

# Spatial scales of genetic structuring in *Bactrocera cucurbitae* (Diptera, Tephritidae): population structure on La Réunion

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## ***Bactrocera cucurbitae* : the Melon fruit fly**

❖ Origin: Asia

❖ First records:

- in Africa: Tanzania (1936)

(<http://data.gbif.org/occurrences/>)

- though not reported in West Africa before 1999 (Vayssieres et al. 2008), it is currently abundant in this region (<http://www.africamuseum.be/fruitfly/AfroAsia.htm>).

- in La Réunion: 1972 (Etienne)



**Up to 90 % losses**



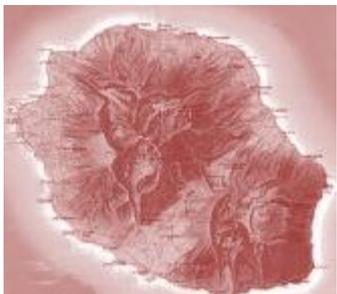
## 3 datasets were analyzed with 2 types of markers:



- **25 worldwide-distributed populations (n=570)** genotyped at 13 microsatellite loci among which, several samples sequenced at 2 mitochondrial gene fragments (COI, ND6) (Virgilio et al., 2010)



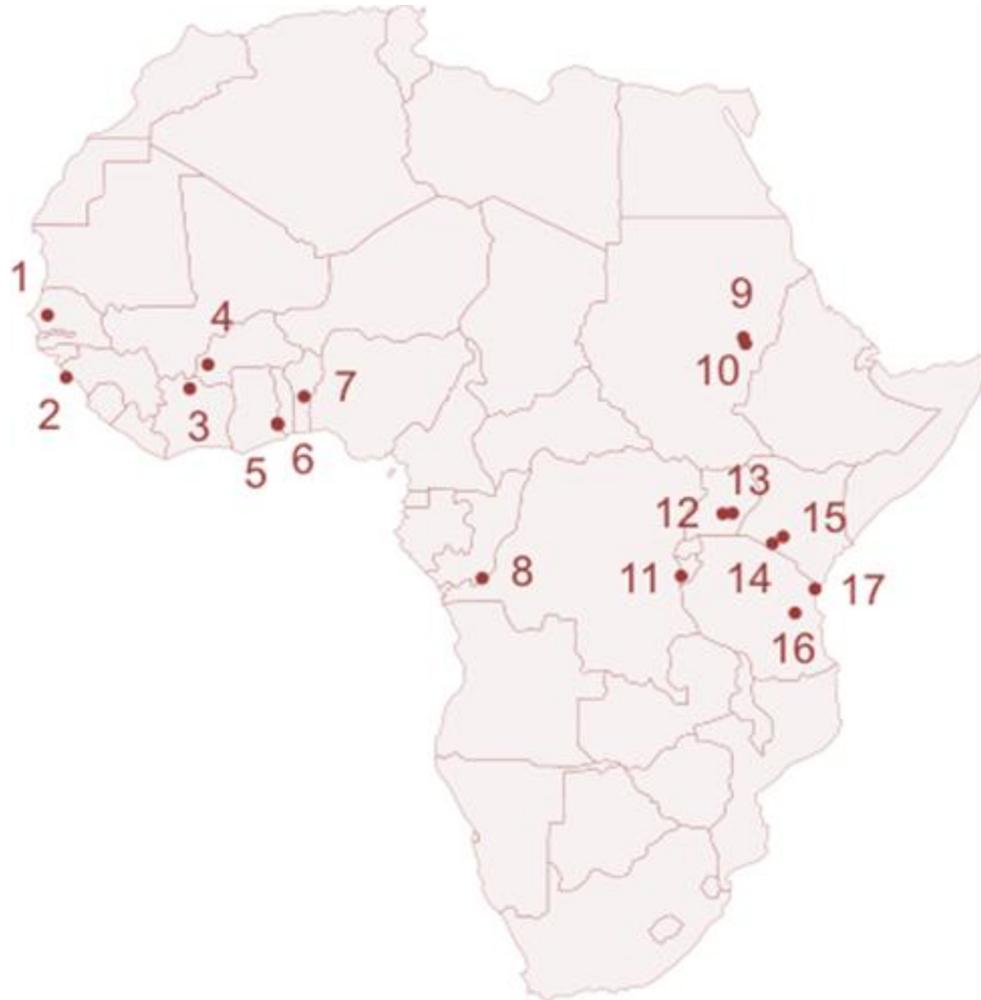
- **17 populations from East, West and Central Africa** genotyped at 19 microsatellite loci and 3 mitochondrial gene fragments (COI, COII, ND6)



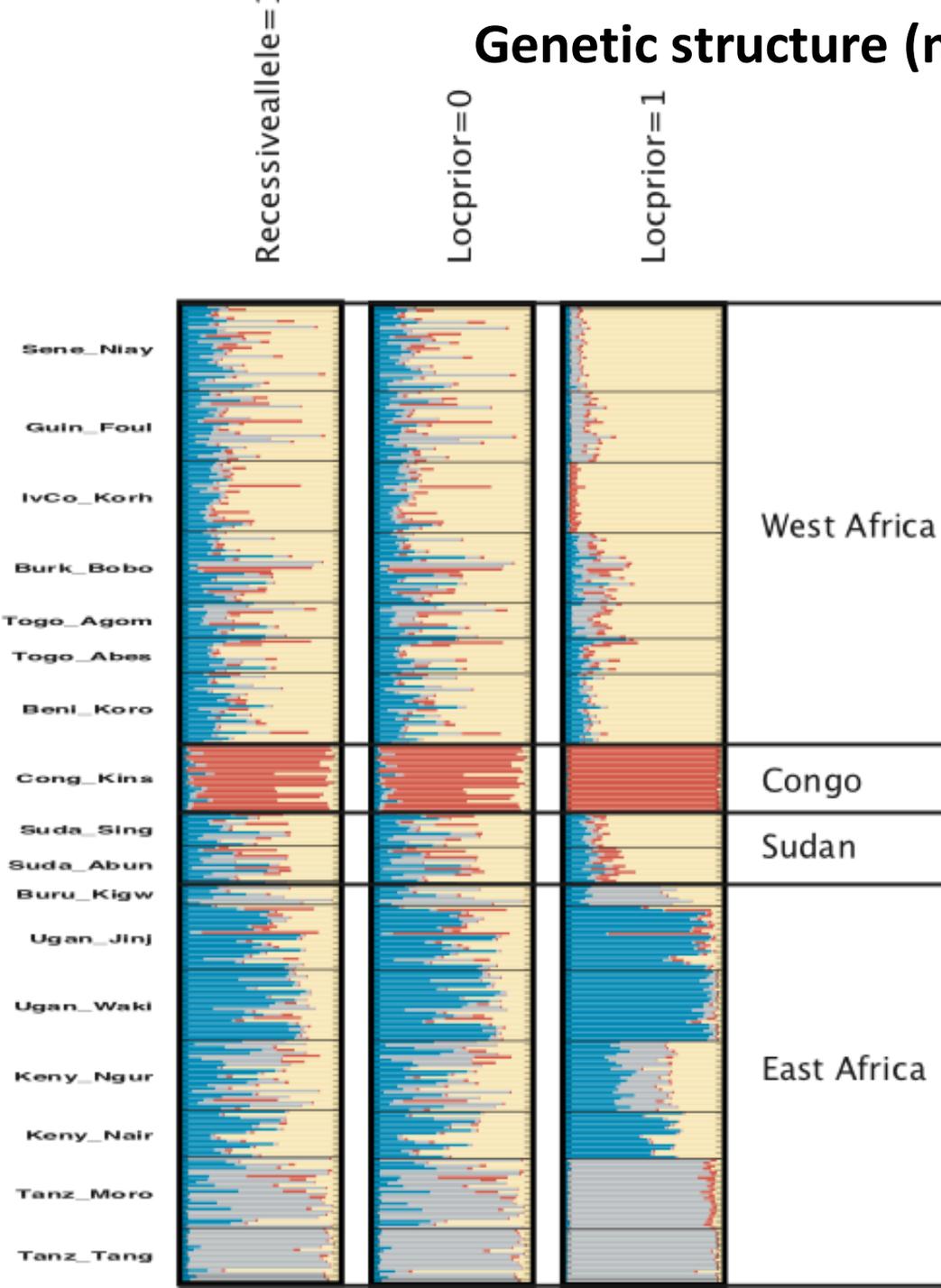
- **2258 specimens sampled in La Réunion** from different wild and cultivated host plants at three altitudinal ranges. Genotyped at 10 microsatellite loci and sequenced at 2 mitochondrial gene fragments (COI, ND6)
- **Global analysis including the 2 datasets : worldwide and Réunion**

## 17 populations from East, West and Central Africa

genotyped at 19 microsatellite loci and 3 mitochondrial gene fragments (COI, COII, ND6)



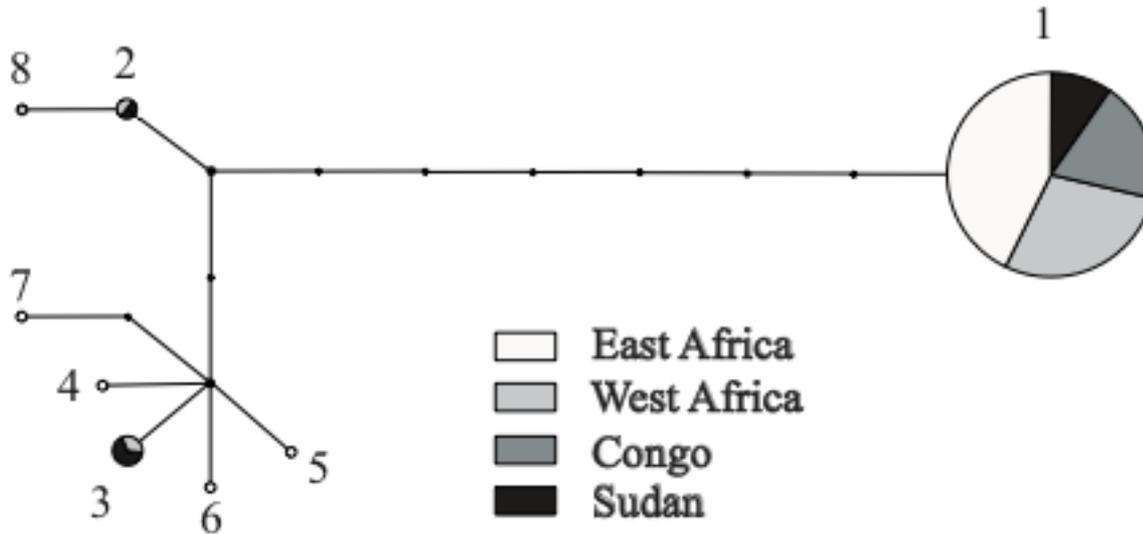
# Genetic structure (microsatellite)



**STRUCTURE → K=4 clusters**

--> **BOTTLENECK** analysis on microsatellite data did not provide indication of recent reductions or population expansions in Africa.

# Mitochondrial analysis



- Low diversity: 8 haplotypes with only 9 polymorphic sites

→ no distinct phylogeographic pattern in the African distribution of *B. cucurbitae*

Minimum Spanning Network 31 specimens of *B. cucurbitae* from 4 African regions (East Africa, West Africa, Congo, Sudan (2026 bp (concatenated COI+COII+ND6))

# Conclusion for African populations (1)

- In Africa *B. cucurbitae* populations are structured **into 4 clusters**

-The analysis of mitochondrial haplotypes suggests that the initial colonization and subsequent demographic expansion of *B. cucurbitae* in Africa originated from a **limited number of introduction events.**

## Conclusion for African populations (2)

-> Overall, genetic data do not suggest a very recent African expansion of *B. cucurbitae* (viz. after 1999 in West Africa) as populations had the time to:

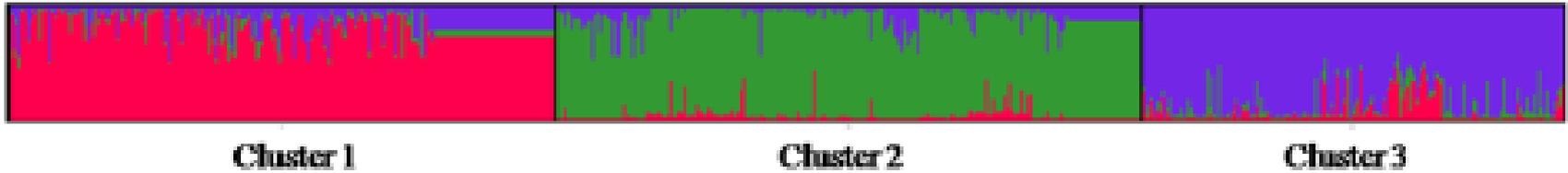
- a) become genetically divergent from the possible world-wide distributed sources and
- b) produce intracontinental genetic structuring not primarily related to genetic drift following population bottlenecks and expansions.

These data suggest that the presence of *B. cucurbitae* in Africa is older than expected or reported (lack of historical records before 1936 in East Africa and 1999 in West Africa might be related to the scarcity of sampling campaigns and to the patchy distribution of this species)

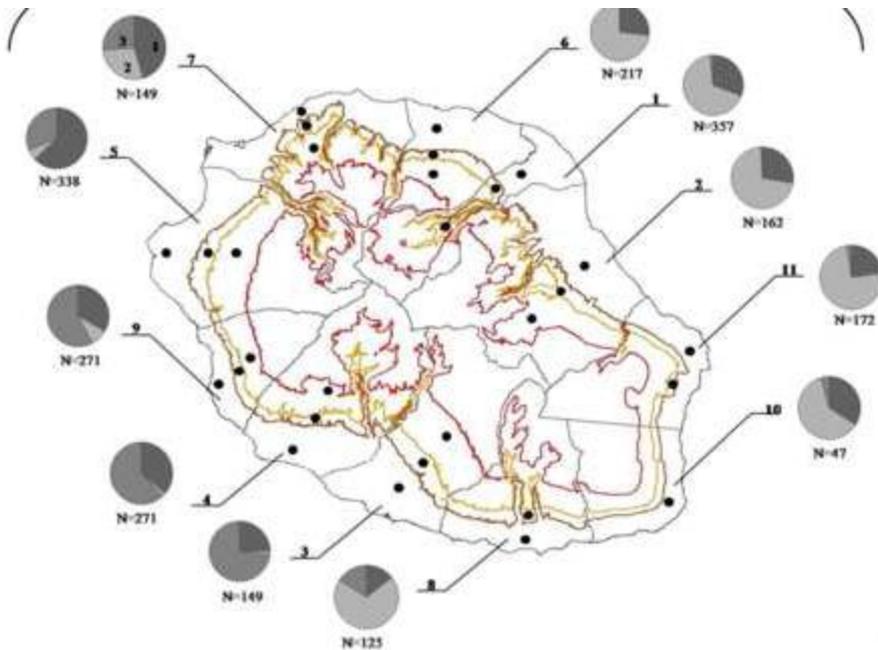
**2258 specimens sampled in La Réunion** from different wild and cultivated host plants and at three altitudinal ranges, genotyped at 10 microsatellite loci



# Genetic structure (microsatellite)



- 3 well differentiated **clusters** of *B. cucurbitae* on La Réunion
- BOTTLENECK analysis did not provide indication of recent reductions or population expansions in the island



→ Structure linked to climatic (rainfall) and topological (zone) factors, with cluster 1 more plastic than the others (present in all sites)

→ But **NOT** linked to the nature of host plant (cultivated / wild)

# Conclusion for La Réunion populations

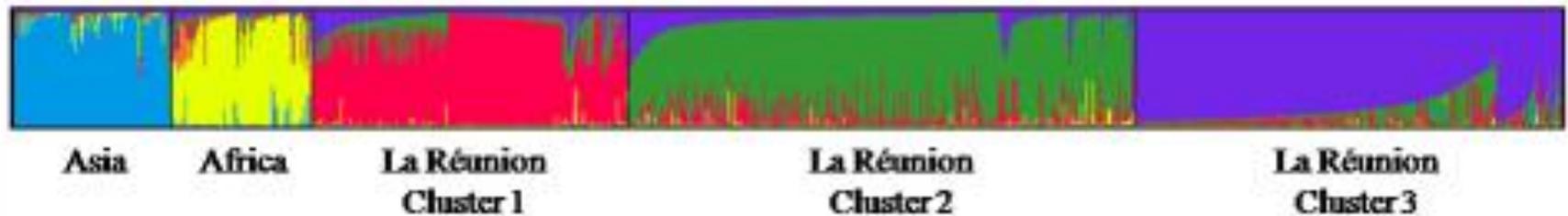
- In La Réunion, *B. cucurbitae* populations are structured **into 3 clusters**
- The distribution of the 3 clusters is only affected by rainfall and site

# Origin of the 3 populations found in La Réunion?

Global analysis including the worldwide and La Réunion datasets (microsatellite and mitochondrial markers)

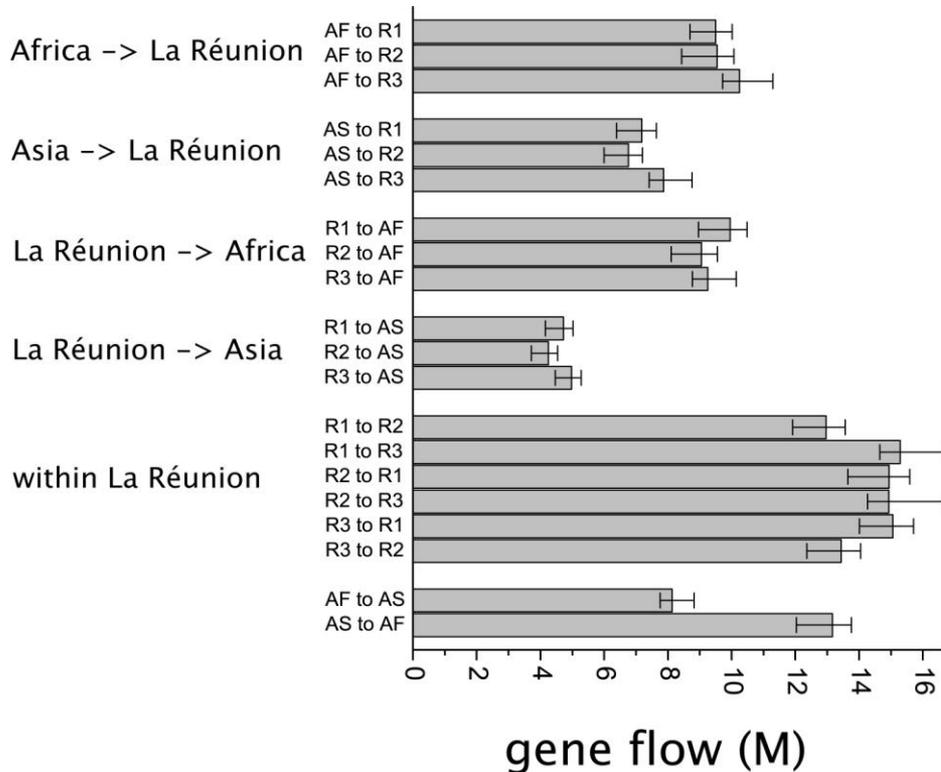


# Genetic structure (microsatellite)



- 3 clusters from La Réunion are again found in a global STRUCTURE analysis

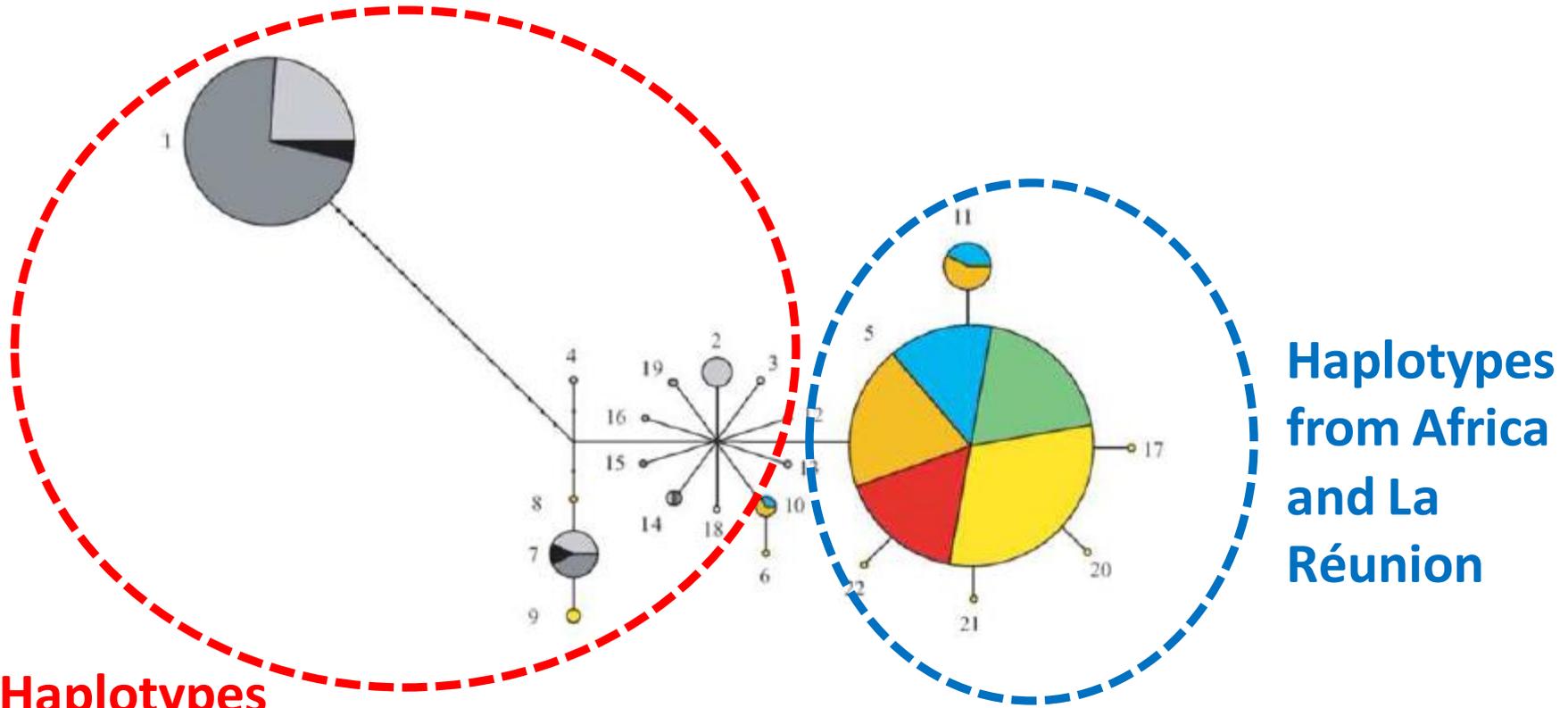
# Gene flow and origin of populations (microsatellite data)



- Migration rates among the sympatric clusters of La Réunion were always higher than migration rates between La Réunion and other parts of the world

- Estimates of gene flow from Africa to La Réunion and from La Réunion to Africa are comparable. They are consistently higher than between Asia and La Réunion.

# Mitochondrial analysis



**Haplotypes  
from Asia  
and Hawaii**

**Haplotypes  
from Africa  
and La  
Réunion**

→ 2 main groups of *B. cucurbitae*

Minimum Spanning network for 100 specimens of *B. cucurbitae* from East (yellow) and West Africa (orange), Congo (red), Sudan (blue), East (medium gray) and Central Asia (light gray), Hawaii (black) and La Réunion (green)

# Conclusion (1)

- The 3 clusters previously found in the study of La Réunion populations were again found in the global analysis
- Gene flow between La Réunion clusters and Africa was higher than between La Réunion and Asia
- Nevertheless with higher gene flow between La Réunion clusters → indicating no complete reproductive isolation on this island

# Conclusion (2)

These data are congruent with **two different scenarios:**

- 1: ancestral Asiatic origin of *B. cucurbitae* in La Réunion and secondary contact with populations from the African continent
- 2: **African origin of *B. cucurbitae* in La Réunion**

The second scenario is more in agreement with the results of the mitochondrial DNA where 2 different groups of haplotypes are found worldwide, one African (including also samples from the 3 clusters of La Réunion) and one Asian with Hawaii populations.

Overall, these data show increasing gene flow at smaller spatial scales and **do not provide evidence of appreciable cryptic speciation within *B. cucurbitae* worldwide.**

# References

Worldwide dataset:

**Virgilio et al., 2010, Molecular Ecology**

La Réunion dataset + origin of populations using the worldwide dataset:

**Jacquard et al., 2012, Biological invasion (Under revision)**

African dataset:

**Virgilio et al. (in preparation)**

**Thanks for your attention**