

'Charismatic' organisms still dominating genomics research

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Decades after the genomics revolution, half of known eukaryote lineages still remain unstudied at the genomic level—with the field displaying a research bias against 'less popular', but potentially genetically rich, singlecell organisms.

This lack of microbial representation leaves a world of untapped genetic potential undiscovered, according to an exhaustive survey conducted by UBC researchers of on-going genomics projects. The survey results are published in the May issue of *Trends in Ecology and Evolution*.

"We're still mostly analyzing the same well-known eukaryotic groups: animals, fungi and plants, in large part because their utility is more obvious, they are closer to us as humans, and frankly because we can see them with the naked eye," says Javier del Campo, lead author on the paper and an expert on the <u>microbial ecology</u> of protists, complex singlecelled organisms.

"But from a <u>biological diversity</u> and a genomic point of view this anthropocentric approach is irrelevant, and potentially holds us back. We're missing the opportunity to study most of the planet's eukaryotic diversity, which means we're missing the opportunity to study a host of alternative life strategies, novel metabolic pathways, new gene functions."

The authors call for a broader, objective and species relationship-based initiative to sequence microbial eukaryotic genomes so that the breadth



of their diversity is covered.

Background

The researchers analyzed all the genome research projects in operation—or projected to launch—and found that 51% of known eukaryotic lineages are not yet represented or studied at a genomic level.

Genomic database holdings are heavily biased against complex single cell organisms, particularly the Rhizaria, Amoebozoa and heterotrophic Stramenopiles lineages.

The study also analyzed the five largest eukaryotic culture collections, and determined that up to 25% of the described eukaryotic lineages have no representatives in culture.

More information: The others: our biased perspective of eukaryotic genomes: <u>www.cell.com/trends/ecology-ev ... /abstract/S0169-5347</u> %2814%2900064-0

Provided by University of British Columbia

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