De novo TE annotation : tackling the fat genomes issue

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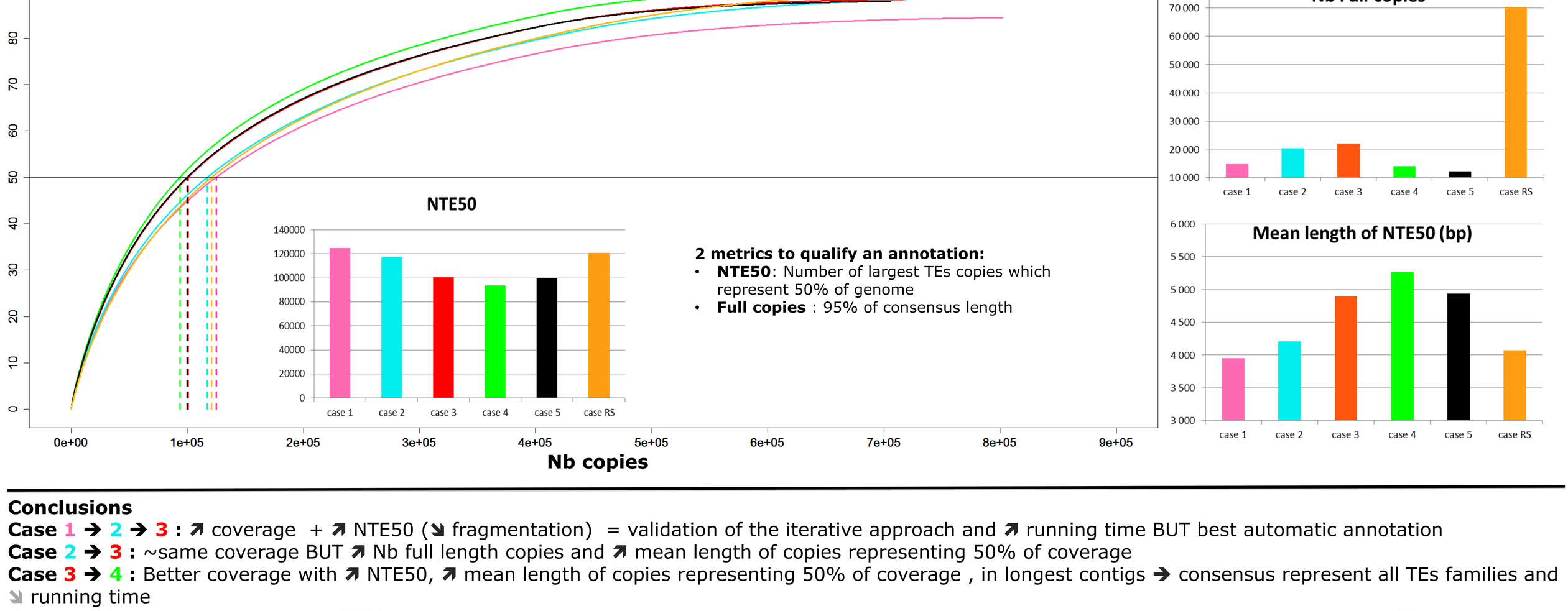
Abstract Transposable elements (TEs) constitute the most dynamic and the largest component of large plant genomes, e.g. 85% of the maize genome [1], and 88% of the wheat genome [2]. *De novo* TEs annotation is therefore a computational challenge. We designed new strategies to this end based on the functionalities of the REPET package [3]. This package includes 2 pipelines: TEdenovo that builds a repeated sequences consensus library, and TEannot that annotates copies of library in the genome.
For our methodological developments, we chose the wheat 3B chromosome sequence (~1Gbp) as an experimental model. We describe the principles and the results of several strategies by different use cases:

Case 1: A library of known TEs [4]
Case RS: RepeatScout [6] consensus library. In each cases the consensus are classified and used in an iterative annotation process. **Case 2**: A library of known TEs concatenated to a *de novo* library built from a genome spliced from their known TEs,
Case 3: A *de novo* LTR-retrotransposon library obtained with the LTRHarvest software [5] then concatenated with the *de novo* library built from a genome spliced from an already identified LTR-Rns library,
Case 4 & **5**: A *de novo* TEs consensus library obtained from a genome part (300 Mbp and 150 Mbp longest contigs),



Legend

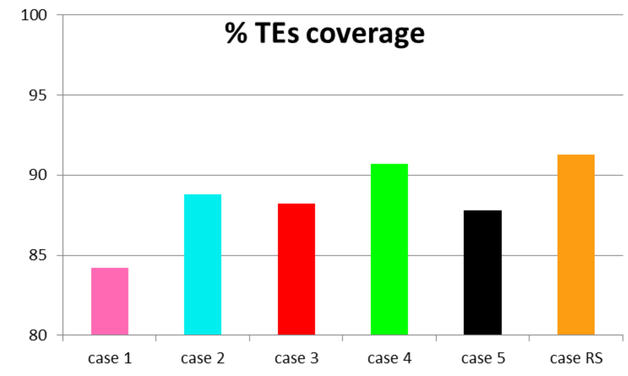
★ 3B chromosome V2.1, first to be fully sequenced, 294 691 contigs, 986.1 Mbp [1]

Cons FLC: consensus having at least 1 Full Length Copy

REPET package V2.0 [7]

2 metrics to qualify an annotation:

- **NTE50**: Number of largest TEs copies which represent 50% of genome
- **Full copies** : 95% of consensus length



Conclusions

Case 1 ➔ 2 ➔ 3 : ↗ coverage + ↗ NTE50 (↘ fragmentation) = validation of the iterative approach and ↗ running time BUT best automatic annotation
Case 2 ➔ 3 : ~same coverage BUT ↗ Nb full length copies and ↗ mean length of copies representing 50% of coverage
Case 3 ➔ 4 : Better coverage with ↗ NTE50, ↗ mean length of copies representing 50% of coverage , in longest contigs ➔ consensus represent all TEs families and ↘ running time
Case 4 ➔ 5 : ↘ coverage with ↗ NTE50 (↗ fragmentation) with ↘ running time = consensus from too small genome part don't represent enought TEs
Case 4 ➔ 6 : ↗ coverage with ↗ NTE50 (↗ fragmentation) with same running time, ↗ nb full length copies but they are too small.
Our analyses show that all our strategies enable us to overcome the current memory and time limitations for *de novo* TEs discovery and annotation using REPET on large plant genomes, effectively. This study paves the route towards comprehensive and high quality automatic TEs annotation in a number of economically and agronomically important species.

Perspectives : We are testing these strategies on the maize genome (2,3 Gbp)

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