Genetic basis of host fruit adaptation in D. suzukii : an Evolve & Resequence study

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Genetic basis of host fruit adaptation in *D. suzukii* : an Evolve & Resequence study

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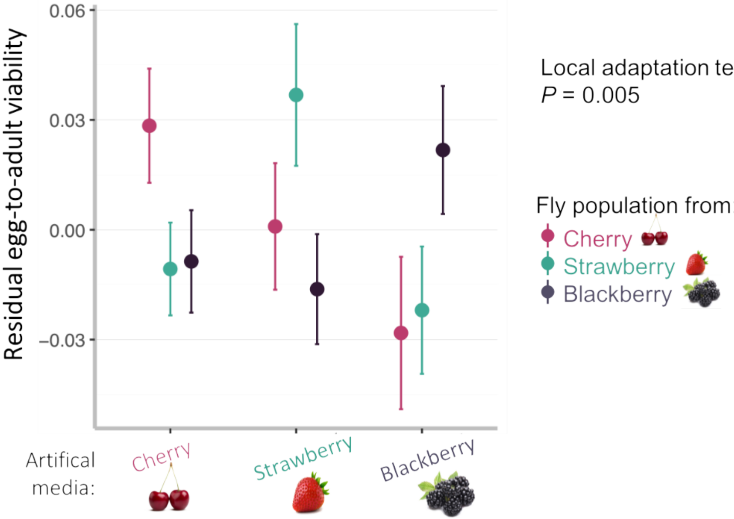
INRAE, CBGP, Montpellier, France

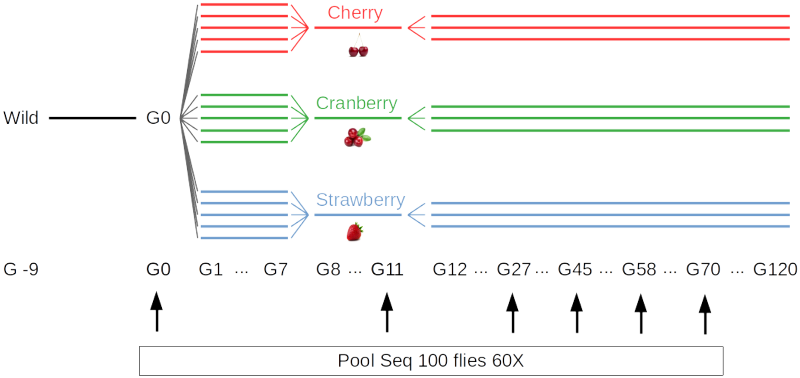
14th DrosEU workshop - 10th DrosEU anniversary
Barcelona, 8th April 2024

Local adaptation to host plant (Olazcuagua *et al*, 2022)

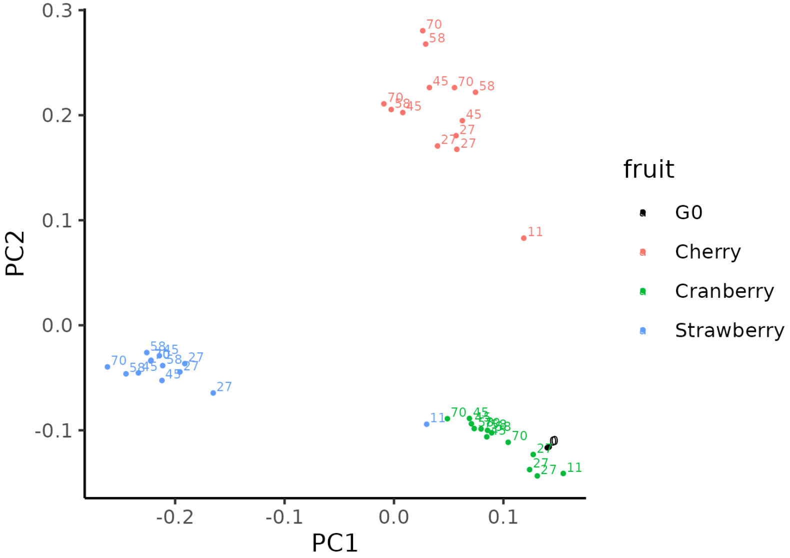


Local adaptation test:
P = 0.005

Evolve & Resequence experiment

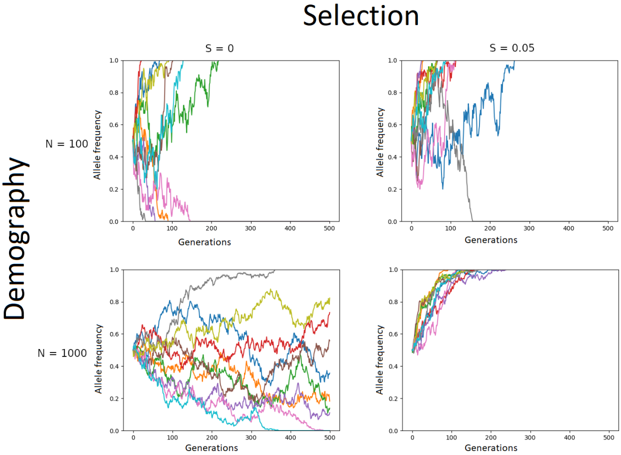


Genetic diversity structuring

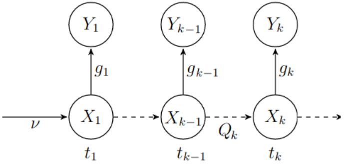


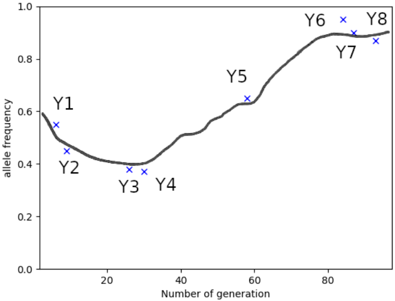
Genomic time series

Temporal trajectories of allele frequencies informative about demography and selection.



Hidden Markov Model (HMM) (Bollback 2008)





- X_k population allele freequency at time t_k (hidden)
- Y_k sampled allele freequency at time t_k (observed)
- Q_k transition matrix from time t_{k-1} to time t_k

Transition matrix

- Computed under a Wright-Fisher model.
- Depends on N, s and $t_{k-1} - t_k$.
- Example for $N = 4$:

$$Q = \begin{array}{c} \\ 0/4 \\ 1/4 \\ 2/4 \\ 3/4 \\ 4/4 \end{array} \begin{array}{c} \begin{array}{ccccc} 0/4 & 1/4 & 2/4 & 3/4 & 4/4 \end{array} \\ \begin{pmatrix} 1 & 0 & 0 & 0 & 0 \\ 0.32 & 0.42 & 0.21 & 0.05 & 0.04 \\ 0.06 & 0.25 & 0.38 & 0.25 & 0.06 \\ 0.004 & 0.05 & 0.21 & 0.42 & 0.32 \\ 0 & 0 & 0 & 0 & 1 \end{pmatrix} \end{array}$$

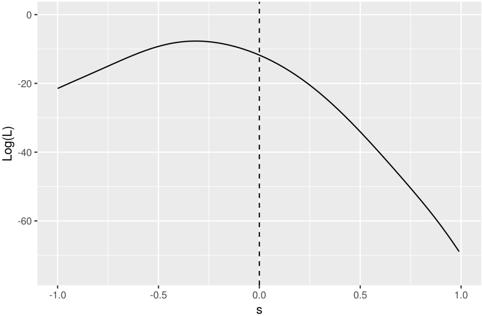
Demography and Selection Inference

Exact (and fast) computation of the likelihood

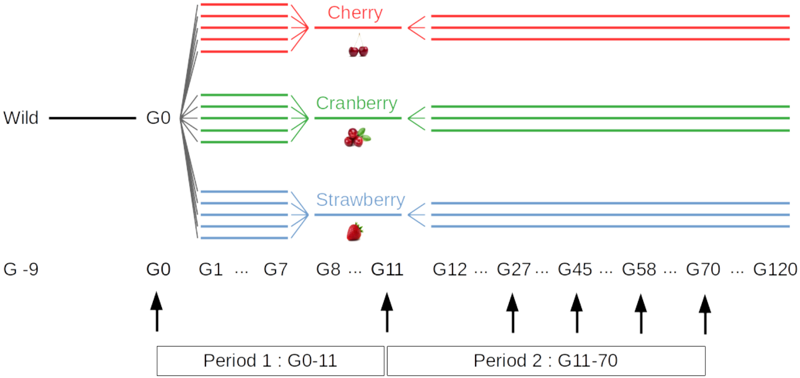
$$P(Y|N,s) = P(Y_1, ..., Y_n|Q_1, ..., Q_n)$$

for any values of N and s

1. **Inference of N** : connsider p independent loci and optimize $P(Y_1|N, s_1 = 0)P(Y_2|N, s_2 = 0) \ldots P(Y_p|N, s_p = 0)$ over N.
2. **Inference of s** : for each locus i, optimize $P(Y_i|\hat{N}, s_i)$ over s.

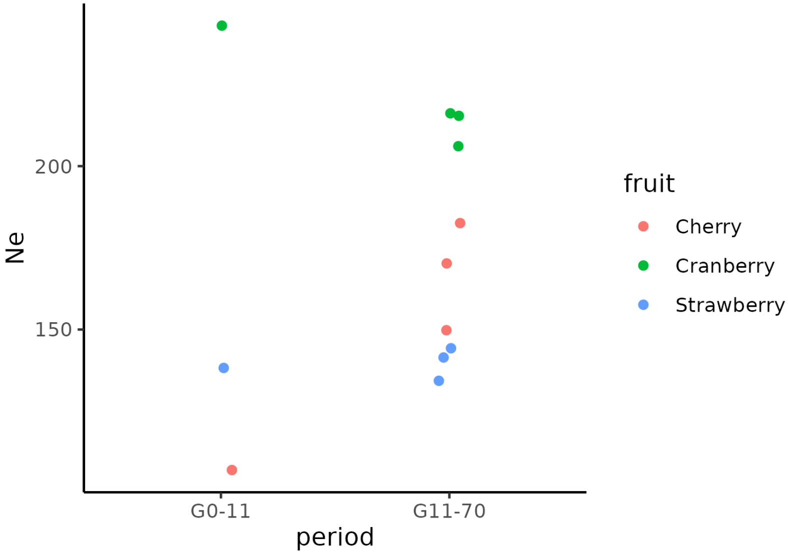


Analysis of Evolve & Resequence data

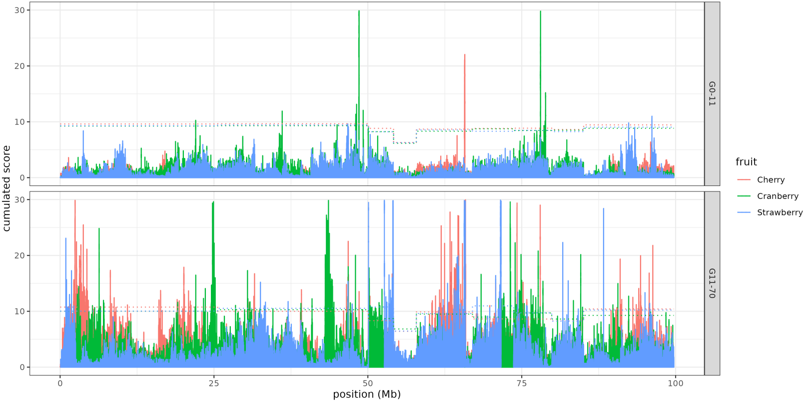


3 lines in period 1, 9 lines (3 per fruit) in period 2

Inferred N


Ne
200
150
G0-11
G11-70
period
fruit
Cherry
Cranberry
Strawberry

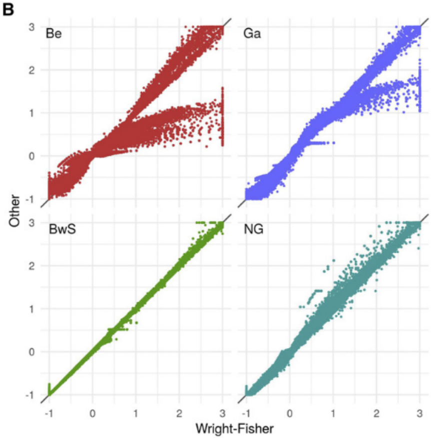
Candidate regions under selection ($\hat{s} \neq 0$)



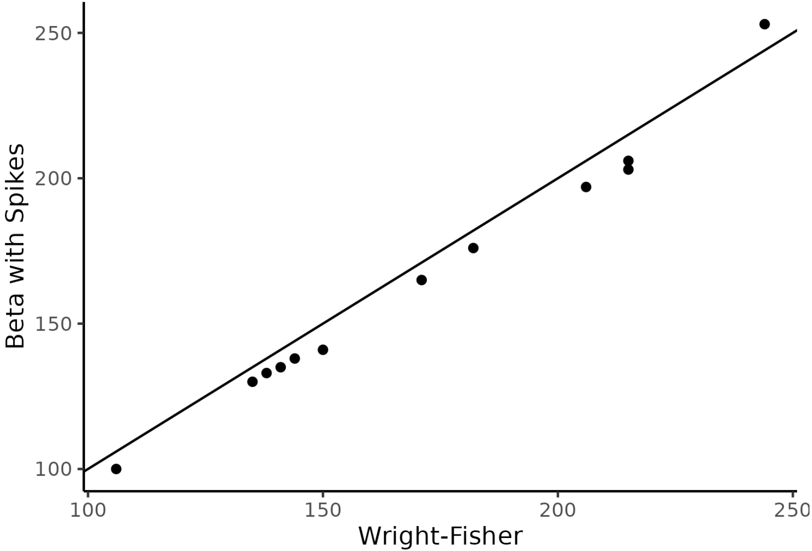
p-values obtained from the HMM and 'cumulated' using a local score approach (Fariello *et al*, 2017).

Wright-Fisher approximations

- Wright-Fisher model limited to $N \approx 300$ for numerical reasons (Q of size $N \times N$).
- The Beta with Spikes distribution (Tataru *et al* 2019) is a very good approximation in this context (Paris *et al*, 2017).



Inferred *N*


250
200
150
100
Beta with Spikes
100
150
200
250
Wright-Fisher

Perspectives

- Evolve & Resequence study:
    - Explore candidate regions, especially those that are specific to one single fruit.
    - Compare with candidate regions detected on wild populations PoolSeq data from different fruits.
- Methodological developments:
    - Linked selection **pervasive** (Elyashiv *et al*, 2016) and **biases demographic inference** (Schrider *et al*, 2016; Pouyet *et al*, 2018; Johri *et al* 2021, Boitard *et al* 2022).
    - Joint estimation of demography and selection from genomic time series: PhD position available!

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