



Genome evolution, taxonomy, and transmission of potexviruses in cacti (Alphaflexiviridae)

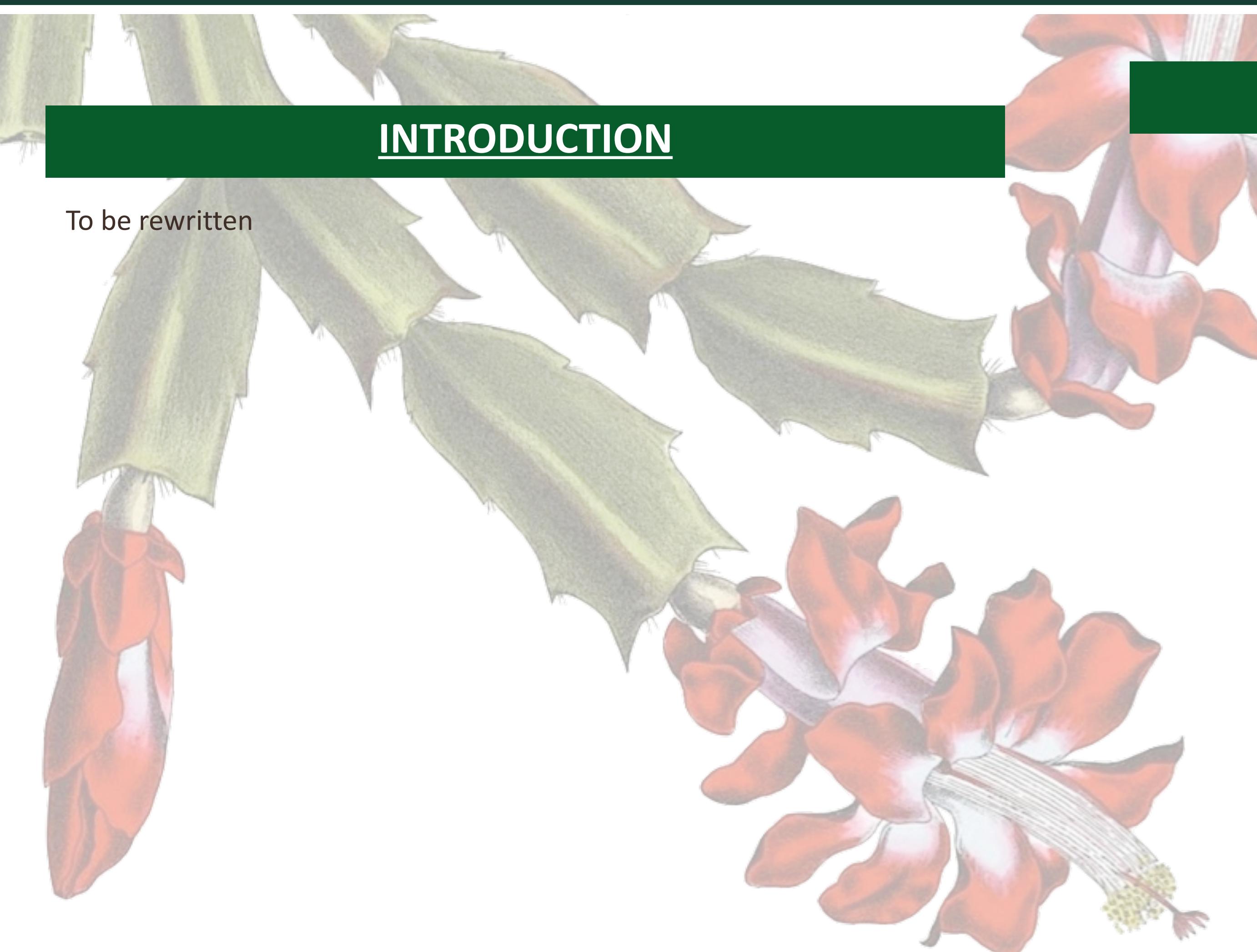
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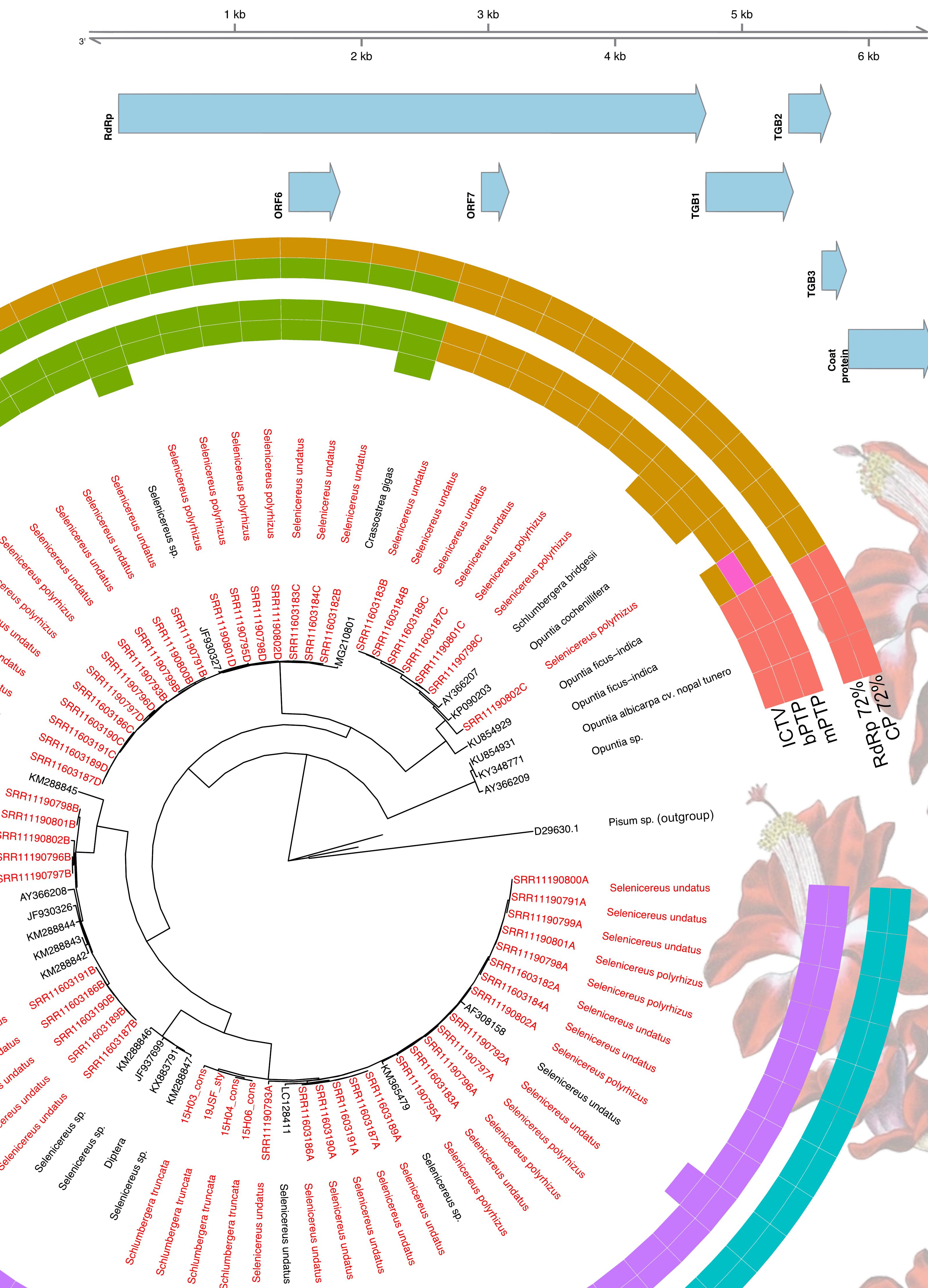


INTRODUCTION

To be rewritten



RESULTS



DISCUSSION

To be rewritten

METHODS

- We sampled from already assembled NCBI Genbank genomic data for cactus-infecting potexviruses (n=37).
- We searched NCBI Genbank for RNA-seq samples within cacti (n=149) and assembled samples with positive hits for viral RNA to reference sequences (n=59).
- We sequenced samples of *Schlumbergera truncata* from BI's personal collection (n=22).
- The *S. truncata* samples were filtered for virus and viral samples were mapped to reference sequences (n=85), which were filtered for quality and collapsed to consensus sequences (n=4).
- We created an alignment using MAFFT and then a phylogeny using IQTree (GTR+F+I+G4).
- We used ICTV guidelines (72% similarity cutoff), as well as mPTP and bPTP algorithms for species delimitation.

REFERENCES

ACKNOWLEDGEMENTS

