



HAL
open science

Flowering intensity and phenology in clonal seed orchards of maritime pine

Jean-François Trontin, Pierre P. Alazard, Sandrine S. Debille, Laurent Bouffier

► **To cite this version:**

Jean-François Trontin, Pierre P. Alazard, Sandrine S. Debille, Laurent Bouffier. Flowering intensity and phenology in clonal seed orchards of maritime pine. 5. IUFRO 2.09.02 conference Clonal trees in the bioeconomy age: opportunities and challenges, Sep 2018, Coimbra, Portugal. hal-03341474

HAL Id: hal-03341474

<https://hal.inrae.fr/hal-03341474v1>

Submitted on 30 Sep 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

Flowering intensity and phenology in clonal seed orchards of maritime pine



5th IUFRO 2.09.02 conference
Clonal trees in the bioeconomy age:
opportunities and challenges

Sept. 10-15, 2018
Coimbra, Portugal

TRONTIN Jean-François¹, ALAZARD Pierre¹, DEBILLE Sandrine¹, BOUFFIER Laurent^{2,3}



¹Biotech & advanced forestry Dpt.

71, Rt. d'Arcachon, Pierroton
33610 Cestas, FRANCE
jean-francois.trontin@fcba.fr

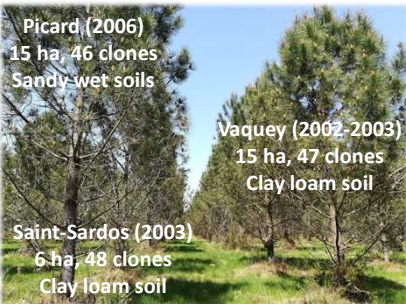
^{2,3}UMR 1202 BIOGECO

69, Rt. d'Arcachon, Pierroton
33610 Cestas, FRANCE

351, Cours de la Libération
33400 Talence, FRANCE



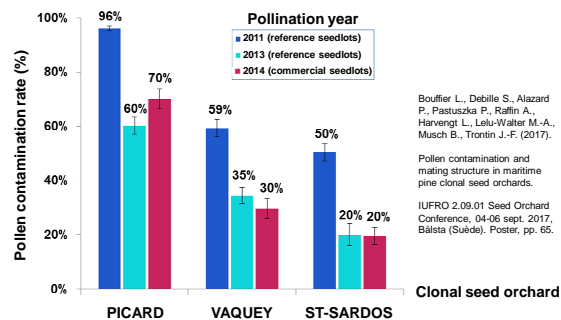
Maritime pine (*Pinus pinaster* Ait.)
Southern Europe: 4.2 Mha
France: 1.1 Mha (mainly Landes de Gascogne)



Third-generation clonal seed orchards currently producing in France (Nouvelle Aquitaine) the maritime pine VF3 (Vigour-Form) seedlots were established between 2002 and 2006 in contrasted pedo-climatic conditions using the same source materials propagated through grafting (52 selected genotypes overall).

These orchards (Picard, Vaquey and Saint-Sardos) have been producing improved seeds since 2011 in an open pollination setting, a method that drastically reduces production costs compared to controlled crossings. The full achievement of the expected genetic gain however assumes that pollen contribution from outside the orchard (pollen contamination) is low, while that of the orchard's clonal progenitors is well-balanced.

In practice, pollen contamination rate of maternal genotypes is high and variable according to the orchard and the year (Bouffier et al. 2017, SNP markers study)



Bouffier L., Debille S., Alazard P., Pastuszka P., Ratto A., Hareng L., Lelu-Walter M.-A., Musch B., Trontin J.-F. (2017).

Pollen contamination and mating structure in maritime pine clonal seed orchards.

IUFRO 2.09.01 Seed Orchard Conference, 04-06 sept. 2017, Båsta (Suède). Poster, pp. 65.

How the flowering intensity and phenology of clonal seed orchards progenitors can affect pollen contamination rate and parental contribution in seedlots?

Flowering traits were scored for all genotypes in the 3 clonal orchards during springs 2015 and 2016:

1. Female flowering phenology (development stage 1-10, from early to late)
2. Intensity of female flowering (number of flowers)
3. Intensity of male flowering (score 0-4, from low to high)

Overall more than 7500 data were collected (mean of 7 trees/clone/condition). Clone ranking (out of 52 clones) was calculated for each trait.

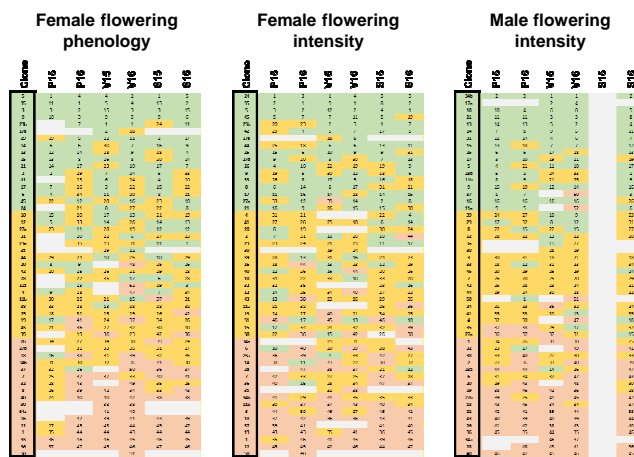


Clone ranking

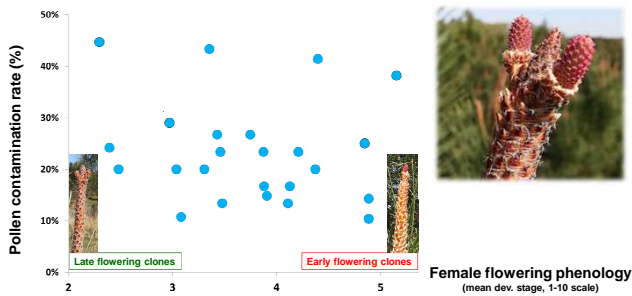
- Earliest- or high-flowering clones
- Late- or low-flowering clones
- Intermediate clones
- Not estimated

P15, P16: PICARD 2015 or 2016
V15, V16: VAQUEY 2015 or 2016
S15, S16: ST-SARDOS 2015 or 2016

Although annual differences are observed among sites, strikingly, average ranking of each clone for female flowering phenology as well as female and male flowering intensities is similar in the 3 orchards for the 2 investigated years suggesting a strong genetic control of flowering traits.

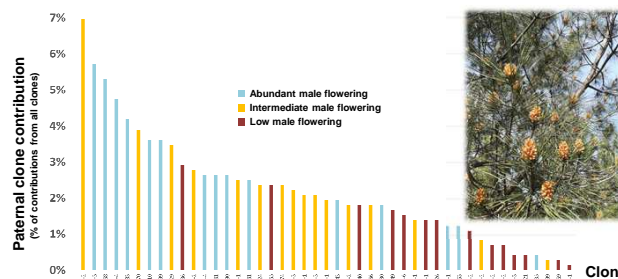


There is no apparent relationship between female flowering phenology of clones and pollen contamination rate (e.g. Vaquey, pollination 2013, SNP analysis of progenies from 24 clones)

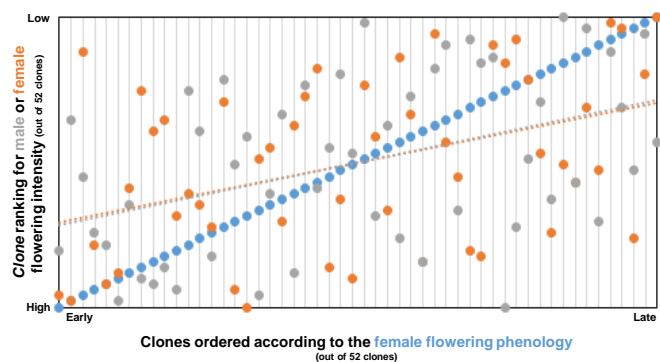


Male flowering intensity partly explains the heterogeneity of paternal contributions to seedlots

(e.g. Vaquey, pollination years 2011 & 2013, SNP analysis of paternal contributions from 45 clones)



A positive relationship is detected between female flowering phenology (●) and male (●) or female (●) flowering intensity (all 2015 and 2016 data from the 3 clonal seed orchards)



Relationships (linear regression) between flowering phenology and male ($R^2 = 0.1858$) or female ($R^2 = 0.1688$) flowering intensities are shown as dotted lines.

Major findings

Open-pollinated clonal seed orchards are a cost-effective way to deliver expected genetic gain in new varieties provided that female and male contributions of selected clones are well balanced and that contamination by foreign pollen is low. Molecular analyses (SNP markers) of maritime pine orchards producing the VF3 variety revealed high pollen contamination rates (Bouffier et al. 2017), therefore questioning the mating structure in relation with flowering phenology and intensity of clones. A strong genetic control of flowering traits is suggested from the survey of 3 VF3 clonal seed orchards during two consecutive seasons. Female phenology could not be related with pollen contamination rate but male flowering intensity could partly explain reproductive success of clones. A positive relationship was observed between female flowering phenology and flowering intensity suggesting some genetic correlation as observed in e.g. eucalypts (Cané-Retamates et al. (2011) *Euphytica* 178: 177; Contreras-Soto et al. (2016) *J. For. Research* 27: 239). Observation bias cannot be however excluded, e.g. underestimated flowering intensity for late clones.

Acknowledgements: This project was supported by the French Ministry of Agriculture (MAADGAL, QUASEGRAINE/2014-352/coord. ONF, B. Musch). We thank the Maritime Pine Breeding Cooperative (GIS Pin Maritime du Futur) for its support through the FORTIUS project granted by Region Nouvelle Aquitaine and MAA. SNP genotyping was performed at the Bordeaux Genomic Facility granted by Region Nouvelle Aquitaine (20030304002FA, 20040305003FA), FEDER funds from European Union (2003227) and ANR (XYLOFOREST/ANR-10-EQPX-16).

