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## Ubiquity or Not Ubiquity: That is the Question

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## NEWS AND VIEWS

## PERSPECTIVE

## Ubiquity or not ubiquity: That is the question

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The nature of population structure in eukaryotic microbes has been the subject of intense debate, but until recently the tools to test these hypotheses were either problematic (e.g., allozymes that cannot detect all genetic changes) or beyond financial and technological limits of most laboratories (e.g., high throughput sequencing). In a recent issue of *Molecular Ecology*, Craig et al. (2019) use a genomic approach to investigate the population structure of a model alga, the chlorophyte *Chlamydomonas reinhardtii* (Figure 1). Using high throughput sequencing, read mapping, and variant calling, they detected strong signals of differentiation at a continental scale, while local patterns of admixture were complex. Population genomic techniques such as these have not been used extensively in studies of microbial eukaryotes and the fields of conservation genetics and evolution stand to benefit vastly from the adoption of these techniques to studies of diverse protist lineages.

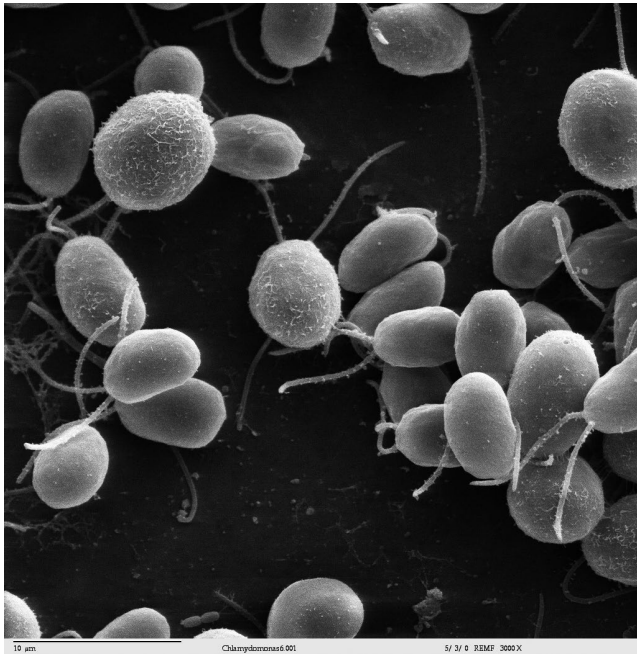
## KEYWORDS

admixture, genetic differentiation, identity by descent, microbial eukaryotes, population structure

The authors explicitly test two competing models of microbial eukaryote distributions: ubiquity vs. moderate endemism. The “ubiquity model” of Fenchel and Finlay (2004) posits that large population sizes are responsible for a flat relationship between species and area for organisms smaller than 1 mm. In this “everything is everywhere” scenario, species occurrence is determined not by distribution history but by local habitat properties, leading to the prediction that microbial eukaryotes will display no geographically-patterned genetic variation. In contrast, the moderate endemism model (Foissner, 2008) predicts that the dispersal of microbial eukaryotes is more limited and as a result, genetic structure arises due to three main types of isolation: distance, adaptation, and/or colonization. Under the moderate endemism model, some protists are predicted to have very wide ranges and thus to have a higher proportion of cosmopolitan species when compared to plants and animals. However, other protist species will have restricted distributions that are not due to specific habitat requirements, but instead are the result of limited gene flow. Evidence exists supporting both models, but advances in population genomics such as in the current study allow a finer grained examination of population structure in microbial eukaryotes.

Although *Chlamydomonas reinhardtii* has a rich history of study as a model organism in studies of plant physiology and cell biology, most of this work has been done using a single strain isolated from eastern North America. As a result, until recently, little was known about the population structure of this soil dwelling alga (Flowers et al., 2015; Jang & Ehrenreich, 2012). In their study, Craig et al. (2019) use 36 available isolates of *C. reinhardtii* sampled from North America and Japan to examine the population structure and evolutionary history of a widespread microbial eukaryote lineage. To our knowledge, the study is among the most marker-rich approaches (5.88 million SNPs) to address free-living microbial eukaryotic population structure, with other examples coming from better-known yeasts, parasites and mesofauna such as nematodes.

To test between the ubiquity and moderate endemism models, the authors performed whole genome resequencing of all available isolates of *C. reinhardtii* using standard Illumina-based high throughput sequencing techniques. Leveraging the previously sequenced, chromosome-level reference genome of Merchant et al. (2007), the authors then mapped reads and called genotypes against this reference. Distance based and ordination techniques revealed three distinct lineages (Figure 2): a northeastern North American population (NA1), a

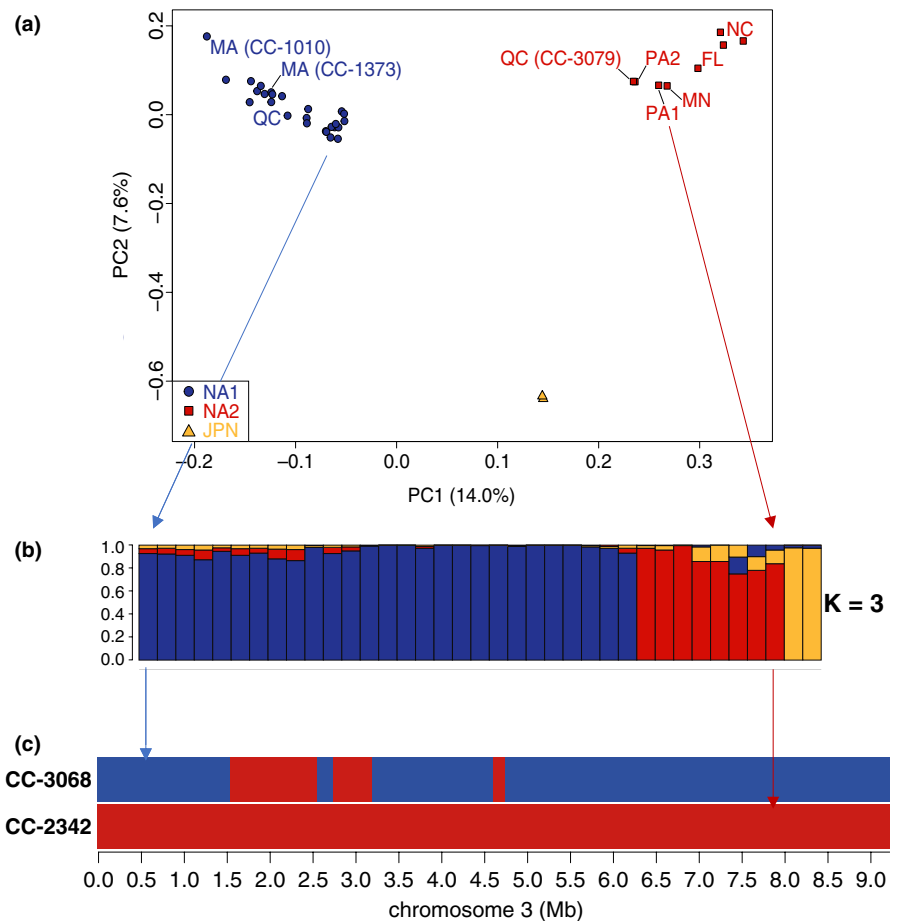


**FIGURE 1** *Chlamydomonas reinhardtii*. By Dartmouth Electron Microscope Facility, Dartmouth College—Source and public domain notice at <http://remf.dartmouth.edu/imagesindex.html>, Public Domain, <https://commons.wikimedia.org/w/index.php?curxm%3Aid%3D2787116>

Midwest/Mid-Atlantic/Southern USA population (NA2), and a Japanese population (JPN). A haplotype-based analysis also recovered three lineages, but revealed interesting patterns of haplotype sharing. At local scales (i.e., among multiple samples within both North Carolina and Quebec) substructure of closely related isolates was detected. Analyses also revealed evidence of isolation by distance in the NA2 populations, but not in the NA1 populations. To more closely examine the admixture between the North American populations, analyses of the proportion of SNPs matching consensus alleles for each population in 20 kb windows, displayed as a heat map for each chromosome, demonstrated the patterns of introgression for each North American isolate.

To examine gene flow at a local scale, the team tested NA1 isolates for identity by descent and found that on average a pair of isolates from the northeastern North American population shared 9.1% of their genomes in long identical haplotypes. This result was at odds with the finding that genetic diversity was very high in the population displaying high identity by descent (NA1). Based on this observation the authors raise an interesting paradox “how can essentially the entire sampled population appear to share recent ancestry, yet genetic diversity be maintained at a high level.” This leads to many intriguing questions that will require refinement of population models for organisms with clonal life stages, a better understanding of the impact of selection on genetic diversity, and functional knowledge of recombination suppression in *C. reinhardtii* and other organisms with similar life histories.

**FIGURE 2** Patterns of population structure in *Chlamydomonas reinhardtii* reveal considerable isolation among populations. (a) Principal components analysis (PCA) delineates two North American populations and one Japanese population. (b) STRUCTURE plot for three populations demonstrates various levels of admixture. (c) Admixture profiles of chromosome 3 for two samples (one from Farnham Quebec, Canada [CC-3068] and one from Pennsylvania, USA [CC-2342]) depicting consecutive 20 kb windows of >60% SNPs matching the northeastern North American population (blue), or the Midwest/Mid-Atlantic/Southern USA population (red). Adapted from figures 2 and 4 of Craig et al. (2019)



In their conclusion, the authors reject the ubiquity model and find support for the moderate endemism model for *C. reinhardtii*. The patterns of North American population structure indicate the possibility of allopatric divergence in glacial refugia during the last glacial maximum, demonstrating that patterns applicable to plants and animals can also apply to populations of microbial eukaryotes. The admixture observed between the North American populations further indicates that substantial dispersal occurs in this microbial eukaryote, and other factors such as local adaptation may be responsible for a lack of structure at local scales.

The insights gained from this study set the stage for additional sampling of geographically-diverse populations of *C. reinhardtii*. An increased sampling density will allow comparisons of introgression in the Midwest/Mid-Atlantic/Southern USA population and may detect further evidence of glacial refugia. Furthermore, additional sampling is sorely needed in Japan and throughout Eurasia to fully understand the global population structure of *C. reinhardtii*. The robust genomic and proteomic resources for *C. reinhardtii* also allow additional studies to examine the impact of SNPs in coding regions to examine how local adaptation is related to fitness. This study demonstrates the power of using population genomics approaches to resolve long-standing questions of microbial evolution and ecology.

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#### REFERENCES

- Craig, R. J., Böndel, K. B., Arakawa, K., Nakada, T., Ito, T., Bell, G., ... Ness, R. W. (2019). Patterns of population structure and complex haplotype sharing among field isolates of the green alga *Chlamydomonas reinhardtii*. *Molecular Ecology*, 28(17), 3977–3993. <https://doi.org/10.1111/mec.15193>
- Fenchel, T., & Finlay, B. J. (2004). The ubiquity of small species: Patterns of local and global diversity. *BioScience*, 54(8), 777–784. [https://doi.org/10.1641/0006-3568\(2004\)054\[0777:Tuossp\]2.0.Co;2](https://doi.org/10.1641/0006-3568(2004)054[0777:Tuossp]2.0.Co;2)
- Flowers, J. M., Hazzouri, K. M., Pham, G. M., Rosas, U., Bahmani, T., Khraiweh, B., ... Purugganan, M. D. (2015). Whole-genome resequencing reveals extensive natural variation in the model green alga *Chlamydomonas reinhardtii*. *The Plant Cell*, 27(9), 2353–2369.
- Foissner, W. (2008). Protist diversity and distribution: Some basic considerations. *Biodiversity and Conservation*, 17(2), 235–242. <https://doi.org/10.1007/s10531-007-9248-5>
- Jang, H., & Ehrenreich, I. M. (2012). Genome-wide characterization of genetic variation in the unicellular, green alga *Chlamydomonas reinhardtii*. *PLoS One*, 7(7), e41307. <https://doi.org/10.1371/journal.pone.0041307>
- Merchant, S. S., Prochnik, S. E., Vallon, O., Harris, E. H., Karpowicz, S. J., Witman, G. B., ... Grossman, A. R. (2007). The *Chlamydomonas* genome reveals the evolution of key animal and plant functions. *Science*, 318(5848), 245–250. <https://doi.org/10.1126/science.1143609>

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