



Pre-breeding strategies for obtaining new resilient and added value berries

Workshop

Advancing Berry Breeding: From Phenotyping to Genomic Innovation

RESULTS FROM THE OPEN CALL #1 Marker-Assisted Selection (MAS) in strawberry

INRAE

Béatrice Denoyes
Juliette Bénéjam



The BreedingValue project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 101000747.

Open Call #1: Marker-Assisted Selection (MAS) in strawberry

Objective Open Call #1

- Delivering the MAS method to breeders from private companies that are not familiar with this method
- 3 companies were selected :   
- Taking advantage of Fluidigm® low-density array for genotyping
- Validation of markers in a broad genetic background

Open Call #1: Marker-Assisted Selection (MAS) in strawberry

What were companies asked to do?

1- Traceability



1 unique advanced line

DNA

Phenotypes

2- DNA extraction for genotyping

3- Phenotypes (ex. Fruit weight, Brix, Resistances, ...)



The Strawberry Fluidigm® array

RESISTANCES TO PESTS	SNPs in BV_v3 array
Rce to <i>Pythophthora cactorum</i>	5
Rce to <i>Colletotrichum acutatum</i>	1
Rce to <i>Fusarium oxysporum</i> f. sp.	4
Rce to <i>Colletotrichum gloesporioides</i>	3
Resistance to <i>Verticillium dahliae</i>	2
Resistance to <i>Xanthomonas fragariae</i>	2
Resistance to <i>Podosphaera aphanis</i> (powdery mildew)	5
Resistance to <i>Macrophomina phaseolina</i>	3
Resistance to <i>Tetranychus urticae</i>	2
VEGETATIVE TRAITS	
Day neutrality, Everbearing	3
Flowering time	3
PRODUCTION TRAITS	
Fruit weight (FW)	3
Yield	4
Fruit number	8
FRUIT QUALITY	
Texture (Firmness, bostwick)	6
Fruit color (int, ext, anthocyanins)	11
Flavor	
Sugars (Brix)	7
Acids (pH, malic acid)	3
Nutritional quality	
Vitamin C	4
Polyphenols	3
Aromas	
VOC derived from fatty acids (γ -decalactone)	1
VOC derived from amino acids (phenylpropanoids)	1
Esters	7
Terpene	2
Furanone	3
	96

General description:

96 genetic markers associated to resistance, flowering, yield and quality

Problematic:

Can the markers identified in study populations predict the phenotypic value of hybrids in selection?

SNPs polymorphism

Additive/non-additive control?

Validation of markers

SNP as trait predictor?
Correlation genetic/phenotypic data

Optimisation of array?
Combination of markers

SNPs polymorphism

Material: **1176 DNA samples** analysed, shared from 3 companies



Groups	No. SNPs per group
No polymorphism (only 1 class of allele)	8
Partial polymorphism (2 classes of alleles)	26
Complete polymorphism but 1 class poorly represented (1 class < 10 samples)	16
Complete polymorphism and classes well represented	56

More than **92%** of SNPs are **polymorphic**

SNPs as trait predictor

Method:

Variance analysis on R software

Trait A ~ SNP(A02) + residuals

Using *lm* function (same results as *aov* function)



A list of SNPs was validated = significant link between SNP allelic class and phenotypic mean

SNPs as trait predictor

Method:

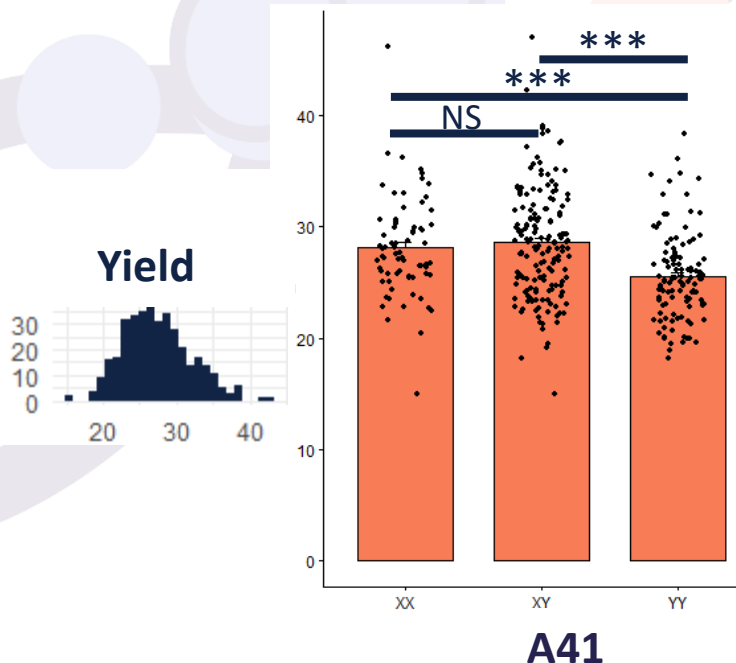
Variance analysis on R software

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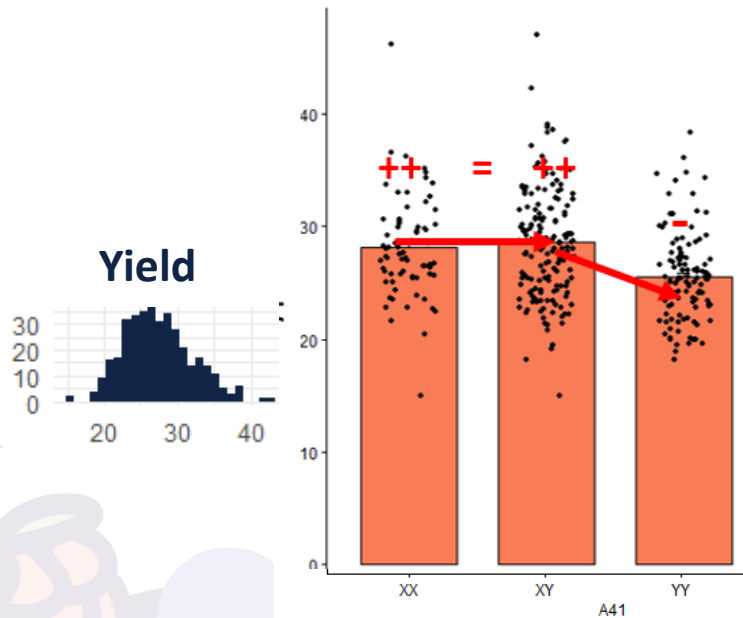
A list of SNPs was validated = significant link between SNP allelic class and phenotypic mean



Mean difference: ~2.5 units between XY and YY

→ Selection of XX or XY genotypes for marker A41 to improve yield

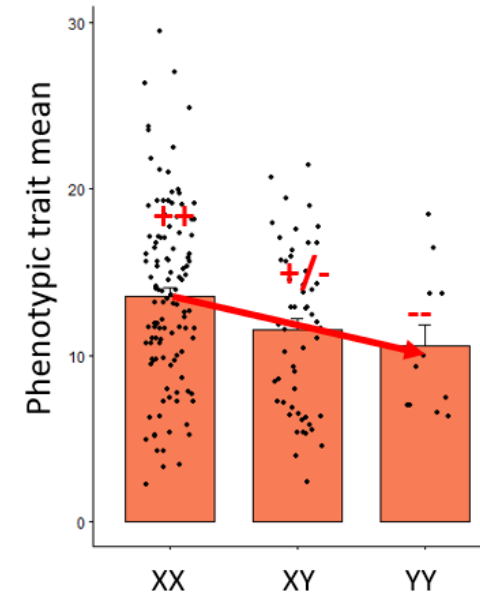
Additive/non-additive



Example 1: dominant effect

$$\text{Mean}_{XX} = \text{Mean}_{XY}$$

$$\text{AND } \text{Mean}_{XX} > \text{Mean}_{YY}$$



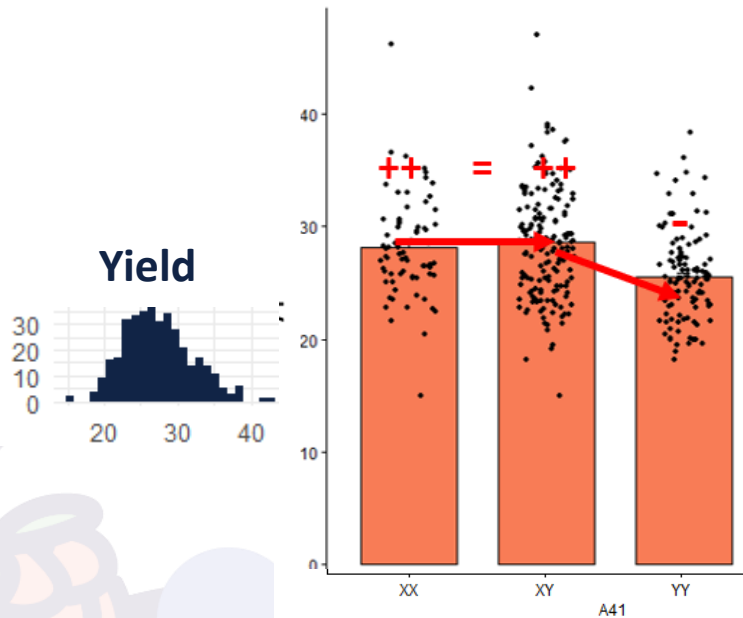
Example 2: additive effect

$$\text{Mean}_{XX} < \text{Mean}_{XY} < \text{Mean}_{YY}$$

Or

$$\text{Mean}_{XX} > \text{Mean}_{XY} > \text{Mean}_{YY}$$

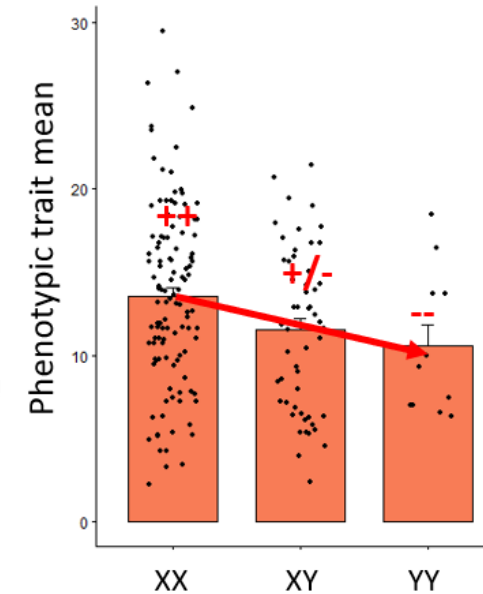
Additive/non-additive



Example 1: dominant effect

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$$\text{AND } \text{Mean}_{XX} > \text{Mean}_{YY}$$



Example 2: additive effect

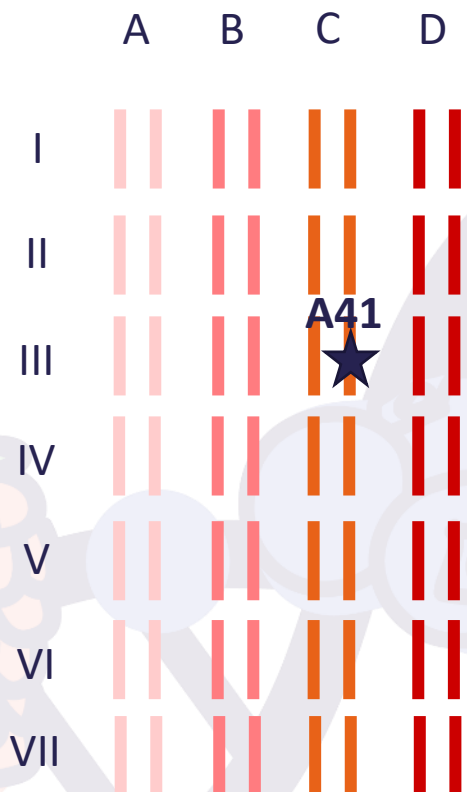
$$\text{Mean}_{XX} < \text{Mean}_{XY} < \text{Mean}_{YY}$$

Or

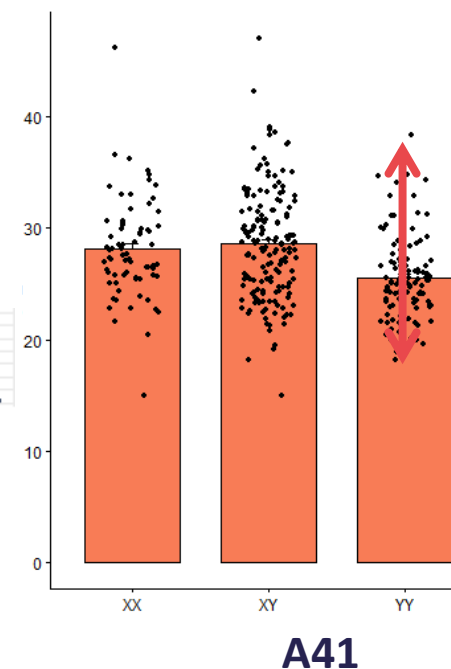
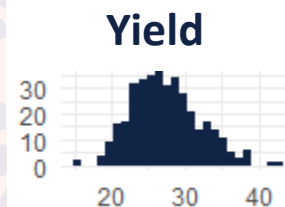
$$\text{Mean}_{XX} > \text{Mean}_{XY} > \text{Mean}_{YY}$$

→ Ability to predict trait with additive or dominant allelic effect

Optimisation of array: SNP combination



A41

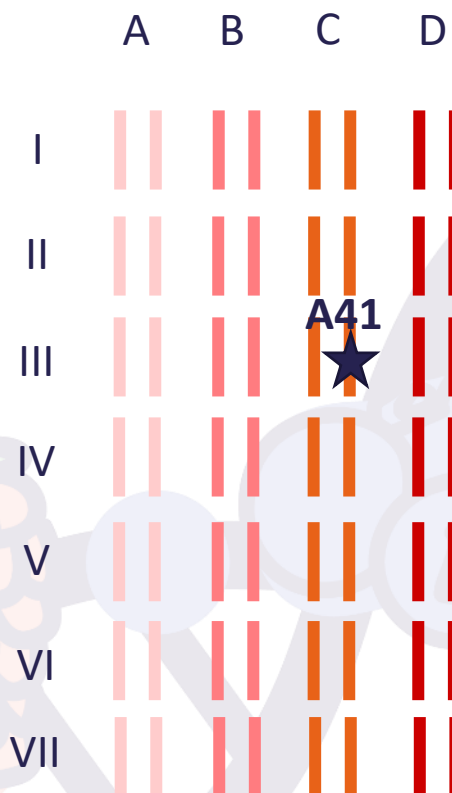


Considering one significant marker

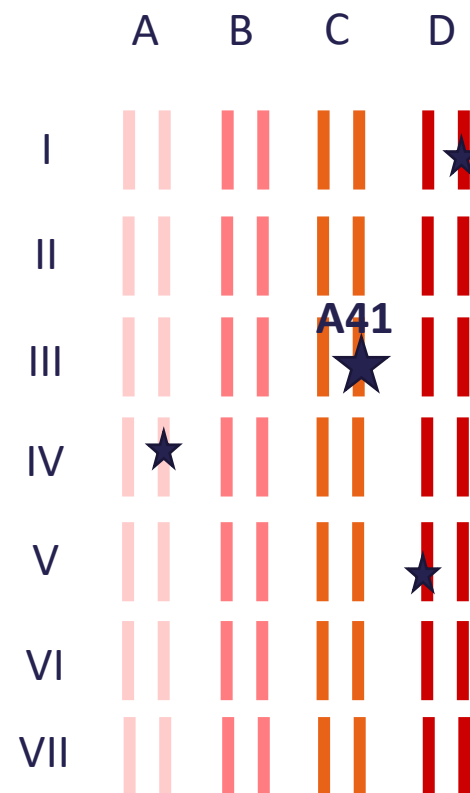
Limits:

- 1- Small difference between means
- 2- Large variability around the means

Optimisation of array: SNP combination



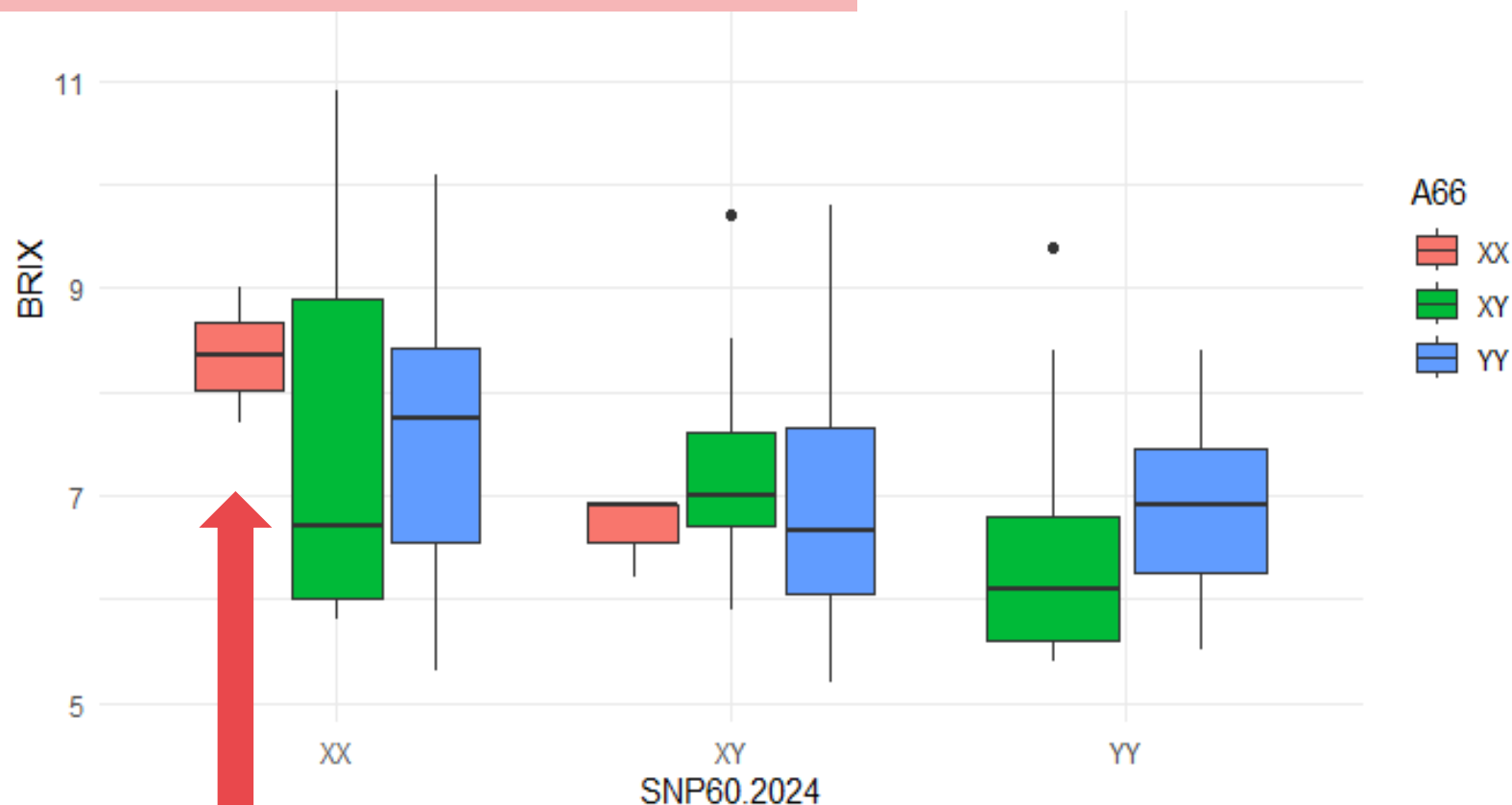
Considering one significant marker



Considering several markers together

Can the prediction of the trait be improved by considering several markers?

Optimisation of array: SNP combination



The combination of 2 SNPs is better than if the SNPs had been considered independently

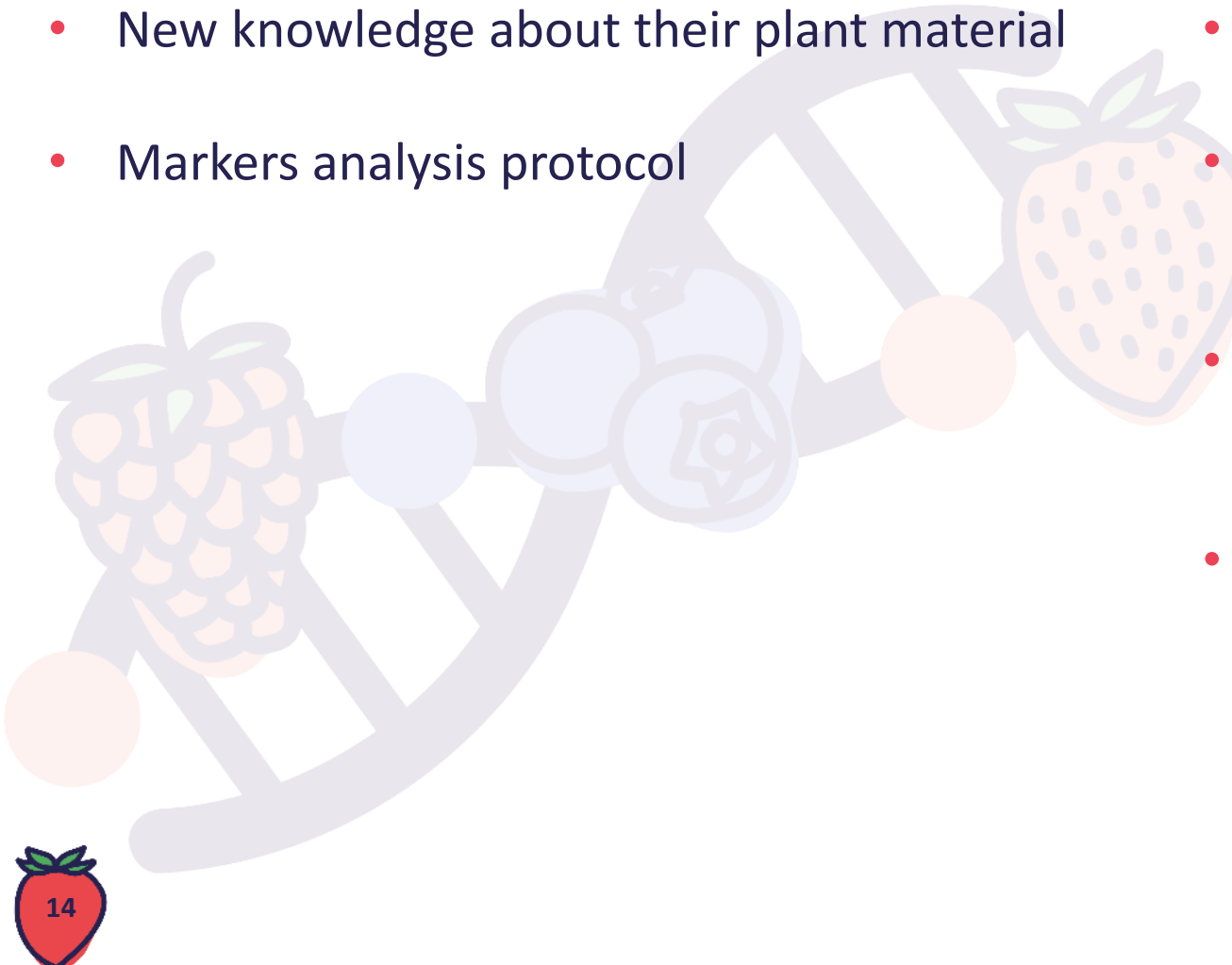
Conclusions

Companies

- New knowledge about their plant material
- Markers analysis protocol

Public community

- 92% markers informative for genetic analysis
- List of markers validated as trait predictor (validation in a large background)
- Additive/dominant information to refine selection strategy
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Béatrice Denoyes
Juliette Bénéjam
Amélia Gaston
Johan Petit
Aline Potier
Pierre Prevost

THANK YOU !



15.02.2024

