Signatures of selection on roses from 19th and 20th centuries

Rose diversity (crédits : Agnès Grapin)

Socio-economic and scientific context

The rose, plant with a strong symbolic value in art and culture has also a remarkable heritage value, with more than 30,000 known old and present varieties, some of which are preserved in rose gardens. The rose represents half of the cut flower market in Europe and rosebush is the leader plant for private garden market.

In the 19th century, intense varietal creation activity took place in Europe, with interbreeding between old European and Asian roses. The 20th century saw a segmentation of the uses of roses: garden roses, cut flowers, perfumes, pot plants, etc. From domestication to the present day, phenotypic characteristics have evolved such as petal colour, number of petals, flowering time, fragrance, resistance to (a)biotic stresses, etc. Molecular markers are still not widely used in ornamental plant breeding, and the impact of the selection on the evolution of the rose genome remains poorly known. The results obtained will be a major step forward for both academic researchers and breeders.

Assumptions and questions

It is hypothesised that anthropogenic breeding activities on roses over time and in relation to use and selected traits may have left selection signatures, e.g. high levels of genetic differentiation in selected genomic regions between contrasting groups of roses or reductions in diversity related to positive selection of alleles involved in advantageous traits.

The scientific questions are: (1) What are the genome-wide selection signatures in roses bred in the 20th- 21st centuries, in relation to type of use and breeding periods? (2) What selection pressures have candidate genes undergone during the 19th century?

The main steps of the thesis and methodological approaches considered

The study will be based on a large sample of roses including the genetic resources used in plant breeding. The first part will consist of searching for selection signatures in 20th and early 21st century roses, using a pool-seq approach. Resequencing data has been produced for 4 pools defined on "type of use": cut flowers, garden plants, pot plants and, for comparison, botanical roses. Further pools are to be defined in the first half of the thesis to address issues such as breeding periods. The second part of the thesis will look for selection signatures in 19th century roses, using a candidate gene approach. A sample of 365 roses from the 19th century was phenotyped and characterised for sequences of 50 randomly selected genes and 11 candidate genes involved in flowering, petal number, colour, fragrance and architecture.

Selection signatures may be looked for based on allele frequencies in previously identified genetic groups or pools, for both research questions. The distinction between the effect of selection and the effect of demographic history on molecular evolution can be made by comparing regions of the genome for the research question (1) or between candidate genes and random genes for research question (2).

The selection signatures detected will be compared with the genomic region already detected in F1' progenies and by GWAS. The selected traits could be assessed in the light of the work carried out with the historians of the University of Angers (UMR TEMOS).

Scientific and technical skills required by the candidate

Basic bioinformatics skills (running Bash/Shell commands on a computing server, managing large datasets, mastery of a programming language such as Python or Perl and R, proficiency in softwares for managing short reads) and in population genetics/genomics, in particular research into selection signatures.

Research Unit

The thesis will be carried out at the Institute of Research in Horticulture and Seeds (IRHS) in Angers, a French leading centre for research and teaching in plant sciences. https://www6.angers-nantes.inrae.fr/irhs

Thesis supervision

Thesis director: Agnès GRAPIN (Associate Professor HDR Institut Agro) agnes.grapin@agrocampus-ouest.fr

Thesis co-supervisor: Jérémy CLOTAULT (Associate Professor Université d'Angers) jeremy.clotault@univ-angers.fr

Thesis funding

Funding already acquired. Gross monthly salary: 2 044.12 € in 2023, 2 100 in 2024 and 2 200 in 2025.

Recruitment procedure

Please send your CV, M1 and M2 transcripts, a letter of recommendation and a covering letter to the two supervisors by 20 September at the latest. Interviews will be organised in the very beginning of October in order to start the thesis before the end of 2023.

Date of start/duration of thesis funding: November or December 2023 / 36 months

Publications of the team on thesis subject

Leroy T, Albert E, Thouroude T, Baudino S, Caissard JC, Chastellier A, Chameau J, Jeauffre J, Loubert T, Paramita SN, Pernet A, Soufflet-Freslon V, Oghina-Pavie C, Foucher F, Hibrand-Saint Oyant L, Clotault J (2023) Dark side of the honeymoon: reconstructing the Asian x European rose breeding history through the lens of genomics. *BioRxiv* 2023.06.22.546162 [doi: 10.1101/2023.06.22.546162]

Clotault J, Foucher F, Grapin A, Hibrand-Saint Oyant L, Malécot V, Paillard S, Pernet A, Soufflet-Freslon V, Oghina-Pavie C (2022) Rose selection in France: a long and beautiful history. *Chronica horticulturae* 62: 28-37 [Lien].

Soufflet-Freslon V, Araou E, Jeauffre J, Thouroude T, Chastellier A, Michel G, Mikanagi Y, Kawamura K, Banfield M, Oghina-Pavie C, Clotault J, Pernet A, Foucher F (2021) Diversity and selection of the continuous-flowering gene, *RoKSN*, in rose. *Horticulture Research* 8: 76 [doi: 10.1038/s41438-021-00512-3].

Smulders MJM, Arens P, Bourke PM, Debener T, Linde M, De Riek J, Leus L, Ruttink T, Baudino S, Hibrant Saint-Oyant L, Clotault J, Foucher F (2019) In the name of the rose: a roadmap for rose research in the genome era. *Horticulture Research* 6: 65 [doi: 10.1038/s41438-019-0156-0].

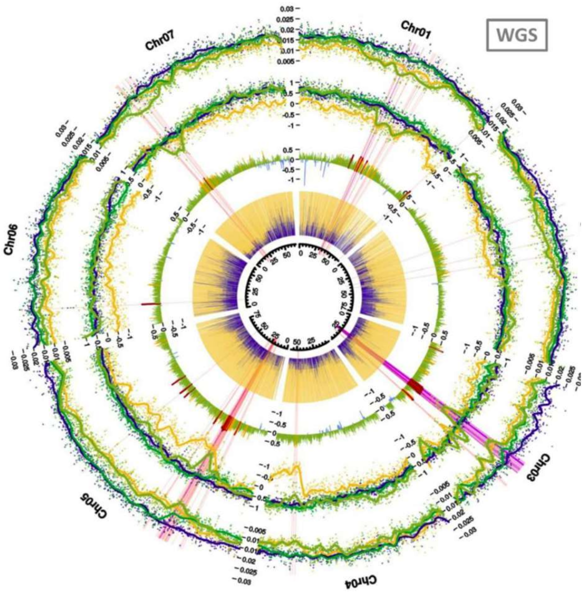

Figure 1: Detection of regions exhibiting footprints of selection in hybrid tea roses. (Leroy et al. 2023)

Hibrand Saint-Oyant L, Ruttink T, Hamama L, Kirov I, Lakhwani D, Zhou N-N, Bourke PM, Daccord N, Leus L, Schulz D, Van de Geest H, Hesselink T, Van Laere K, Debray K, Balzergue S, Thouroude T, Chastellier A, Jeauffre J, Voisine L, Gaillard S, ..., Clotault J, ..., Aubourg S, Sakr S, ... Foucher F (2018). A high-quality genome sequence of *Rosa chinensis* to elucidate ornamental traits. *Nature Plants* 4: 473–484 [doi: 10.1038/s41477-018-0166-1].

Liorzou M, Pernet A, Li S, Chastellier A, Thouroude T, Michel G, Malécot V, Gaillard S, Briée C, Foucher F, Oghina-Pavie C, Clotault J, Grapin A (2016) Nineteenth century French rose (*Rosa* sp.) germplasm shows a shift over time from a European to an Asian genetic background. *Journal of Experimental Botany*, 67 :47114725 [doi: 10.1093/jxb/erw269]