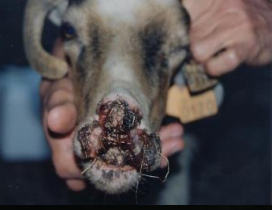
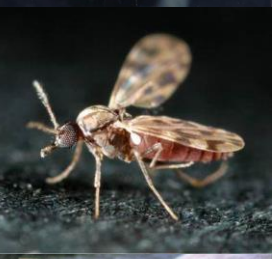
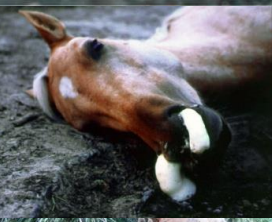






Is *Culicoides imicola* (Diptera: Ceratopogonidae) a recent invasive species in the Mediterranean basin?

Stéphanie Jacquet, Karine Huber, Jérémy Bouyer, Christine Chevillon, Thomas Balenghien, Claire Garros

Funded by
Cirad and CHERCHAV Convention

19th E-SOVE Conference 2014
13th-17th October 2014 Thessaloniki-Greece

UNIVERSITÉ MONTPELLIER 2 SCIENCES ET TECHNIQUES

INRA SCIENCE & IMPACT

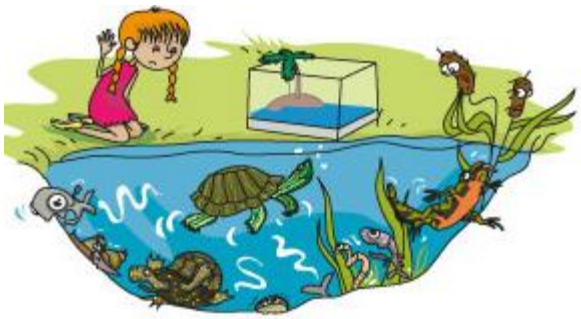
cnrs

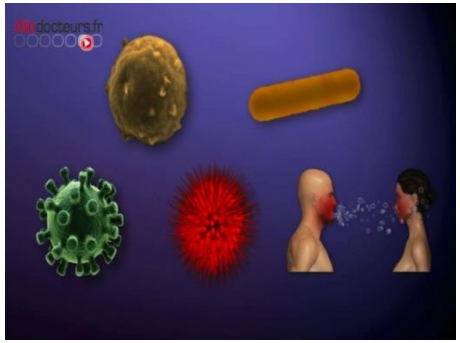
cirad

Biological invasions

❖ Their consequences

- Ecosystem modification and/or deterioration
- Detrimental effects on agriculture
- Impacts on health





❖ The causes

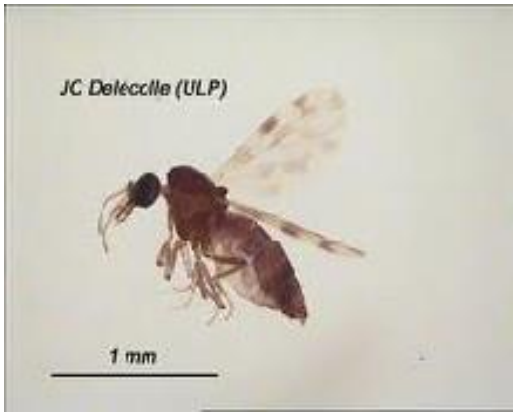
- Phenotypic traits, evolutionary change
- Migration
- Environmental change

An example: *Culicoides imicola* and bluetongue virus

C. imicola, a vector species

Arthropoda: Diptera: Ceratopogonidae

- Small biting midge with passive dispersal through winds
- Vector of economically important viruses of livestock :
  - African horse sickness virus (AHSV)
  - Bluetongue virus (BTV)
  - Epizootic hemorrhagic disease virus (EHDV)



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- Small biting midge with passive dispersal through winds
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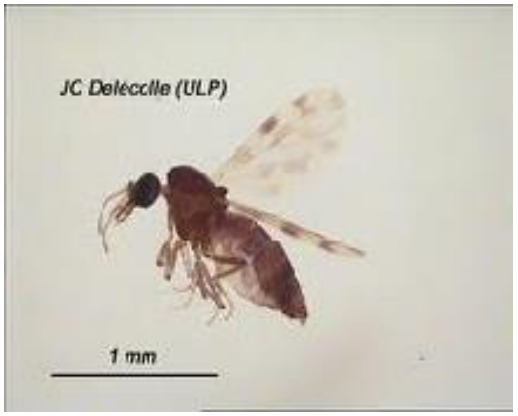
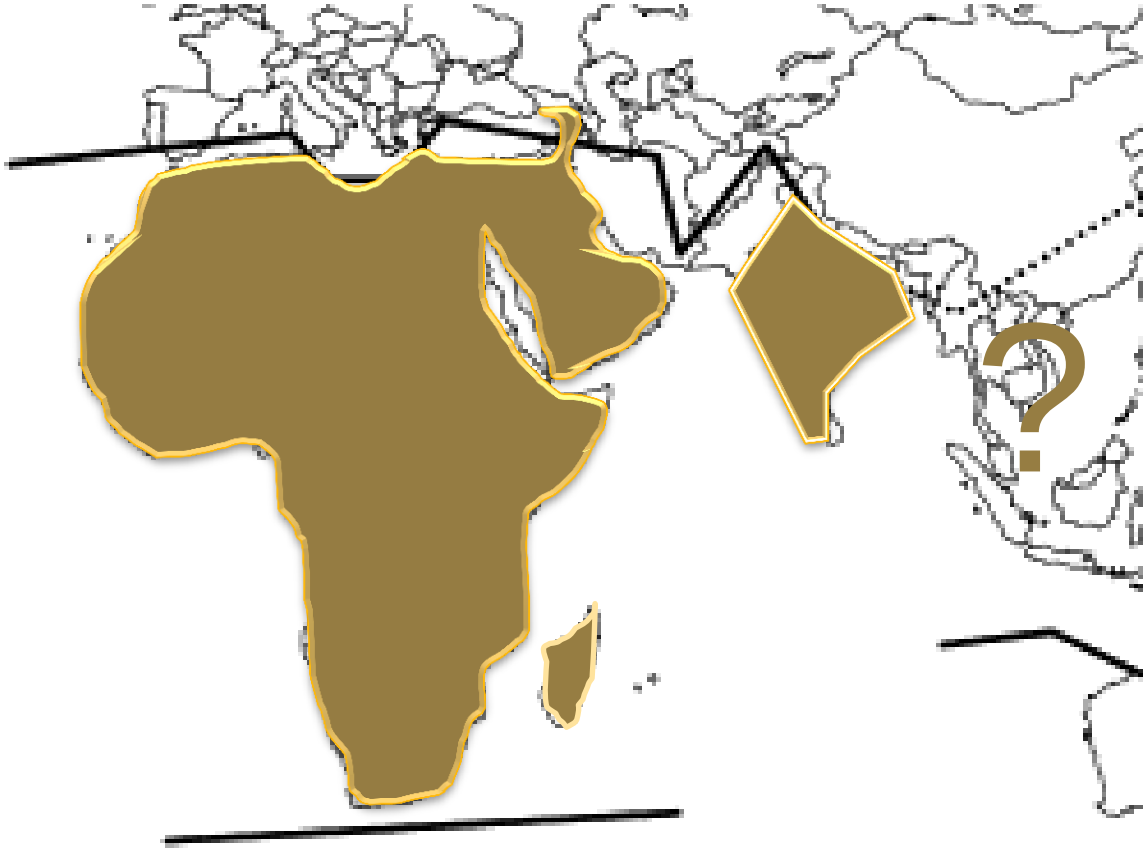


C. imicola and BTV distribution before 1998

- *C. imicola* limited to North Africa and Arabic peninsula
- BTV distributed in America, Asia, Australia and Africa

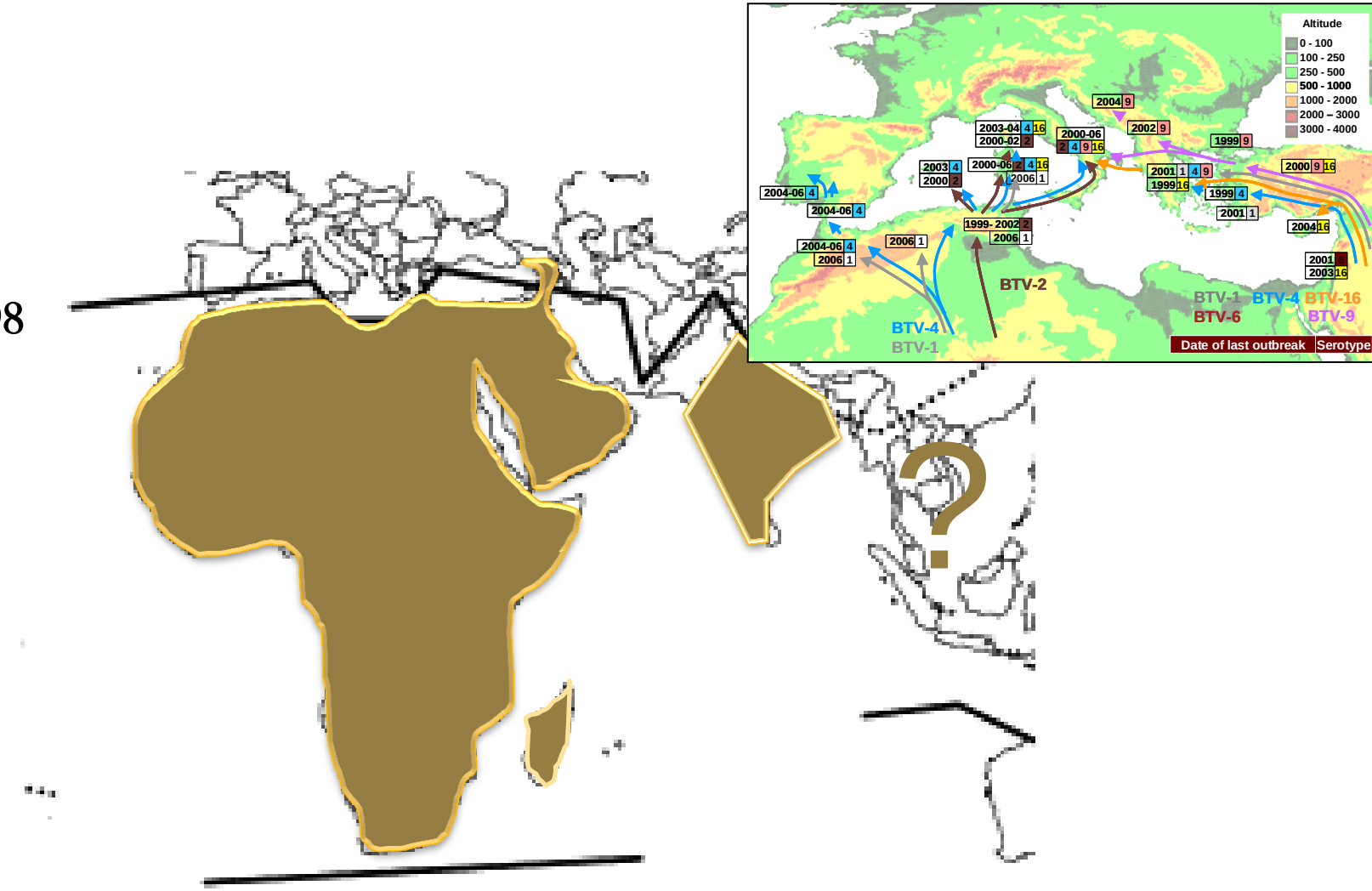
1998



C. imicola and BTV distribution since 1998

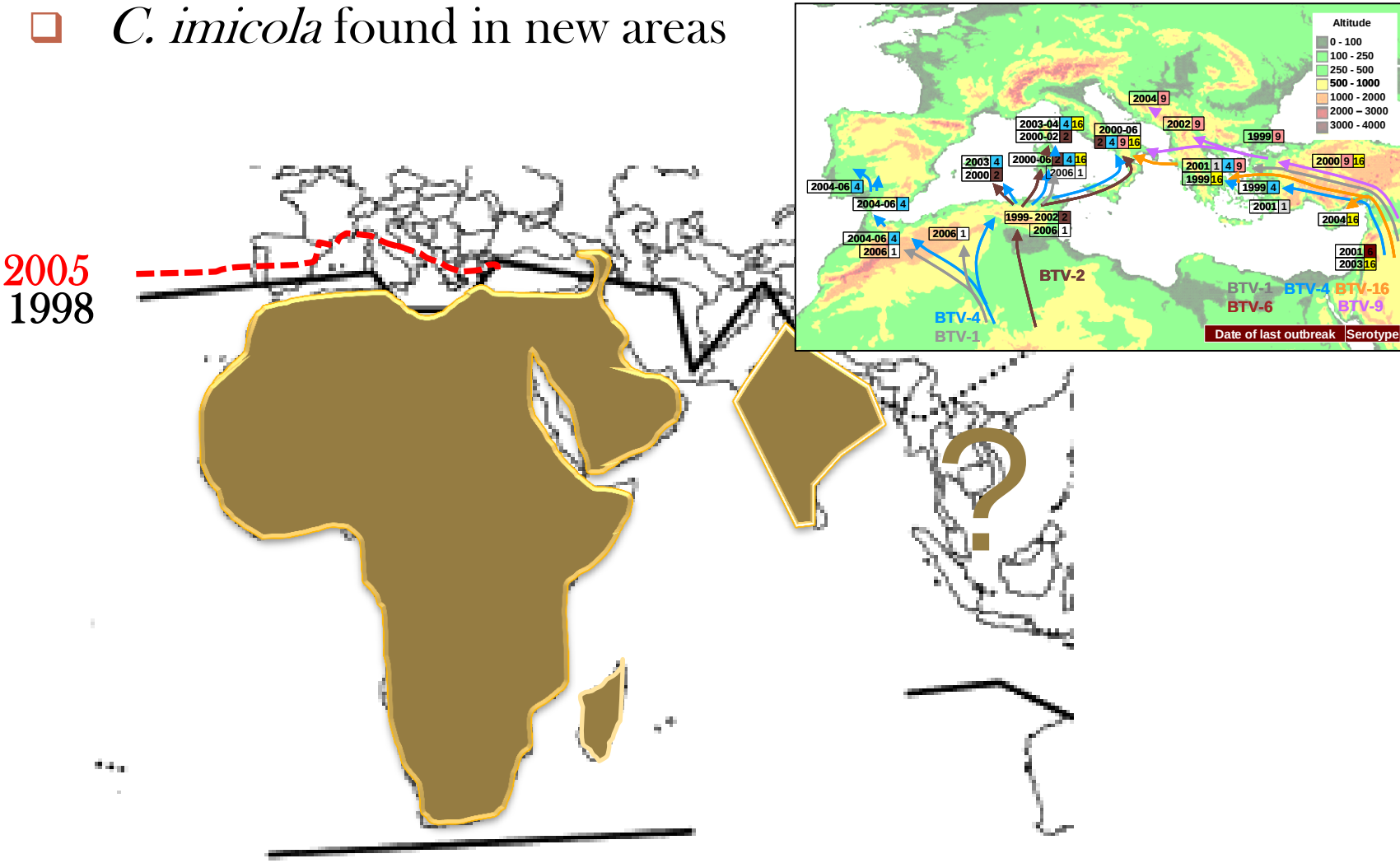
- In 1998, BT outbreaks in southern Europe

1998



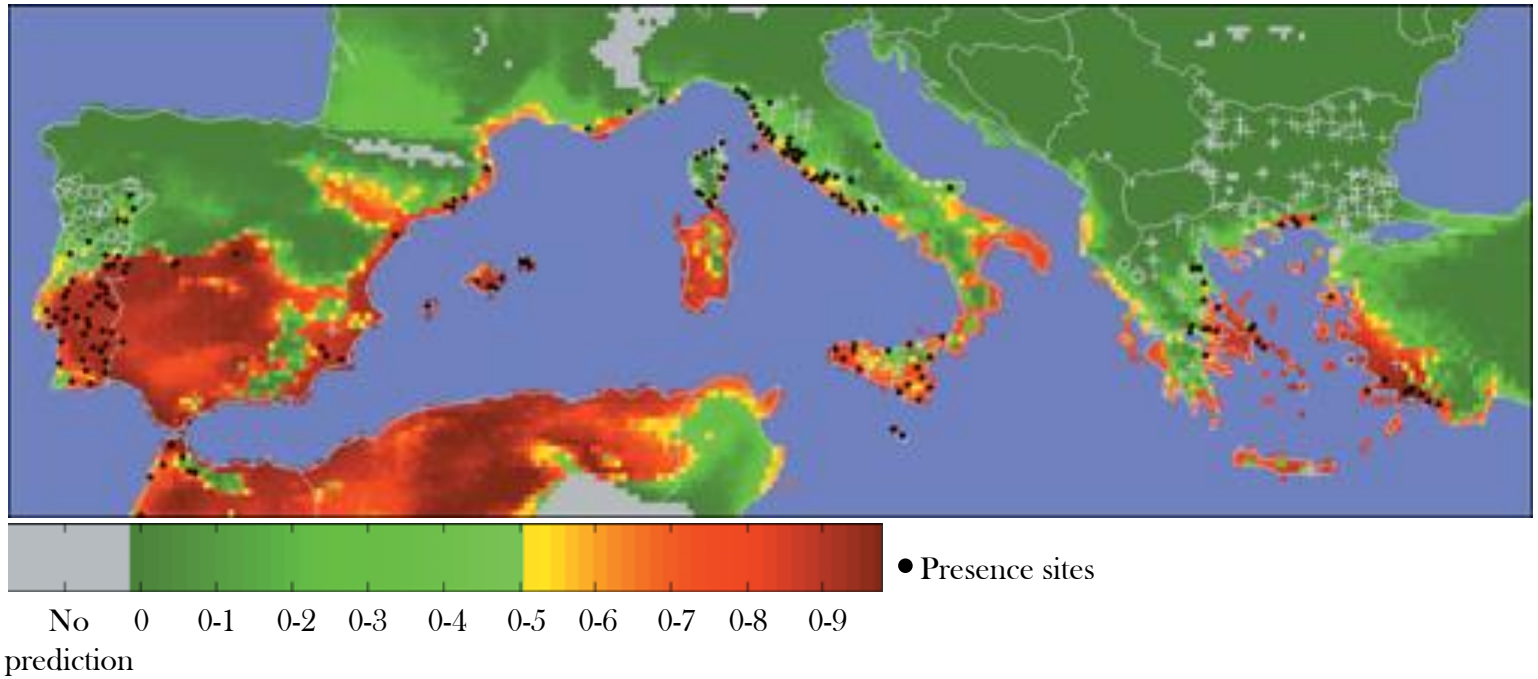
C. imicola and BTV distribution since 1998

- In 1998, BT outbreaks in southern Europe
- *C. imicola* found in new areas



An hypothesis: climate change

- Increase temperature have lead to *C. imicola* range expansion



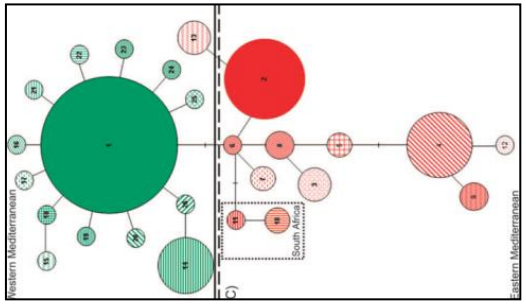
Predicted probability of the presence of *Culicoides imicola s.s*

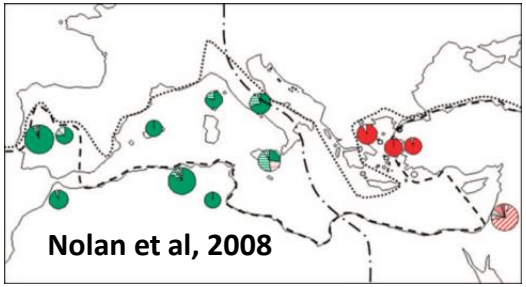
Purse et al.. 2007, Purse et al.,2005

Recent or ancient colonization ? knowledge from genetic data

Phylogeographic studies based on COI

- Recent colonization
- Two routes of colonization

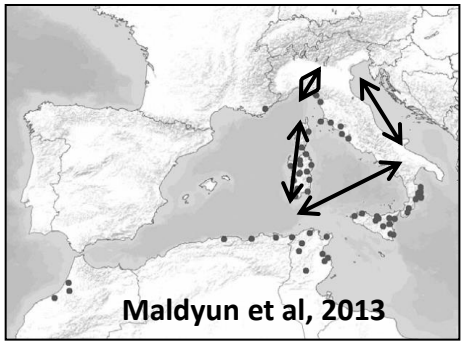




Population genetics study based on microsatellites

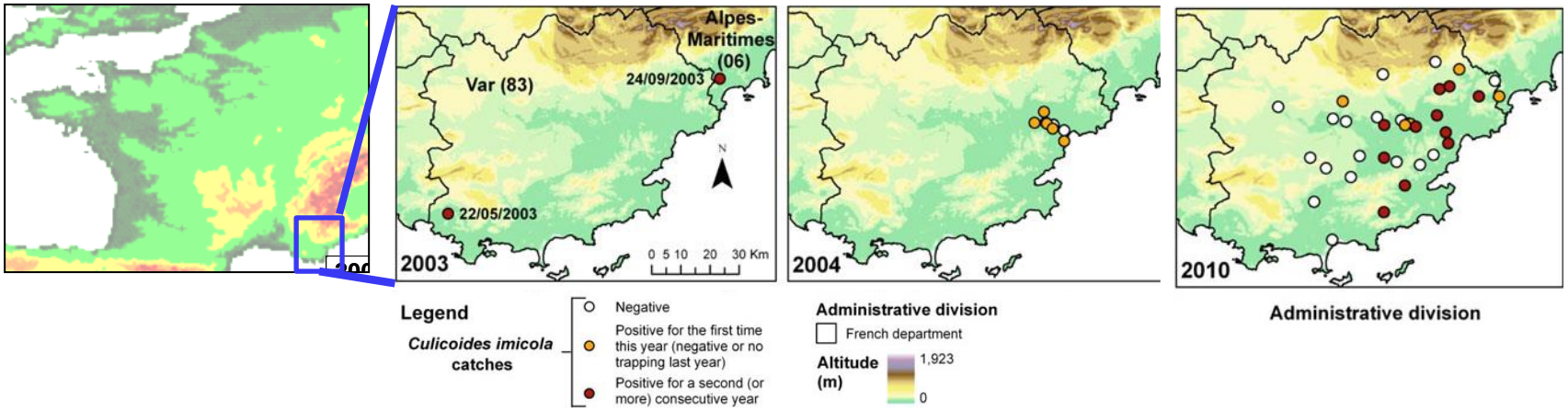
- Observed diversity and structure

suggest long time presence of *C. imicola*



Recent colonization *vs* entomological surveys bias ?

- Population expansion in Var department (France)



- Populations stable in space and time in Italy

Journal of Applied Ecology
British Ecological Society
Journal of Applied Ecology 2009, **46**, 1332–1339 doi: 10.1111/j.1365-2664.2009.01723.x

Eight years of entomological surveillance in Italy show no evidence of *Culicoides imicola* geographical range expansion

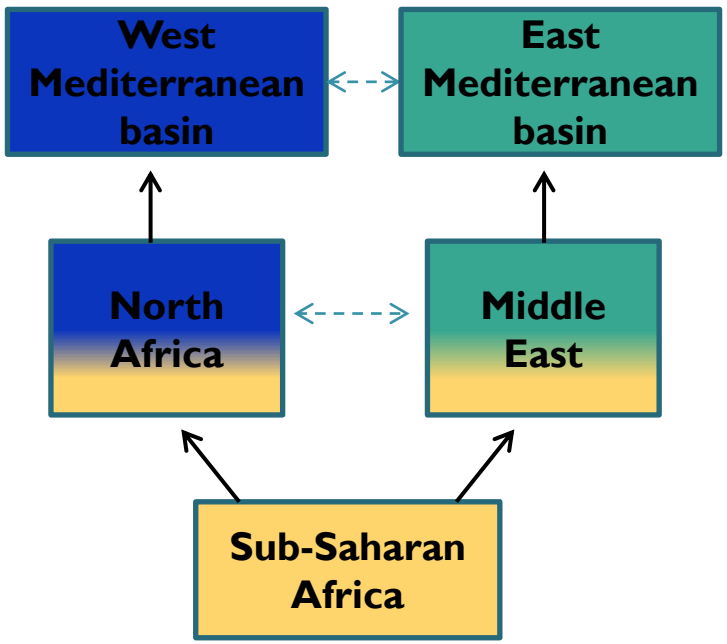
A. Conte[1,*], M. Gilbert[2,3] and M. Goffredo[1]

[1]*Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise 'G. Caporale', Via Campo Boario, 64100 Teramo, Italy;*
[2]*Biological control and Spatial ecology, Université Libre de Bruxelles, av FD Roosevelt 50, B-1050 Brussels; and*
[3]*Fonds National de la Recherche Scientifique, rue d'Egmont 5, B-1000 Brussels, Belgium*

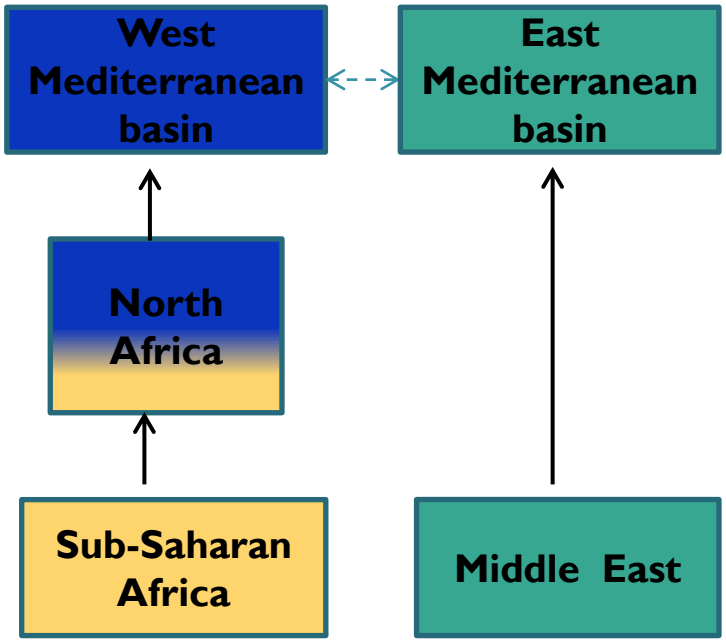
Venail et al.. 2012. Conte et al.. 2009

Aims and scenarios

- Determine if *C. imicola* is a recent invader
  - Spatial scenarios : origin ?
  - Temporal scenarios : recent vs ancient ?



Hypothesis (1):
One source = Sub-Saharan Africa



Hypothesis (2):
Two sources = Sub-Saharan Africa and Middle-East

Material

- 55 populations

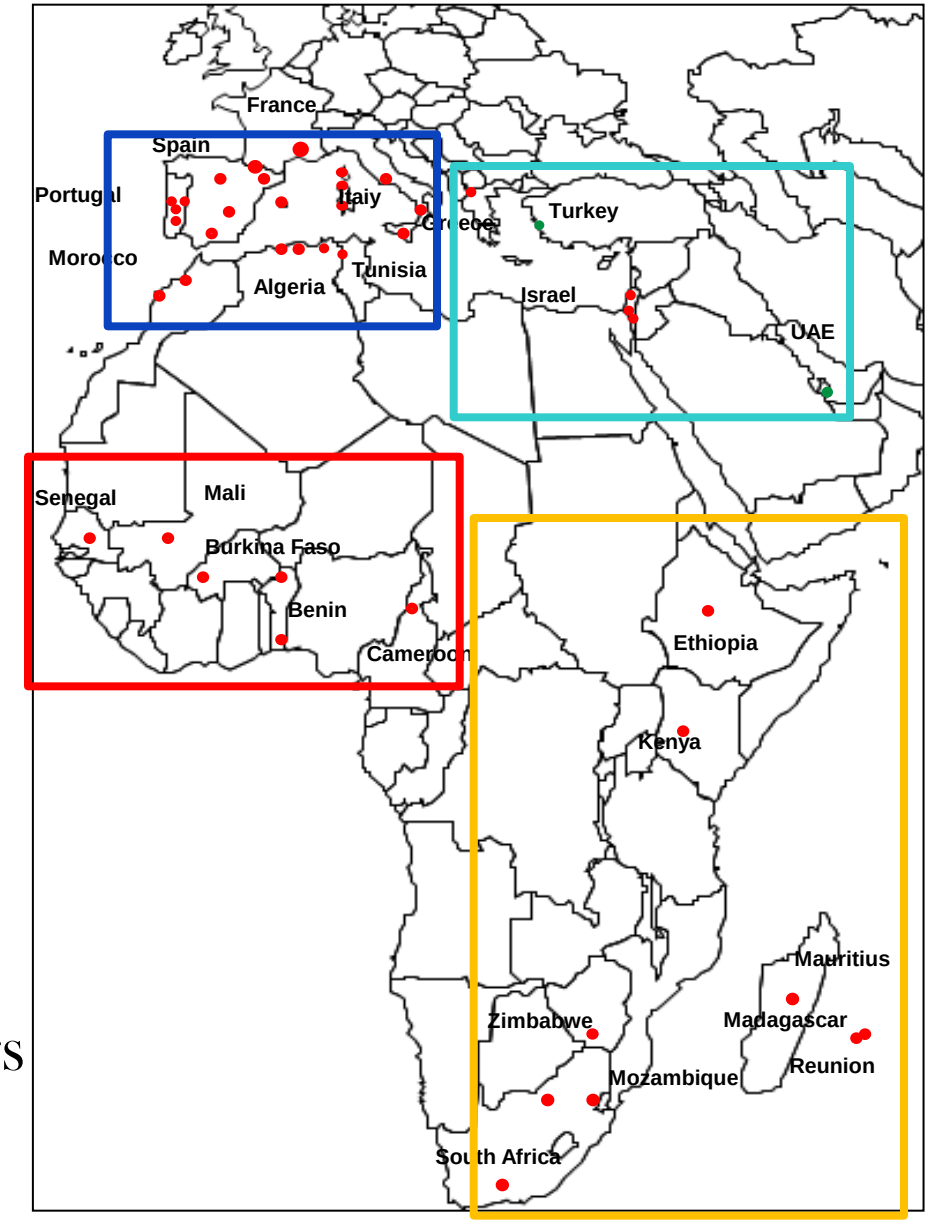
West Mediterranean basin (WMB)
East Mediterranean basin (EMB)
West Africa (WA)
South-East Africa (SEA)

- 2 mitochondrial and 1 nuclear genes

8 individuals/site
Cytochrome Oxidase subunit I (**COI**, 476bp) , Cytochrome B (**CytB**, 635bp), Elongation factor alpha (**Efα**, 556bp)

- 9 microsatellites markers

32 individuals/site

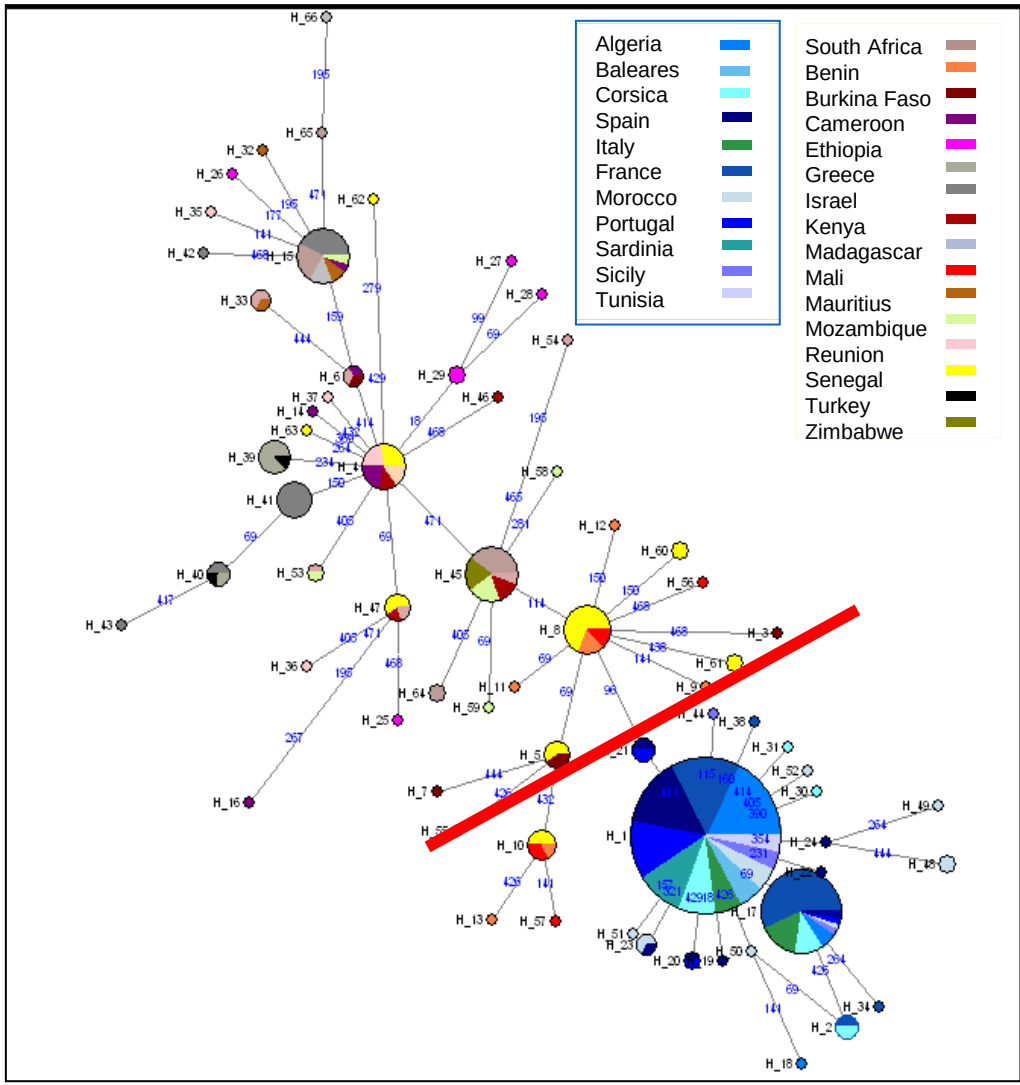


Methods

- Diversity index
- Genealogy relationships: haplotype network, phylogeny
- Demographic features: neutrality and mismatch test
- Populations structure: bayesian clustering analysis, genetic differenciation test (Fst)

Results : Population genetic relationships

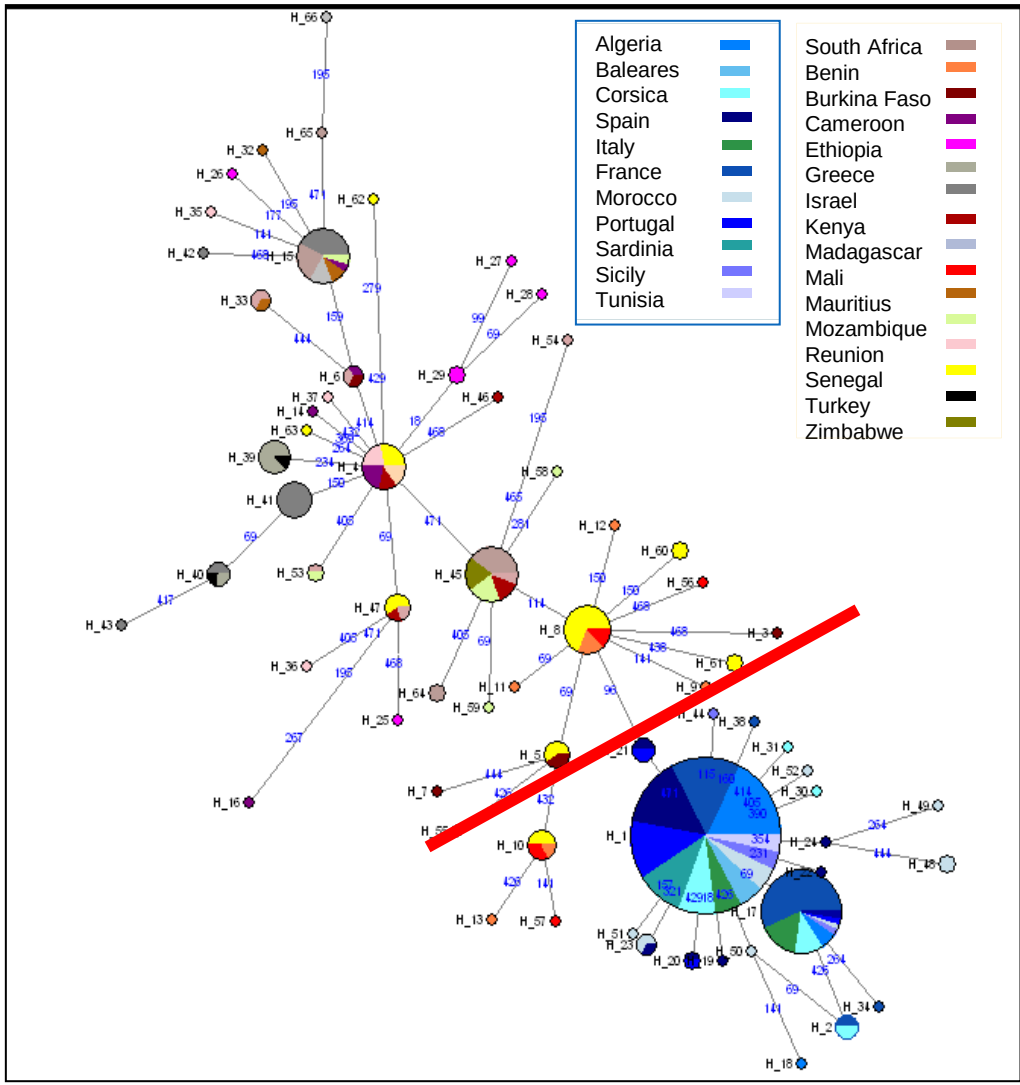
- Higher diversity in Sub-Saharan Africa => historical range



N J network COI polymorphism

Results : Population genetic relationships

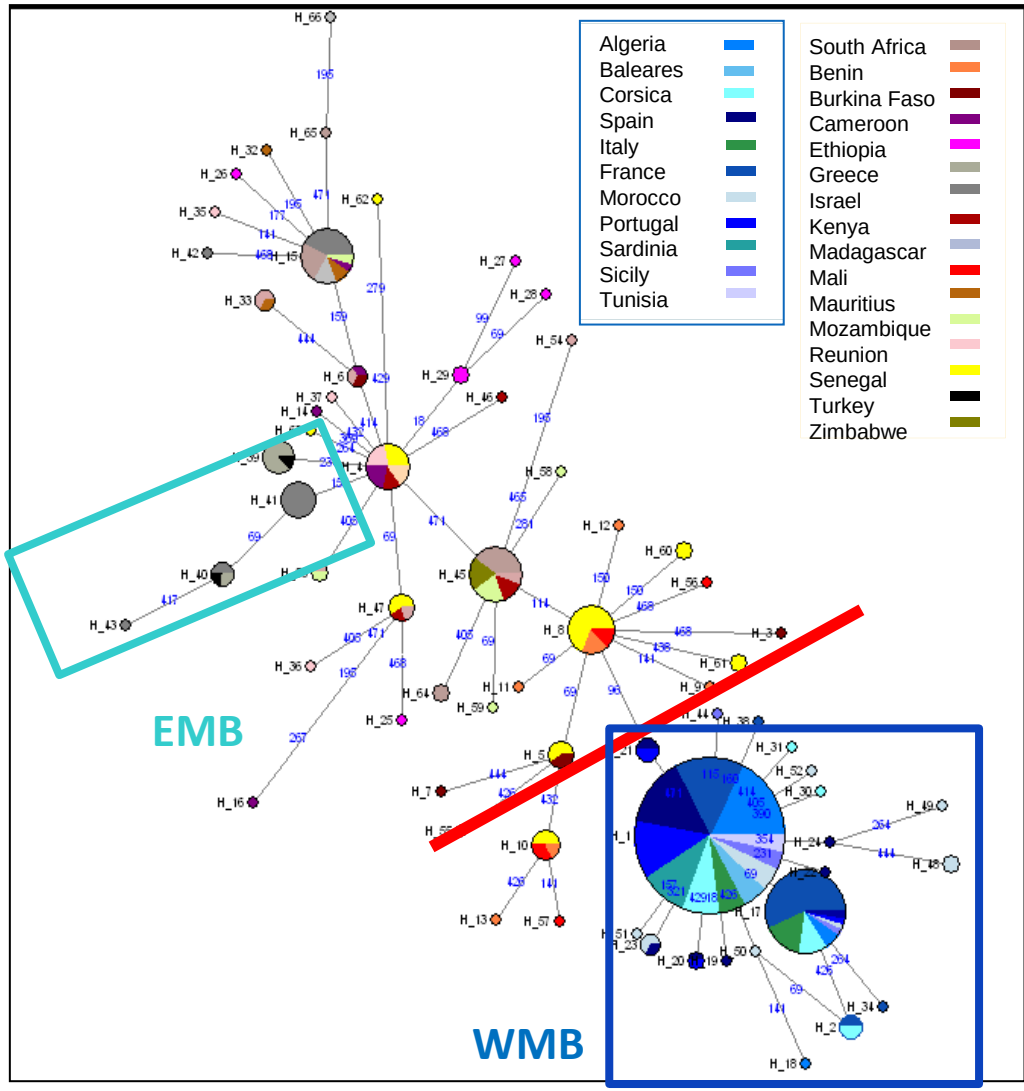
- Higher diversity in Sub-Saharan Africa => historical range
- Two genetic groups



N J network COI polymorphism

Results : Population genetic relationships

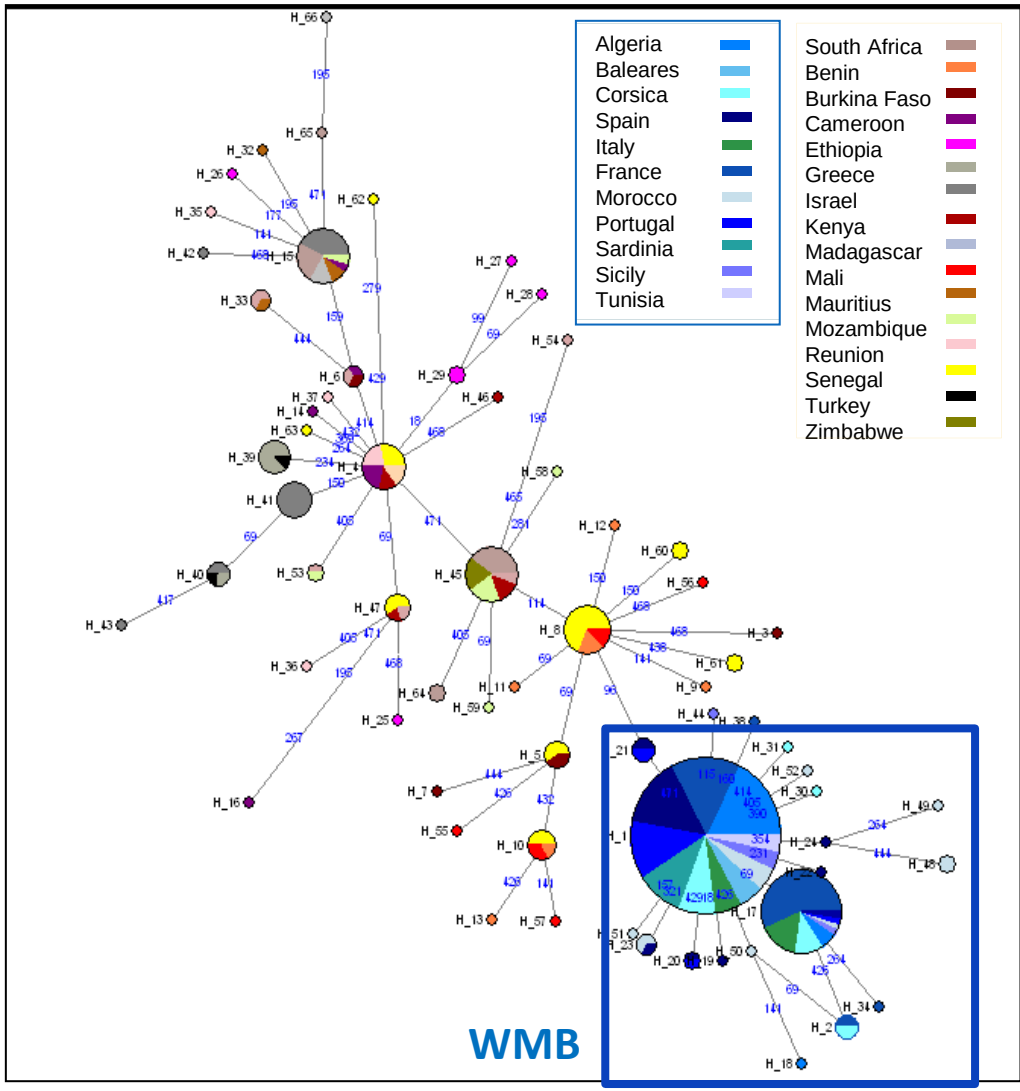
- Higher diversity in Sub-Saharan Africa => historical range
- Two genetic groups
- No shared haloptypes between WMB and EMB



N J network COI polymorphism

Results : Population genetic relationships

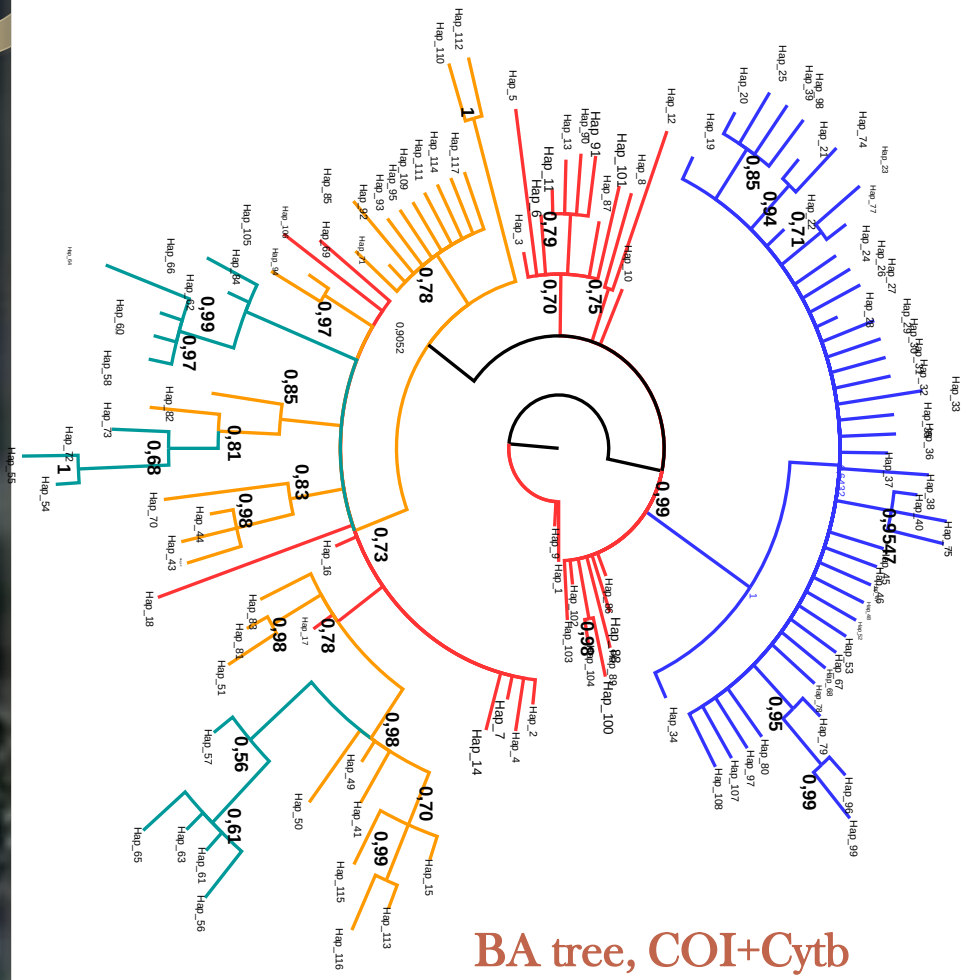
- Higher diversity in Sub-Saharan Africa => historical range
- Two genetic groups
- No shared haloptypes between WMB and EMB
- Star-like network in the WMB => recent demographic expansion?



N J network COI polymorphism

Results : Population genetic relationships

- WMB genetically closer to WA
- EMB genetically related to WA and SEA

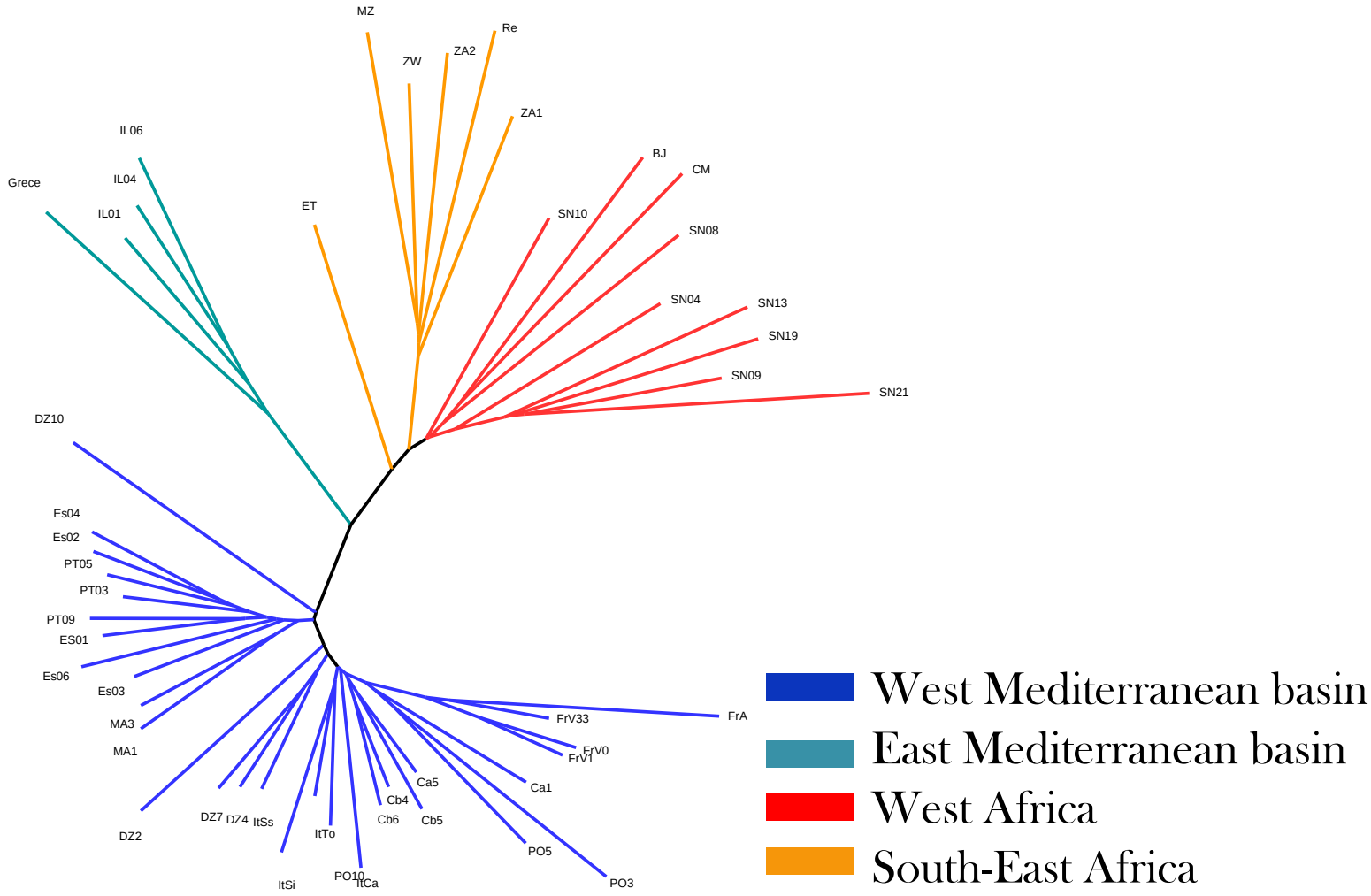


BA tree, COI+Cytb

- West Mediterranean basin
- East Mediterranean basin
- West Africa
- South-East Africa

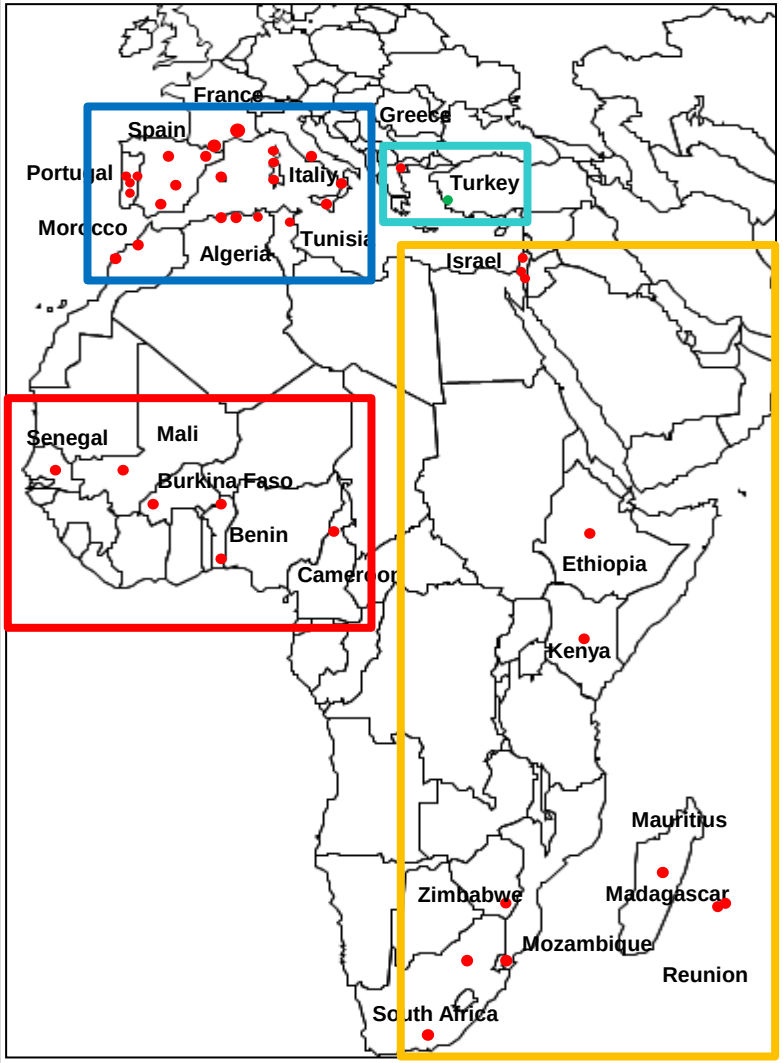
Results : Population genetic relationships

- Genetic differentiation in Sub-Saharan Africa



NJ based on microsatellite polymorphism

Results : Population genetic structure

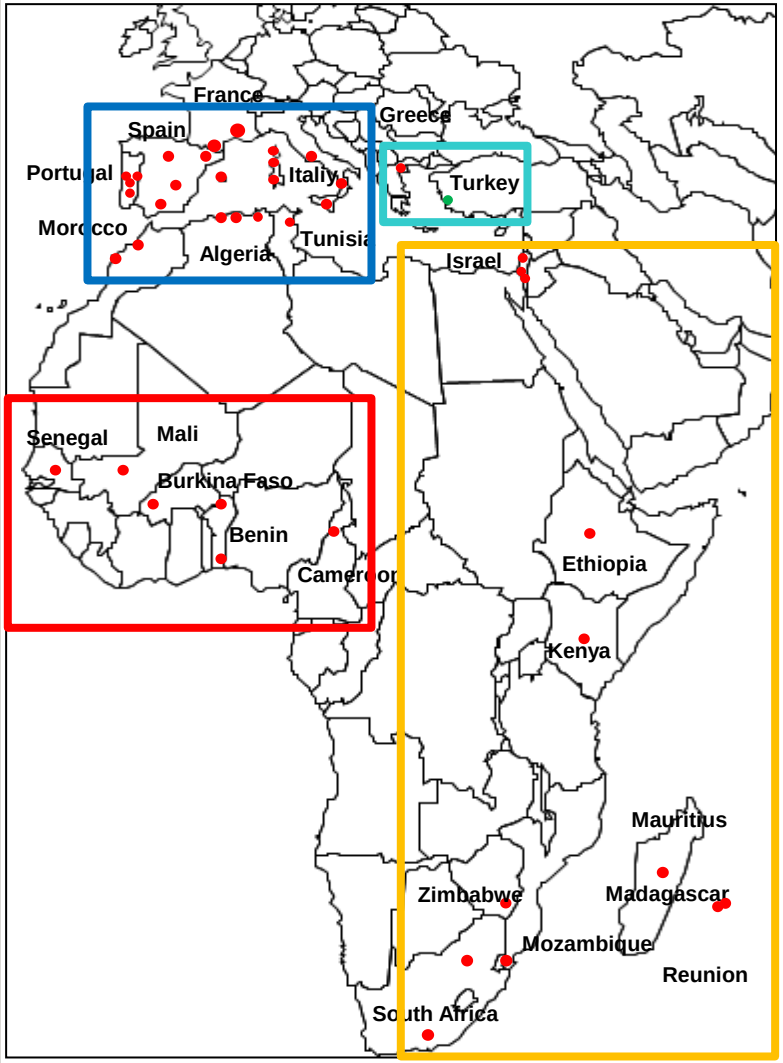


Clusters based on COI polymorphism

- Low genetic differentiation between Mediterranean basin populations

	North Africa	Southern Europe	WA	SEA
Southern Europe	0.051*	-		
WA	0.520**	0.603**	-	
SEA	0.614**	0.700**	0.236**	-
EMB	0.635**	0.715**	0.358**	0.167**

Results : Population genetic structure



Clusters based on COI polymorphism

- Low genetic differentiation between Mediterranean basin populations
- High genetic diffentiation between WMB and EMB + African populations

	North Africa	Southern Europe	WA	SEA
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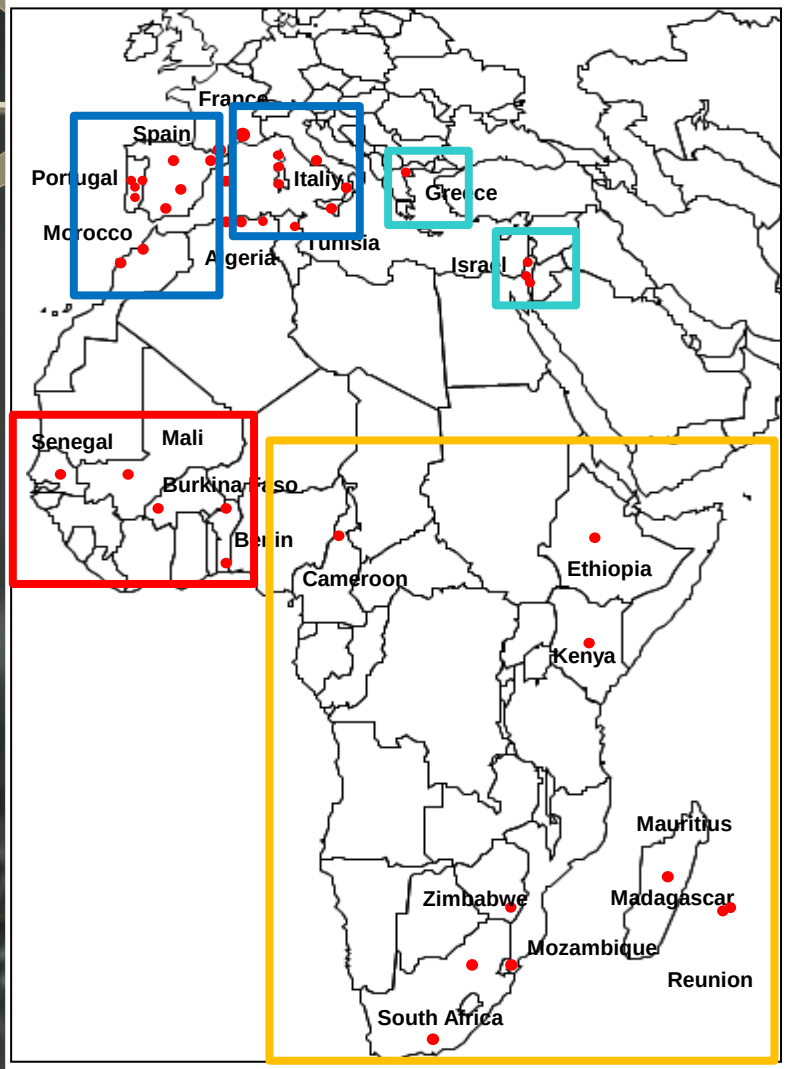
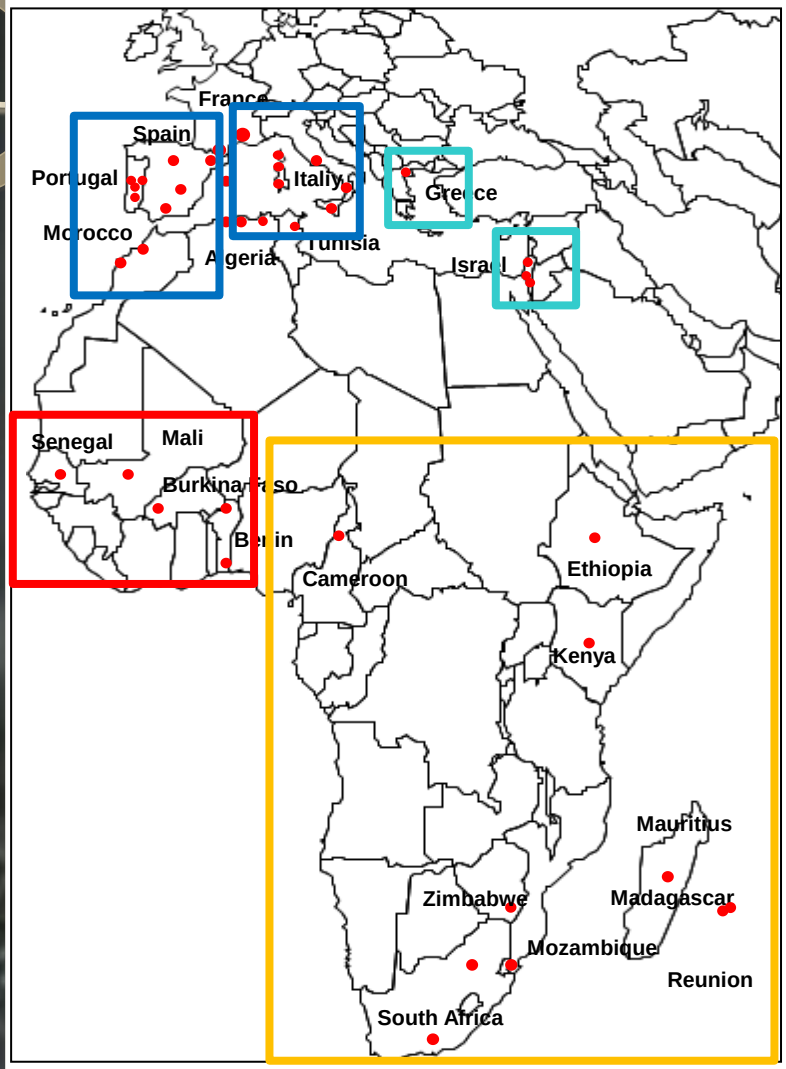


- High genetic differentiation between WMB and EMB

	WMB	Central MB	Greece	Israel	SEA
Central MB	0.016**	-			
Greece	**0.147****	**0.113****	-		
Israel	**0.148****	**0.114****	0.078**	-	
SEA	0.097**	0.077**	0.137**	0.092**	-
Senegal	0.104**	0.078**	0.131**	0.128**	0.034**

Clusters based on microsatellite polymorphism

Results : Population genetic structure



- High genetic differentiation between WMB and EMB
- High diffentiation between WMB, EMB and sub-Saharan Africa

	WMB	Central MB	Greece	Israel	SEA
Central MB	0.016**	-			
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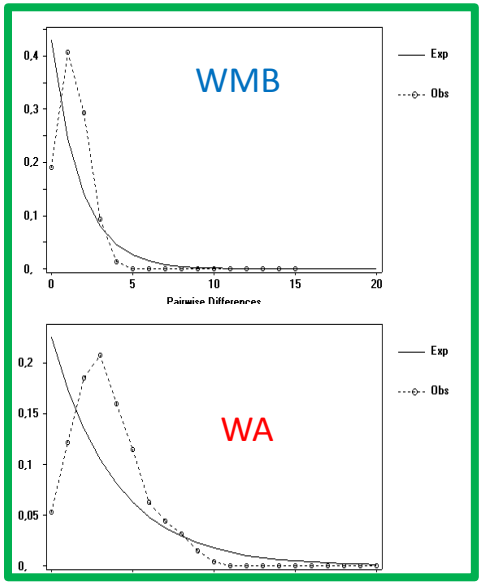
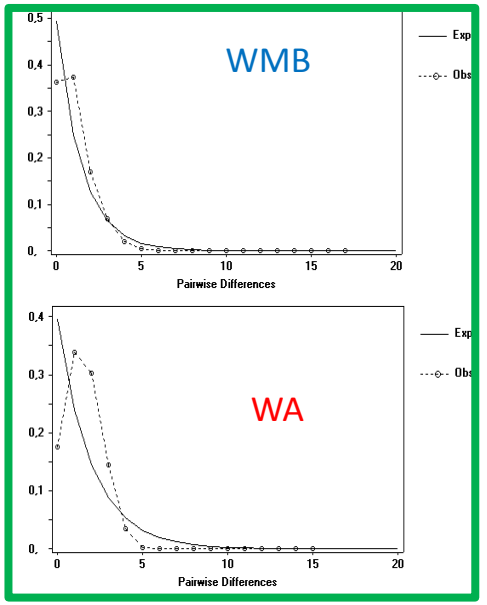
SEA	0.097**	0.077**	0.137**	0.092**	-
Senegal	0.104**	0.078**	0.131**	0.128**	0.034**

Clusters based on microsatellite polymorphism

Results: Populations demographic history

- Significant deviation from neutrality (COI+Cytb, Efα) for WA and WMB
- Demographic stability for SEA and EMB, while signature of population expansion for WMB and WA





Conclusion

Population diversity and demography

- High diversity in Sub-saharan Africa but low diversity in the Mediterranean basin
- Star like shape network + significant neutrality and mismatch tests

➔Sub-Saharan Africa = historical range

➔Recent demographic expansion of West Mediterranean basin populations only

Conclusion

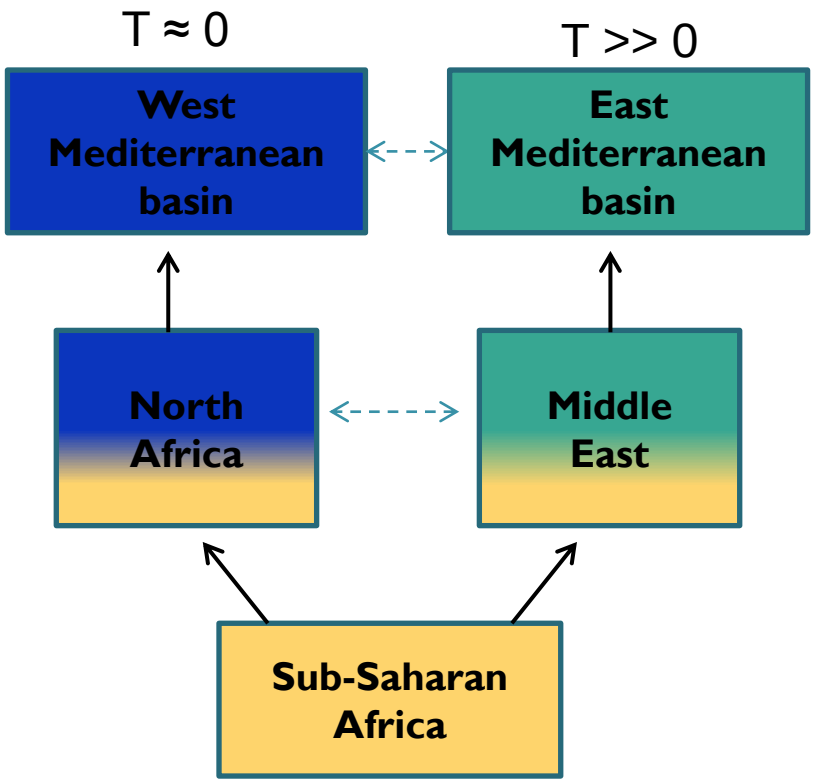
Population origin and structure

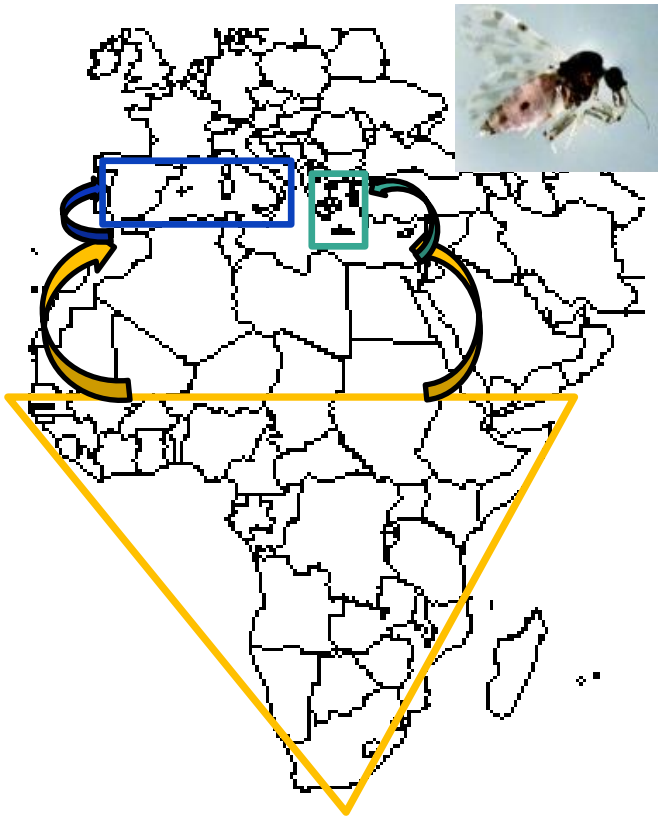
- No shared haplotypes between Sub-saharan Africa and West Mediterranean basin but West Mediterranean basin genetically closer to West Africa
- No shared haplotypes + high genetic differentiation between West and East Mediterranean basin
- East Mediterranean basin genetically closer to South-East Africa

➔ **Long time presence of *C. imicola* in EMD**
➔ **Genetic subdivision between WMD and EMD**

Conclusion

➔Support one source hypothesis with two routes of colonization : Atlantic coast and Nile valley





=> supported by ABC analyses P=0,56

Acknowledgements

A Tabbabi
Tunisia

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UZ, Spain

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UIB, Spain

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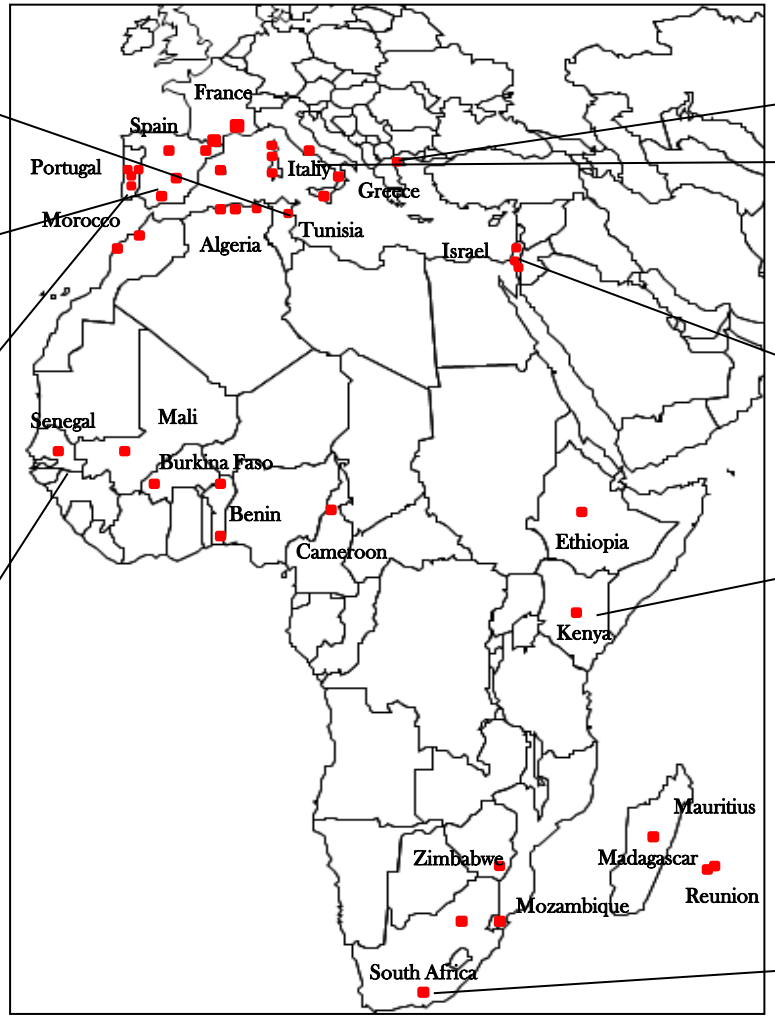
CReSA,
Spain

D Ramilo,
I Fonseca
CIISA, Portugal

A Gueye Fall
M Fall
M Tallar Seck
ISRA, Senegal



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IZS, Italy

Y Gottlieb
HUJ, Israel

M Kasina
KARI, Kenya

G Venter
K Labuschagne
OVI, South Africa

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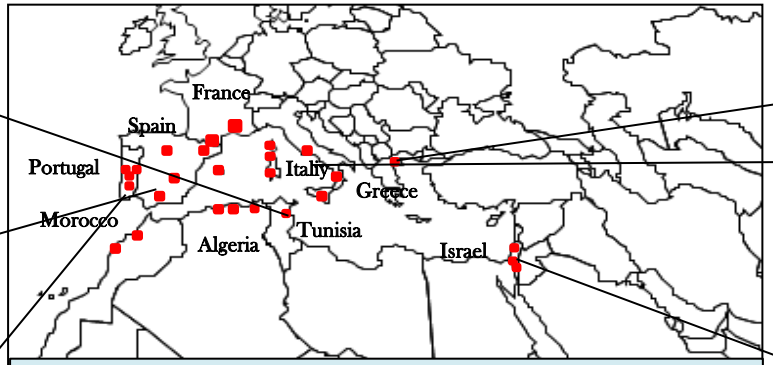
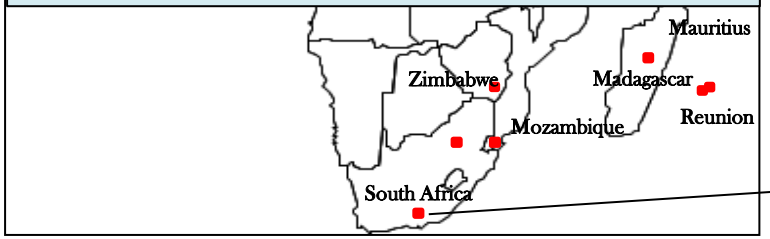


M-L Setier-Rio (EID-Méd, France)
M de Garine-Wichatitsky, T Martin, C Cêtre-Sossah, T Baldet, A Desvars, F Starchurski (Cirad, France)
B Mathieu, J-C Delécolle (UdS, France)



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Thank you for your attention !