Evolutionary innovation in the long-term absence of sex in the oribatid mite *Platynothrus peltifer*

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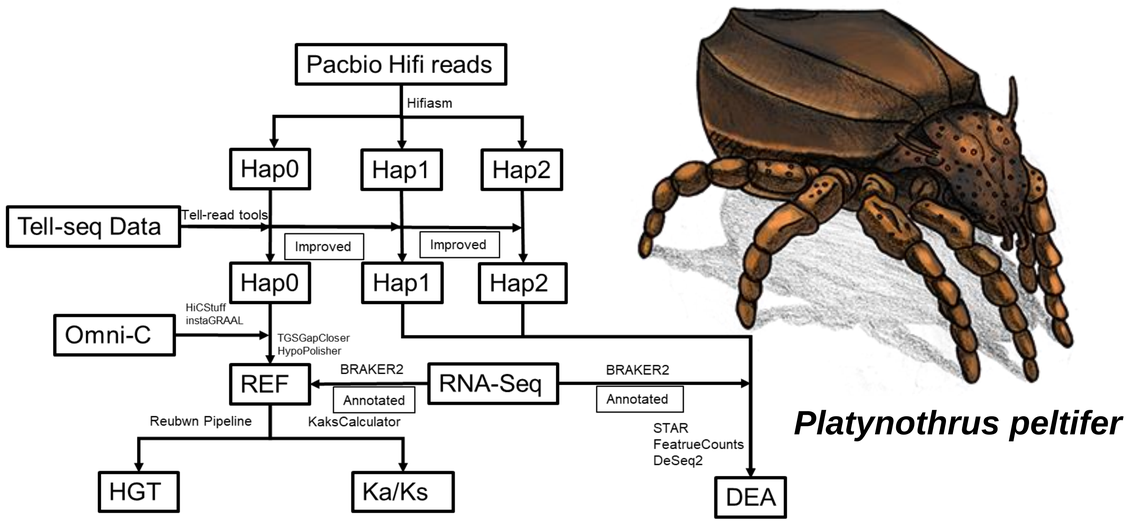
Introduction

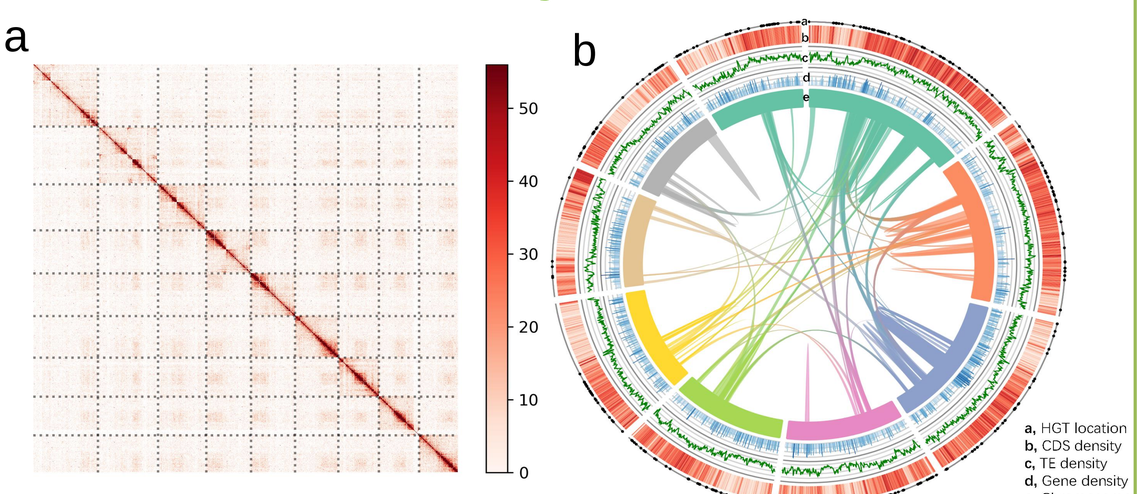
Asexuality is considered an evolutionary dead-end, but some **'ancient asexual organisms',** like oribatid mites, have persisted and diversified over time. Very little is known about the processes that could generate evolutionary novelty and adaptability in the absence of sex. We analyzed potential genomic footprints of innovation in the haplotype-resolved, chromosome-scale genome of the ancient asexual oribatid mite ***Platynothrus peltifer***. Large-scale structural variants might not play a major role, as there are few rearrangements within and between chromosomes as well as between haplotypes. However, heterozygosity is maintained and divergent haplotypes, as well as **differential allele expression (DEA)** with an functional enrichment in e.g. metabolic pathways, resource uptake and immune system. We further analyzed the evolutionary trajectories of these alleles, as these processes might contribute to adaptation and evolutionary novelty in the absence of sex. Moreover, **Transposable element(TE)** and **Horizontal Gene Transfer (HGT)** could supply the substrate for novelty via modulating gene regulation of these mites. Overall, identifying such signatures of evolutionary innovation will help to understand why some asexual can escape the dead-end fate and to identify the benefits of sex vice-versa.

Workflow



Platynothrus peltifer

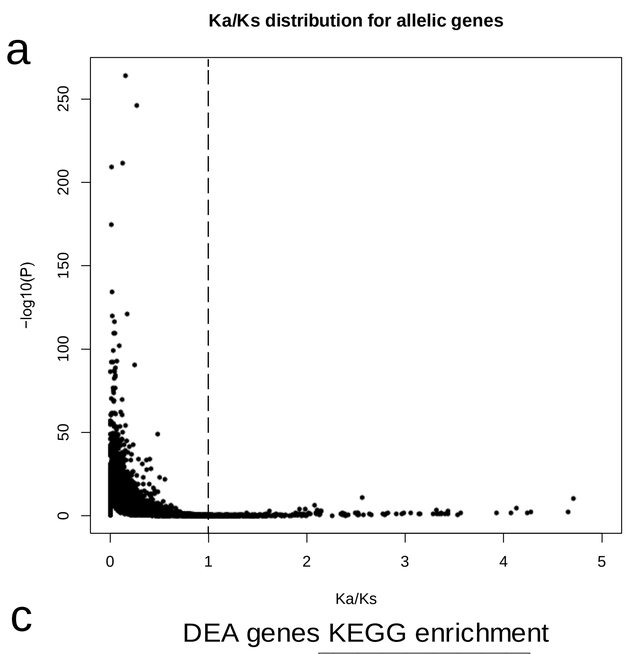
1. Genome assembly

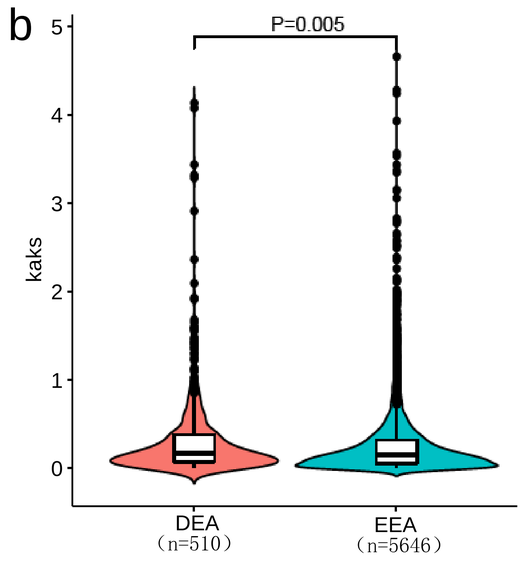


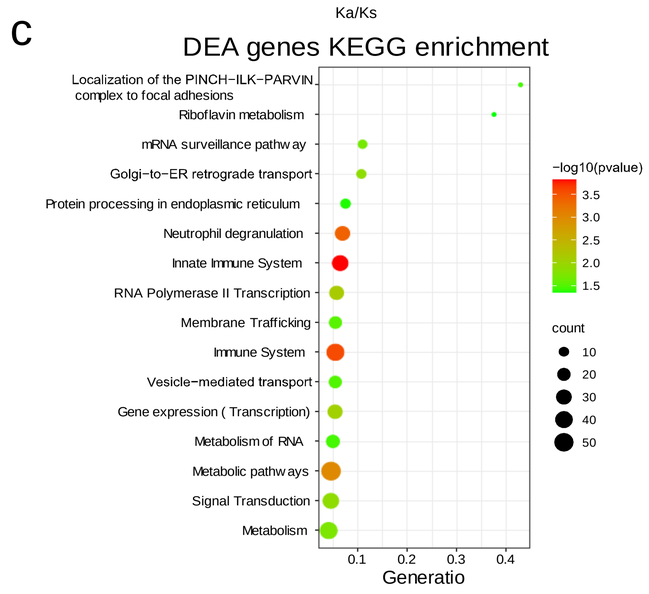
Features	Hap0	Hap1	Hap2
total length [Mb]	220	208	200
N50 [Mb]	23	14	14
Transposable elements	52Mb(25%)	48Mb(23%)	45Mb(23%)
BUSCO [%] (assembly)	97	97	96
BUSCO [%] (protein)	98	98	97
Nr annotated genes	24139	24357	22553

a, Contact map of Hi-C links among 9 chromosomes. **b,** Rearrangement of the *Platynothrus peltifer* and genomic features.

2. Differential expression of alleles(DEA)

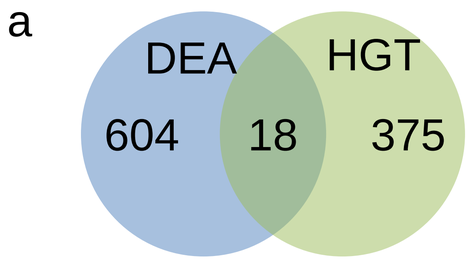




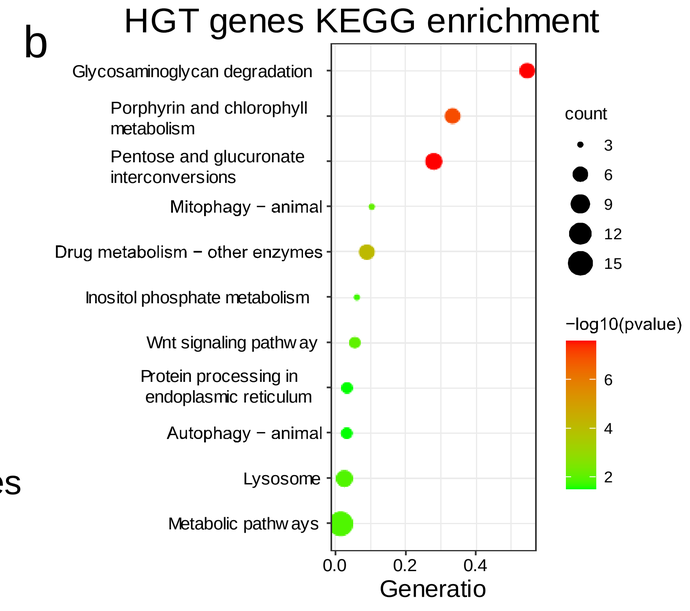


a, Pairwise comparison the Ka/Ks of distribution for allelic genes.
b, DEAs are of relatively higher Ka/Ks value. *P* values were calculated with Wilcoxon's t-test.
c, KEGG enrichment of DEA genes (*P-adjust*<0.05).

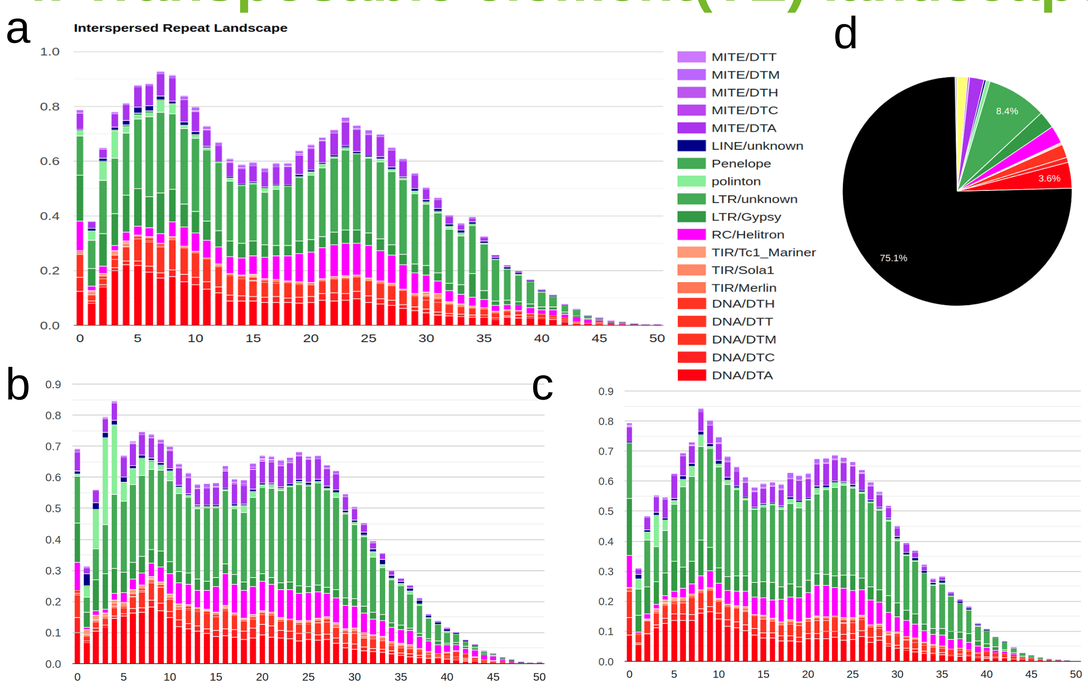
3. Horizontal Gene Transfer (HGT)



a, Venn plot of the DEA and HGT genes.
b, KEGG enrichment of HGT genes (*P-adjust*<0.05).



4. Transposable element(TE) landscape



a, b, c are Transposable element(TE) landscapes of Hap0, Hap1 and Hap2 **d,** The pie chart of the TE types

5. Conclusion and outlook

- **Single individual chromosome-level scale reference genome and two high quality haplotypes assembles.**
- **K_a/K_s of DEA relatively higher EEA genes.**
- **10% single copy genes between two haplotypes show DEA**
- **77.5% HGT with intron and 1.8% HGT show DEA**
- **The two haplotypes show different TE styles**

Outlook: construct Pan-genome for the *Platynothrus peltifer*