

Copy number variation appears increased in clonal lineages over sexual lineages of *Phytophthora infestans*

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Rationale and methodology

Phytophthora infestans is the most devastating pathogen of potato. We set out on a genomics project and realized that copy number variation (CNV) may be more important than single nucleotide polymorphisms. Our project focused on:

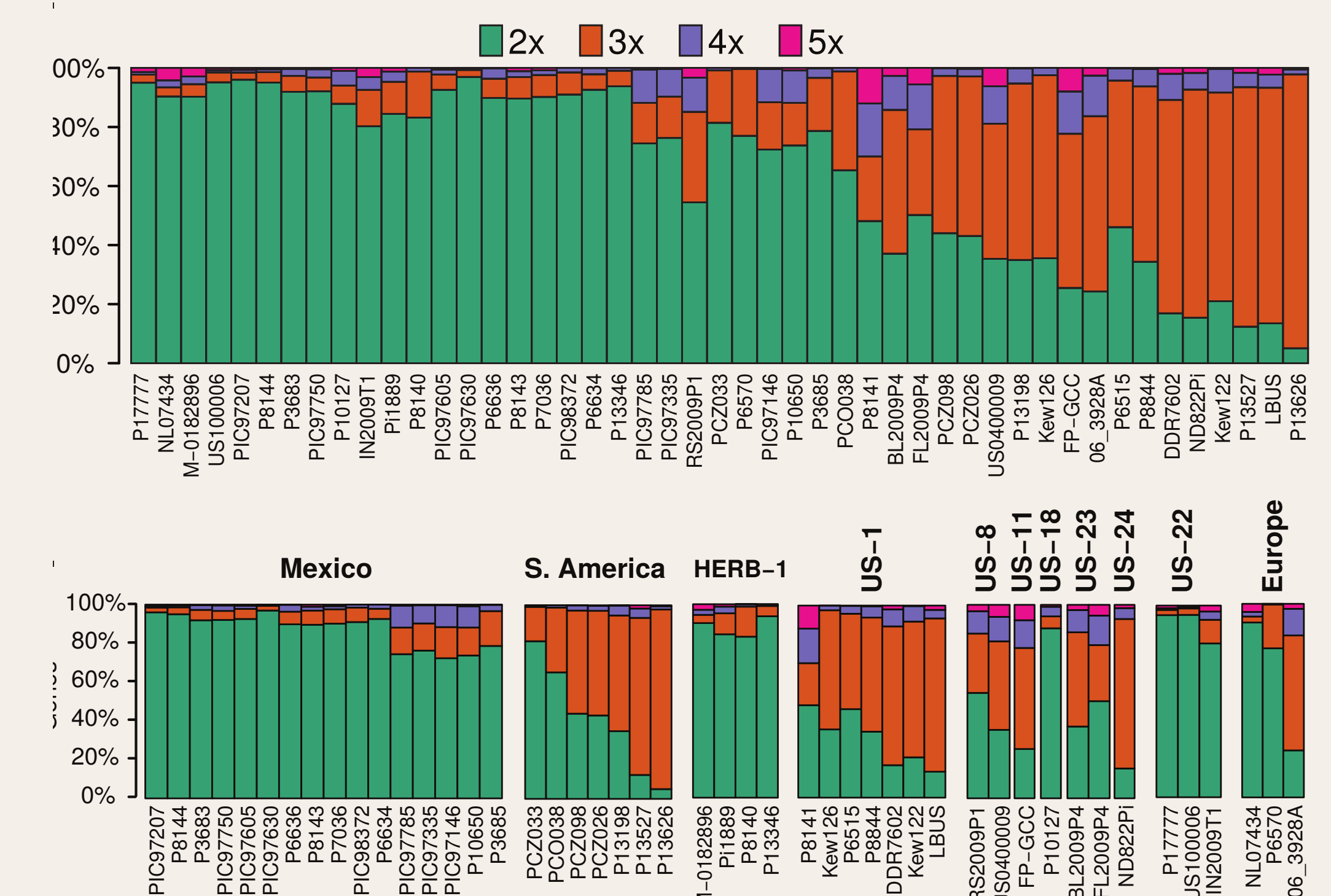
- Determine copy number for all *P. infestans* genes
- Determine if certain categories of genes had more CNV
- Ask if CNV occurred in other species of *Phytophthora*

We sequenced genomes of isolates of *P. infestans* collected from Mexico and added these to genomes already published. We used the method of Knaus and Grünwald (2018) to assign copy number to genomic windows in *P. infestans*. We then used the genomic coordinates of each gene to determine which window and what its copy number was for all *P. infestans* genes. We also determined copy number for genomic windows of several other *Phytophthora* species available at the SRA.

Copy number varies continuously

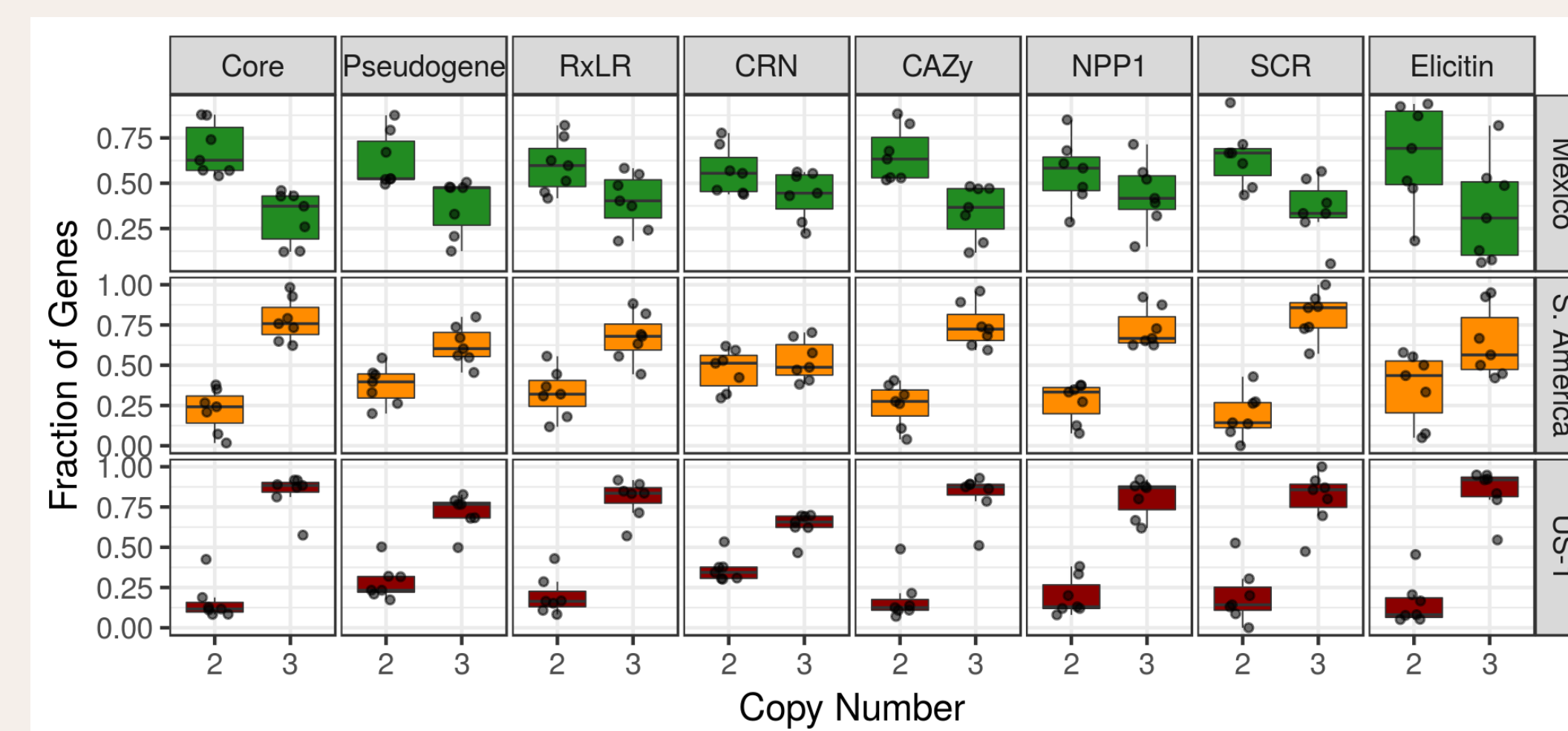
Copy number determined for each gene did not result in isolates that were diploid or triploid. Instead, we found a gradient of isolates from predominantly diploid to predominantly triploid. This indicated that this was not simply a matter of ploidy, but instead was copy number variation within each genome.

Sexually reproducing isolates from Mexico were predominantly diploid while clonal lineages outside of Mexico tended to have three copies of each gene suggesting a link between copy number and mode of reproduction.

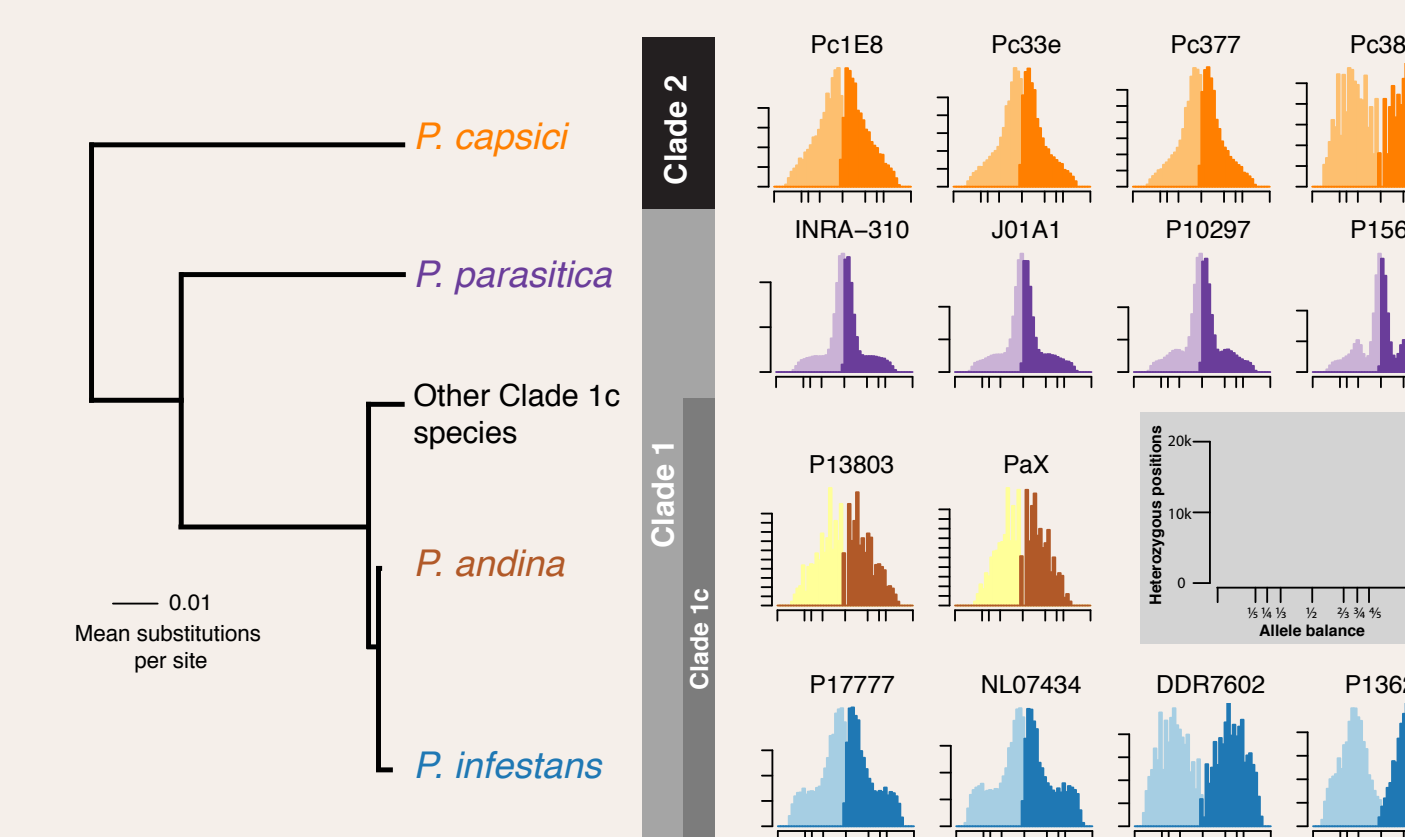


Copy number does not vary by gene category

Isolates from Mexico typically having two copies of each gene also tended to have two copies of each gene within several annotation categories. Isolates from South America and US-1 typically had three copies of each gene and also tended to have three copies of each gene within annotation categories. This indicated that CNV does not prefer particular gene classes.



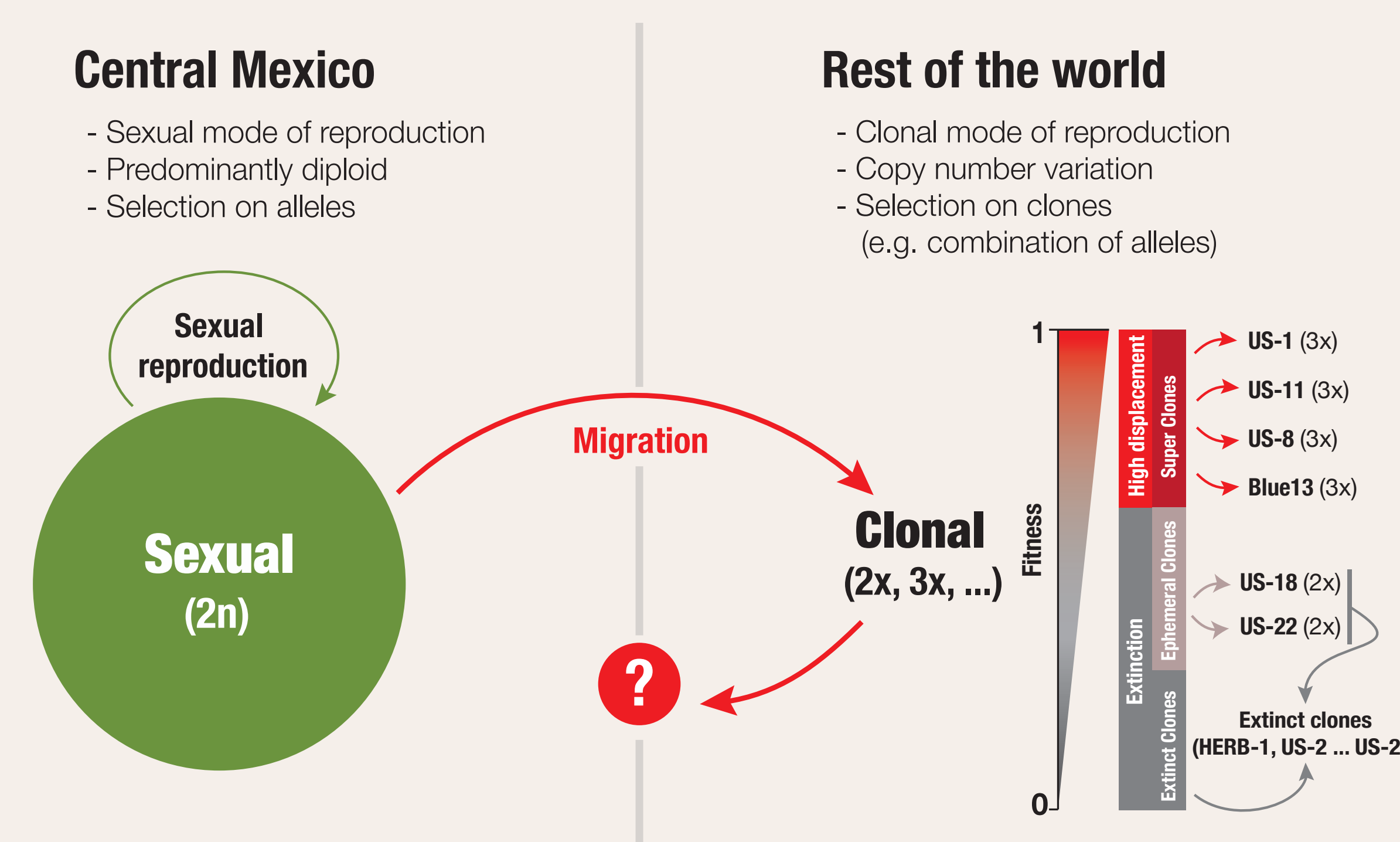
CNV occurs in other species



P. andina and *P. parasitica* appeared predominantly diploid. *P. parasitica* included minor peaks at the expectation for three copies. Three out of the four *P. capsici* samples appeared predominantly diploid but one appeared triploid. This indicates that CNV occurs throughout *Phytophthora*.

A model for emergence

Most emergences of *P. infestans* may be ephemeral. Occasional emergence of high fitness lineages displace preceding lineages. Our work shows that these high fitness clones are also associated with high CNV. This research also indicates a link between a copy number of two and a sexual mode of reproduction. It is currently unknown whether a copy number of three drives fitness or it accumulates after highly fit lineages emerge. It is also unknown if lineages of high copy number can revert back to a copy number of two.



Acknowledgments

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References

Knaus, B. J., & Grünwald, N. J. (2018). Inferring variation in copy number using high throughput sequencing data in R. *Frontiers in Genetics*, 9.

vcfR can be found at:
<https://CRAN.R-project.org/package=vcfR>