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Low genetic variation is associated with low mutation rate in the giant duckweed

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Mutation rate and effective population size (N_e) jointly determine intraspecific genetic diversity, but the role of mutation rate is often ignored. Here we investigate genetic diversity, spontaneous mutation rate and N_e in the giant duckweed (*Spirodela polyrhiza*). Despite its large census population size, whole-genome sequencing of 68 globally sampled individuals reveals extremely low intraspecific genetic diversity. Assessed under natural conditions, the genome-wide spontaneous mutation rate is at least seven times lower than estimates made for other multicellular eukaryotes, whereas N_e is large. These results demonstrate that low genetic diversity can be associated with large-N_e species, where selection can reduce mutation rates to very low levels. This study also highlights that accurate estimates of mutation rate can help to explain seemingly unexpected patterns of genome-wide variation.

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