

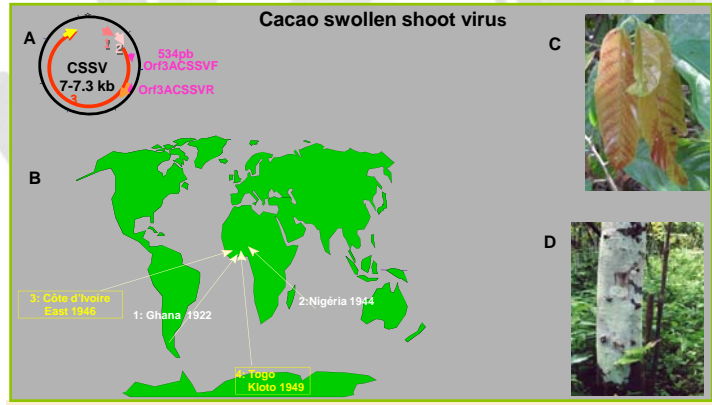
# Origin of the emergence of badnaviruses such as *Cacao swollen shoot virus (CSSV)* and *Banana streak virus (BSV)*

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*Cacao swollen shoot virus (CSSV)* and *Banana streak virus (BSV)* are two members of the family *Caulimoviridae*, genus *Badnavirus*. CSSV and BSV are naturally transmitted to their respective hosts, cacao (*Theobroma cacao*) and banana (*Musa* sp.), in a semi-persistent manner by several mealybug species.

**Cacao swollen shoot disease (CSSD)** occurs in all the main cacao growing areas of West Africa where it has caused enormous economic damage. Despite numerous "cutting out" campaigns specially in Ghana, the virus is still a serious constraints to cocoa production in West Africa and renewed outbreaks of CSSD caused problems in Ghana, Togo and Côte d'Ivoire. As this disease only exists in Africa and appeared soon after the introduction of cacao from America to West Africa, it is likely that CSSV came by host shift from indigenous hosts

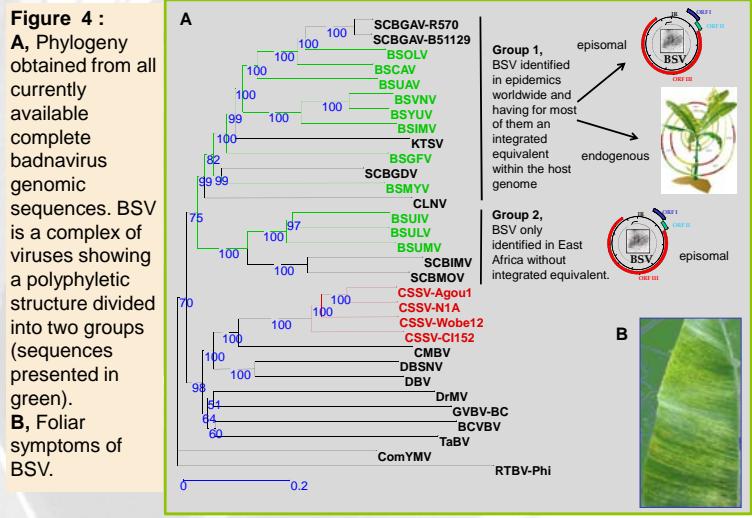
**Banana streak virus** recently became emergent in East Africa. The biodiversity of BSV higher than for the other badnaviruses is the consequence of two phenomena: the epidemic process of the disease - contamination of plant to plant by vector- and the release of infectious viral genomes by the banana genome harboring endogenous sequences.



**Figure 1:** A, CSSV genome showing the 5 ORFs and the position of the primers used for variability studies. B, History of the appearance of the disease in West Africa. C et D, Characteristic symptoms of the disease, red vein banding of the young leaves et swellings on stems or chupons.

## Do the primary and recent CSSV outbreaks have the same origin: host shift versus contamination by pods bearing infected mealybugs?

Analysis of CSSV populations is based on sequence comparisons of the first part of ORF3 (Figure 1A). Their spatial repartition in Togo and Côte d'Ivoire are presented in Figure 2 and 3.

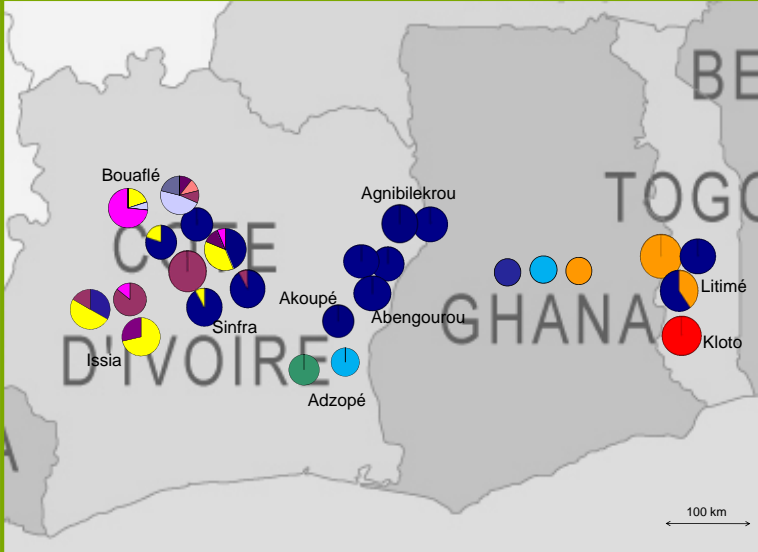
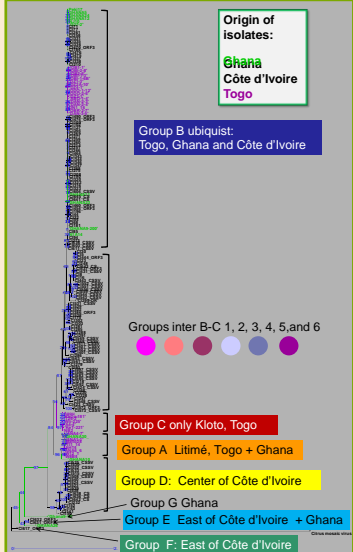


**Figure 4:** A, Phylogeny obtained from all currently available complete badnavirus genomic sequences. BSV is a complex of viruses showing a polyphyletic structure divided into two groups (sequences presented in green). B, Foliar symptoms of BSV.

## Could the second group of BSV originate from integrated equivalent within alternative host genome?

*Work in progress*

**Figure 2:** maximum likelihood phylogeny constructed with PhyML (after alignment of 534pb of the first part of ORF3). Using the 80% nucleotide identity threshold in the RT/RNase H domain for discriminating badnavirus species, groups B-C, A, D, F, G, and E correspond to different CSSV species. *Citrus mosaic virus* is used as outgroup



**Figure 3:** Geographic repartition of CSSV groups in different foci in West Africa (Togo, Côte d'Ivoire). In Ghana, only few isolates were studied.

We cannot answer the question on the basis of these results.  
 - The hypothesis that each homogeneous diversity group could originate from a different original host species should be tested.  
 - We now need to study additional isolates from Ghana, the first country where CSSV was reported, to have a more complete idea of the geographical repartition of CSSV populations.

