

Isolates of cocoa swollen shoot virus from tolerant/resistant cocoa trees (*Theobroma cacao* L.) collected in cocoa orchards in Côte d'Ivoire show a genetic diversity

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Context and justification

Since its upsurge in 2003, cocoa swollen shoot virus disease (CSSVD) has caused enormous production losses in Côte d'Ivoire. The study of the genetic diversity of isolates from CSSV in cocoa trees is a fundamental approach for effective genetic control (Muller & Sackey, 2005). The objective of this study is to identify and characterize the different CSSV isolates present in the potentially tolerant accession to CSSVD and to determine the existing phylogenetic relationships.

Plant Materials

◆ 168 cocoa tree potentially tolerant (APT) or susceptible (APS) to CSSVD

Origins	APT	APS	APT/APS	Total
Bangolo	3	0	0	3
Bouaflé	25	93	3	121
Duekoué	3	0	0	3
Guezabo	2	0	0	2
Meagui	7	7	2	16
Sinfra	18	1	3	22
Soubré	0	1	0	1
Total	58	102	8	168

Methods

- Viral DNA extraction (Matab)
- Rolling Circle Amplification
- **PCR: Primers UNI1F/R:** Tm: 55°C, 650pb; designed in the intergenic region of the viral genome. **Primers BADNA ¼ CSSV deg2 :** Tm: 57°C, 626pb, designed in the reverse transcriptase region of the viral genome
- Sequencing
- Sequences alignment and phylogenetic tree construction (logiciel Seq Man Pro, Seaview, Muscle alignment)

Results

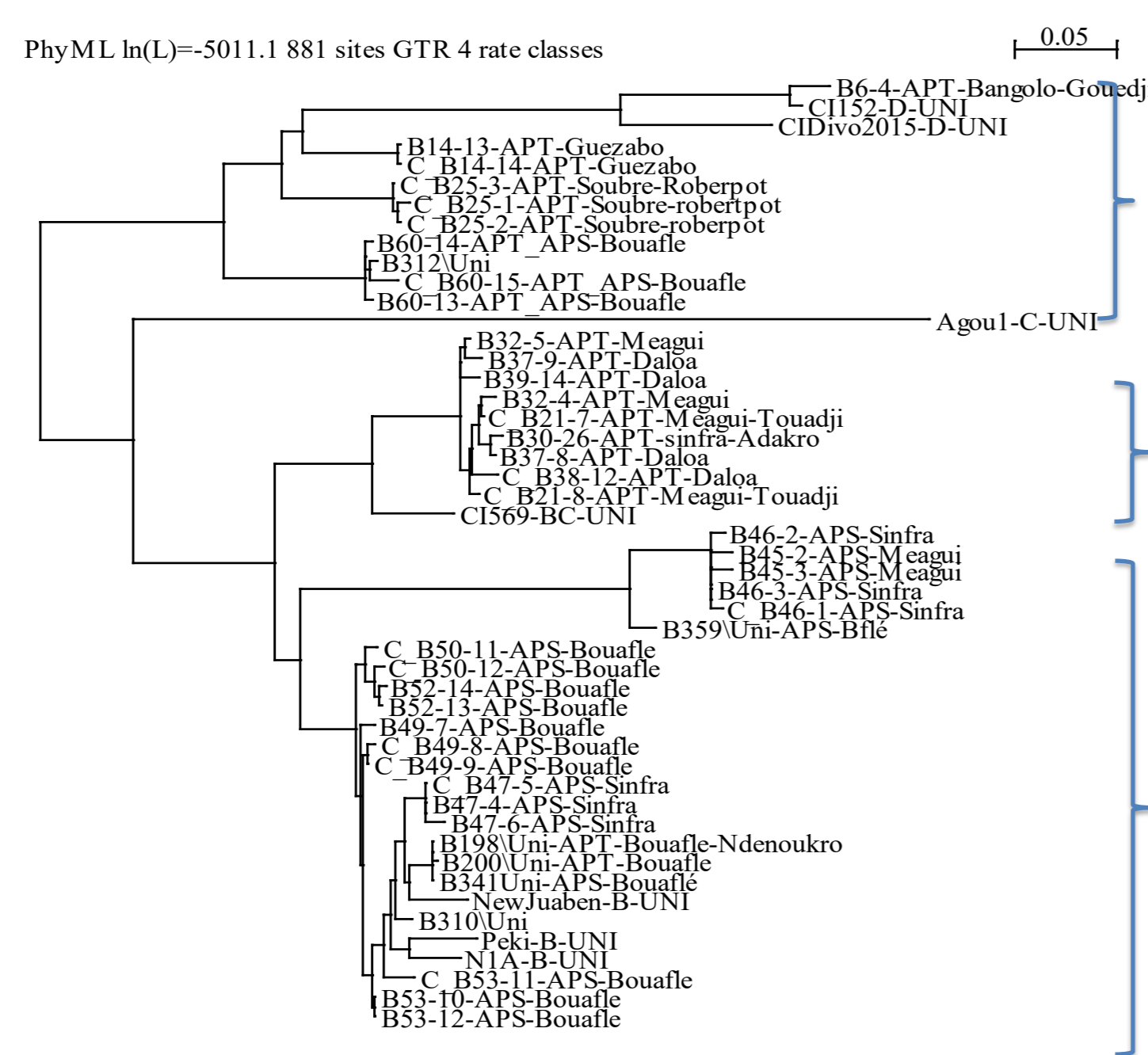


Fig 2: Dendrogram (PhyML) showing genetic diversity (primer pair UNI 1F/R) of CSSV from potentially tolerant and susceptible accessions to CSSVD in Côte d'Ivoire

- **Primers UNI 1 F/R:** group D, B and BC, with a prevalence of group B.

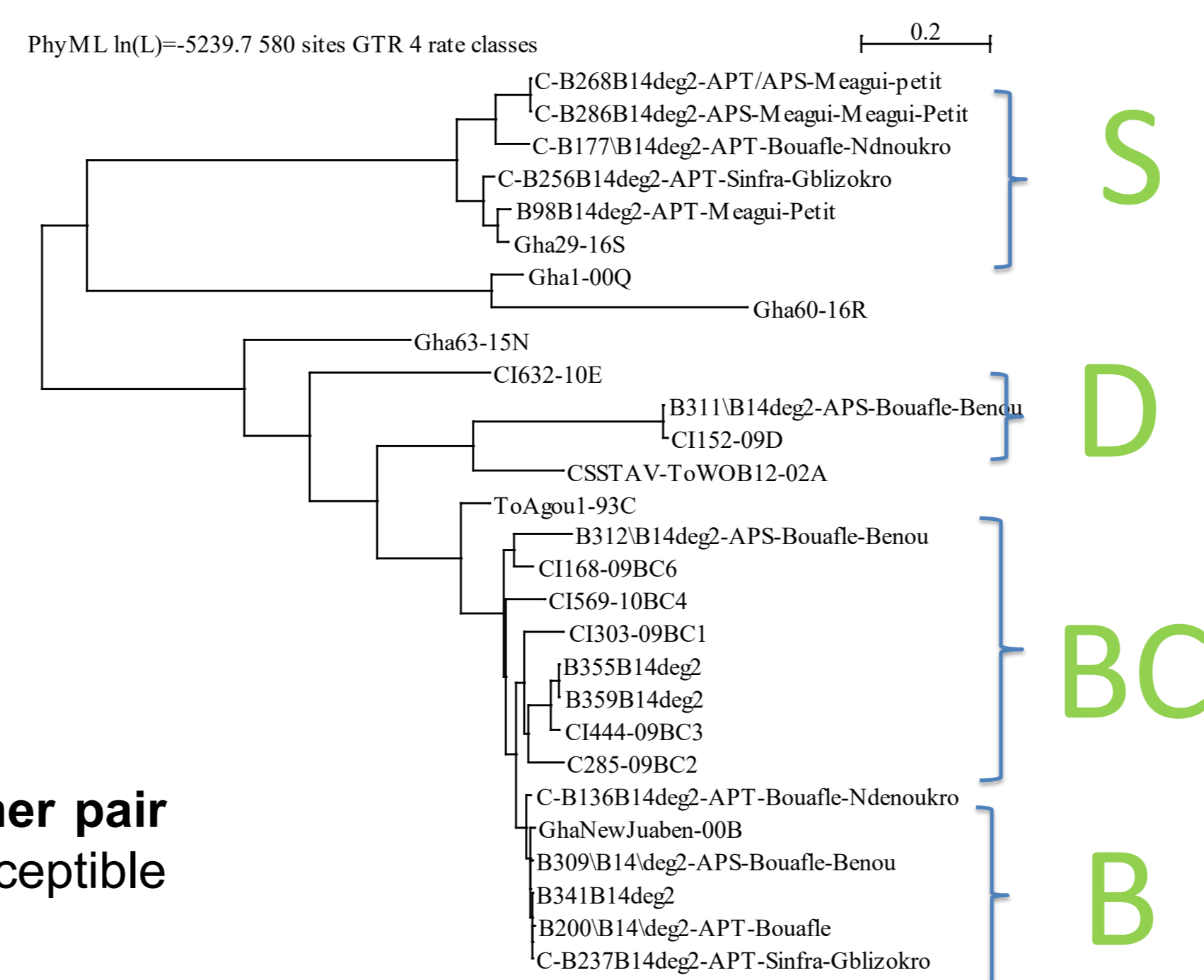


Fig 3: Dendrogram (PhyML) showing genetic diversity of CSSV (Primer pair Badna ¼ CSSV Deg2) from potentially CSSVD tolerant and susceptible accessions in Côte d'Ivoire

- **Primers Badna ¼ CSSV Deg 2:** groups D, B and a new group S (integrated sequence in the genome).

- **Group D:** species CSSCDV,
- **Group B and B-C:** species CSSTBV

Conclusion: Two species have been obtained (CSSCDV & CSSTBV). The group S is sequence integrated in the cocoa genome. These results confirm those (Muller, 2021).

Perspectives: Set up multi-local trials in areas infected with cssv in order to confirm the performance of tolerant cocoa trees



Fig 1. Symptoms of CSSVD in field (A) and greenhouse (B)

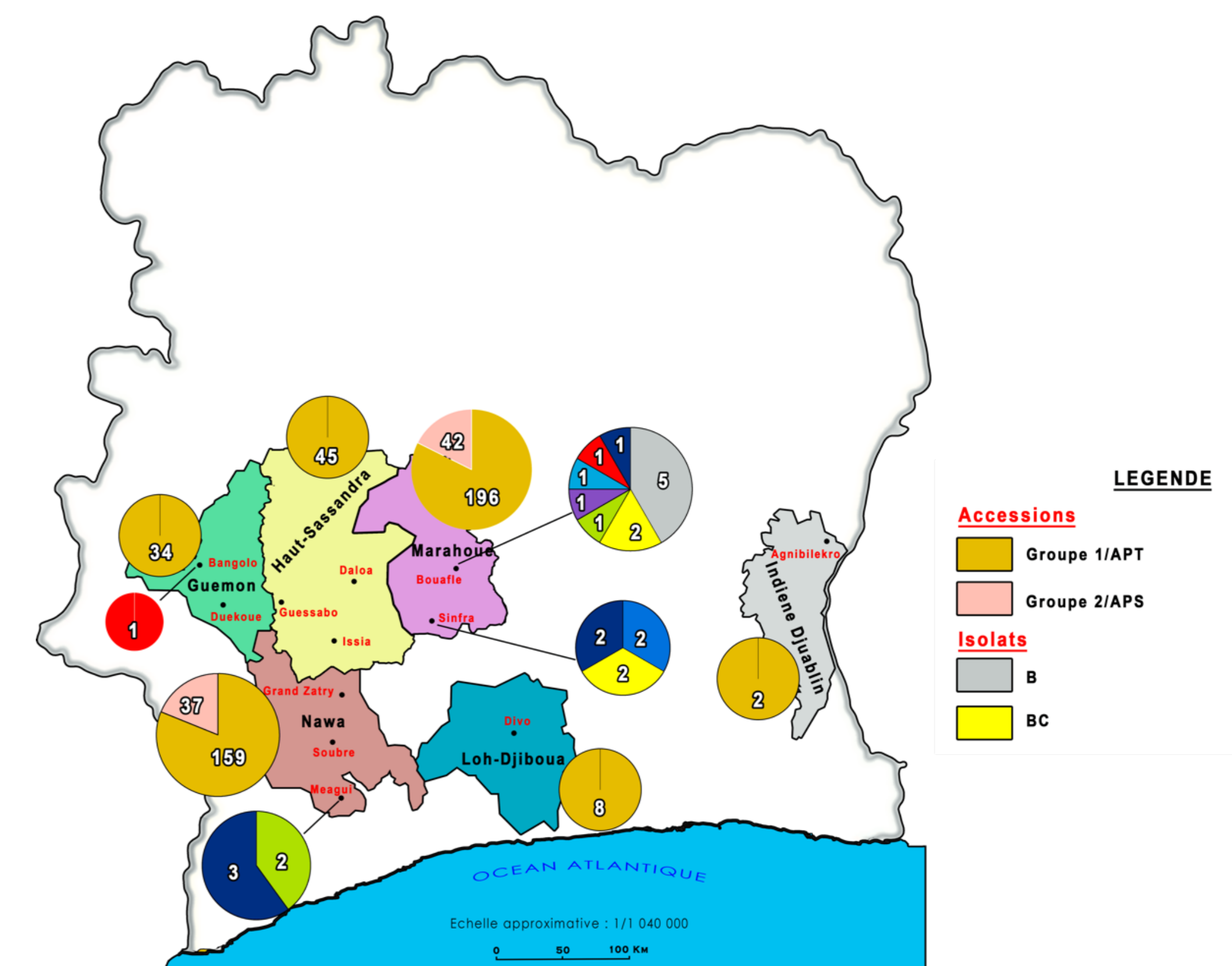


Fig 4: Geographical distribution of isolates identified within potentially CSSV tolerant and susceptible accessions

- Marahoué –(Sinfra et Bouaflé): **B et S**
- Nawa (Soubré Grand Zatry Meagui): **S et BC**
- Guemon (Bangolo, Duekoué): **D**