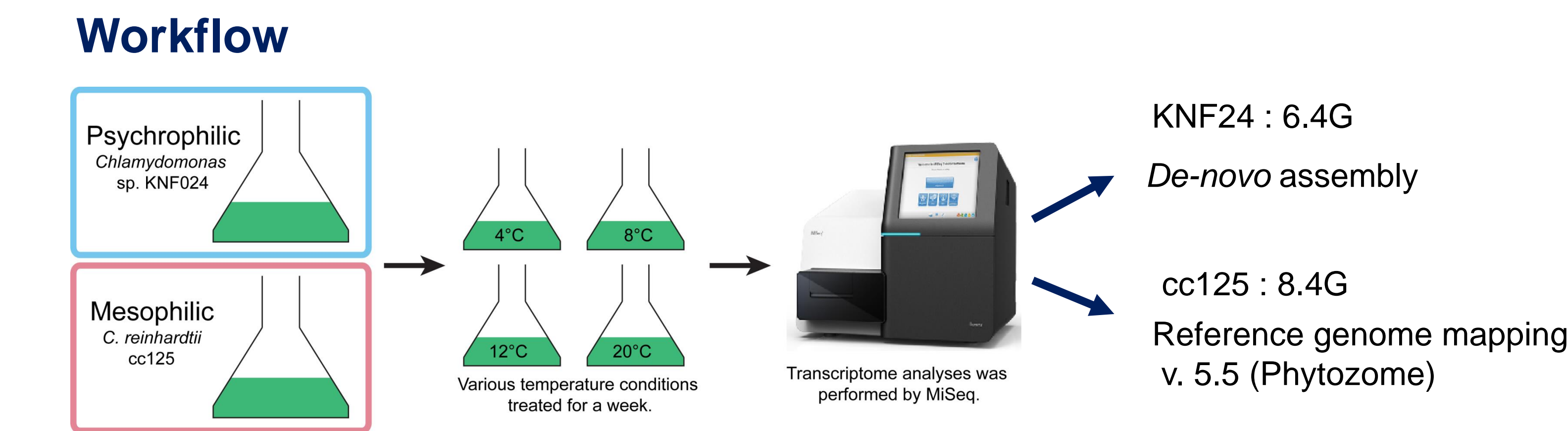


Chlamydomonas sp. is widely present in the Earth’s aquatic ecosystem and is worth as a model species based on environmental factors related to environmental stresses. As a part of a study on the environmental adaptation mechanisms that exist in polar *Chlamydomonas*, we selected an Arctic *Chlamydomonas* sp. strain from the KOPRI culture collection of polar microorganisms (KCCPM, KNF0024), which had been isolated from ice-covered freshwater from the Arctic. This strain shows psychrophilic growth. To explore its adaptation strategy in freezing environments and identify the genes related cold acclimation, we investigated its temperature-dependent transcriptome changes. Uni-gene sets of this strain were established through *de-novo* assembly. The assembled contigs were annotated and functionally classified according to the biological functions. We examined the candidate target genes whose expression differs in accordance with the temperature, clustered them by expression patterns. In addition, we compared the temperature-dependent transcriptome response between this Artic *Chlamydomonas* sp. with those of *Chlamydomonas reinhardtii*, a mesophilic species. This dataset would be a valuable resource to understand the molecular mechanism behind *Chlamydomonas*’ adaptation under extreme and changing environment.

Characteristics of Arctic *Chlamydomonas* sp.



RNA-seq analysis to study temperature response of arctic *Chlamydomonas* sp.



Characterization of arctic *Chlamydomonas* sp. transcriptome

