

## Background

- Currently, genomic and genetic resources available to understand or combat the damage caused by *Moniliophthora perniciosa* are lacking and phylogenies are largely unresolved. Genome size prediction is a fundamental task in genome assembly. Fungi display a great variety of genome sizes (from 8 to 177.6Mbp).
- Assumptions: *M. perniciosa* biotypes have a significant variation in genome size.

## Theobroma cacao

- The chocolate tree, native to the humid tropical forests of South America, is the raw material for manufacturing chocolate, one of the main crops in Brazil. Cacao diseases are one of the main problems limiting its production;
- Witches' broom disease, caused by *M. perniciosa*, is one of the main problems in cacao plantations.

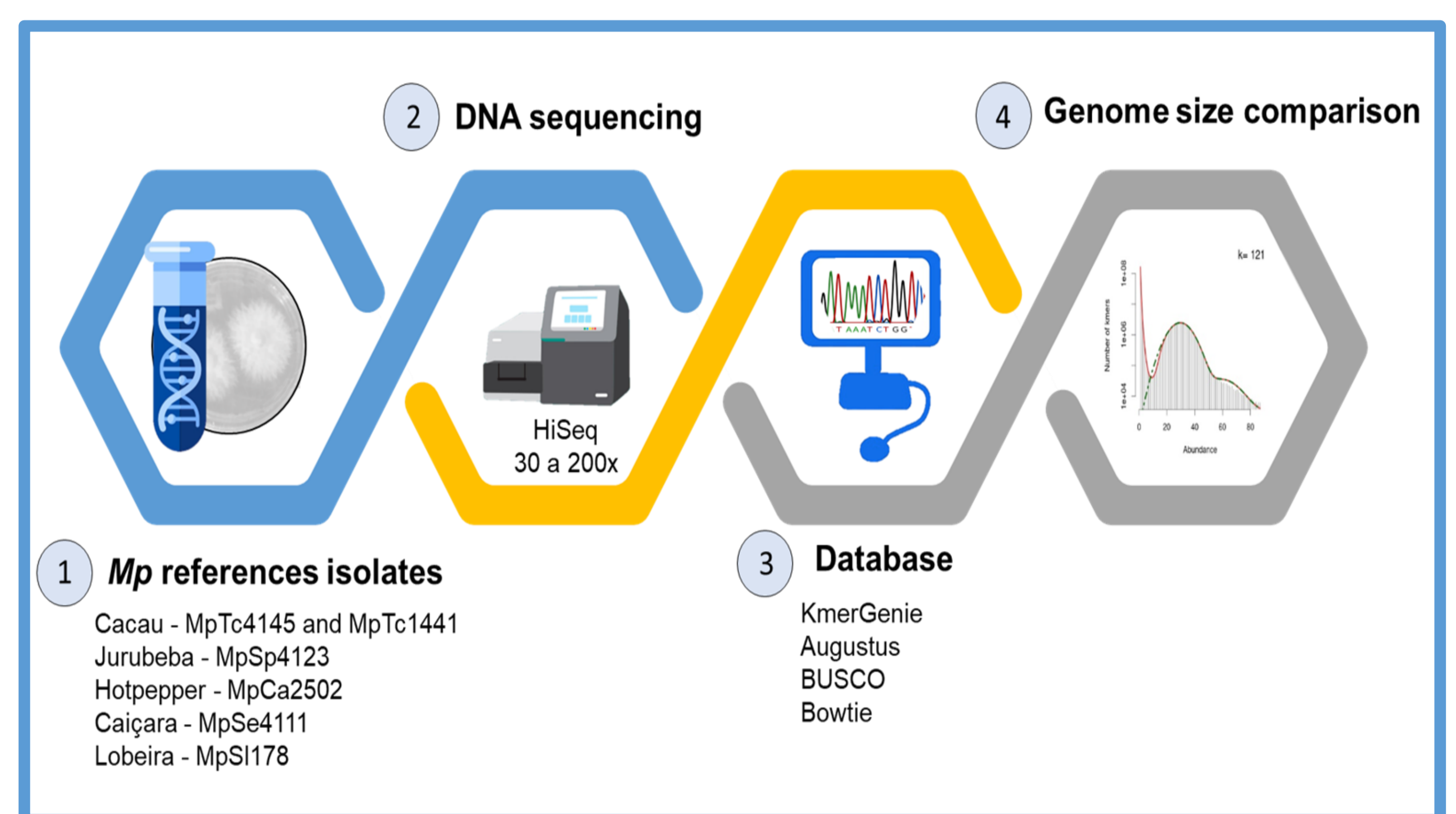
## Moniliophthora perniciosa

- Basidiomycota, hemibiotrophic fungi;
- Primary hosts: *Theobroma* and *Herrania* species;
- Wide host range, including *Solanaceae*, *Bignoniaceae*, and *Malpighiaceae* families;
- Pathogenic variability leads to biotypes: C (Cacao), S (Solanum), and L biotype (Lobeira).

## OBJECTIVE

To generated draft genome sequences of six *M. perniciosa* isolates obtained from cacao (2) and solanaceous hosts (4) and to compared the *in silico* genome size of *M. perniciosa* from different hosts.

## MATERIALS AND METHODS

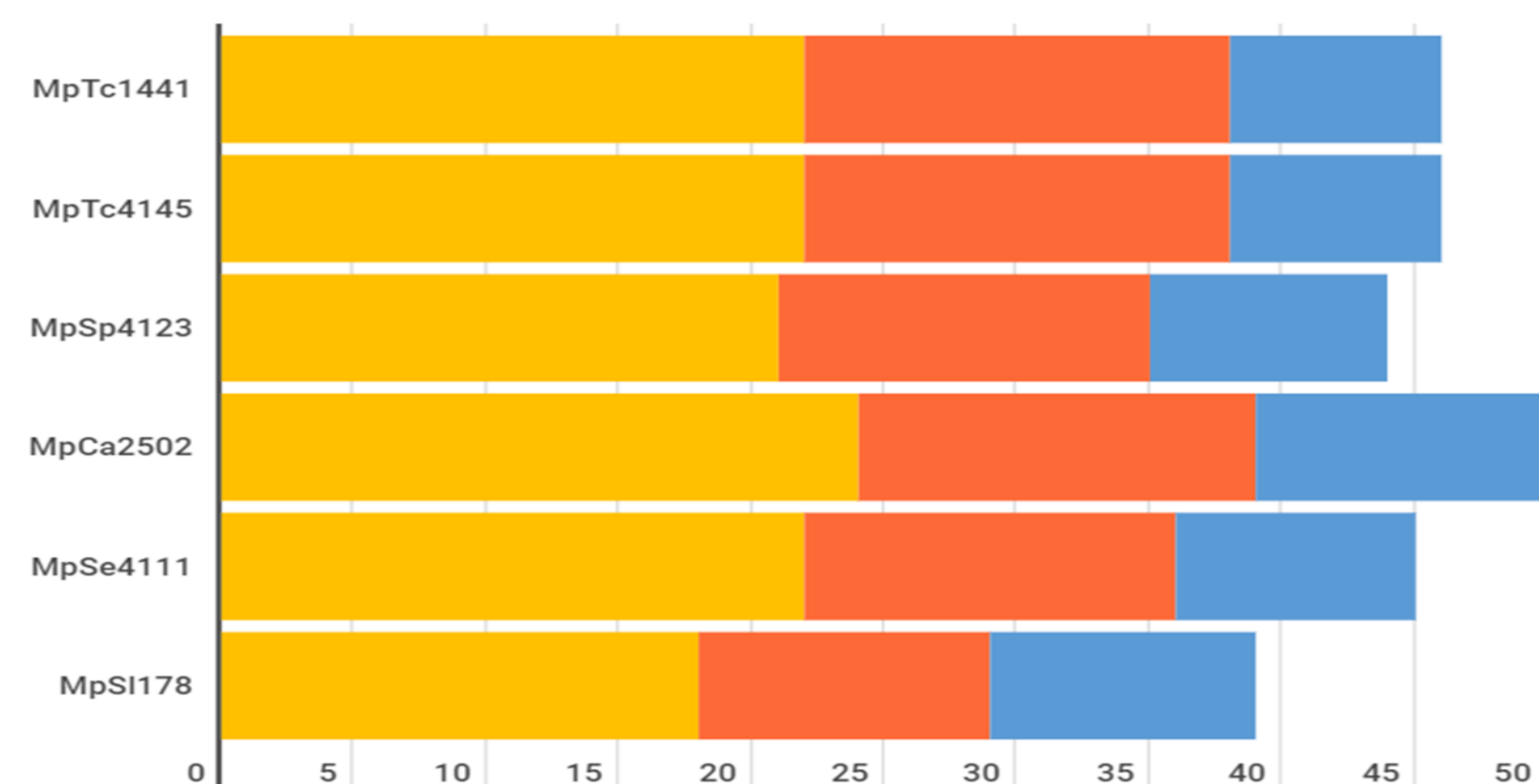


## RESULTS AND DISCUSSION

- The draft genome assemblies varied from 38.19-47.97 (Figure 1);
- The comparative genomic analysis of six Mp isolates showed that the total TE content and genome size varied widely among them.
- Repeated elements: most commonly simple repeats, followed by Interspersed repeats/ Transposable elements (Tes). In addition to these, other types of repetitive sequences observed were LTR elements, Low Complex, and small RNAs;
- The variation in genome size might reflect the evolution in the pathogenicity of *M. perniciosa*;
- Isolates of cultivated *Solanaceae* are pathogenic to cacao and vice-versa. But, the isolates from wild nightshades Lobeira is not pathogenic to cacao.

Table 1 Genetic features of genomes

	MpTc1441	MpTc4145	MpSp4123	MpCa2502	MpSe4111
Assembled genome size (Mb)	47.34	47.97	45.84	51.53	46.17
N50 scaffold size (Kb)	100.65	103.83	67.37	56.52	70.51
Longest scaffold size (Kb)	598.20	916.10	554.50	571.80	554.50
GC %	47.70	47.70	47.80	47.80	47.80
Busco (%)	93.00	92.90	92.30	92.90	92.50



## CONCLUSIONS

- These genomes will be a useful resource for those studying genome expansion of *M. perniciosa* and host adaptation;
- Likewise, the addition of these genomes from different hosts will be useful for future comparative genomics projects investigating how the pathogenic lifestyle evolved in the Basidiomycetes.

## ACKNOWLEDGMENTS