

# Determination of genetic loci in the control network of grapevine flowering

Anna Schwandner<sup>1</sup>, Iris Ochßner<sup>1</sup>, Ludger Hausmann<sup>1</sup>, Nadia Kamal<sup>2</sup>, Boas Pucker<sup>2</sup>, Daniela Holtgräwe<sup>2</sup>, Felix Bemm<sup>3</sup>, Detlef Weigel<sup>3</sup>, Bernd Weisshaar<sup>2</sup>, Reinhard Töpfer<sup>1</sup>

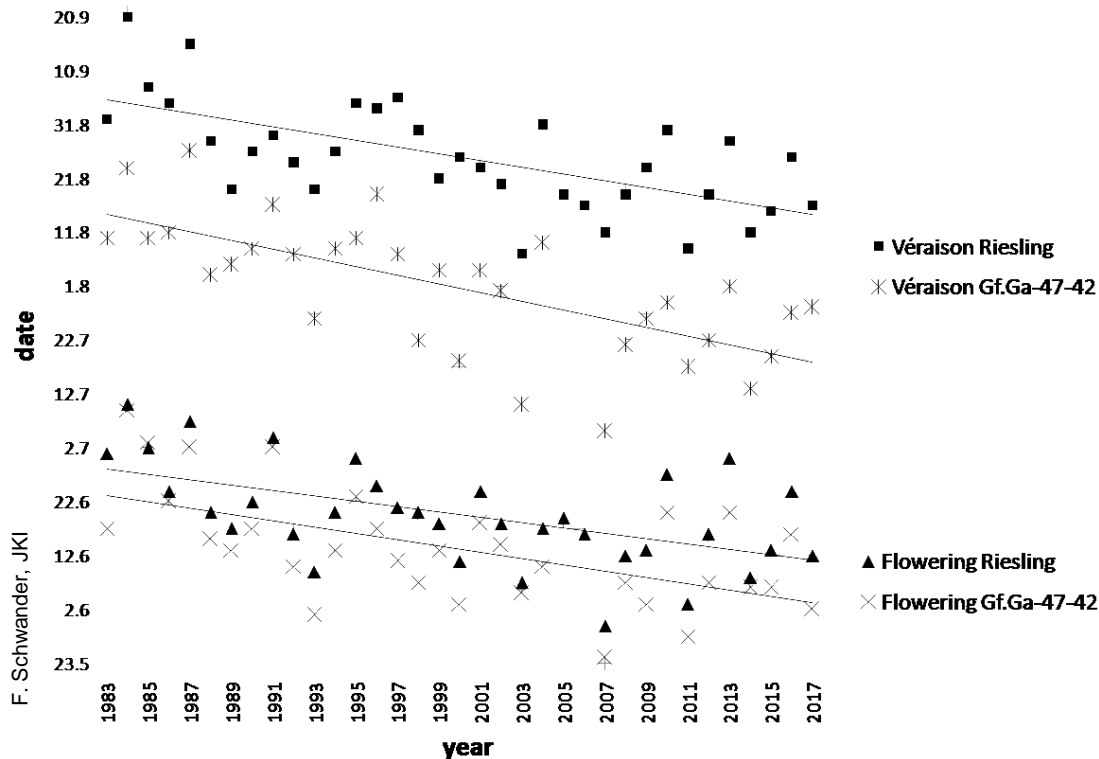
<sup>1</sup> Julius Kühn-Institut, Institute for Grapevine Breeding Geilweilerhof, Siebeldingen

<sup>2</sup> Bielefeld University, Faculty of Biology & Center for Biotechnology

<sup>3</sup> Max Planck Institute, Institute for Developmental Biology, Tübingen

# Motivation

- Temperature is the main environmental factor affecting grapevine development
- Climatic changes and global warming



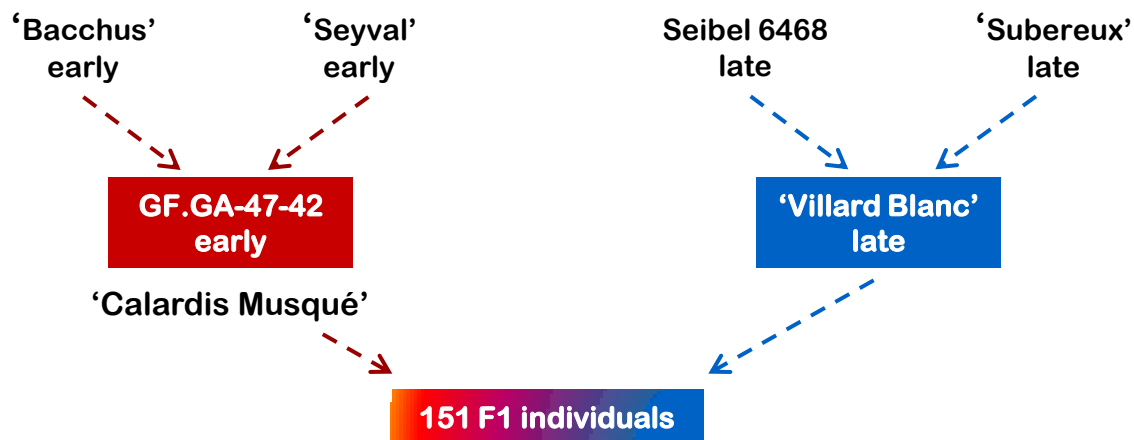
- Timing of flowering participates in timing of ripening
- Knowledge-based breeding of new, adjusted grapevine varieties

# Aims

- Find genetic loci/genes contributing to the timing of grapevine development especially timing of flowering
  - QTL analysis
  - Correlation of alleles/haplotypes and flowering time phenotype
  - Differential gene expression studies over the whole developmental cycle



# Mapping population GF.GA-47-42 x 'Villard Blanc'



# QTL analysis

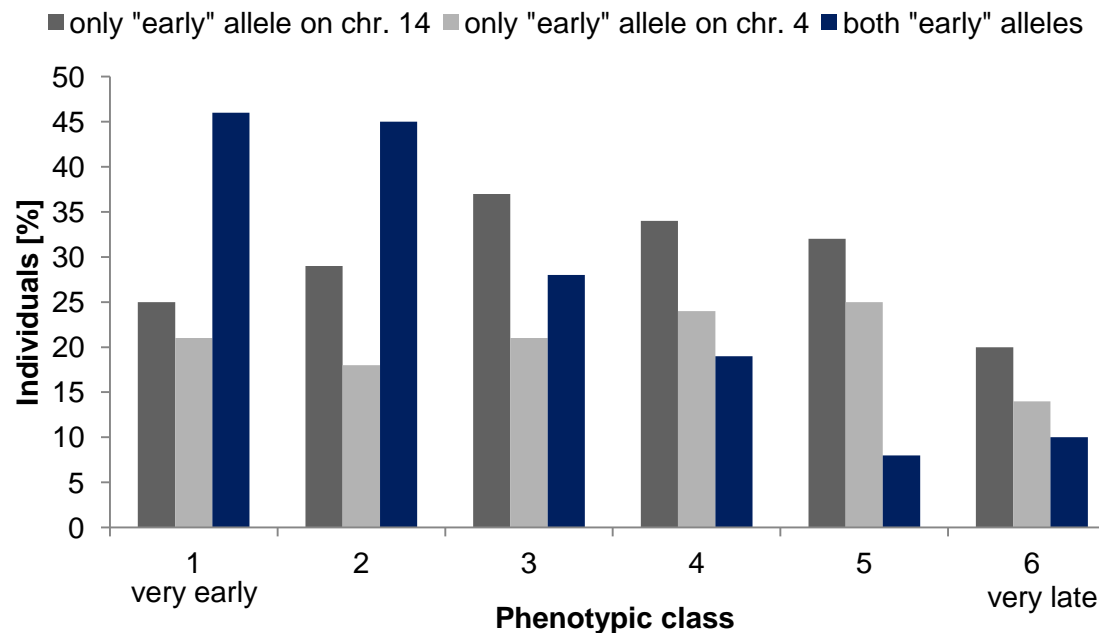


- QTL on several chromosomes of GF.GA-47-42 x 'Villard Blanc'
- Some regions coincide with QTL detected in a second population (Fechter et al. 2014)
- Indicates general function of these regions in *Vitis* flowering
- Additive effects of detected QTL observed

# Additive effects of flowering time QTL



- Only one “early” allele (in the QTL on chr. 4 or 14) doesn’t lead to an early phenotype
- F1 individuals with both “early” alleles present tend to actually flower earlier
- Impact of further QTL possible



# Main QTL on chr.14



- Consistently recurring QTL in all 10 years
- Appears to have the highest impact on time of full bloom
- Here only maternal (GF.GA-47-42, early flowering) influence on flowering time

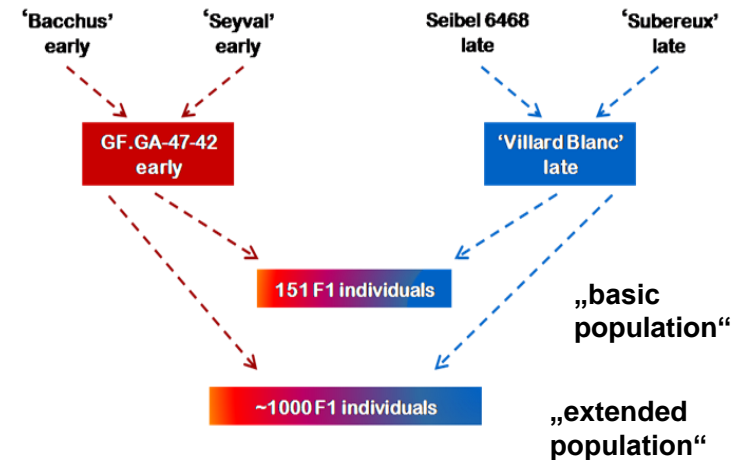
# Extension of the mapping population



- Validation of flowering time QTL on 6 chromosomes in the extended population
- QTL on chromosome 14 is again the most prominent
- No change in QTL positions

|   | 2015 | 2016 | 2017 | 2018 |
|---|------|------|------|------|
| F1 individuals with „mature“ inflorescences | 122  | 545  | 394  | 691  |

|      | Chromosome |   |   |    |    |    |    |
|------|------------|---|---|----|----|----|----|
|      | 1          | 4 | 8 | 14 | 17 | 18 | 19 |
| 2015 |            |   |   | x  |    |    |    |
| 2016 |            | x | x | x  | x  |    |    |
| 2017 | x          | x |   | x  | x  |    | x  |
| 2018 | x          | x | x | x  | x  |    | x  |





# Season spanning RNA-Seq experiments

- Four years, two genotypes, buds and inflorescences
- Which genes show differential expression over time and between genotypes?
- Find FTC candidate genes involved in different developmental steps

GF.GA-47-42  
early

'Villard Blanc'  
late



# Season spanning RNA-Seq experiments

- New FTC candidate genes revealed by their expression patterns
- Gene expression patterns of both genotypes support each other in the respective developmental stage
- Gene expression relatively stable over the rather long period before dormancy
- During and after dormancy genes cluster into two groups:
  - Genes up-regulated during bud dormancy
  - Genes up-regulated towards single flower development
- Some FTC homologs not expressed in grapevine buds/inflorescences

# Further approaches



Max Planck Institute for  
Developmental Biology

- Generation of whole genome sequences of the early and late parent of the mapping population
- Creation of a high resolution genetic map based on SNPs derived from RAD-Seq
- Association studies with amplicon sequences of selected candidate genes showed a significant correlation with specific flowering time phenotypes
- Testing if genetic markers can be applied in MAS

# Summary



- Several QTL for time of full bloom
- Proposing putative flowering time and developmental genes on the basis of:
  - Location within QTL regions
  - Association of specific alleles with a particular flowering time phenotype
  - Season-spanning RNA-Seq experiments

# Thank you for your attention!



## Acknowledgements

Reinhard Töpfer  
Ludger Hausmann  
Eva Zyprian  
Iris Ochßner  
Andreas Preiß  
Carina Mook  
Florian Schwander  
Daniel Zender  
Franco Röckel  
Robert Richter  
Florian Rist



Nadia Kamal  
Daniela Holtgräwe  
Boas Pucker  
Bernd Weisshaar  
Willy Keller  
Prisca Viehöver



Universität Bielefeld

Felix Bemm  
Detlef Weigel



MAX-PLANCK-GESellschaft  
Max Planck Institute for  
Developmental Biology

And the DFG for funding the project.

