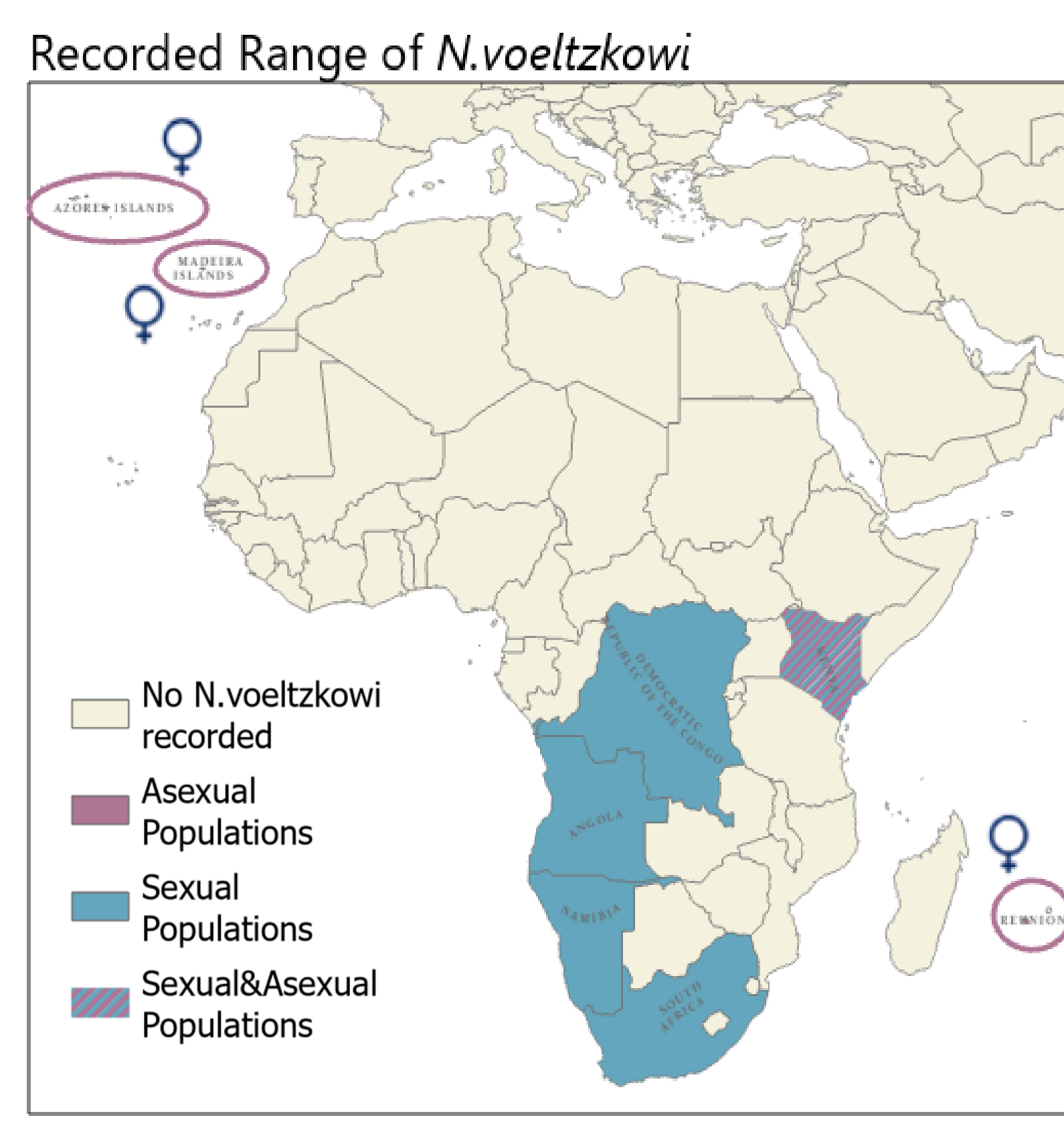# Unraveling the Mechanisms Driving Transitions to Parthenogenesis:
A Case Study of Hybridization, Triploidy, and *Wolbachia* Infection in the Ladybug *Nephus voeltzkowi*

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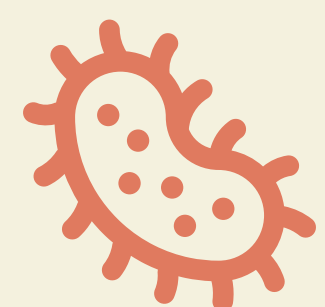
Background

- Bisexual populations of the ladybug *Nephus voeltzkowi* Weise have previously been recorded in several countries[1].

- Newly discovered populations have been found to be capable of obligate thelytokous parthenogenesis[2].

- There are several known triggers to the transition to parthenogenesis[3]:
  - ❑ **Mutation**
  - ❑ **Hybridization**
  - ❑ **Bacterial infection** with a parthenogenesis-inducing endosymbiont

- There are features often associated with parthenogenetic lineages:
  - ❑ **Odd polyploidization**, increasing selective pressures for other reproductive modes

- Which features are present in these sexual vs parthenogenetic populations?

- Which might have caused the transition from sex to parthenogenesis?

Recorded Range of *N.voeltzkowi*

No *N.voeltzkowi* recorded
Asexual Populations
Sexual Populations
Sexual&Asexual Populations
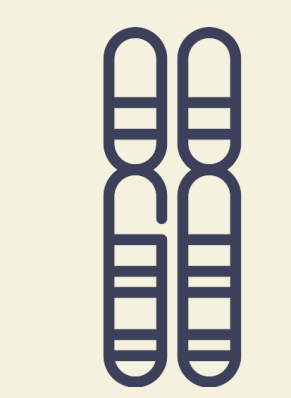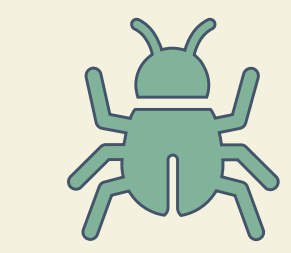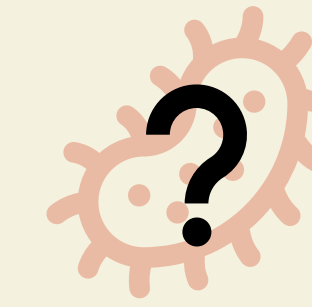
Sexual Populations — **Parthenogenetic Populations**

Wolbachia infection
Hybrid status
Ploidy level

Results

Ploidy level analysis

Sexual and parthenogenetic individuals were sequenced. Kmer coverage and frequency were analyzed with Genomescope2[4].

Two major peaks indicates a diploid genome. Three major peaks indicates a triploid genome.

All sexual individuals appear <u>diploid</u>

All parthenogenetic individuals appear <u>triploid</u>

Sexual Individual Genomescope Graph 2n

Parthenogenetic Individual Genomescope Graph 3n
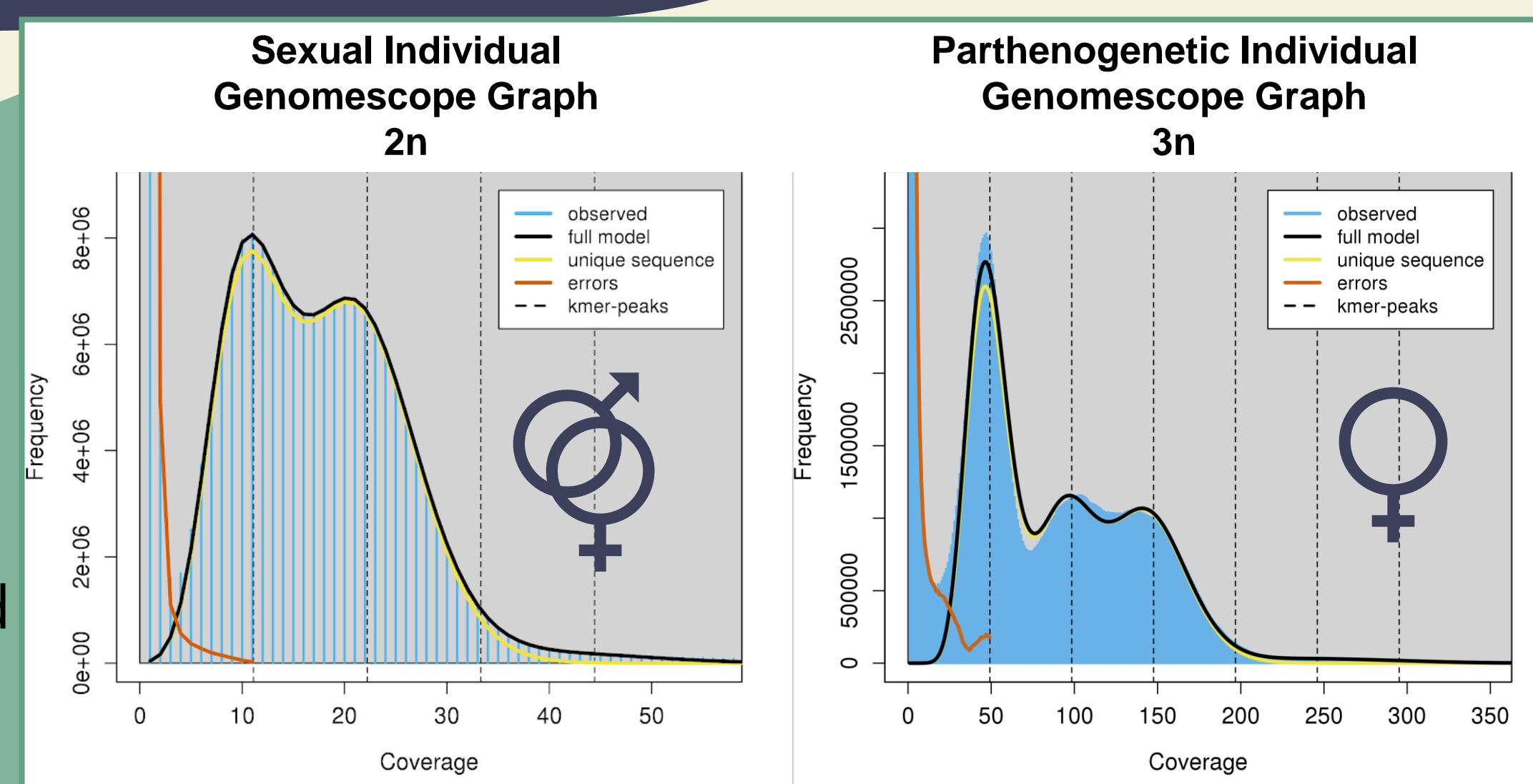
Hybridization indication analysis

The genomic heterozygosity of sexual and parthenogenetic individuals was determined with Genomescope2[4].

Heterozygosity in parthenogenetic individuals was significantly higher than in sexuals, (mean parthenogenic=2.97%, mean sexual=1.50%) **suggesting** <u>hybrid origin</u>.
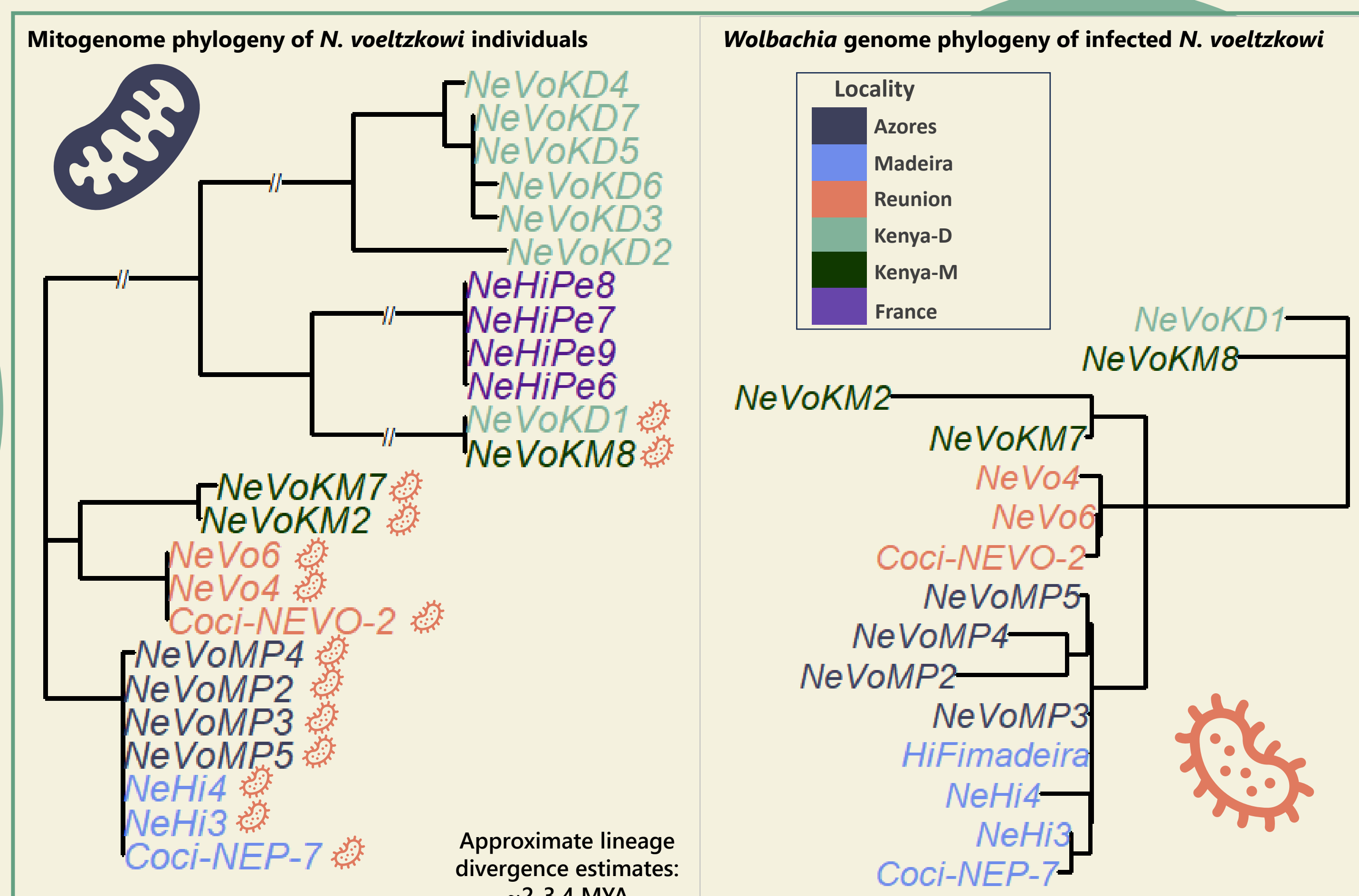
Kmer analysis suggest **the genome is** <u>AAB or AA'B.</u>

Wolbachia infection

In PacBio HiFi sequence data of parthenogenetic *N. voeltzkowi,* one scaffold was a complete *Wolbachia* genome, and no other scaffold contained any *Wolbachia* sequences.

In parthenogenetic populations, **there is only a *Wolbachia* infection with <u>no horizontal gene transfer</u> into the *N. voeltzkowi* genome.**

<u>No *Wolbachia* DNA was found in sexual individuals</u> when mapped against the bacterial genome.

Mitogenome phylogeny of *N. voeltzkowi* individuals

NeVoKD4
NeVoKD7
NeVoKD5
NeVoKD6
NeVoKD3
NeVoKD2
NeHiPe8
NeHiPe7
NeHiPe9
NeHiPe6
NeVoKD1
NeVoKM8
NeVoKM7
NeVoKM2
NeVo6
NeVo4
Coci-NEVO-2
NeVoMP4
NeVoMP2
NeVoMP3
NeVoMP5
NeHi4
NeHi3
Coci-NEP-7

Approximate lineage divergence estimates: ~2-3.4 MYA

Wolbachia genome phylogeny of infected *N. voeltzkowi*

Locality
Azores
Madeira
Reunion
Kenya-D
Kenya-M
France

NeVoKD1
NeVoKM8
NeVoKM2
NeVoKM7
NeVo4
NeVo6
Coci-NEVO-2
NeVoMP5
NeVoMP4
NeVoMP2
NeVoMP3
HiFimadeira
NeHi4
NeHi3
Coci-NEP-7

Phylogeny of mitochondrial genomes and *Wolbachia* genomes across *N. voeltzkowi* populations

The mitochondrial and *Wolbachia* genomes were used to create Maximum Likelihood trees across populations with MAFFT[5] and IQ-TREE[6].

Wolbachia appears to <u>codiverge</u> with each infected population.

<u>No local strains</u> of *Wolbachia* based on population location

Conclusion

Transition to Parthenogenesis
Features confirmed in *N. voeltzkowi:*

- ✓ *Wolbachia* infection
- ✓ Hybridization
- ✓ Odd polyploidization

Continuing research aims to determine:

- **What was the order of events?**
- **Which trigger directly caused the transition to parthenogenesis?**

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