

# Collection inspection: extracting DNA from cycads in living collections for phylogenetic analysis and detection of hybrids

Jay An<sup>1</sup>, Stephan Girard<sup>2, 3</sup>, Jeremie Fant<sup>2, 3</sup>

<sup>1</sup>Stanford University, <sup>2</sup>Northwestern University - Department of Plant Bio. & Conservation, <sup>3</sup>Chicago Botanic Garden



## Background

- Cycads are highly threatened; over half of species are critically endangered (Baillie *et al.* 2004)
- Seeds become inviable in seed banks, making living collections necessary for conservation (Griffith *et al.* 2015)
- Pollination occurs in collections despite lack of obligate pollinators, indicating that hybridization is possible
- Hybridization in collections can harm reintroduction efforts by causing genetic swamping, where local genotypes are replaced by introduced hybrid genotypes (Levin *et al.* 1996)

## Objectives

- Verify methods to extract cycad DNA of sufficient quality for sequence analysis
- Sequence cycads from various collections and compare with existing phylogenetic and sequence data to:
  - Identify unknown and mislabeled individuals
  - Detect hybrid individuals and identify whether hybridization occurs in collections

## Methods

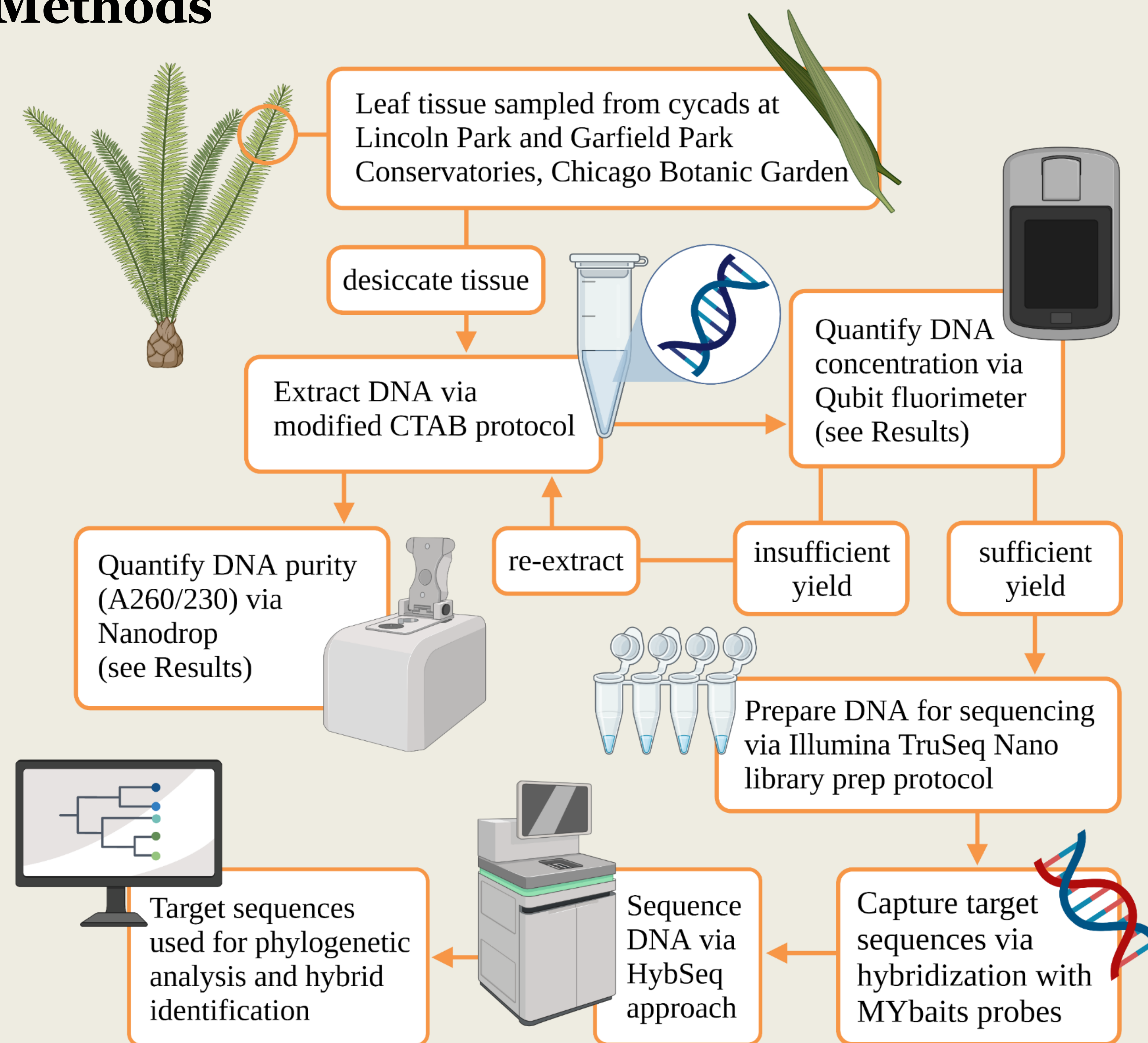
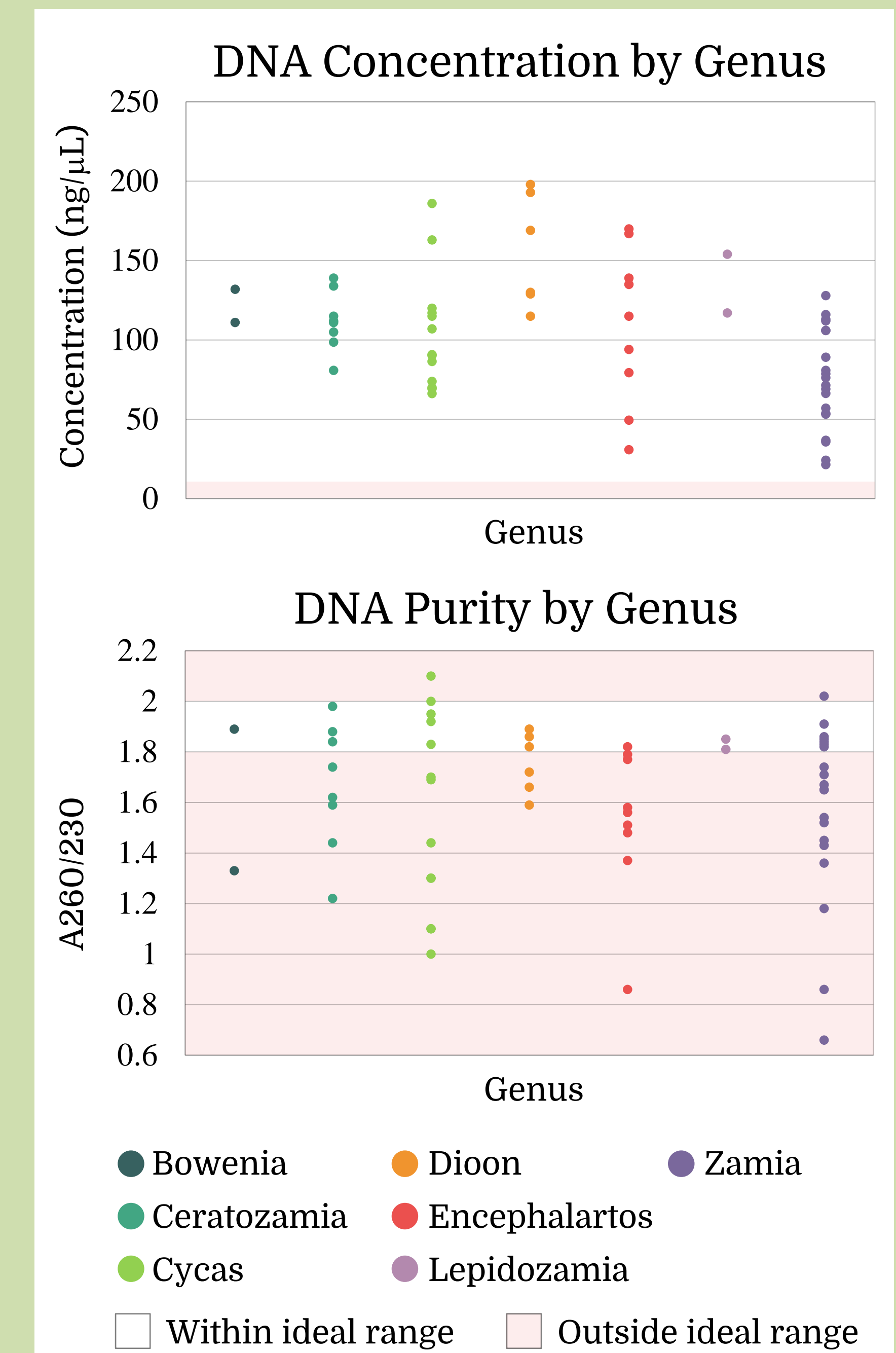


Figure created in BioRender

## Results



## Conclusions

- Modified CTAB extraction yielded DNA of sufficient quantity for sequencing
  - In cases of insufficient yield, repeated extraction produced sufficient DNA
- DNA extracted from cycads via modified CTAB protocol is often of substandard purity
- Sequence data (in progress) needed to further assess the effectiveness of modified CTAB protocol

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## References

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