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# INTEGRATIVE OVERVIEW OF GENETIC AND GENOMIC OF AGRONOMIC TRAITS IN EDIBLE CHERRIES

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## INTRODUCTION

- Cherry trees include species that can be used for their fruits, their flowers as ornamental trees or as rootstocks.

- Fruits from edible cherry can be consumed as fresh fruits or after processing like jam, dried or candied fruit for pastry, juice or brandy.

- They belong to four main species: sweet cherry (*Prunus avium* L.), Chinese cherry (*P. pseudocerasus* L.), sour/tart cherry (*P. cerasus* L.), and Nanking cherry (*P. tomentosa* Thunb.).

- Genome data, genetic maps, QTLs, GWAS loci and validated functional genes were integrated to provide a global genetic architecture of various agronomic traits related to phenology, physiology, abiotic stress and fruit quality traits such as fruit color, cracking, firmness or fruit size.

## RESULTS

- To date, *P. avium*, *P. cerasus* and *P. pseudo cerasus* have been sequenced (A) but most of the genetic and genomic data are on *P. avium*. However, new genome assembly for the tetraploid *P. pseudocerasus* is now available (Jiu et al. 2024).

- By compiling results already reported on the sweet cherry 'Tieton' genome, we observed syntenic regions between *P. avium* and *P. cerasus* for several traits.

- For example, for flowering date, QTLs were reported on *P. avium* and *P. cerasus* on chromosomes 1, 2 and 4, while QTLs on chromosomes 6 and 7 were detected only for *P. avium*, and QTL on chromosome 5 only on *P. cerasus* (B).

## CONCLUSION




- The complex tetraploid genomes of *P. cerasus* and *P. pseudocerasus* have slowed genetic progress, but their recent genome sequences offer opportunities to address limitations like small fruit size, soft texture and short shelf life.

- Genetic studies on *P. tomentosa* remain limited but its unique shrub form and the medicinal properties of its seeds provide promising avenues for future exploration.

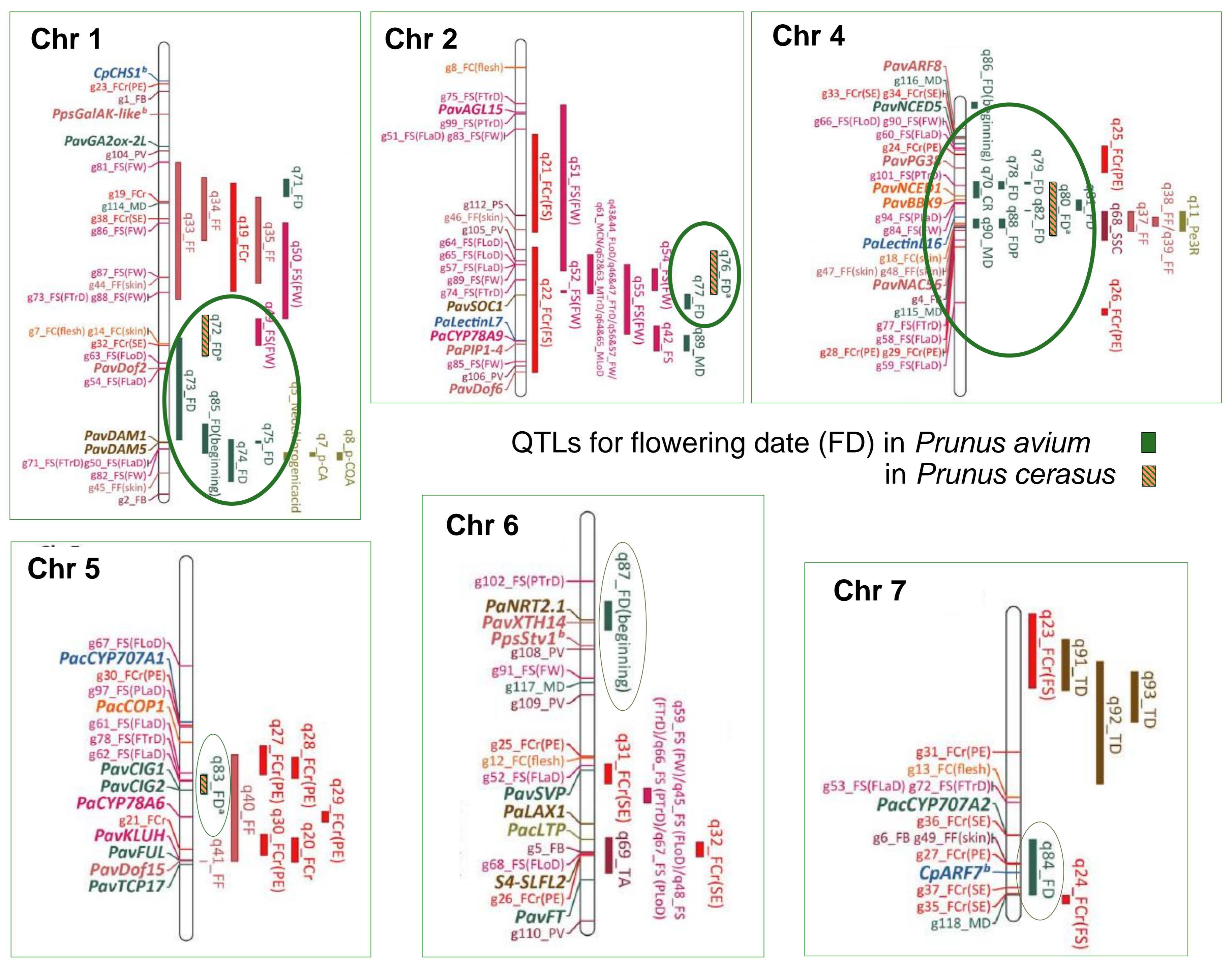
- The availability of sequence data and targeted genomic regions involved in the variation of agronomic traits will allow the construction of an interspecific pangenome of edible cherries.

- Thanks to an integrated analysis of these data, common genomic regions appear under selection pressure between the species.

## A- Edible cherries

| Origin                      | Europe around the Caspian and Black Seas  |   | South  | China   | North  |
|-----------------------------|---|---|--|---|--|
|                             |  |  |   |  |  |
|                             | <b>Sweet cherry</b><br>( <i>P. avium</i> L.)<br>2n=2x=16                            | <b>Sour/tart cherry</b><br>( <i>P. cerasus</i> L.)<br>2n=4x=32                      | <b>Chinese cherry</b><br>( <i>P. pseudocerasus</i> Lindl.)<br>2n=4x=32   |   | <b>Nanking cherry</b><br>( <i>P. tomentosa</i> Thunb.)<br>2n=2x=16   |
| <b>Main characteristics</b> | Firm and large fruits, sweet taste<br>Chilling requirement, cracking                | Sour taste<br>Small and soft fruits   | Early bloom and maturity, disease and pest resistance, small trees easily harvested, no fruit cracking<br>Sour taste, soft, short shelf-life |   | Well adapted to every climate and condition (extreme cold, or heat, arid), pit with high flavonoid content, source of bioactive compounds<br>Small and soft fruits |
| <b>Genomes</b>              | Satonishiki<br>Tieton<br>Regina<br>Big Star   | Montmorency   | Zhuji Duanbing   |   |  |
| Cultivar                    |   |   |  |   |  |
| Estimated size (Mb)         | 322~353   | 621   | 1090   |   |  |
| Assembled size (Mb)         | 272~344   | 1066 (subgenomes A, A', B)  | 994  |   |  |

## B- Focus on the genetic architecture of the flowering date



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