Combining categories of crossbred females to improve the overall performance of the dairy cattle herd : how to benefit from genetic diversity induced by the use of three breed crossbreeding into purebred Holstein herd ?

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Combining categories of crossbred females to improve the overall performance of the dairy cattle herd

How to benefit from genetic diversity induced by the use of three-breed crossbreeding into purebred Holstein herd ?

J. Quénon,[1*] S. Ingrand,[2] and M.-A. Magne[3]

[1] Université de Toulouse, INPT, INP-PURPAN, INRAE, AGIR, F-31320 Castanet-Tolosan, France

[2] Université Clermont Auvergne, AgroParisTech, INRAE, VetAgro Sup, UMR Territoires, F-63000 Clermont-Ferrand, France

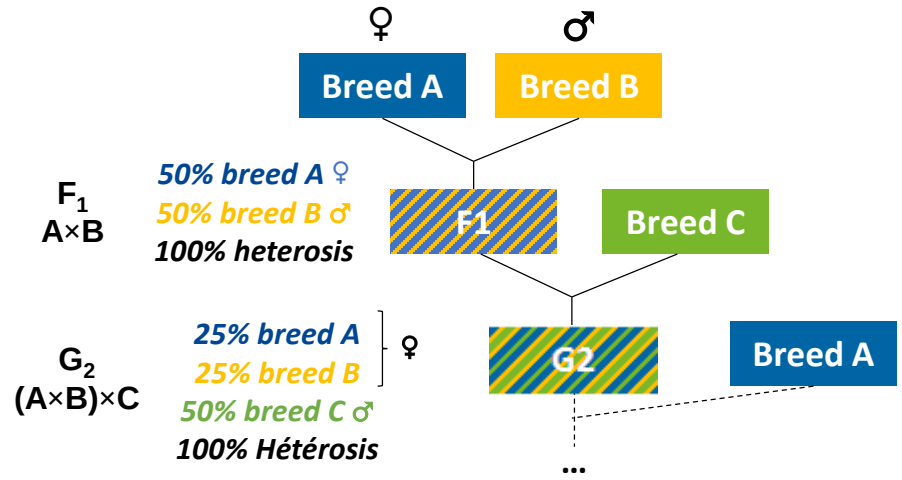
[3] Université de Toulouse, ENSFEA, INRAE, UMR AGIR, F-31320 Castanet-Tolosan, France

Introduction

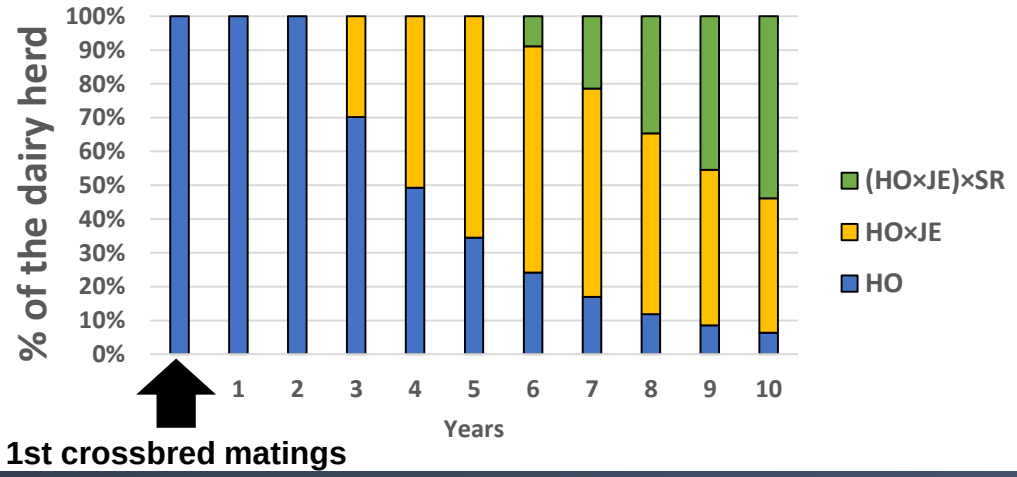
- Low fertility *(Lucy, 2001)* and health *(Oltenacu et al., 2010)* in purebred Holstein dairy cattle herds
- Resilience of dairy cattle systems require enhancing robustness of cows *(Friggens et al., 2017)* and functional diversity within the herd *(Tichit et al., 2011)*

  ➡ **Renewed interest in rotational crossbreeding**
- Crossbreeding to benefit from **heterosis effect** *(Penasa, 2010)* and the complementarity of dairy cattle breeds *(Magne et al., 2016)*
- Three-breed rotational crossbreeding **(3BC)** : compromise to ensure high heterosis (83% in 3rd generation) while keeping management of crossbreeding simple
- Uncommon in Western countries
- **Induce genetic diversity within the herd** over time

Three-breed rotational crossbreeding



Genetic diversity induced by using a Holstein, Jersey, Scandinavian Red 3BC program



Introduction

- Studies on crossbreeding :
  - Mostly assessing performances at animal level : comparison between purebreds and F_1 *(Hazel et al., 2014; Clasen et al. 2019; McClearn et al., 2019)* and more rarely G_2 crosses *(Shonka-Martin et al. 2018)*
  - To a lesser extent at herd level with simulation modelling *(Dezetter et al., 2017; Clasen et al., 2020)*

  ➡ In both cases: a crossbreeding program-based approach
- Diversity in technical transition paths towards rotational crossbreeding *(Quénon et al., 2020)*: several crossbreeding programs simultaneously, trial-and-error of breed combinations

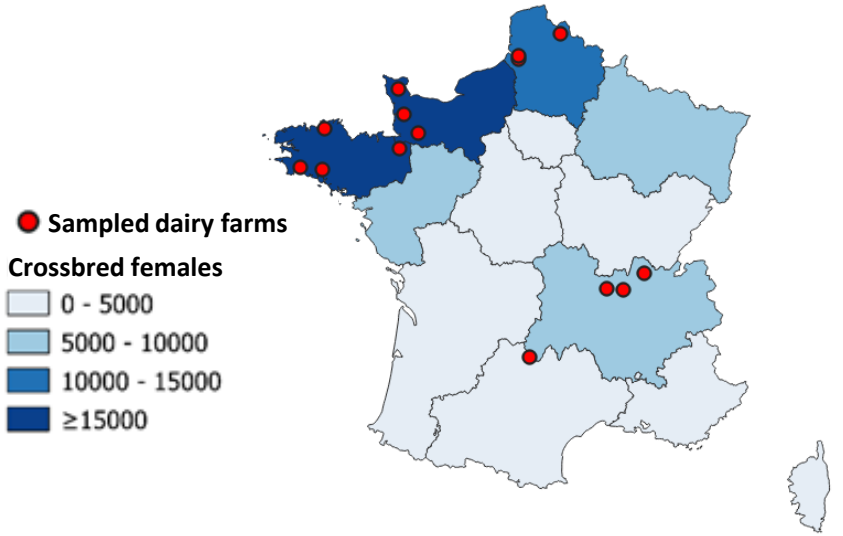
  ➡ Diversity in genotypes challenge categorisation method using 3BC program and crossbreeding generation

How to categorise such genetical diversity?

Does it support functional diversity at herd level?

Materials and methods

- **14 French dairy herds enrolled in milk record**
  - 100% Holstein before using crossbreeding
  - In 2018 : **all crosses > 1/3 herd size**
  - In 2018 (at least): **lactating G_2 cows in herd**
- Data extraction for the 2009-2018 period
  - Lactations data : **performances**
  - Genealogical and breed data : **crossbred genotypes identification**
- 2 datasets
  - Dataset #1 (n = 4476 lactations, 2010 females) for reproduction performances
  - Dataset #2 (n = 4487 lactations, 2051 females) for yield and udder health performances



7/14 organic farming
7/14 conventional famring

2018 characteristics in sampled farms	Med	Min	Max
UAA *(ha)*	98	43	225
Grassland *(% LFA)*	91	16	100
Herd size	70	25	139
Milk yield *(kg/cow)*	6 192	5 000	11 352

Materials and methods

1 Categorisation of diversity in crossbred genotypes induced by 3BC programs : genetic classes

Genotype	HO	HO×A	(HO×A)×B
Heterosis (%)	0	100	100
% of HO genes	100	50	25
Genetic class	HO	F_1	G_2

- HO

- HO × MO
- HO × SI
- HO × SR
- HO × Unkn
- HO × BS
- HO × BR
- HO × NO
- HO × AB
- HO × VO
- HO × JE

- (HO × AB) × NO
- (HO × NO) × Unkn
- (HO × Unkn) × SR
- (MO × HO) × AY
- (HO × AB) × SI
- (HO × MO) × Unkn
- (HO × NO) × AB
- (HO × NO) × MO
- (HO × NO) × SR
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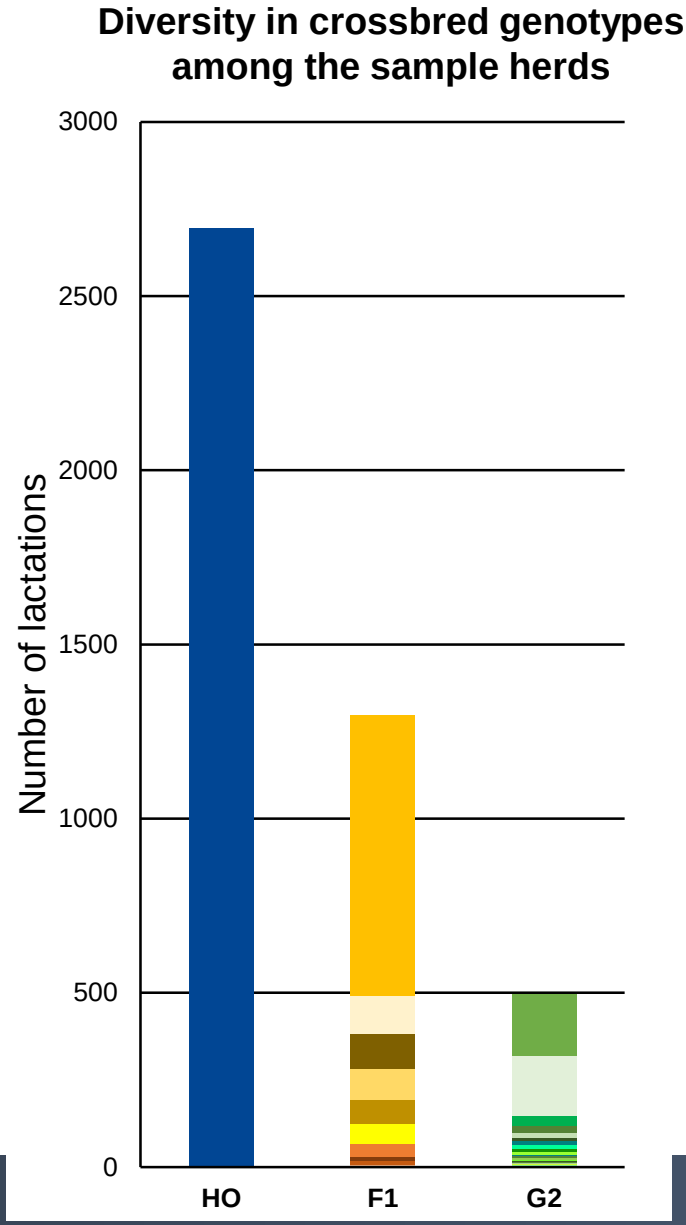

Materials and methods

2 **Estimation and paired comparison of the zootechnical performances between genetic classes**

- **Investigated traits :**
  - 305-d milk yield (MY) in kg/cow
  - 305-s fat (FC) and protein contents (PC) in g/kg/cow
  - Days open (DO) in days
  - SCS
- For each :
  - **Linear regression** (y = μ + Σfixed effects) adjusted of the French genetic evaluation models (UMT eBis and Geneval, 2019)
  - **Least square means** (LSM) for genetic classes
- **Test for differences in performance between genetic classes** (Tukey's tests, $p < 0.05$)

Results : performances profiles of the genetic classes

Classe génétique	**Milk yield** *(kg/cow)*	**Fat content** *(g/kg/cow)*	**Protein content** *(g/kg/cow)*	**SCS**	**DO** *(days)*
HO	**7513^{a}** +	**38.2^{a}** –	**31.3^{a}** –	**2.77^{ab}**	**143^{a}** ☹
F_1	**7 289^{b}** –	**40.4^{b}** +	**32.4^{b}** +	**2.72^{a}**	**127^{b}** ☺
G_2	**6 697^{c}** – –	**41.4^{c}** ++	**33.0^{c}** ++	**2.91^{b}**	**129^{b}** ☺

- Contrasted performances' profiles between genetic classes
- Trends in performances consistent with "crossbreeding program-based approach" studies

➡ **Although less precise and genetically accurate, our *a priori* categorisation of genetical diversity support phenotypical diversity**

How to combine these genetic classes in the herd to optimise its performances?

Materials and methods

3 Simulation of herd compositions and their mean performances

Herd compositions	Composition in genetic classes		
	% HO	% F_1	% G_2
#1	100	0	0
#2	99	1	0
…	…	…	…
#5150	0	1	99
#5151	0	0	100

Classe génétique	Milk yield *(kg/cow)*	Fat content *(g/kg/cow)*	Protein content *(g/kg/cow)*	SCS	DO *(days)*
HO	7513^{a} +	38.2^{a} –	31.3^{a} –	2.77^{ab}	143^{a} ☹
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G_2	6 697^{c} – –	41.4^{c} ++	33.0^{c} ++	2.91^{b}	129^{b} ☺

N= 5151 herds

N° troupeau	Composition du troupeau			MY	FC	PC	DO	SCS
	% HO	% F_1	% G_2					
#1	100	0	0					
#2	99	1	0					
…	…	…	…					

Mean performances of each simulated herd compositions

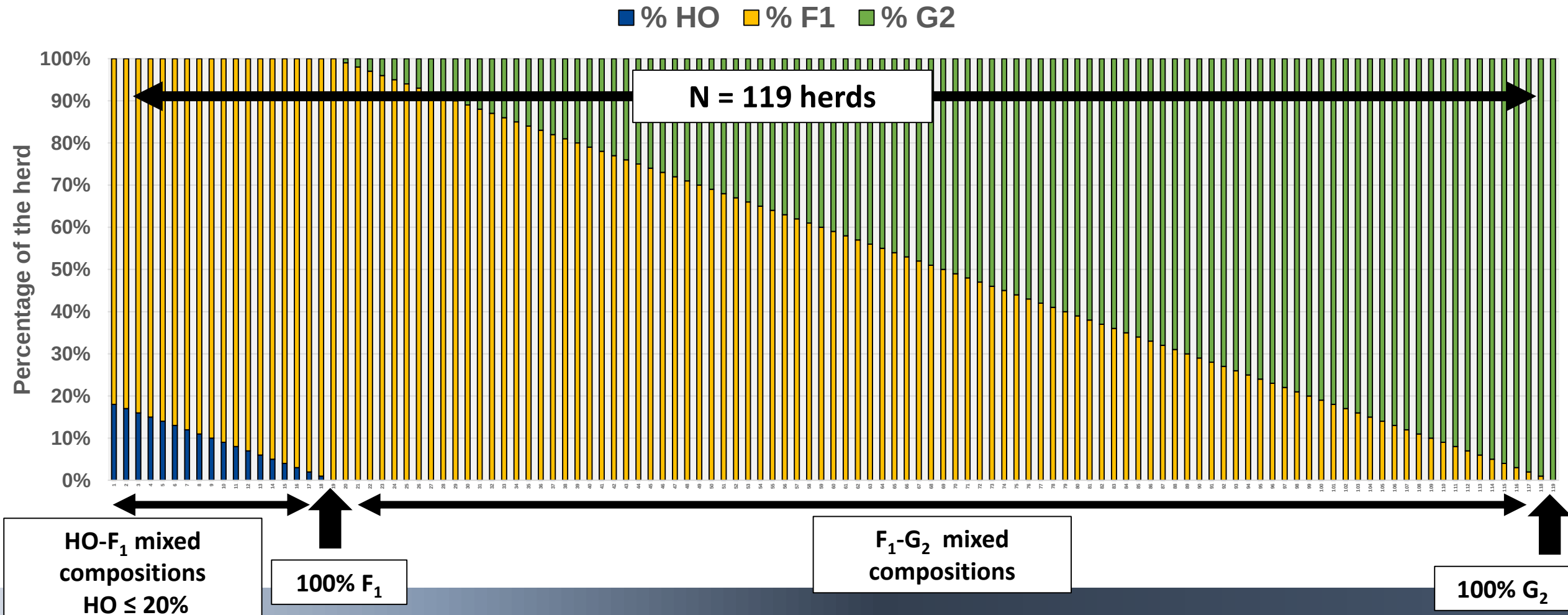
Materials and methods

4 Selection of "optimal herds":

1. Herds with mean DO < 130 days → ~~N= 5151 herds~~ **N= 1286 herds**

2. **Outranking herds with unweighted optimisation methode** → ~~N= 1286 herds~~ **N= 119 herds**
   - Pareto optimal solutions *(Williams et Kendall, 2017)*
   - On 5 objectives functions = 5 performances :
     - Milk yield
     - Fat content
     - Protein content
     - Days open
     - SCS

Results : which combinations of genetic classes optimise herd mean performances?



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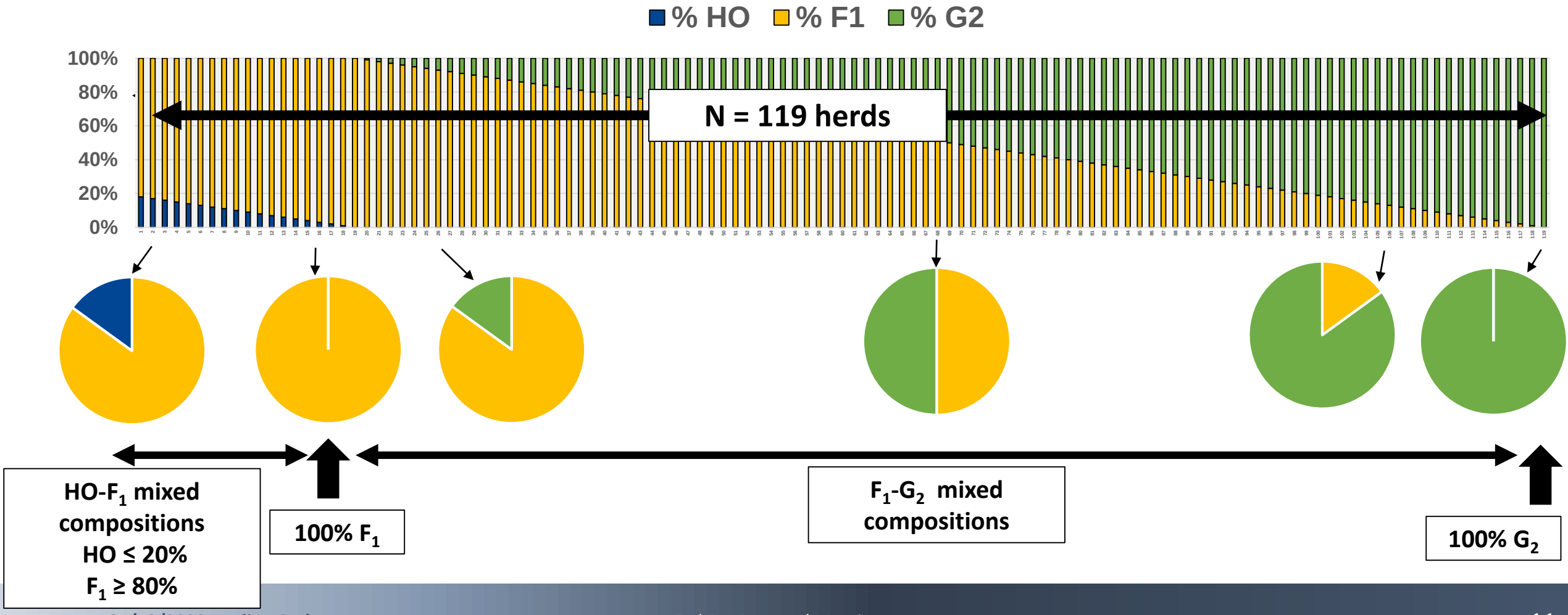
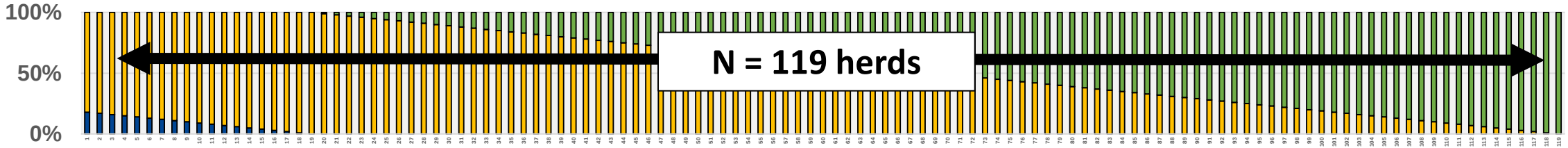
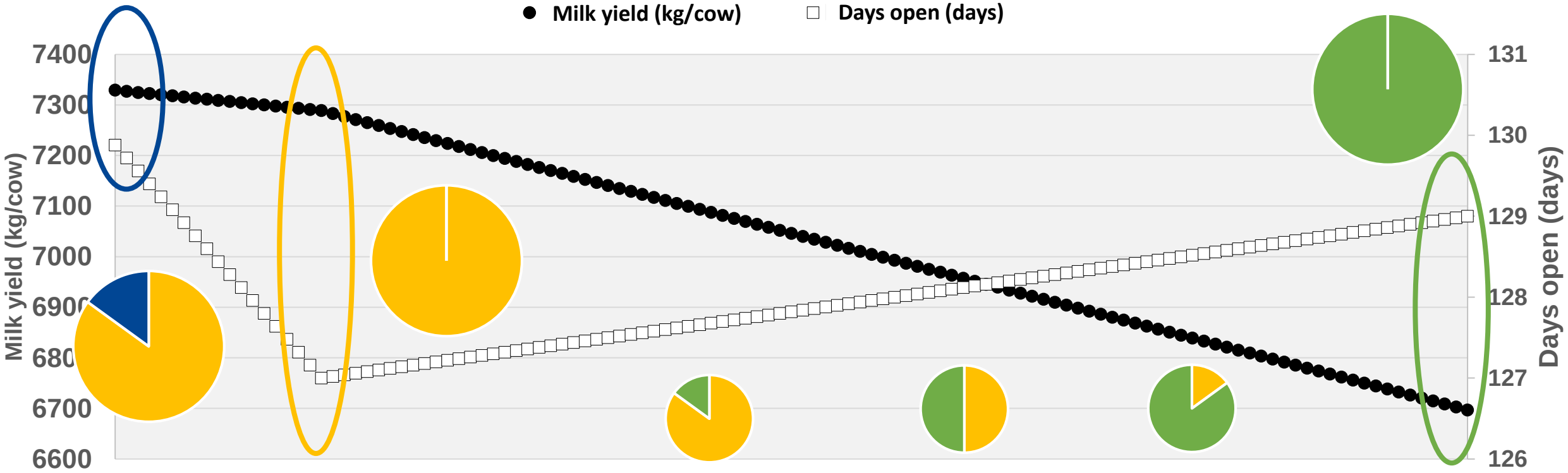


Results : trade-offs between performances





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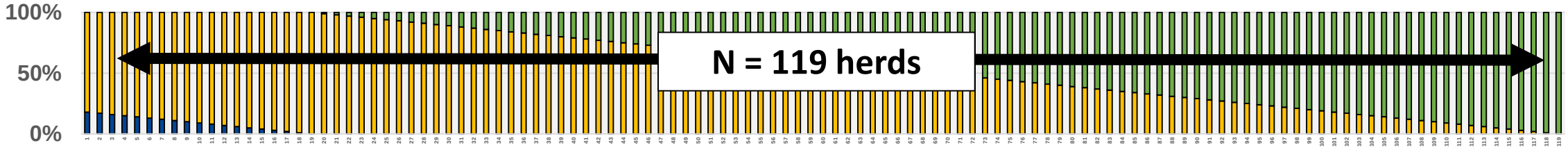
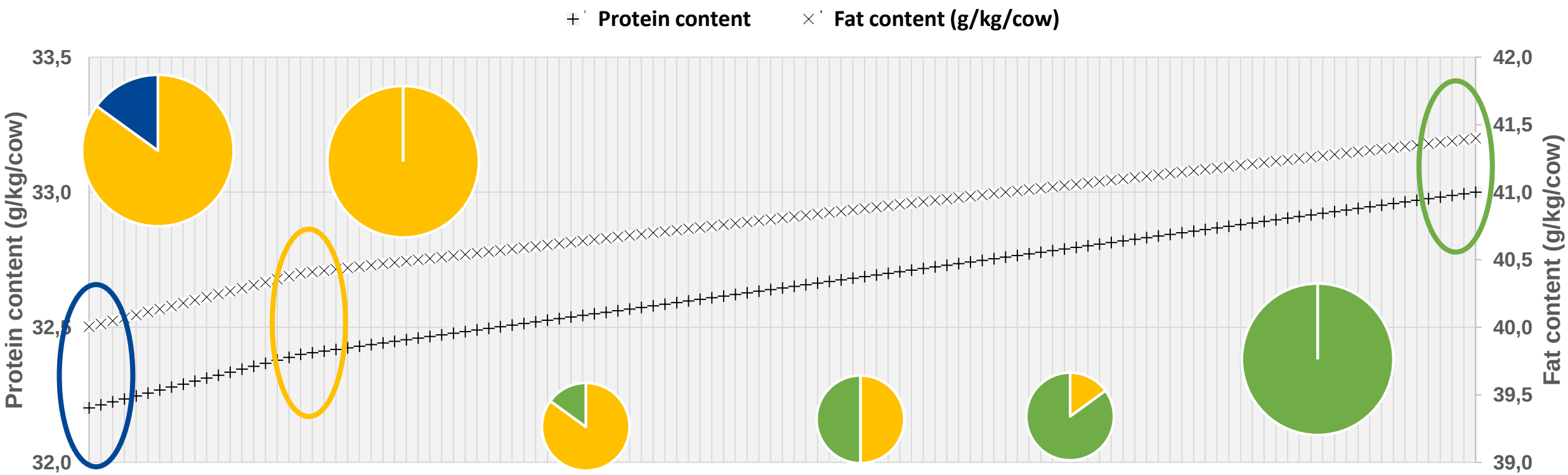
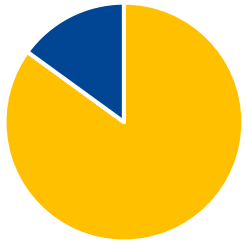
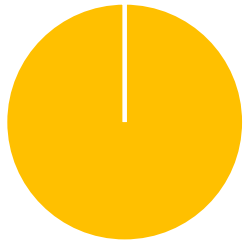
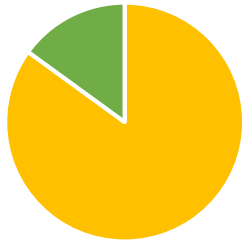
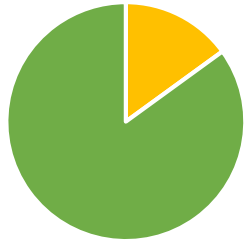
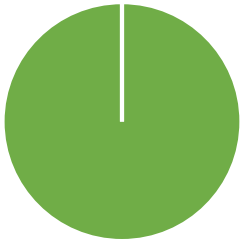




Results : trade-offs between performances

Herd compositions in HO, F_1 and G_2						
Milk yield	+++	+	-	-	- -	- - -
Milk contents	-	+	++	++	+++	+++
Fertility	- -	+++	++	++	++	++

Thank you for your attention

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