Molecular analysis of bunch architecture in grapevine

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BÖLN
Bundesprogramm Ökologischer Landbau und andere Formen nachhaltiger Landwirtschaft

Max Planck Institute for Plant Breeding Research

GBG 2018, Bordeaux, France, July 15-20, 2018

Why study bunch architecture?

Loose clusters

- Dry off quickly
- Don´t squeeze each other
- Have less micro cracks
- Have intact wax layers
- Are better covered by protective sprays

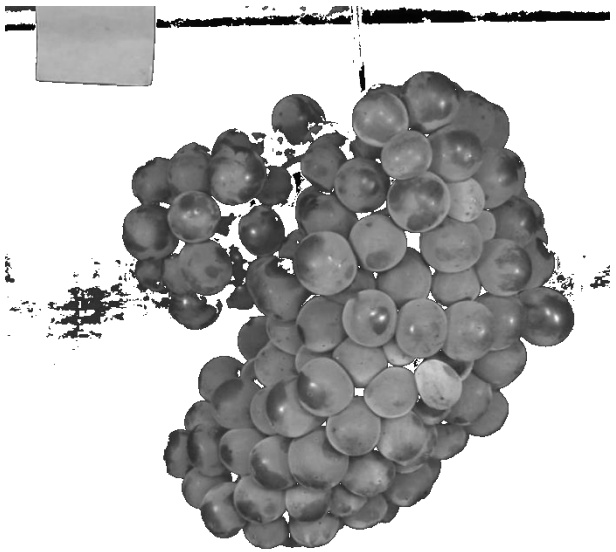
- Are more resilient to ***Botrytis*** bunch rot and other infections

- Represent a physical factor of resistance

QTL Analysis in population GF.GA-47-42 x `Villard blanc´

- 150 F_1 individuals with considerable (transgressive) segregation of cluster architecture traits
- genetic map available (Zyprian et al., 2016)
- eight vines per genotype
- 46 females, 104 hermaphrodite plants

OIV class 1
Individual 0212



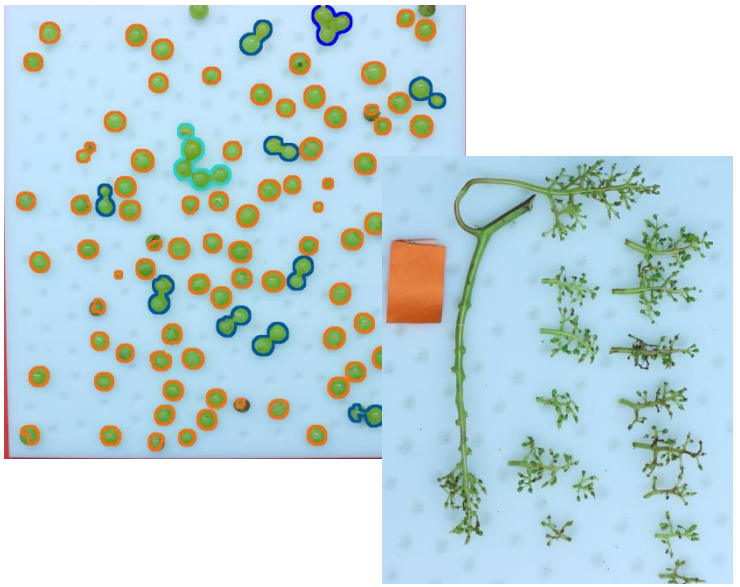
OIV class 9
Individual 0324

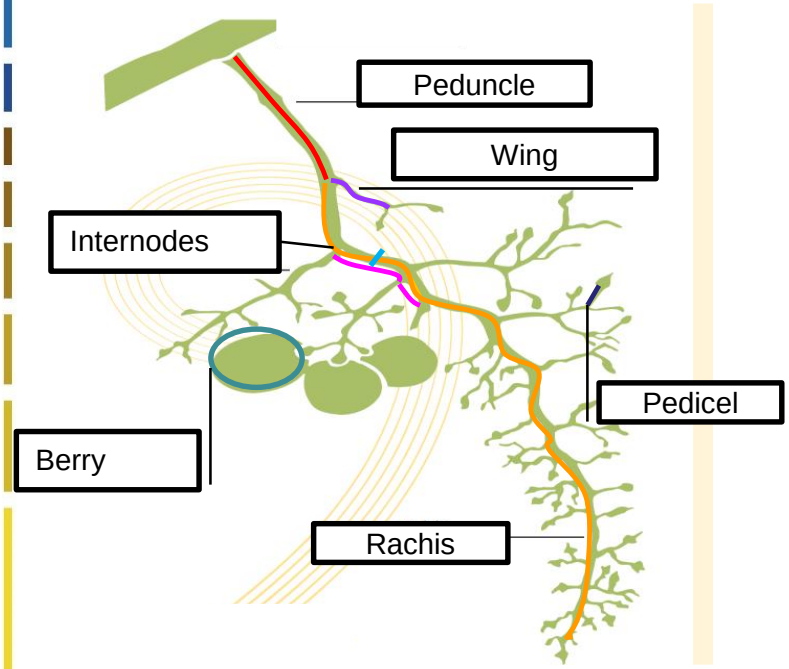
QTL Analysis in population GF.GA-47-42 x `Villard blanc´

Sampling:
6 basally inserted clusters at 6 different trunks

BBCH81 – BBCH87

Phenotyping of cluster architecture sub-traits, over two to four years





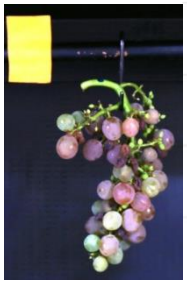
- Image based assessment of sub-traits using
  - BAT software for volume (Kicherer et al. 2013)
  - ImageJ for length parameters
- Reference measurements: volume, weight
- **→ in total 19 ampelometric measurements**

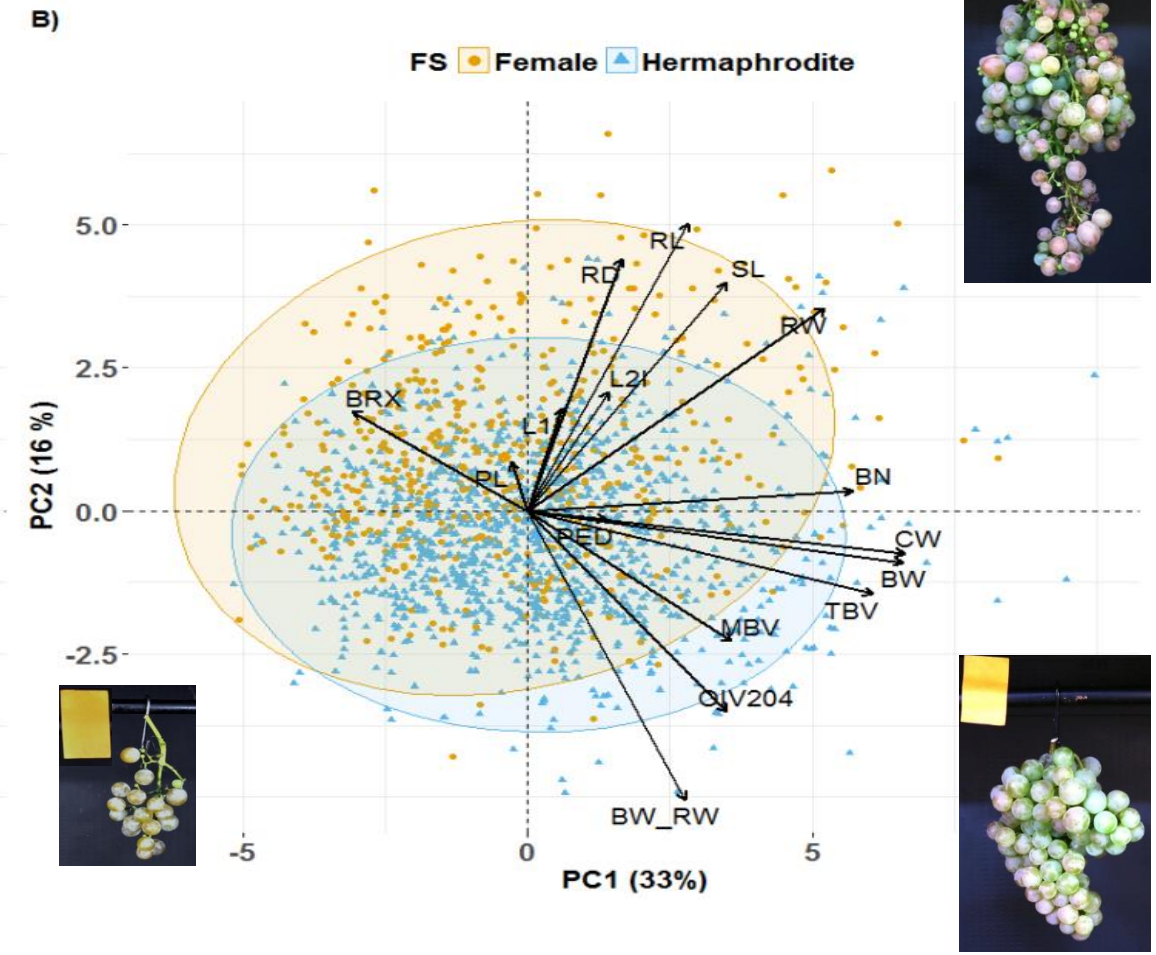
Cluster architecture sub-traits

Sub-trait [Unit]	Notation	2013 n=12	2014 n=3	2015 n=6	2016 n=6	2017 n=6
berry number per bunch	**BN**	x	x	x	x	
sugar content of juice [°Bx]	**Brix**			x	x	
berry weight [g]	**BW**			x	x	
berry weight/rachis weight	**BW/RW**			x	x	
cluster weight [g]	**CW**	x	x	x	x	
mean single berry volume [cm³]	**MBV**	x	x	x	x	
compactness	**OIV204**	x		x	x	x
pedicel length [cm]	**PED**	x	x	x	x	
peduncle length [cm]	**PL**	x	x	x	x	
length 1st internode of rachis [cm]	**L1I**	x		x	x	
length 2nd internode of rachis [cm]	**L2I**	x		x	x	
length 3rd internode of rachis [cm]	**L3I**	x			x	
diameter 2nd internode of rachis [cm]	**RD**			x	x	
rachis length [cm]	**RL**	x	x	x	x	
rachis weight	**RW**			x	x	
shoulder length	**SL**		x	x	x	
total berry volume	**TBV**	x	x	x	x	
total length of laterals	**TLL**	x			x	
presence/ absence of a “shoulder”	**Wing**				x	x

Sub-traits with large effect on CA (OIV204) after statistical evaluation and modeling

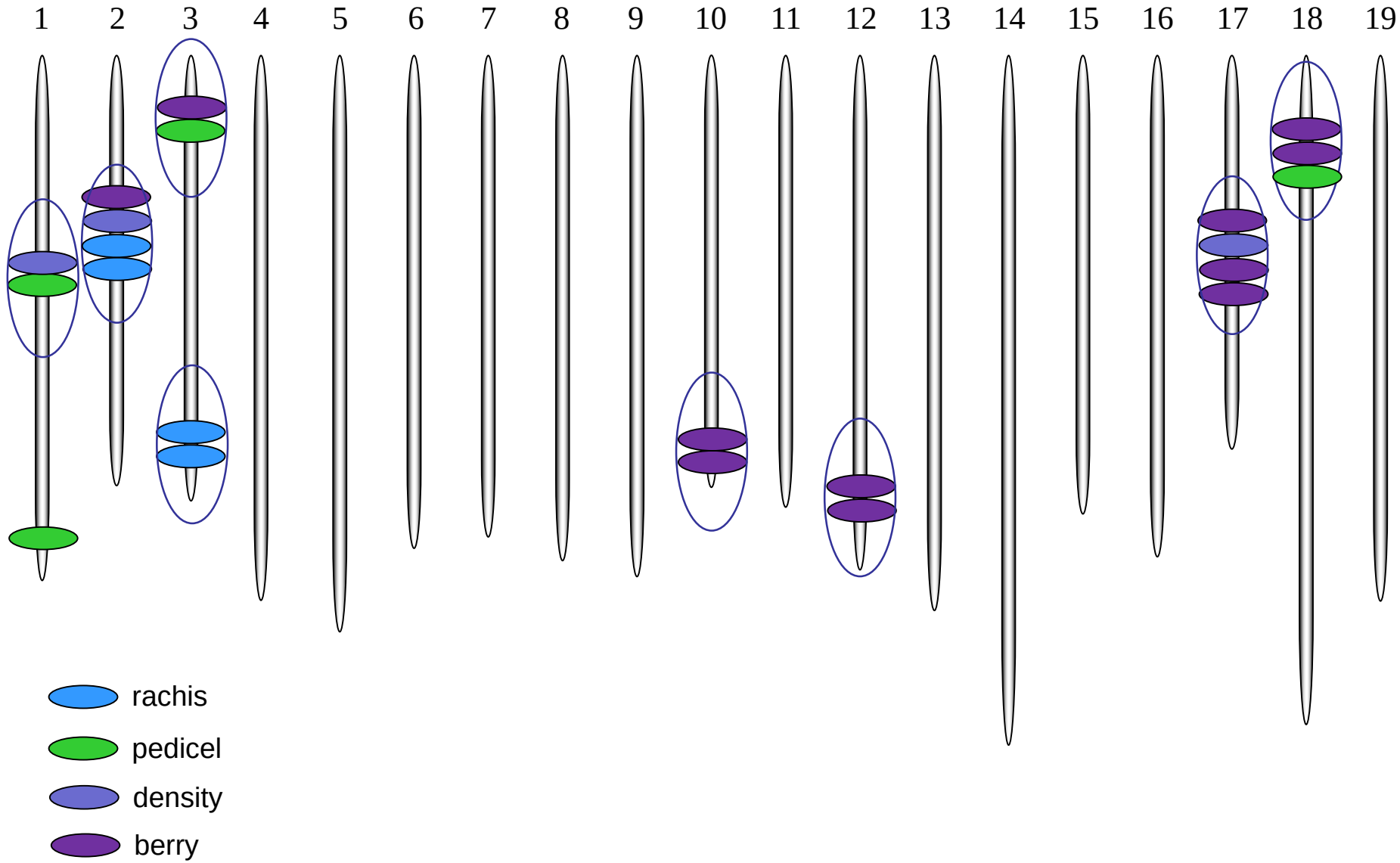
Statistical evaluation of cluster architecture sub-traits

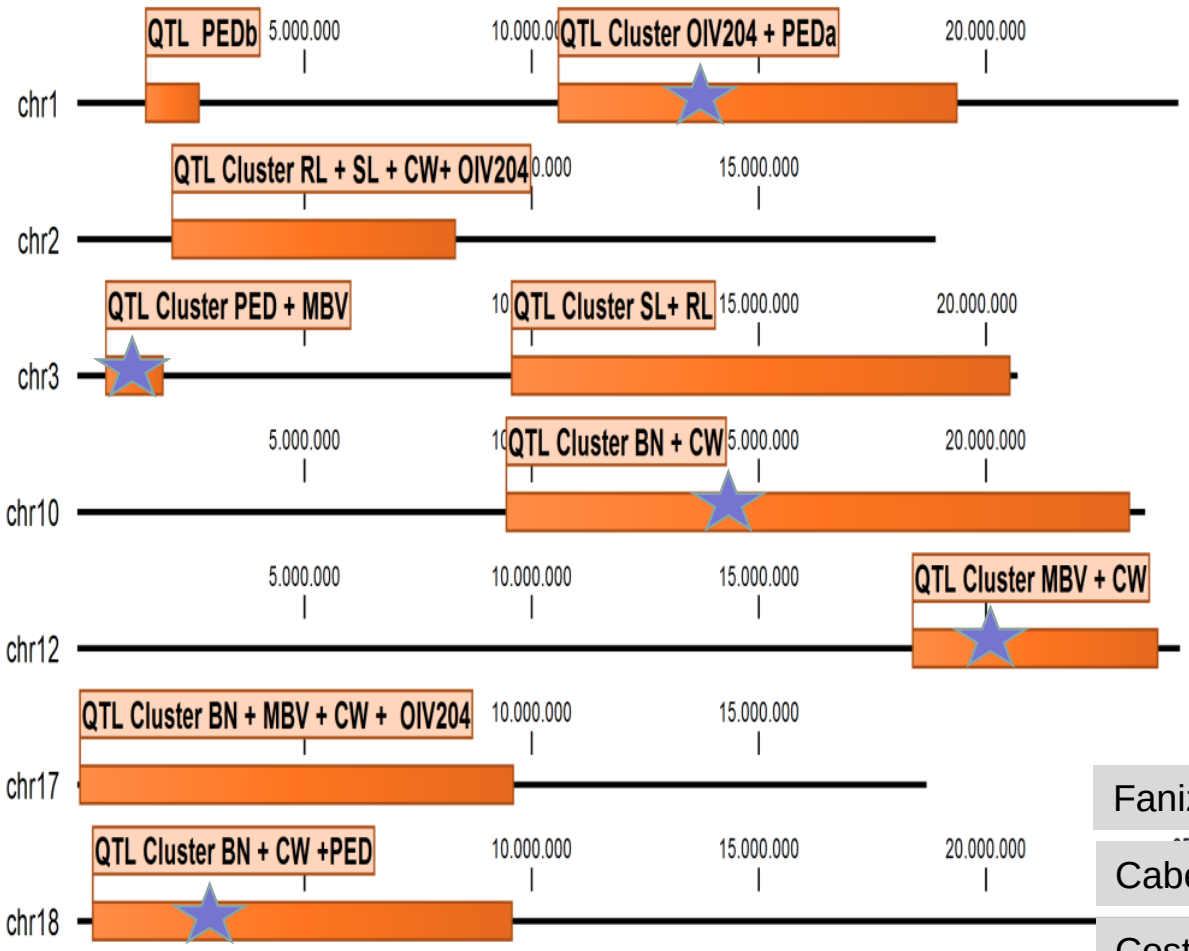




Flower sex affects cluster architecture: Females are more loose!

23 QTLs for large effect sub-traits in eight clusters





newly identified QTL region

Markers flanking QTL clusters are available

- Fanizza et al. 2005 table grape
- Cabezas et al. 2006 table grape
- Costantini et al. 2008 table grape
- Marguerit et al. 2009 hybrid cross
- Doligez et al. 2013 table/wine
- Correa et al. 2014 table grape

Expression Analysis in `Pinot noir´

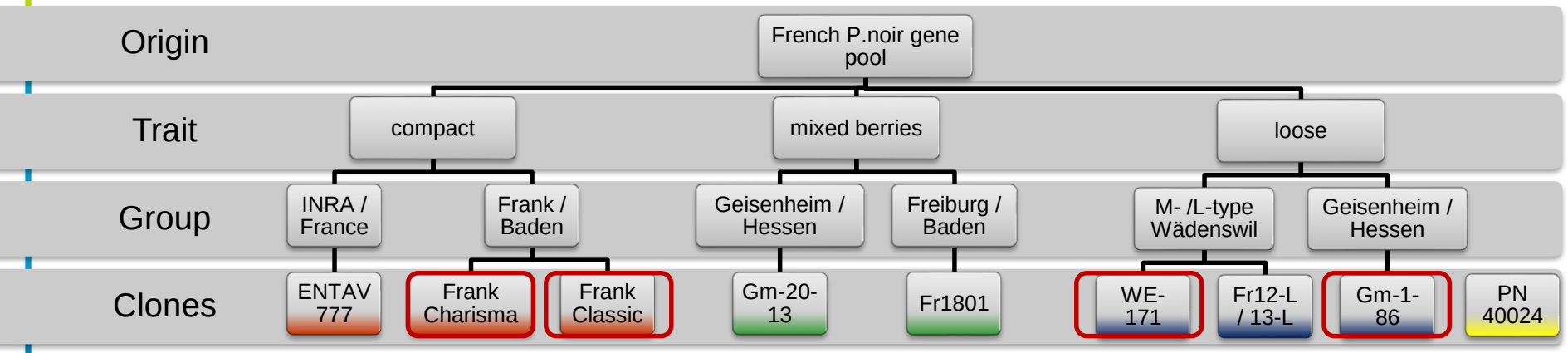


Foto: Antes

Foto: E. Wennesheimer Worms

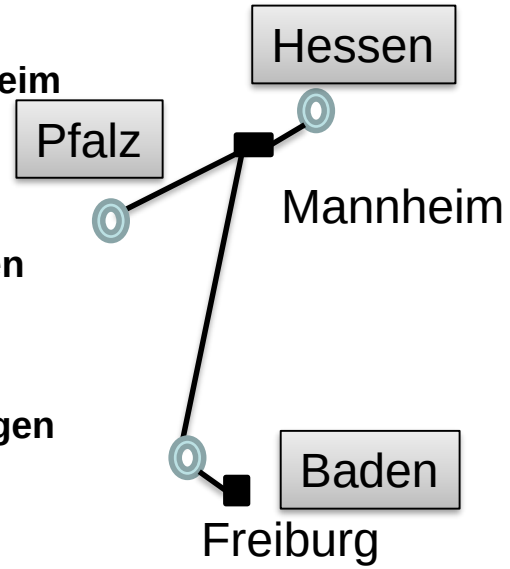
Foto: R.Richter , JKI Geilweilerhof

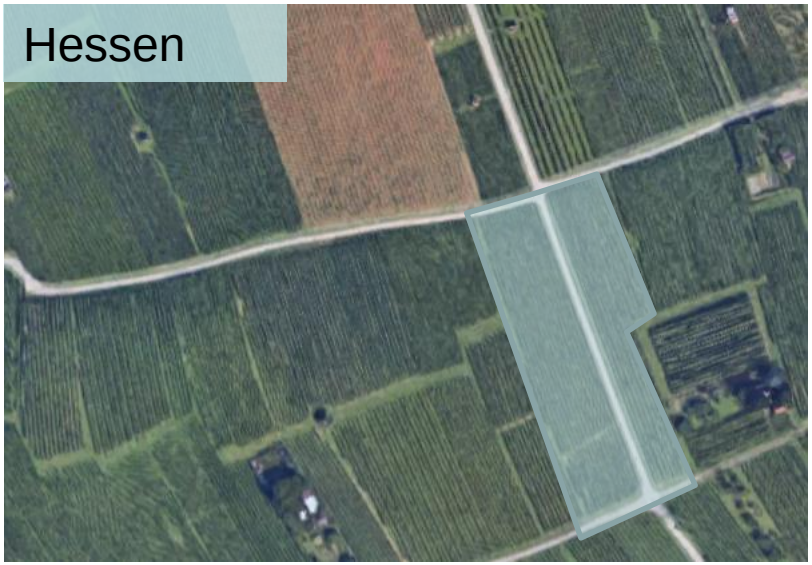
Plants in three different locations

Antes Heppenheim
1995
125AA /1,8m²

JKI Siebeldingen
2005
125AA/1,8 m²

Sibbus Jechtingen
1997
125AA/2,2m²





Sampling harmonized according to degree/days (Molitor, 2014)

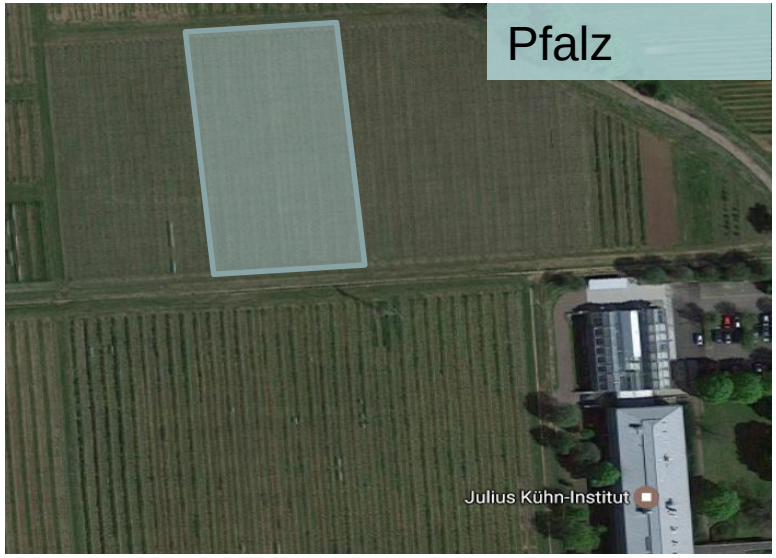


Foto: google earth

Phenotyping in ‘Pinot noir’

- Eight of 20 sub-traits show significant differences between clones
- Grouping in loose and compact clustered clones reveals **four sub- traits** as significantly different

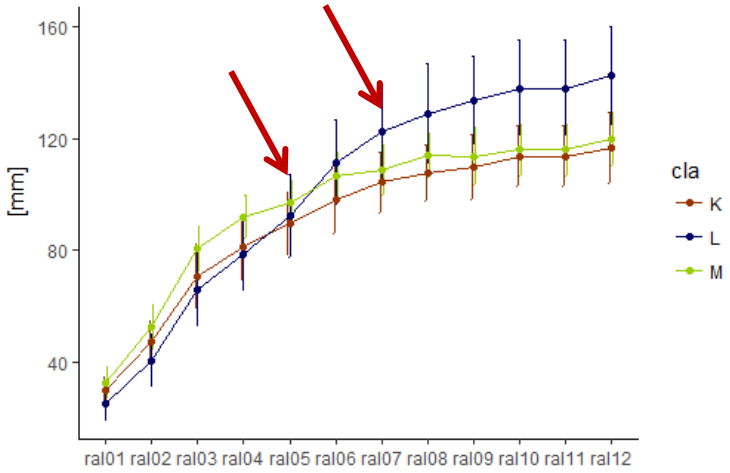
Variance analysis (ANOVA) indicates

- **Berry volume**
- **Pedicel length**
- **Rachis length**
- **Total berry volume**

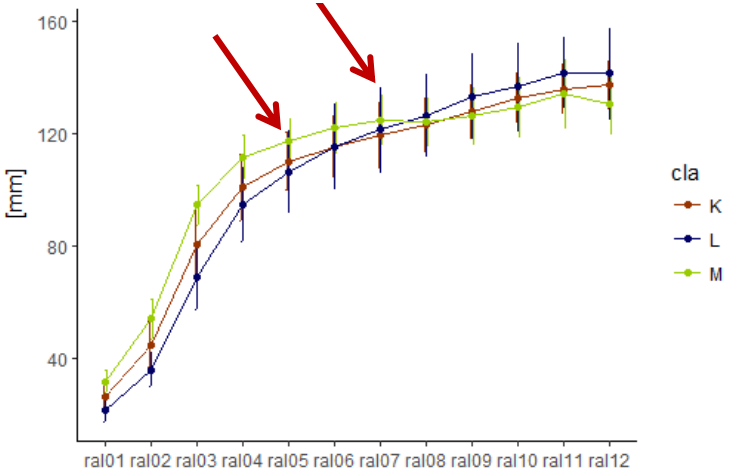
as determinants of CA

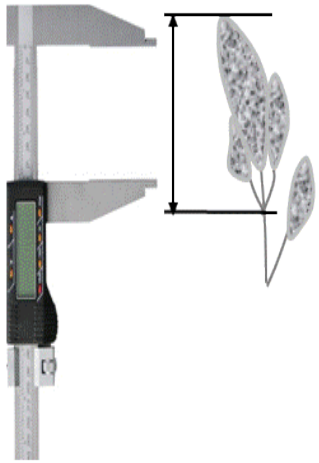
Investigation of rachis elongation

Weekly rachis length 2015

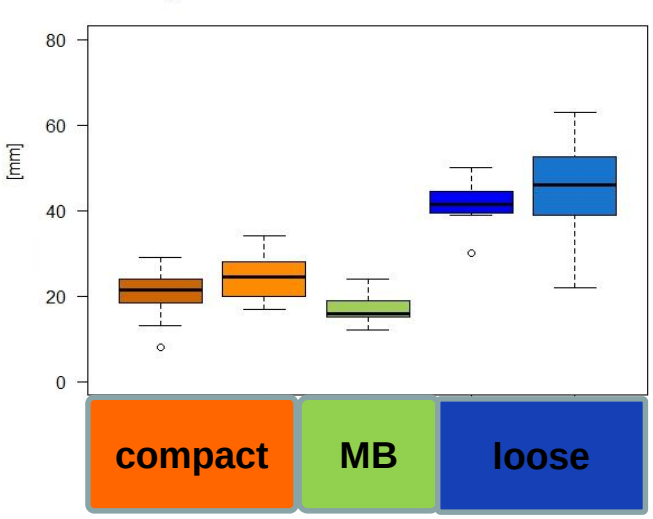


Weekly rachis length 2016

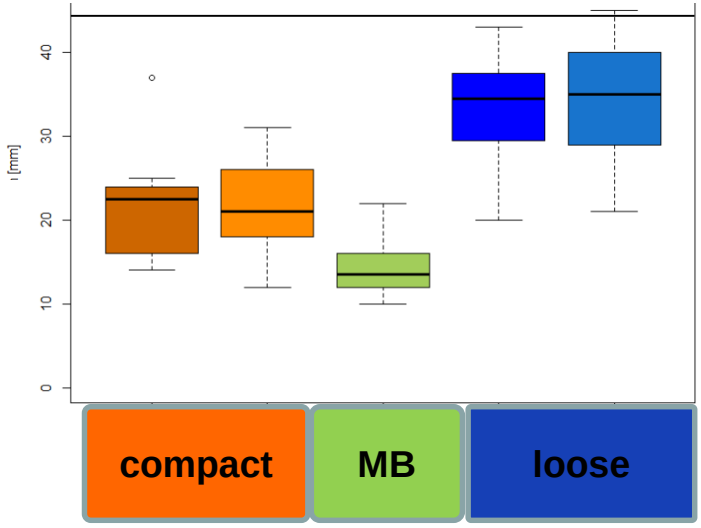




Difference to week before 2015



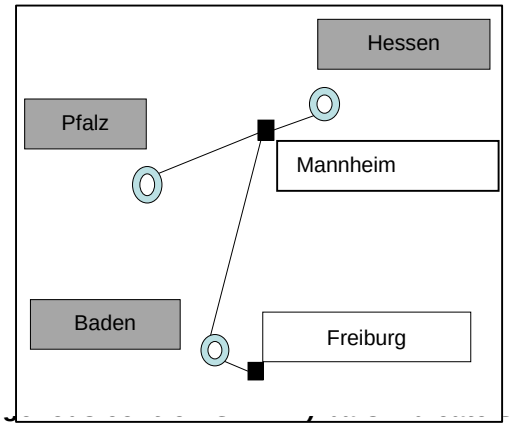
Difference to week before 2016



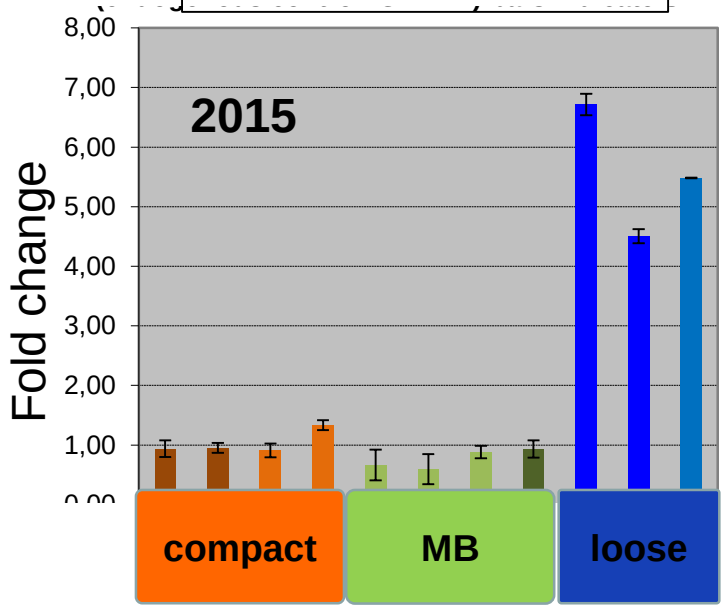
Measurement of rachis length at Geilweilerhof each week from May to August 2015 and 2016 at the same bunch (n = 16)

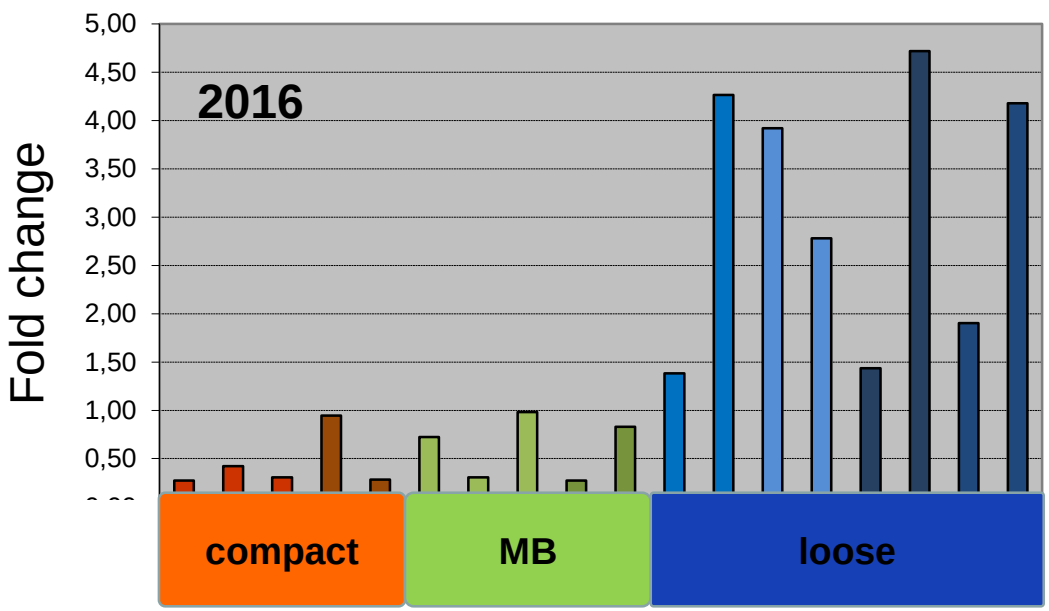
RNA-Seq, RT-qPCR: Candidate gene expression in ‘Pinot noir’ clones

2015/ 2016/ 2017



A candidate gene is consistently higher expressed in loose PN clones over three years and three locations





Conclusions

- Eight QTL regions contain genetic determinants of cluster architecture in GF.GA.47-42 x `Villard blanc´

  Markers from these regions may now be tested for transferability of their linkage to the trait in extended breeding material

- Two candidate genes are differentially expressed in loose versus compact `Pinot noir´ clones, over three locations

Thank you for your attention!

Thanks to…

Grapevine nursery Antes, Heppenheim

Grapevine nursery Sibbus, Jechtingen

Doreen Gabriel

Sarina Elser
Florian Rist
Margit Schneider

Daniel Zendler
Anna Schwandner
Anna Kicherer

Gefördert durch:

Bundesministerium
für Ernährung
und Landwirtschaft

aufgrund eines Beschlusses
des Deutschen Bundestages