Freek T. Bakker (PhD)
Biosystematics Group, Wageningen University, NL

Herbarium genomics, skimming & plastomics

Herbarium genomics is a promising field, as next generation sequencing approaches are well-suited to deal with the usually fragmented nature of archival DNA. We show that routine assembly of plastome sequences from herbarium specimens is feasible, from total DNA extracts and apparently only weakly depending on specimen age. We use genome skimming and an automated bioinformatics pipeline, comprising Iterative Organelle Genome Assembly, that assembles paired-end reads into a series of candidate assemblies, the best one of which is selected based on assembly likelihood estimation. Using a range of herbarium specimens, from 12 different Angiosperm families and some of which up to 146 years old, we show that routine plastome sequencing from herbarium specimens using genome skimming is feasible and cost-effective, and can be performed with highly limited sample destruction. Comparison of fresh DNA with both old and young herbarium from the same tree individuals shows that post-mortem damage in herbarium DNA is negligible.