Genetic diversity and population structure of 18 Tunisians *Orobanche foetida* populations using RADseq

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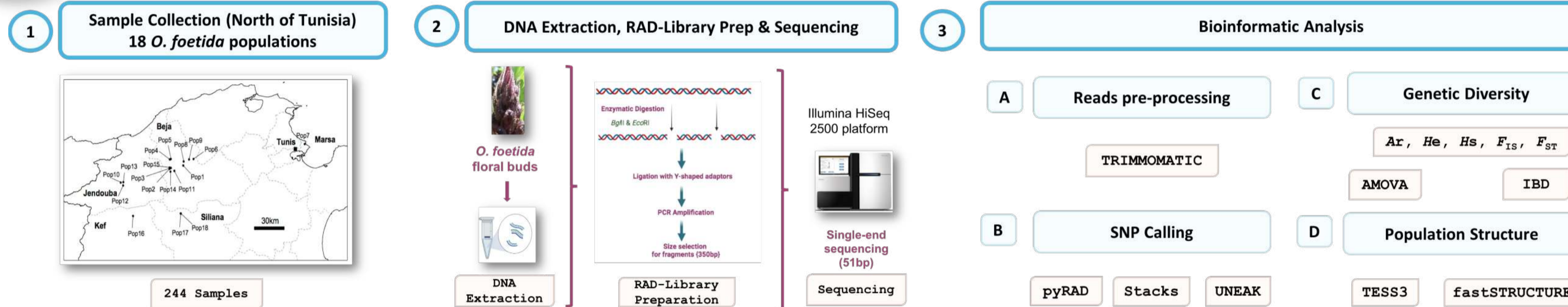
1 · *Orobanche foetida* Poiret, a real threat for legume crops in Tunisia

. *Orobanche foetida* Poiret is a holoparasitic plant devoid of chlorophyll and **totally depending on its host** for its growth.

. *O. foetida* is distributed in the **Mediterranean region** as a wild plant parasite. **In Tunisia,** it parasitizes **faba bean** and may cause **90% yield losses**.

❖ **Aim: Describe the current distribution and the genetic variation of *O. foetida* in Tunisia**

2 · Experimental & Data Analysis Plan

1. Sample Collection (North of Tunisia) 18 *O. foetida* populations — 244 Samples
2. DNA Extraction, RAD-Library Prep & Sequencing — *O. foetida* floral buds — DNA Extraction — RAD-Library Preparation — Illumina HiSeq 2500 platform — Single-end sequencing (51bp) — Sequencing
3. Bioinformatic Analysis
   - A. Reads pre-processing — TRIMMOMATIC
   - B. SNP Calling — pyRAD · Stacks · UNEAK
   - C. Genetic Diversity — Ar, He, Hs, F_{IS}, F_{ST} — AMOVA — IBD
   - D. Population Structure — TESS3 · fastSTRUCTURE

3 · Variances in SNPs Count (Stacks, pyRAD & UNEAK)

The number of the detected SNPs varied among the three data sets; Stacks (10,755 SNPs), pyRAD (1,785 SNPs), and UNEAK (206 SNPs)

4 · Genetic differentiation occurred among the Tunisian *O. foetida* populations

The AMOVA analysis revealed a significant level of genetic differentiation (Monte Carlo test $p < 0.05$) using the three data sets.

The molecular variance :
- Within populations between 96.29% and 96.74%
- Among populations between 3.25% and 3.70%

5 · No strong population clustering was detected using the three data sets (pyRAD, Stacks & UNEAK) and clustering methods (DAPC, fastSTRUCTURE, TESS3 & PCA)

5.1
A differentiation is observed among the 18 populations indicating a potential grouping pattern. Thus, we suggested the distribution of the 18 populations accordingly in four groups.

5.2
A slight divergence is detected among the assessed groups with an overlapping especially among the three groups representing north-west Tunisian populations

5.3
. PyRAD and Stacks data sets showed almost similar clustering patterns without confirming the existence of a strong genetic structure.
. UNEAK did not show any clear clustering.

6 · No Strong evidence for grouping pattern

- Low pairwise F_{ST} values are detected among the 4 potential groups using the three data sets

- Similar genetic variability parameters (Ar, Ho, He and F_{IS}) were detected among the 18 populations
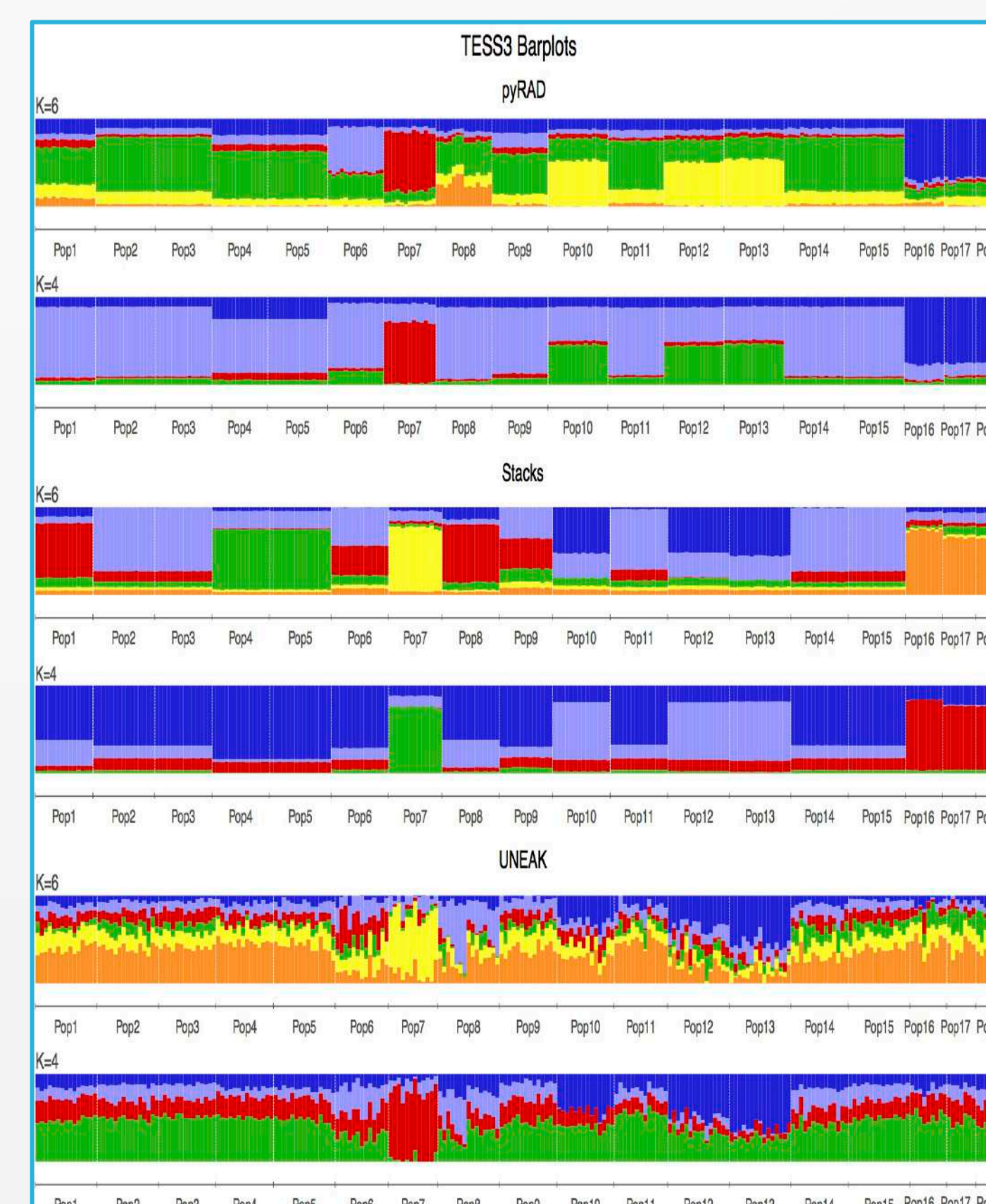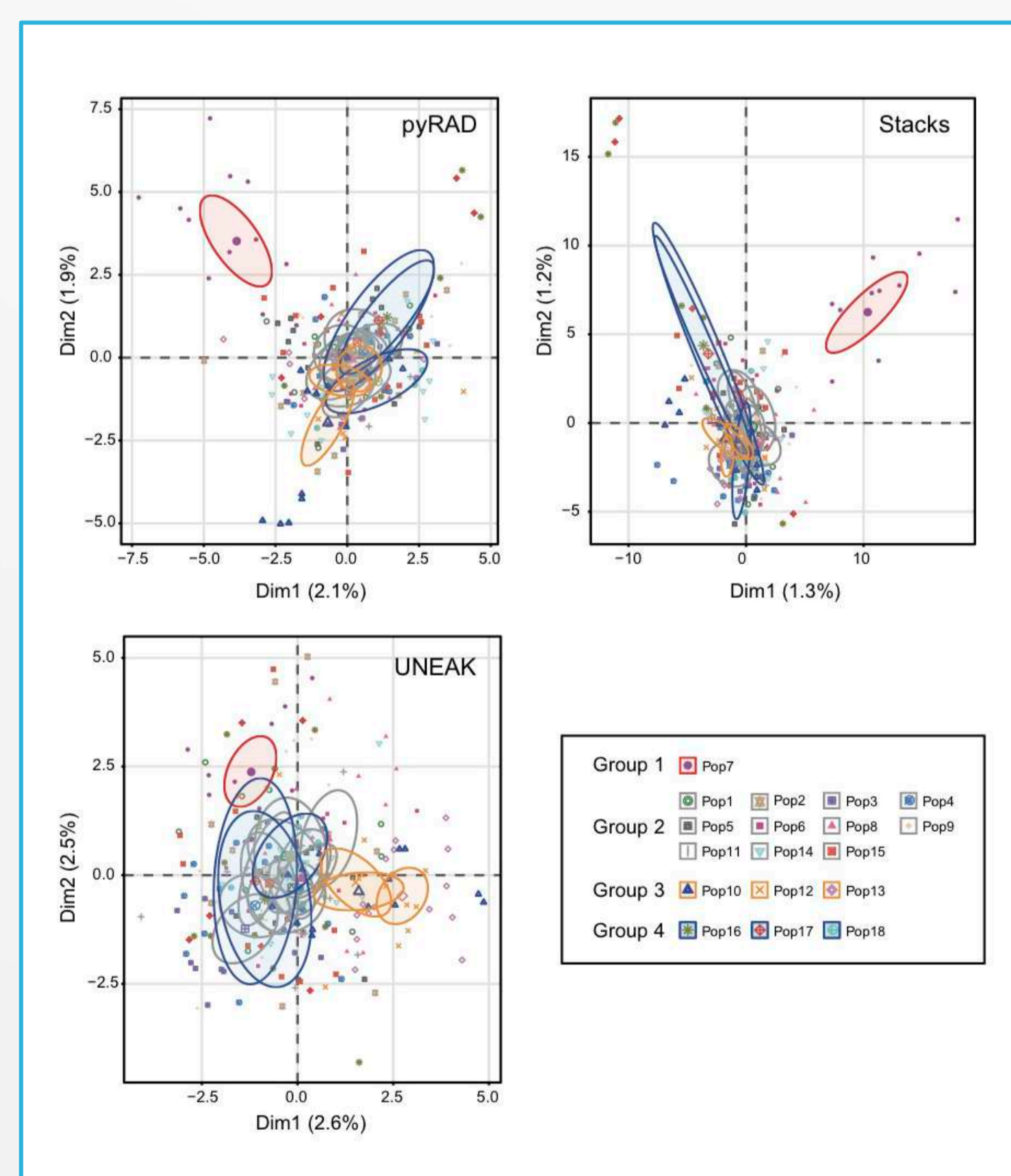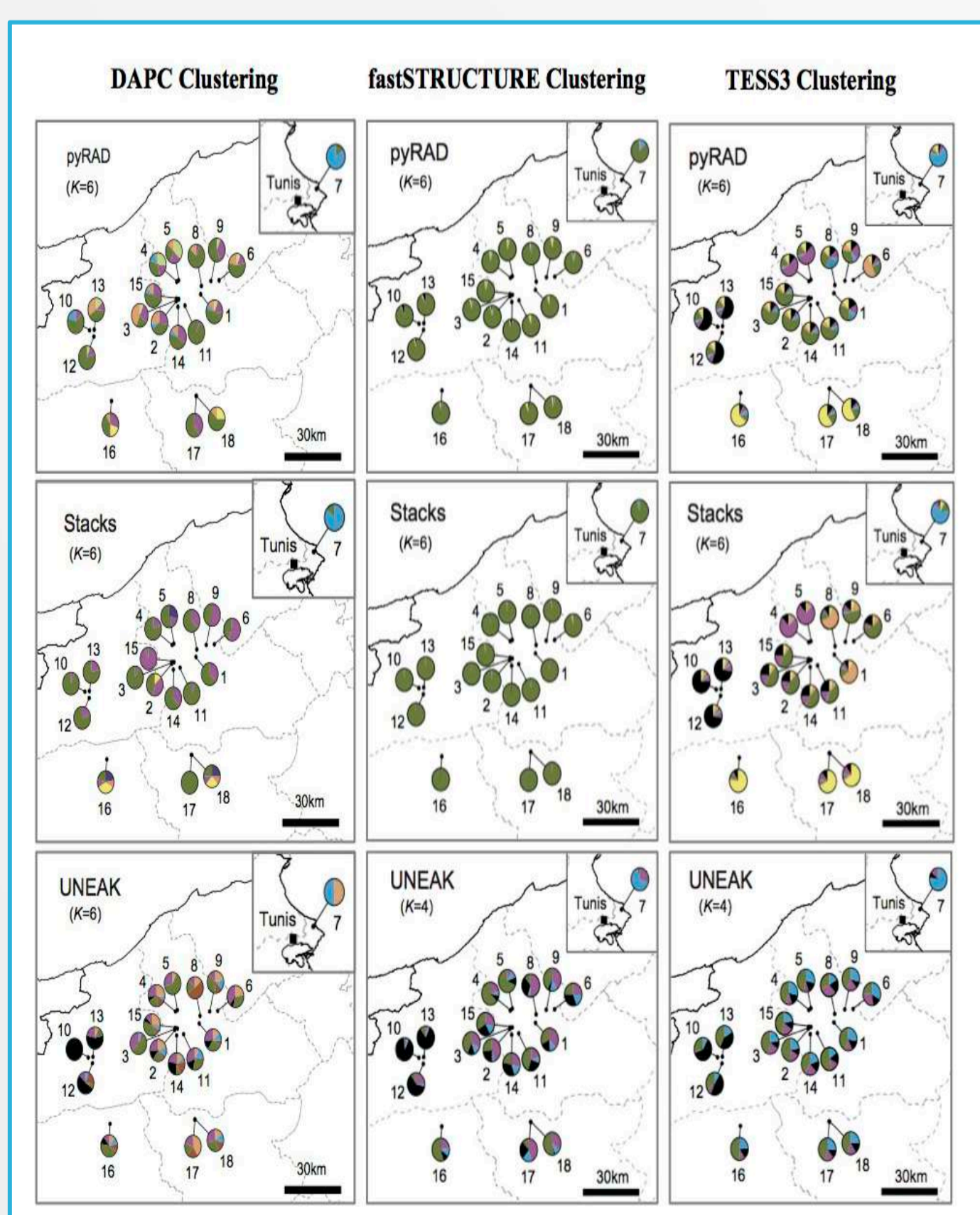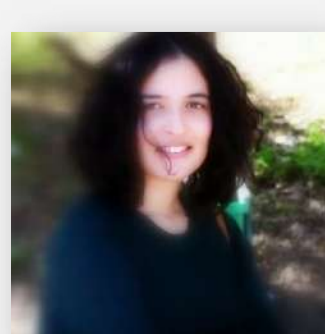
7 · Isolation by distance effect

- Significant and positive association between genetic and geographic distances were observed among the 18 collected populations

- Mantel Test:
UNEAK: r = 0.573, $p = 0.001$;
Stacks: r = 0.558, $p = 0.018$;
pyRAD: r = 0.596, $p = 0.007$

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❖ **The present study could be a valuable reference for the upcoming research projects focusing on this parasitic plant and targeting the release of new faba bean resistant varieties**

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