

Genetic structure of codling moth populations from worldwide to farm spatial scales



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Codling moth ecology & evolution

- > Damage on fruit caused by larva

Apple – Pear – Quince – Walnut
(Barnes, 1991)



- > One to five generations per year

Depending on temperature and latitude (Shel'Deshova, 1967)

- > Insecticide resistances

Depending on the intensity of pesticide treatments
(Reyes et al., 2007; Eberle & Jehle, 2006)

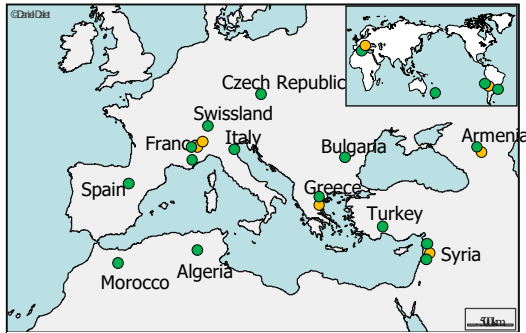
- > Dispersal at adult stage after mating and selection

Depending on landscape features (Mani & Wildbolz, 1977)

Cydia pomonella
Lepidoptera, Tortricidae



Population genetic structure: spatial levels analysed



At worldwide level

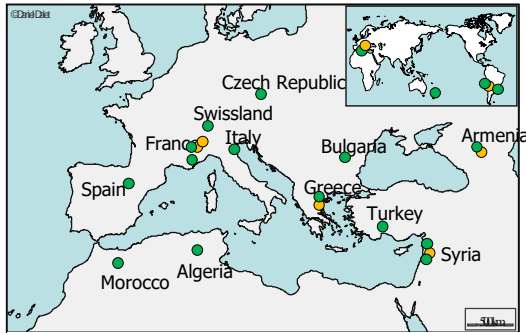
(Franck et al, 2007 and news results)

Apple and walnut orchards in temperate zones

17 countries, 25 orchards, 715 moths, 13 μ sat loci

> **Biogeography**

Population genetic structure: spatial levels analysed



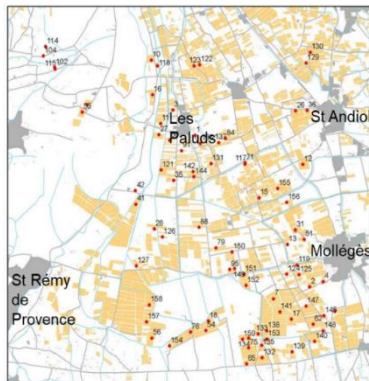
At worldwide level

(Franck et al, 2007 and news results)

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At a river basin level

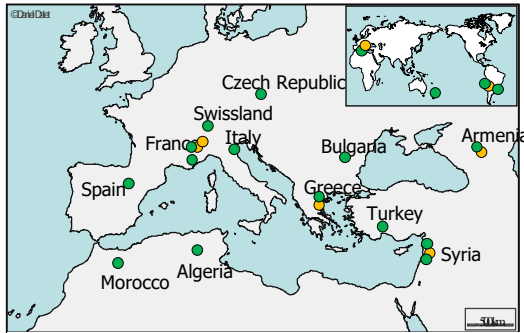
(unpublished results)

Apple orchards in the Basse Durance Valley (70 km²)

51 orchards, 2 years, 900+545=1445 moths, 20 μ sat loci

> **Landscape ecology**

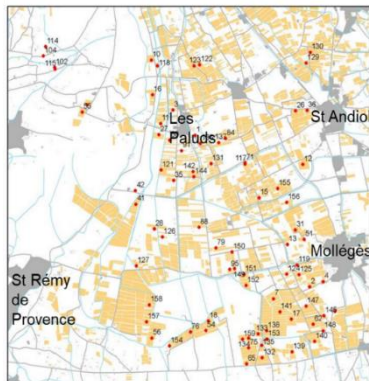
Population genetic structure: spatial levels analysed



At worldwide level (Franck et al, 2007 and news results)

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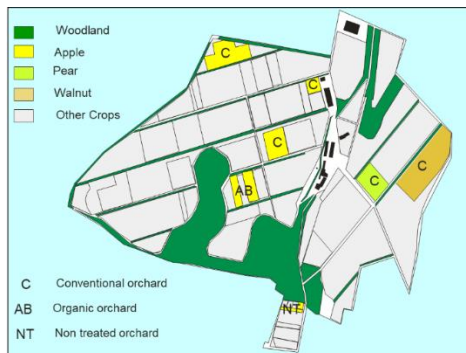
> **Biogeography**



At a river basin level (unpublished results)

Apple orchards in the Basse Durance Valley (70 km²)
51 orchards, 2 years, 900+545=1445 moths, 20 μ sat loci

> **Landscape ecology**



At a farm level (Franck et al, 2011)

Gotheron farm (80 hectares)

8 orchards, 1097 moths, 4 generations, 13 μ sat loci

> **Population dynamics**

Methodology

Sampling: corrugated cardboard traps



(Ricci et al., 2009)

- 30-50 trees sampled per orchard
- 10-30 CM diapausing larvae selected per orchard

Methodology

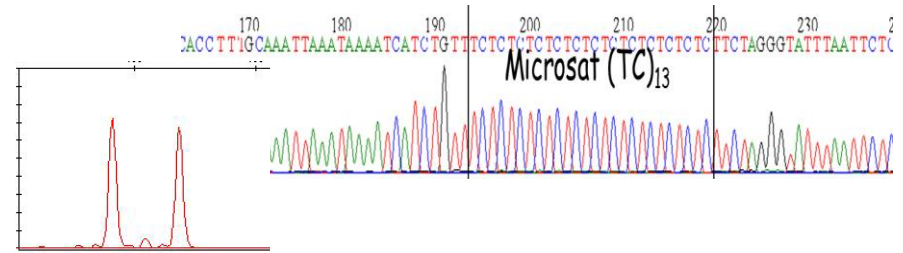
Sampling: corrugated cardboard traps



(Ricci et al., 2009)

- 30-50 trees sampled per orchard
- 10-30 CM diapausing larvae selected per orchard

Genotyping: microsatellite loci



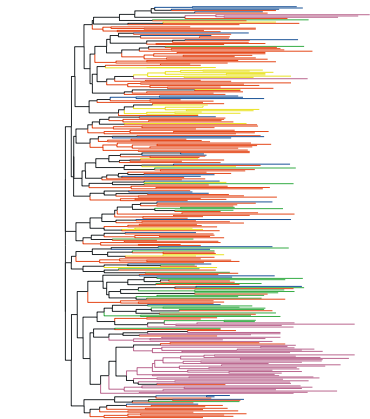
(Franck et al., 2005; 2011; Wan et al. 2019)

Selection of 13-20 loci:

- No linkage disequilibrium
- Up to 3 loci on the same chromosome
- Less than 10% null allele per locus per population

Genetic analyses

- Population approaches: genetic diversity, allele richness indicators
- Classification approaches based on individual genotypes: STRUCTURE, COLONY
- Genetic distances approaches: *Fst*, relatedness (Ritland, 1996)
- Isolation by distance : auto-correlogram (Rousset 1997; Vekemans & Hardy 2004)

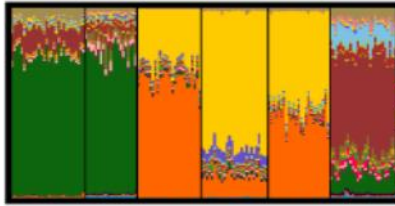
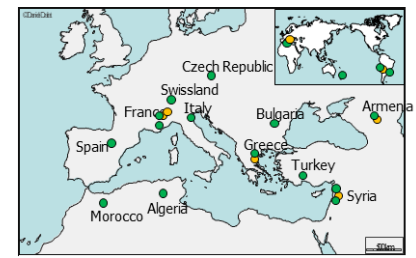


(Franck et al., 2007; 2011)

At worldwide level: genetic structure

715 individuals, 25 orchards, 13 μ sat loci

Classification using Structure : $K=19$



Middle East: Armenia, Syria, Turkey

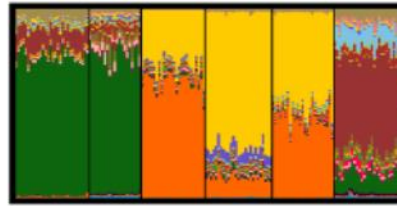
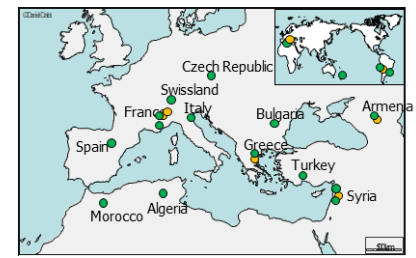
Armenia_A
Armenia_W
Syria_A1
Syria_A2
Syria_W
Turkey_A

- Huge genetic differentiation between populations from countries in the apple domestication origin zones

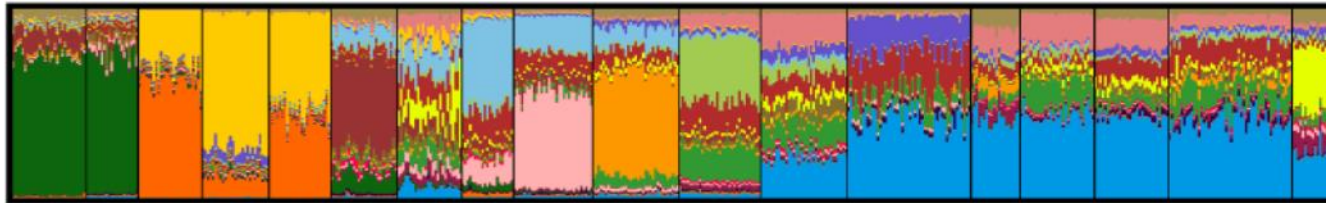
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Middle east



Europe

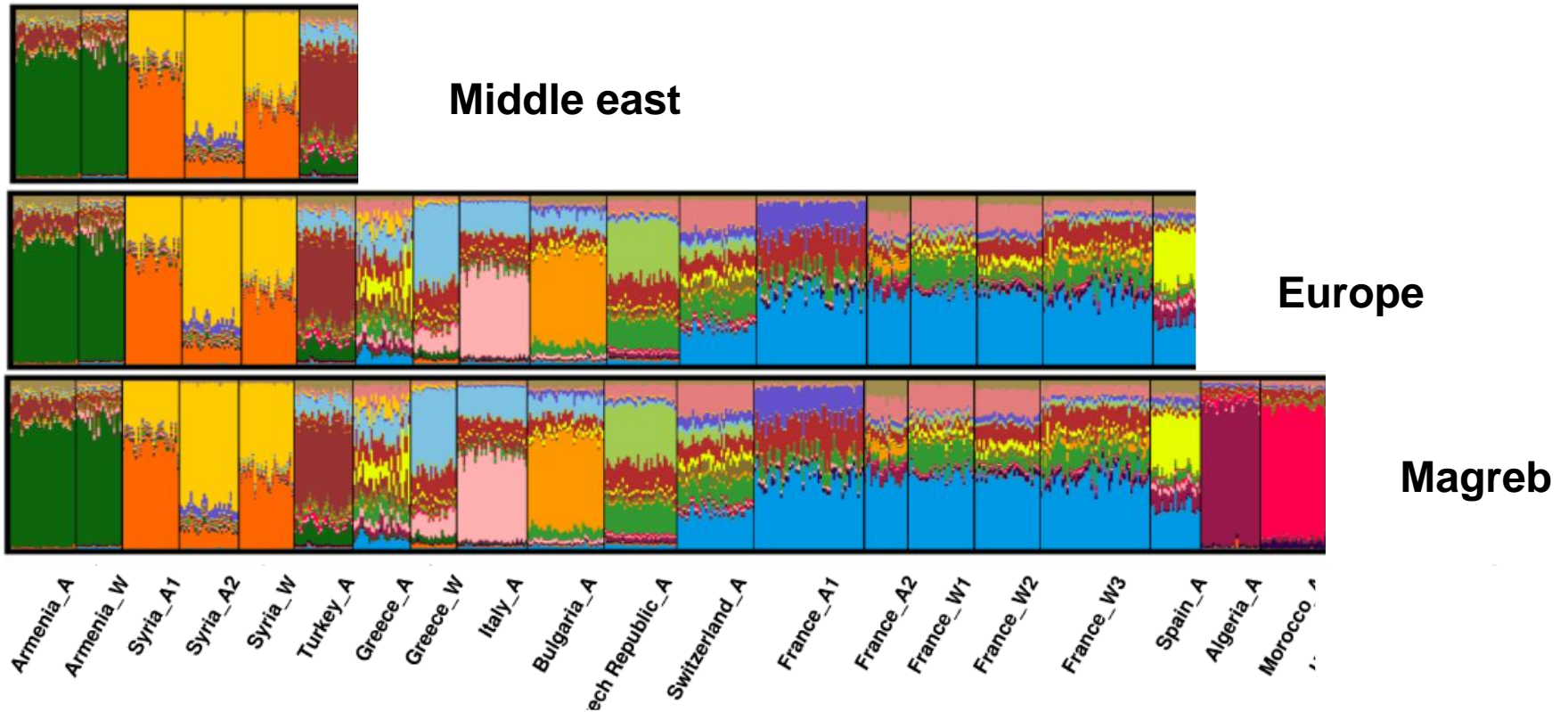
Armenia_A
Armenia_W
Syria_A1
Syria_A2
Syria_W
Turkey_A
Greece_A
Greece_W
Italy_A
Bulgaria_A
Czech Republic_A
Switzerland_A
France_A1
France_A2
France_W1
France_W2
France_W3
Spain_A

- High genetic differentiation between populations in **Europe** linked with high levels of **admixture**

At worldwide level: genetic structure

715 individuals, 25 orchards, 13 μ sat loci

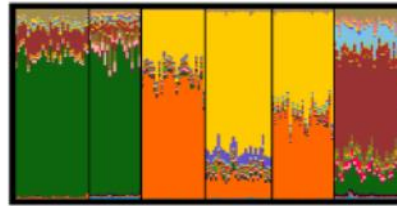
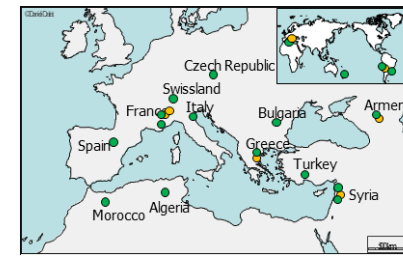
Classification using Structure : $K=19$



- Several additional centers of differentiation in Magreb

At worldwide level: genetic diversity

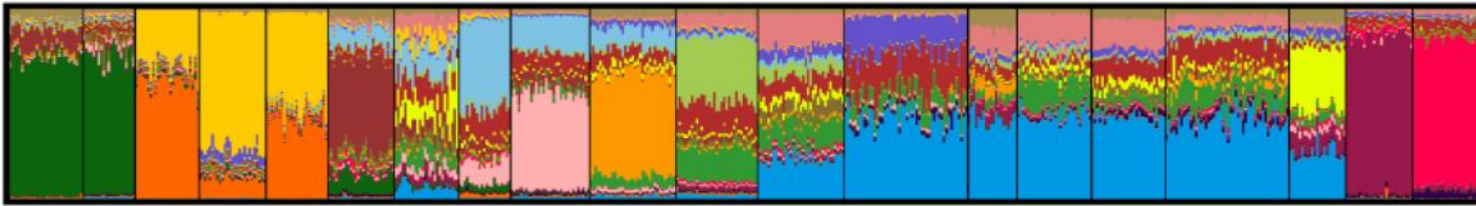
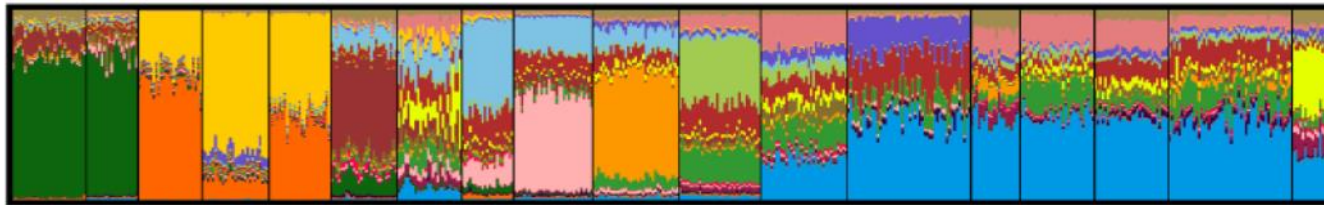
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Classification using Structure : $K=19$



Old World

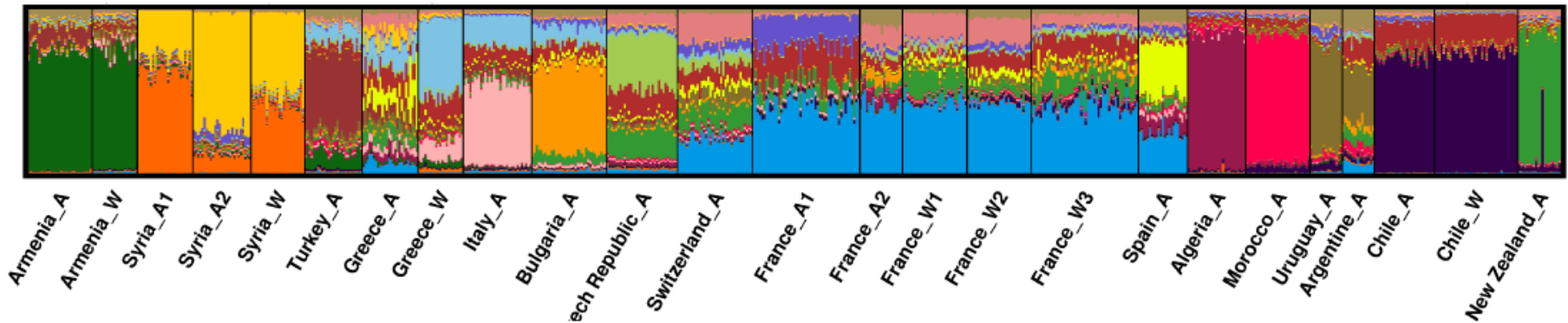
$\hat{\alpha}=6.5$

allele richness (average per locus and per population)



New World

$\hat{\alpha}=5.2$

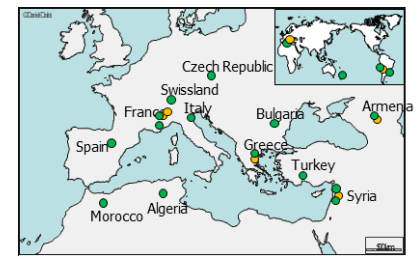


- High genetic differentiation between populations from New and Old Worlds: $F_{st}>0.15$
- Multiple colonization events of New World linked with bottleneck

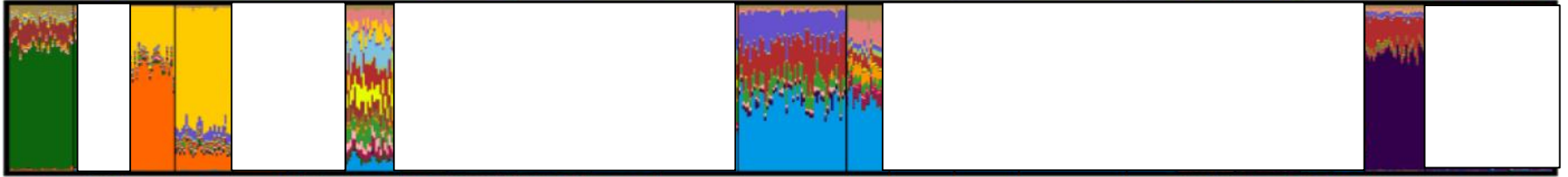
At worldwide level: host-plant differentiation

715 individuals, 25 orchards, 13 μ sat loci

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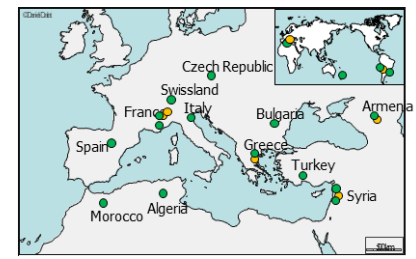


Apple orchards (A)

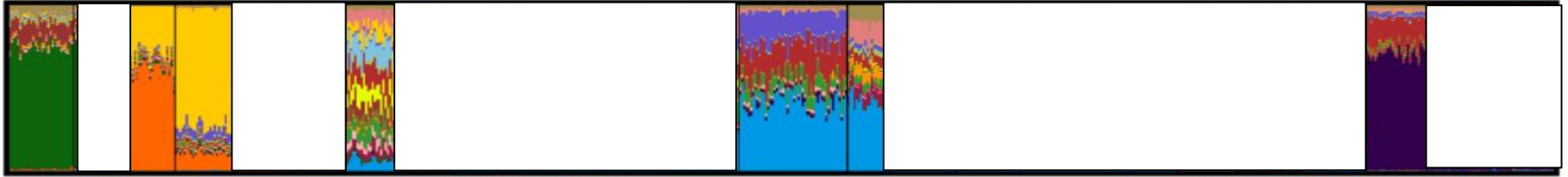


At worldwide level: host-plant differentiation

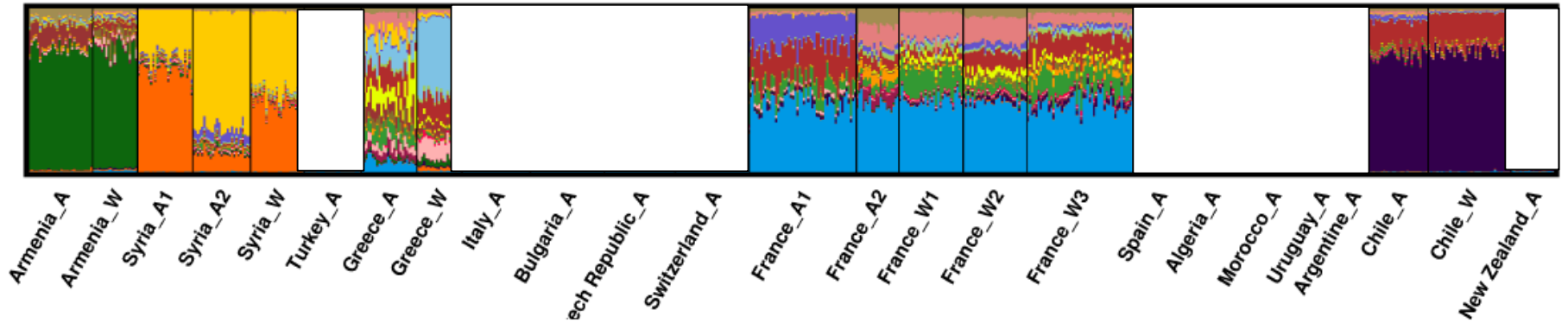
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Classification using Structure : $K=19$



Apple orchards (A)



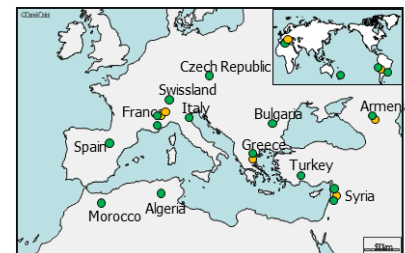
+ Walnut orchards (W)



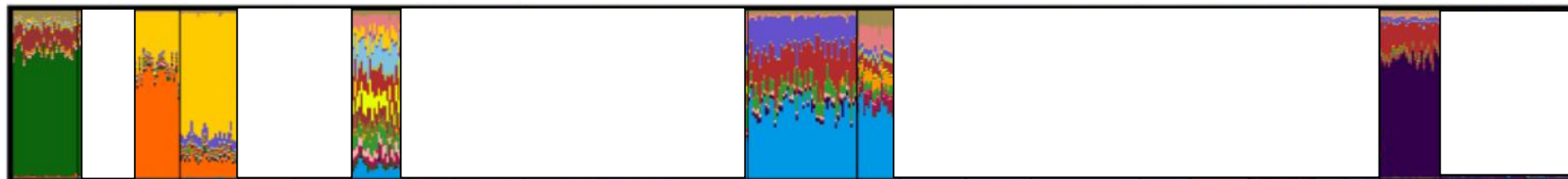
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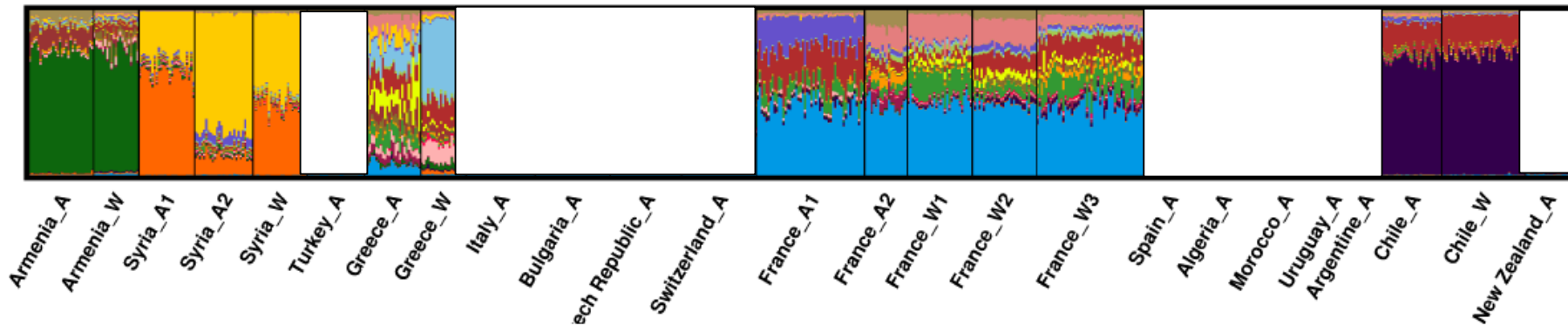
Classification using Structure : $K=19$



Apple orchards (A)



+ Walnut orchards (W)



➤ Low differentiation between populations from apple and walnut orchards in the same country:

- F_{st} apple-apple: 0.04
- F_{st} walnut-walnut: 0.02
- F_{st} apple-walnut: 0.02

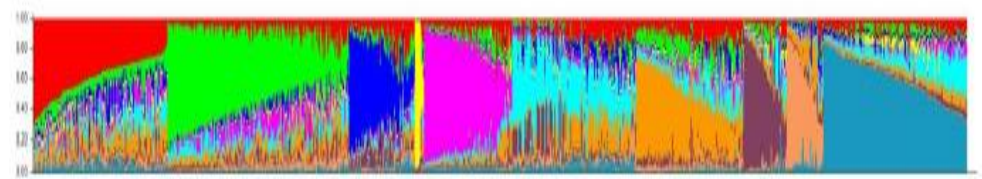
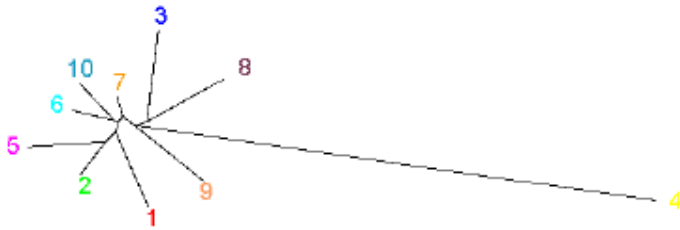
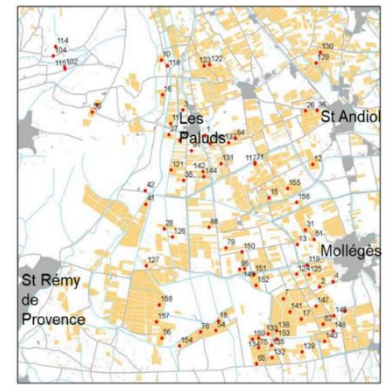
At a river basin level: genetic structure

900 individuals, 51 orchards (2006), 20 μ sat loci

Classification using Structure : $K=10$

F_{st} between orchards: 0,01; F_{st} between clusters: 0.09

Gene diversity: 0.65



Classification of 900 individuals according to 10 clusters

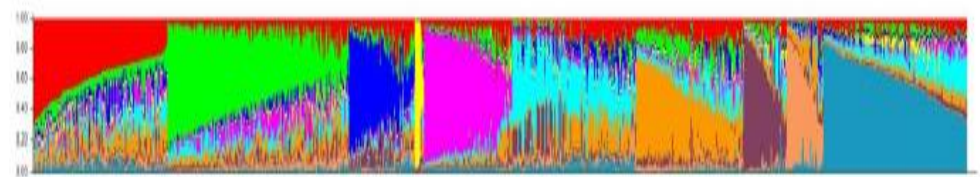
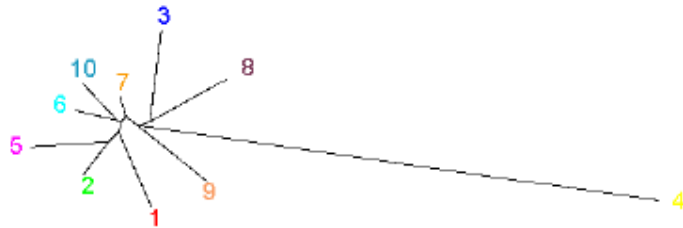
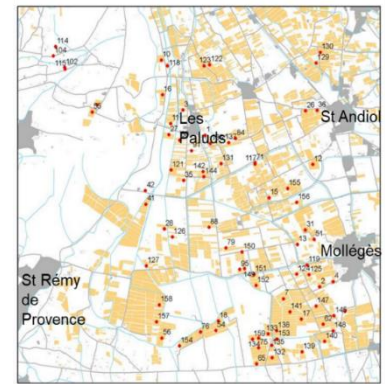
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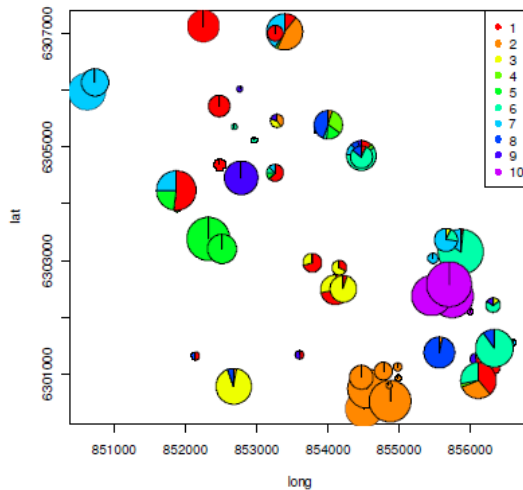
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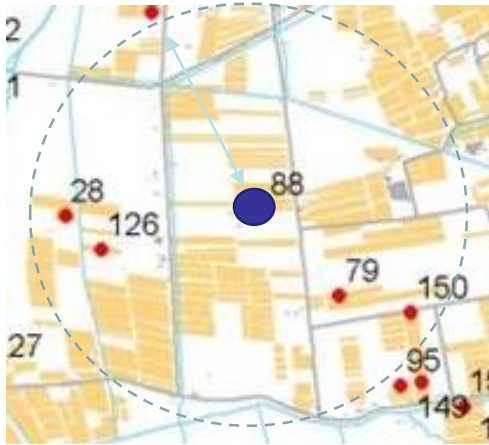
Spatial distribution of the 10 clusters

- Low genetic structure between orchards, which is spatially organized
- Population structure correlated to the number of pesticide treatments (Franck et al. 2007)

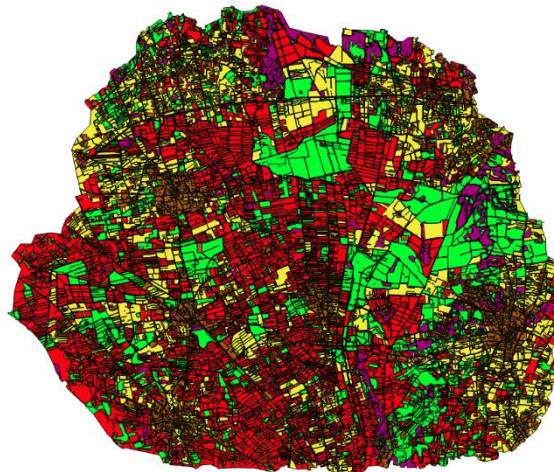
At a river basin level: landscape effect on genetic diversity

Land use characterization in 1km² around each orchard: 51 buffers

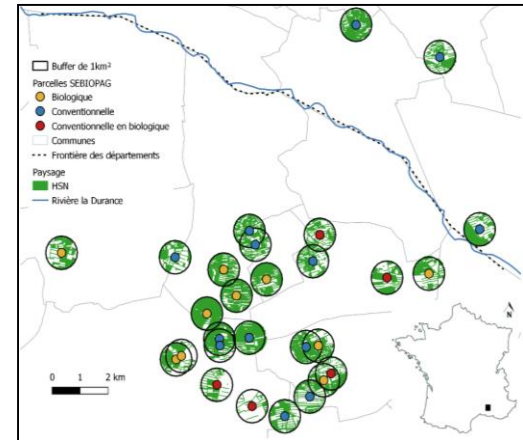
1km² buffer



crop, orchard (organic/conventional),
woodland, meadow, urban



Landscape in 51 buffers



Population genetic prediction:

Population size

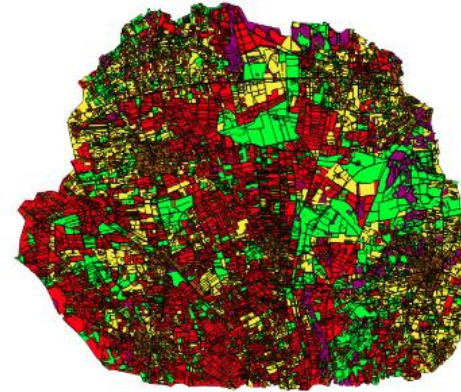
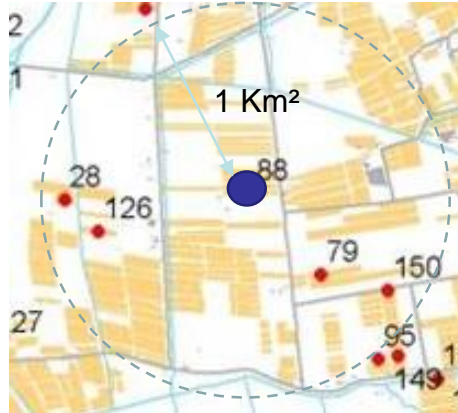
+

Immigration

+

Gene diversity

At a river basin level: genetic structure



Statistical Model (GLM):

Allele richness ~ Landscape in 1km² buffer [Urban, Conventional orchard, Hedgerow]

Results:

Urban +

=> Moth are attracted by urban lights, which increase population diffusion

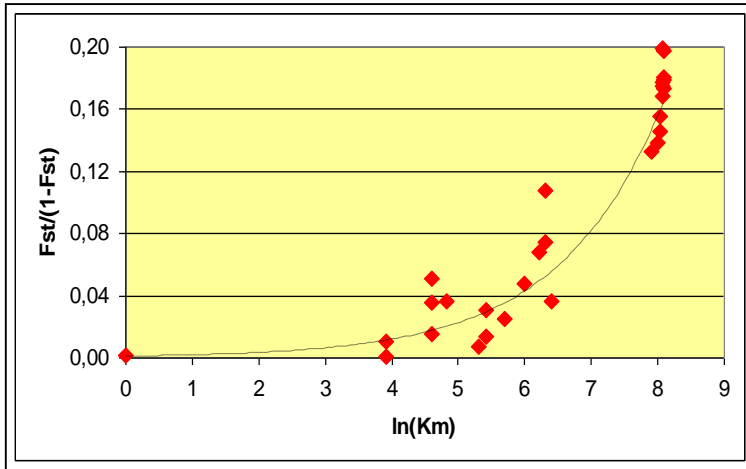
Conventional Orchards –

=> Moth population sizes are reduced by pesticide treatments in conventional orchards

Isolation by distances

=> Individual-based (at landscape or farm level) or population-based genetic approaches (at continental level)

At continental level: Europe

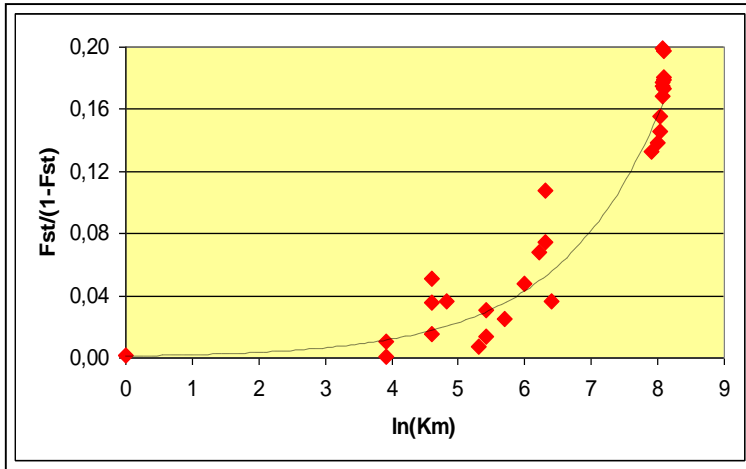


(Franck et al., 2007)

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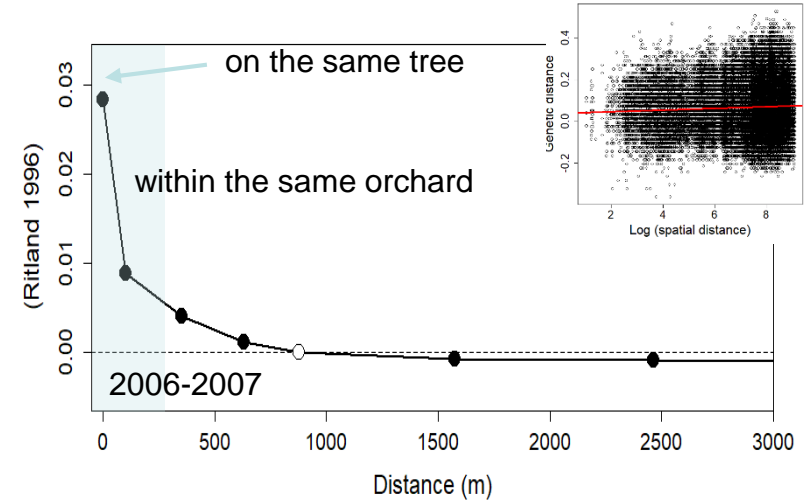
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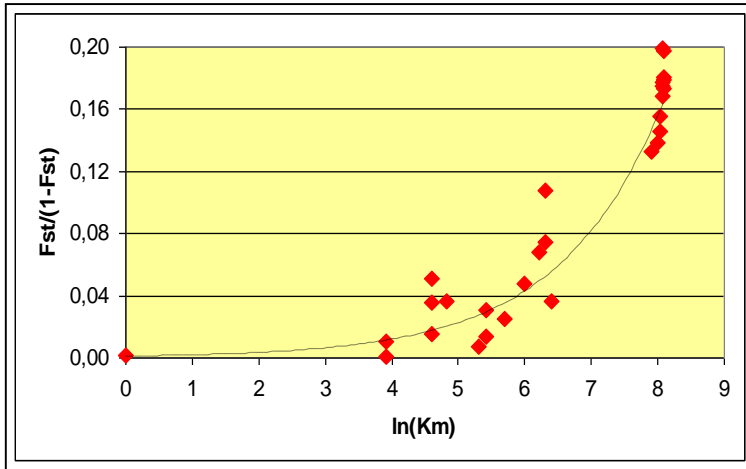
At a river basin level: Basse Durance Valley



Isolation by distances

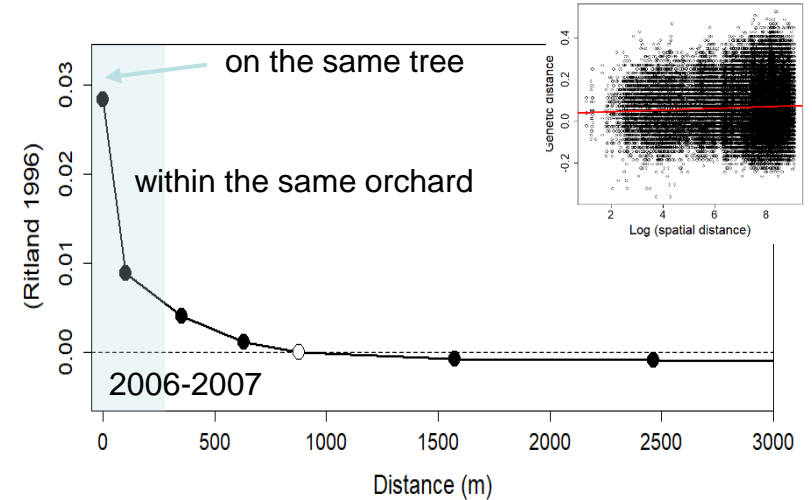
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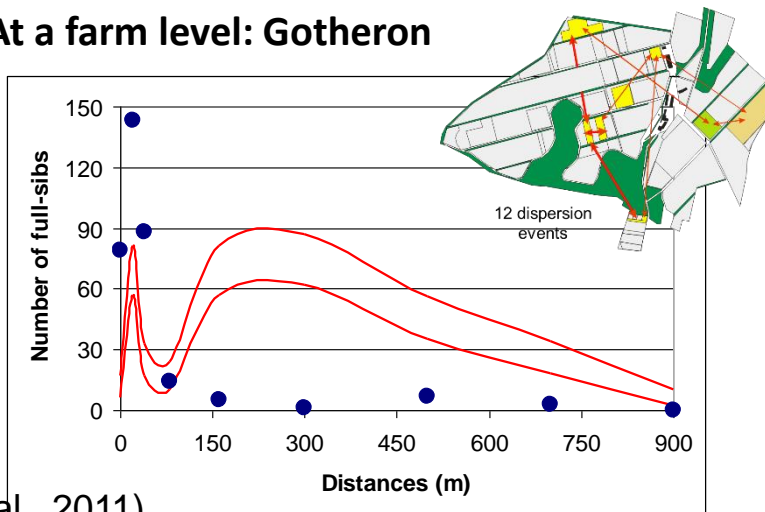


(Franck et al., 2007)

At a river basin level: Basse Durance Valley



At a farm level: Gotheron

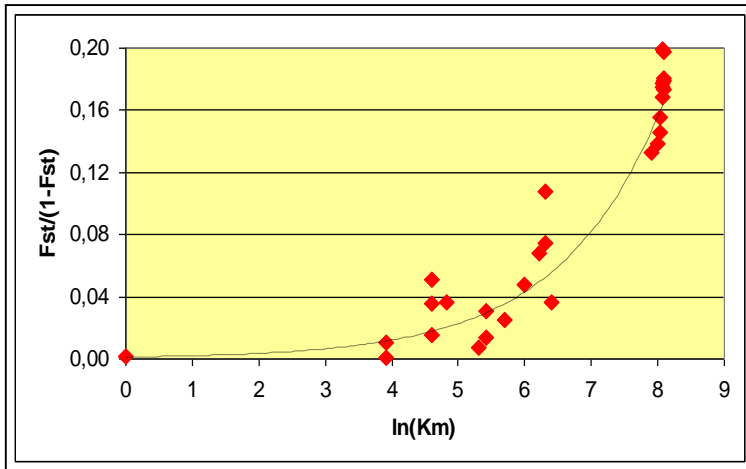


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Isolation by distances

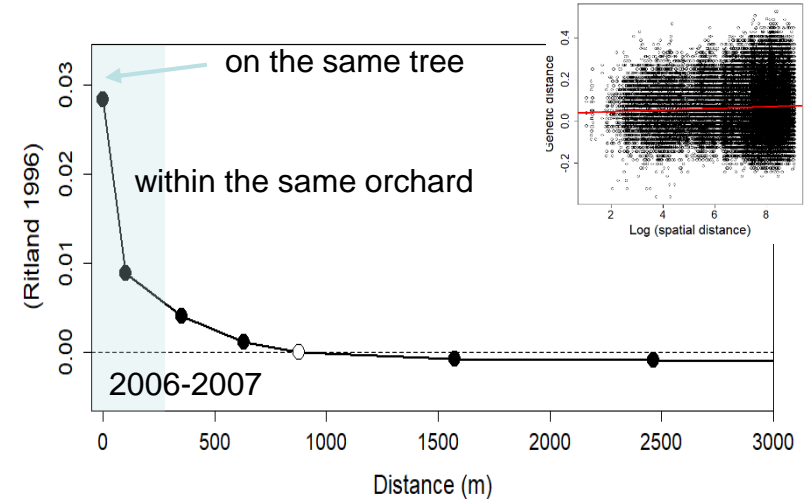
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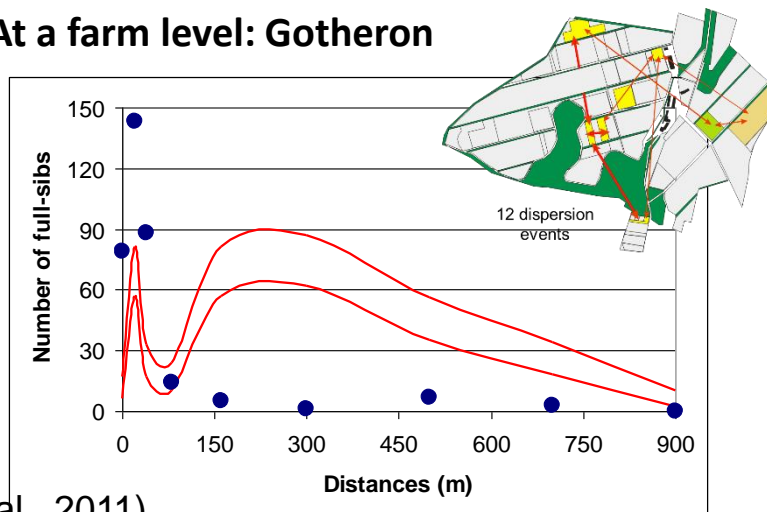


(Franck et al., 2007)

At a river basin level: Basse Durance Valley



At a farm level: Gotheron



(Franck et al., 2011)

- Isolation at continental level between populations distant by more than 100 km
- gene flow between orchards distant by less than 1 km
- **Area-wide pest management at territory and landscape levels**
~ 100-1000 Km²

At farm level: full sibs inference and population size estimate

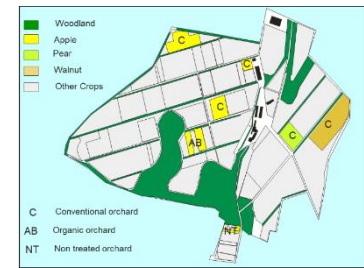
Kinship inferences

1063 individuals, 7 orchards, 4 generations, 13 μ sat loci

Classification using Structure : 302 full sib pairs in total

Proportion of full sibs per generation: 0.7%-1.9%

F_{st} between orchards: 0.01



(Franck et al., 2011)



At farm level: full sibs inference and population size estimate

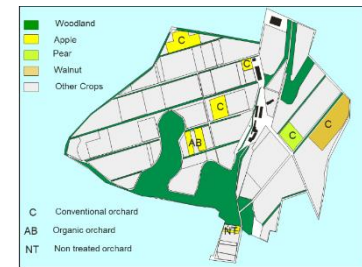
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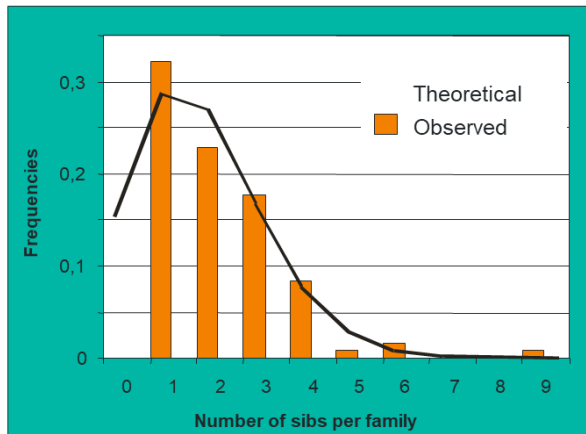
F_{st} between orchards: 0.01



(Franck et al., 2011)



Classification of individual pairs into family clusters



(Baudry et al., 1998)

> Adjusting number of full-sibs by family to a Poisson law

>> λ estimates the average number of offspring by mother in the sample of size N

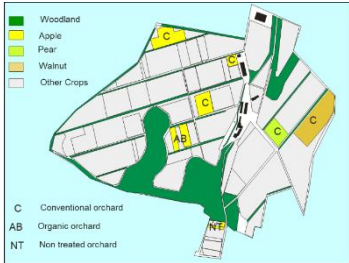
>> estimates of the effective number of mothers in the population $N_f = N / \lambda$

At farm level: female fertility estimates

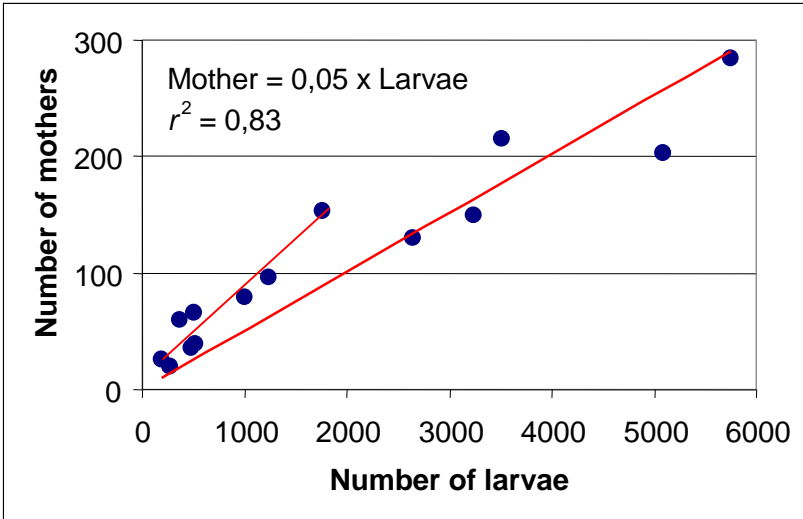
Genetic estimates of the number of mothers

1st generation larvae were sibs of ~ 130 mothers
 2nd generation larvae were sibs of ~ 230 mothers

Up to 150 mothers by orchard - Up to 40 mothers by tree



Estimate of the fecundity rates (r ~ 20)



	Nb of larvae	Nb of mothers	Fecundity	
	mean	mean	mean	95% interval
1st generation	2643	130	20	[18-23]
2nd generation	4786	234	20	[14-24]
Pear	234	23	11	[3-23]
Walnut	1808	105	14	[3-39]
Apple	1385	116	13	[10-17]
Conventional	521	52	10	[6-19]
Organic	864	66	13	[7-36]
Non-treated	1997	88	23	[14-42]

- No difference of fecundities between generations and host-plants
- Around twice higher in non-treated than conventional apple orchards



Etienne Klein
Lionel Roques
Emily Walker
Olivier Bonnefon
Olivier Martin



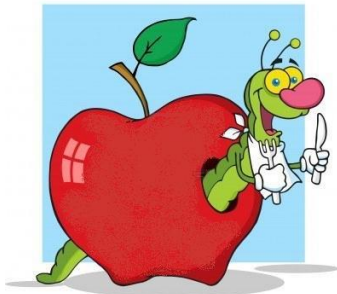
Jérôme Olivares
Claire Lavigne
Bertrand Gauffre



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Predictive Ecological Engineering for
Landscape Ecosystem Services and
Sustainability



Thank you for your attention!