

Introduction

Oxalis (~230 species) in the Greater Cape Floristic Region (GCFR), South Africa – a hotspot of plant diversity. In the recent decades the collaboration of South African and European botanists have increased our knowledge about distribution, morphology, cytogenetics, ecology and taxonomy of *Oxalis*, making it an ideal model for the application of modern sequencing methods that could provide improved phylogenies to study trait evolution. Moreover, unlike other

Zeisek, Vojtěch^{1,2} (vojtech.zeisek@ibot.cas.cz); Oberlander, Kenneth² (kco@sun.ac.za); Schneeweiss, Hanna³ (hanna.schneeweiss@univie.ac.at); Dreyer, Leanne⁴ (ld@sun.ac.za); Schmickl, Roswitha^{1,2} (roswitha.schmickl@ibot.cas.cz);

1 – The Czech Academy of Sciences, Institute of Botany, Zámek 1, Průhonice, 252 43, Czech Republic

2 – Charles University, Faculty of Science, Department of Botany, Benátská 2, Prague, 12800, Czech Republic

3 – University of Vienna, Department of Botany and Biodiversity Research, Rennweg 14, Vienna, 1030, Austria

4 – Stellenbosch University, Botany and Zoology, Natural Sciences Building, Merriman avenue, Stellenbosch, WC, 7600, South Africa

floras, the GCFR appears to have low levels of polyploidisation.

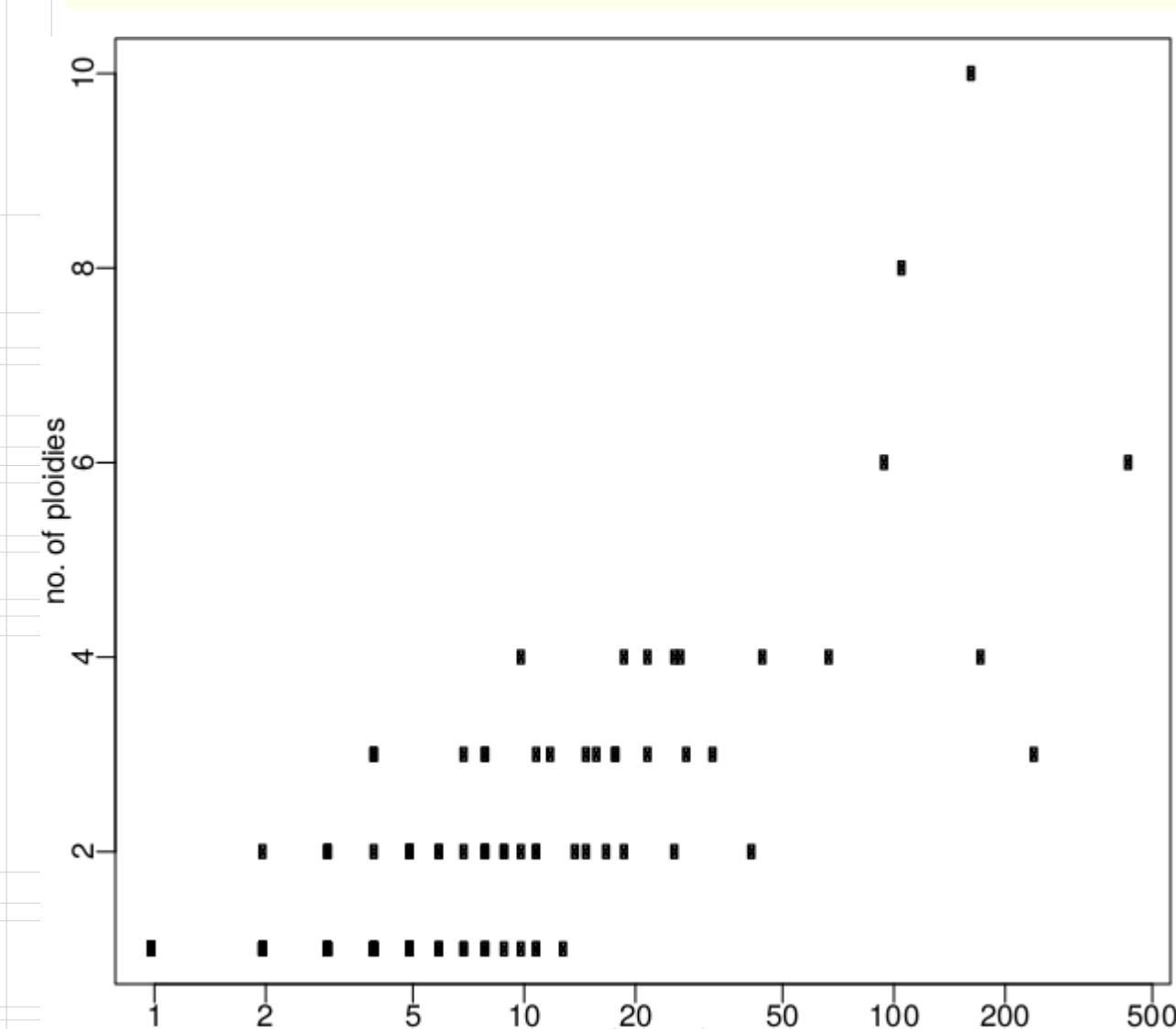
Oxalis is a notable exception, and the frequency of polyploidisation in *Oxalis* and its relationship to diversification is a major focus of our current study.

Materials and Methods

For generating the phylogeny, we used > 1,100 orthologous nuclear **genes** (> 1.1 Mb) for Hyb-Seq (probes generated using the Sondovač pipeline; [Schmickl et al. 2016](#)). The **ASTRAL species tree** (426 accessions shown) was obtained using HybPhyloMaker ([Fér & Schmickl 2018](#)). The genome sizes (> 2,200 accessions) was obtained with DAPI flow cytometry. Mitotic chromosomes were counted from 140 accessions.

Results and Discussion

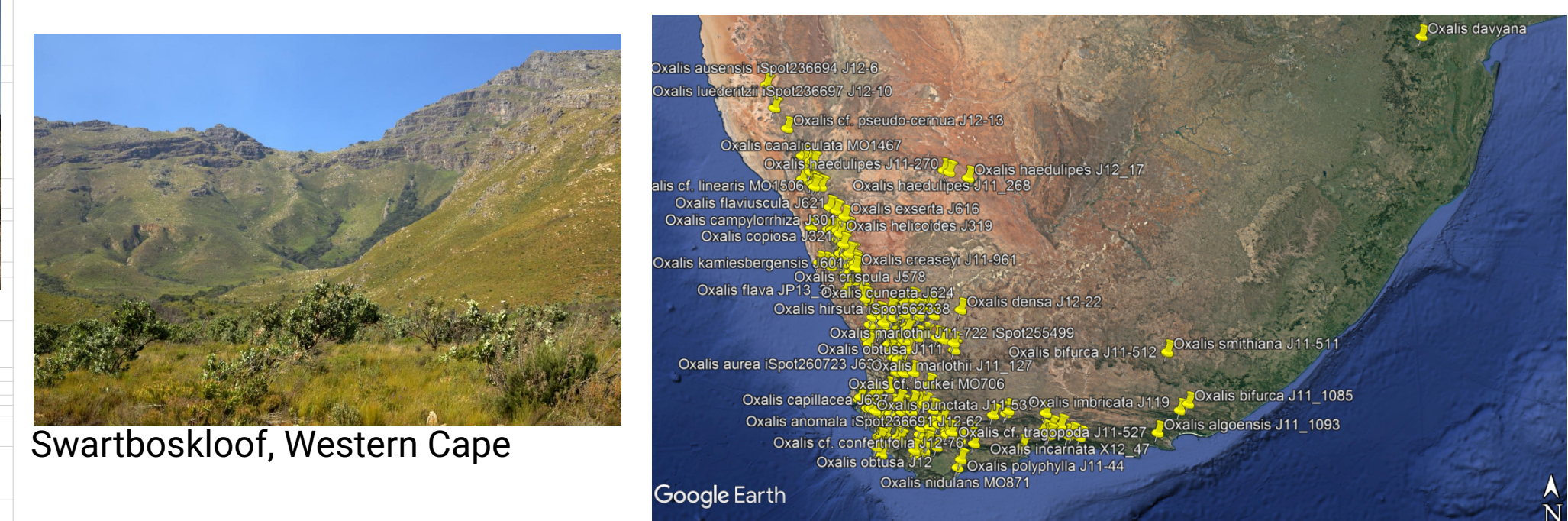
The *Oxalis* species tree is well-resolved, robust and consistent across methods. Most species are monophyletic, some appear to be polyphyletic. We also found several new species. Nearly every well-sampled species has multiple ploidy levels (from diploids to dodecaploids), with the number of ploidy levels rising linearly with the number of measured accessions (see plot below). Higher polyploids seem to arise within particular species and very few species/clades are exclusively polyploid, suggesting that polyploidy is not playing a strong role in diversification dynamics (possible evolutionary dead ends?). We have not detected any allopolyploids or hybrids, although there is possible evidence for chloroplast capture. We found two major karyotypes, x=7 and x=5. Rare karyotypes (x=4, x=6) were also observed. Inflorescence types appear to be useful, whereas characters that are currently considered taxonomically important, like the number and position of peduncular bracts, have actually evolved multiple times and showed a substantial degree of homoplasy.



The number of detected ploidies correlates strongly with number of samples measured by FCM. Each point is one species (some species overlap).

Upcoming work

We are continuously adding more and more data (FCM, Hyb-Seq, chromosome counts, traits, etc.). We are preparing our dataset for analysis in chromEvol and hisse R package to formally test chromosome and genome size evolution (see talk by R. Schmickl). Surprisingly, Hyb-Seq provides sufficient resolution for phylogeographic studies (strong geographic pattern observed in *O. incarnata* / *O. hirta* and its relatives).



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