Genomic consequences of long-term asexuality in the bdelloid rotifer *Adineta vaga*

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Heterozygosity, on the other hand, is predicted to increase freely through time in ameiotic species (the "Meselson effect"). The Meselson effect was first described based on genetic studies of bdelloid rotifers, that are considered as an "evolutionary scandal" because of their apparent persistence and diversification for more than 40 million years without sex.

Bdelloids are extremely resistant to radiations and desiccation, which allows them to survive in semi-terrestrial environments that dry out frequently.

Heterozygosity poses a major challenge to genome assembly, which is why most genome sequencing projects target haploid or inbred individuals. Unfortunately, asexual individuals cannot be crossed to reduce their heterozygosity.

In heterozygotes, alleles that are divergent assemble in distinct contigs, whereas alleles that are similar are fused during assembly.

Hence, allelic divergence should make genome assembly easier in long-term ameiotic species such as bdelloids than in sexually reproducing species.

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The genome of *Adineta vaga* was initially thought to contain two divergent sets of alleles A and B that had accumulated a large amount of differences in the absence of recombination. In such case, assembling this genome would have posed no problem.

Our genomic data are rather compatible with an organisation in four sets A, A', B and B' (as proposed by previous cytogenetic and genetic studies). The divergence between A and A' and between B and B' is only 3%, whereas the divergence between As and Bs is larger.

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The heterozygosity is too high for the alleles to be fused and too low for them to be assembled separately, resulting in this example in 10 small contigs instead of two large ones!