# 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 ?

Julien Quénon, Stéphane Ingrand, Marie-Angélina Magne

# 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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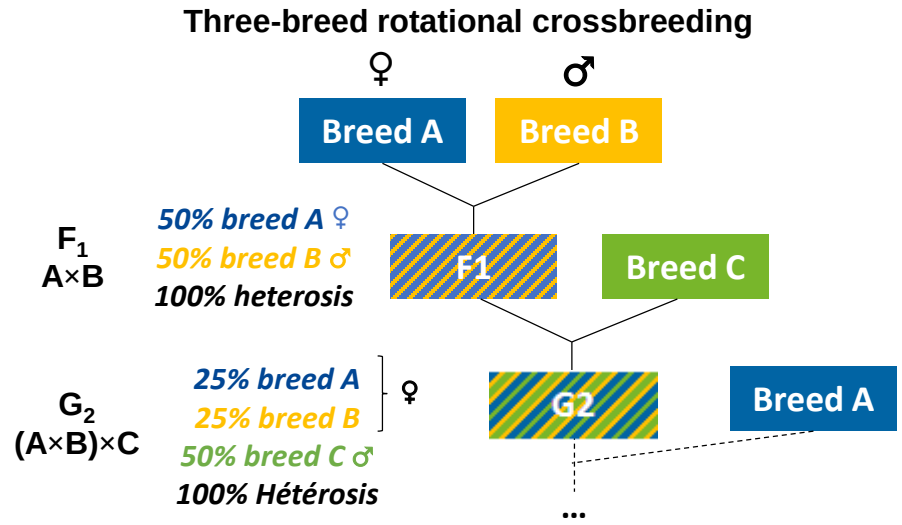
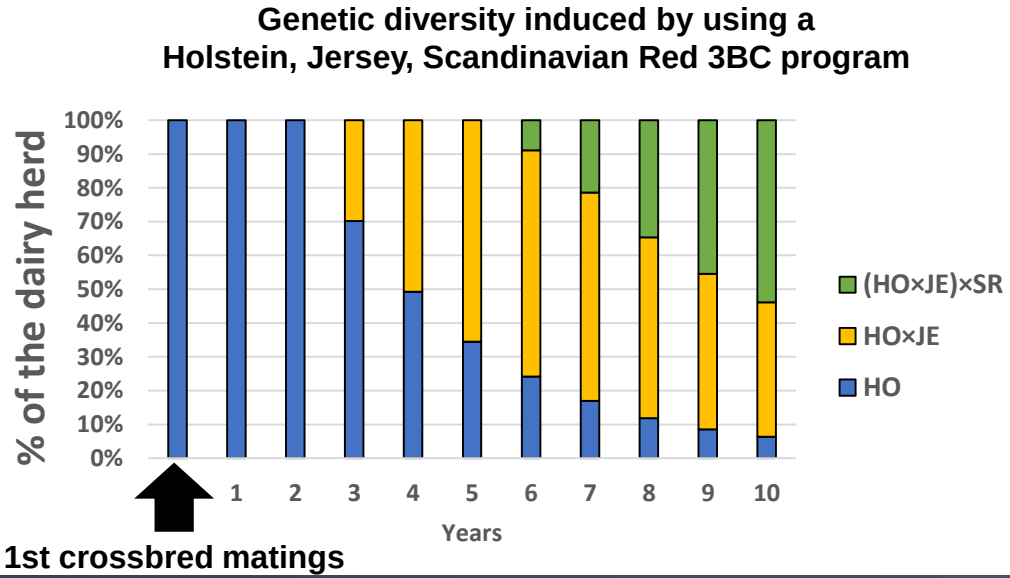
# Introduction

- 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



# 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

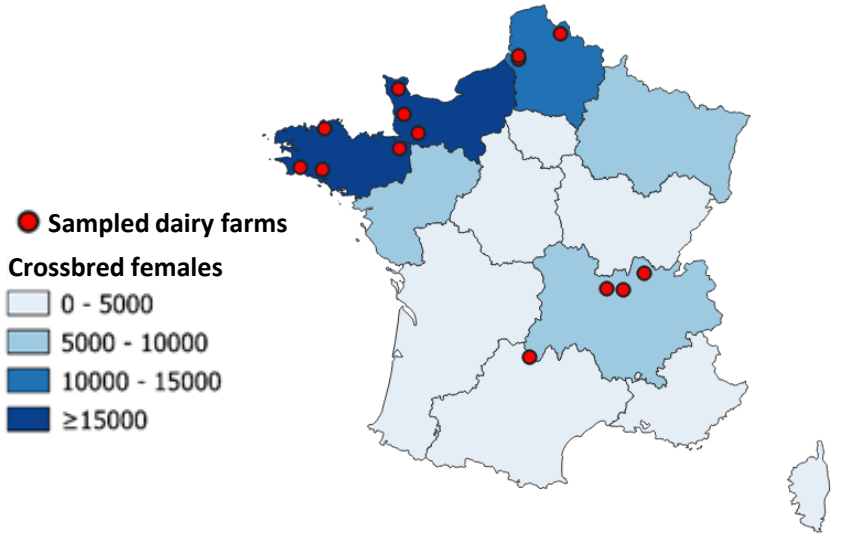
  ➡ Diversity in genotypes challenge categorisation method using 3BC program and crossbreeding generation

***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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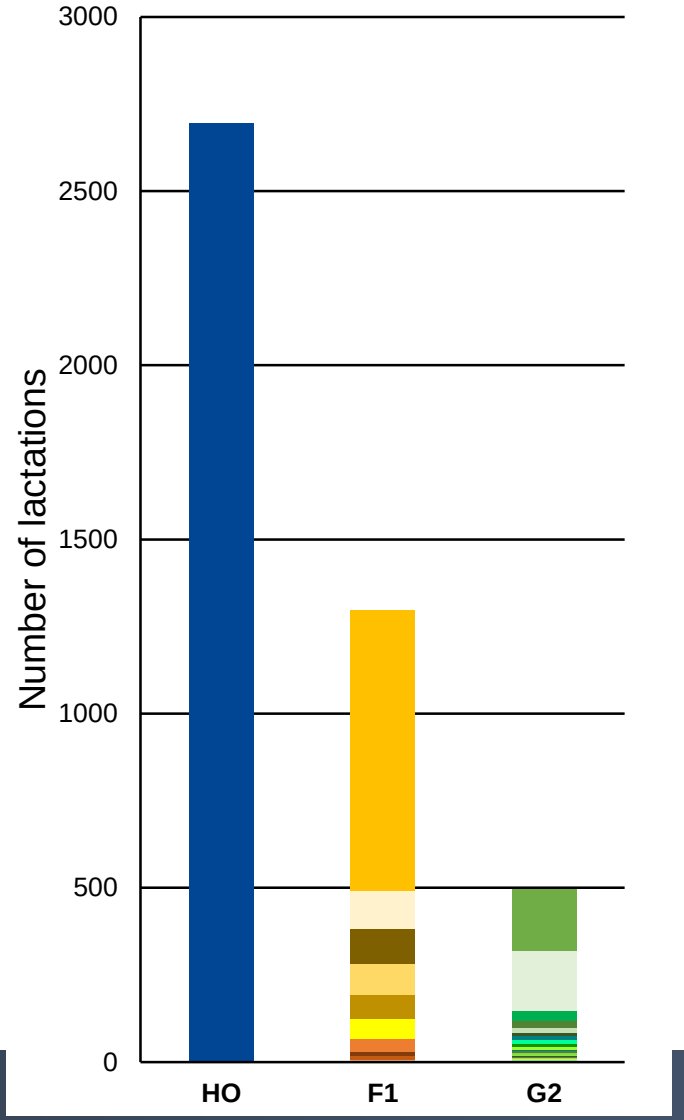
- (HO × SR) × MO
- (HO × BS) × JE
- (HO × BR) × SR
- (HO × AB) × MO
- (HO × SI) × MO
- (HO × MO) × AY
- (HO × BS) × AB
- (HO × SI) × SR

**Diversity in crossbred genotypes among the sample herds**



# 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 + $\Sigma_{\text{fixed effects}}$) 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 | $7513^{a}$ + | $38.2^{a}$ – | $31.3^{a}$ – | $2.77^{ab}$ | $143^{a}$ ☹ |
| $F_1$ | $7\,289^{b}$ – | $40.4^{b}$ + | $32.4^{b}$ + | $2.72^{a}$ | $127^{b}$ ☺ |
| $G_2$ | $6\,697^{c}$ – – | $41.4^{c}$ ++ | $33.0^{c}$ ++ | $2.91^{b}$ | $129^{b}$ ☺ |

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**

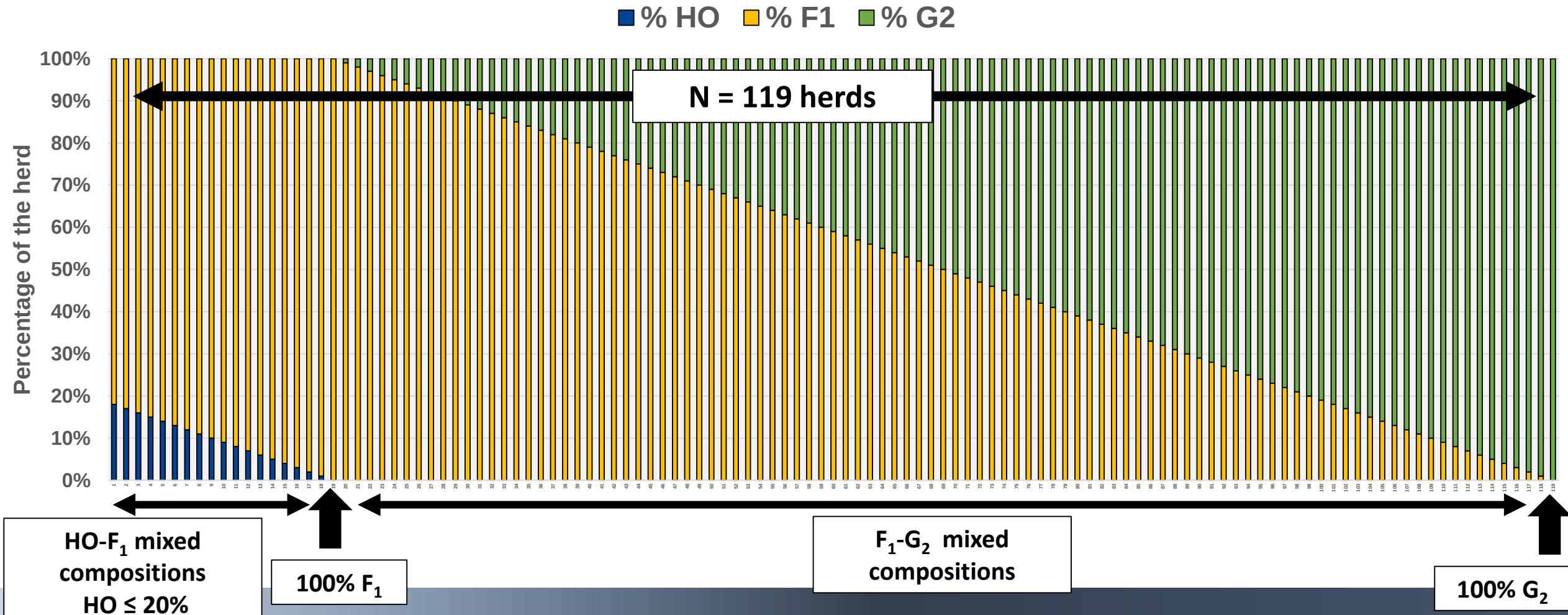
# Materials and methods

## 4 Selection of "optimal herds":

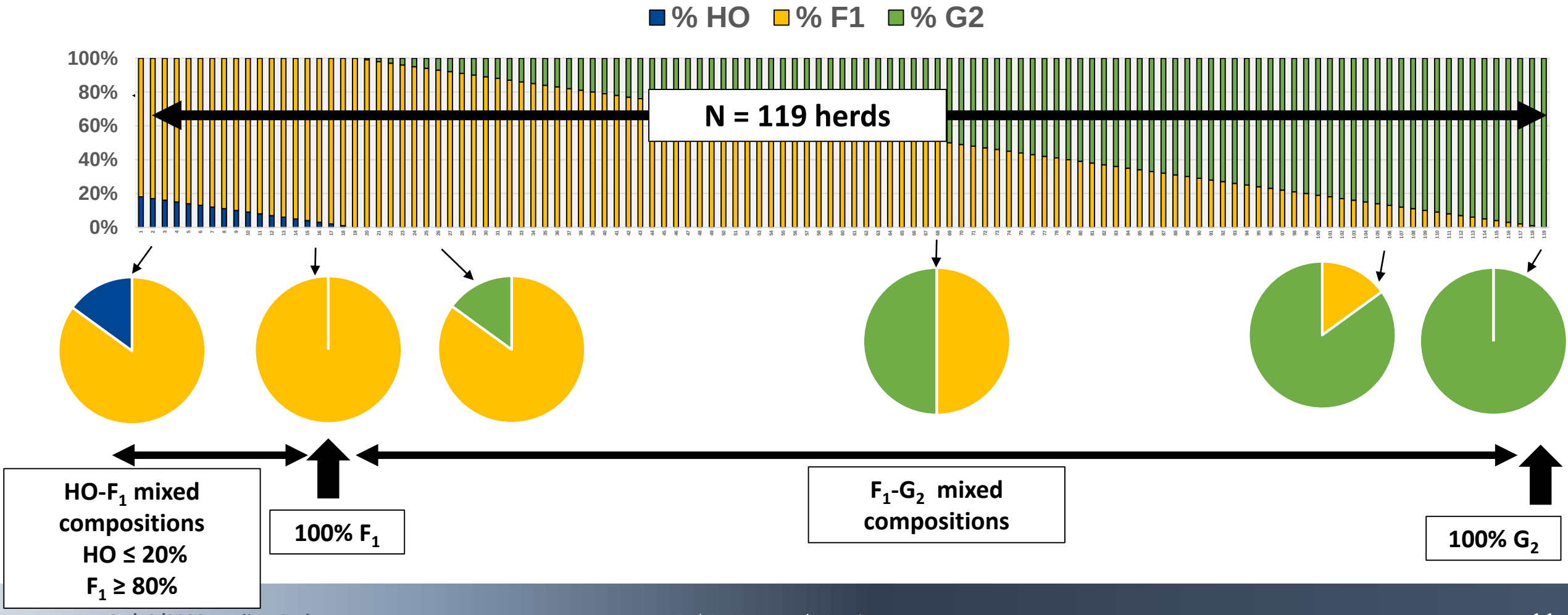
1. Herds with mean DO < 130 days → ~~N= 5151 herds~~ **N= 1286 herds**

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

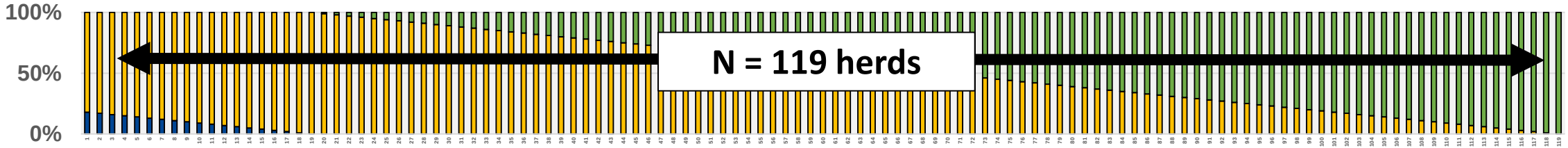
# Results : which combinations of genetic classes optimise herd mean performances?

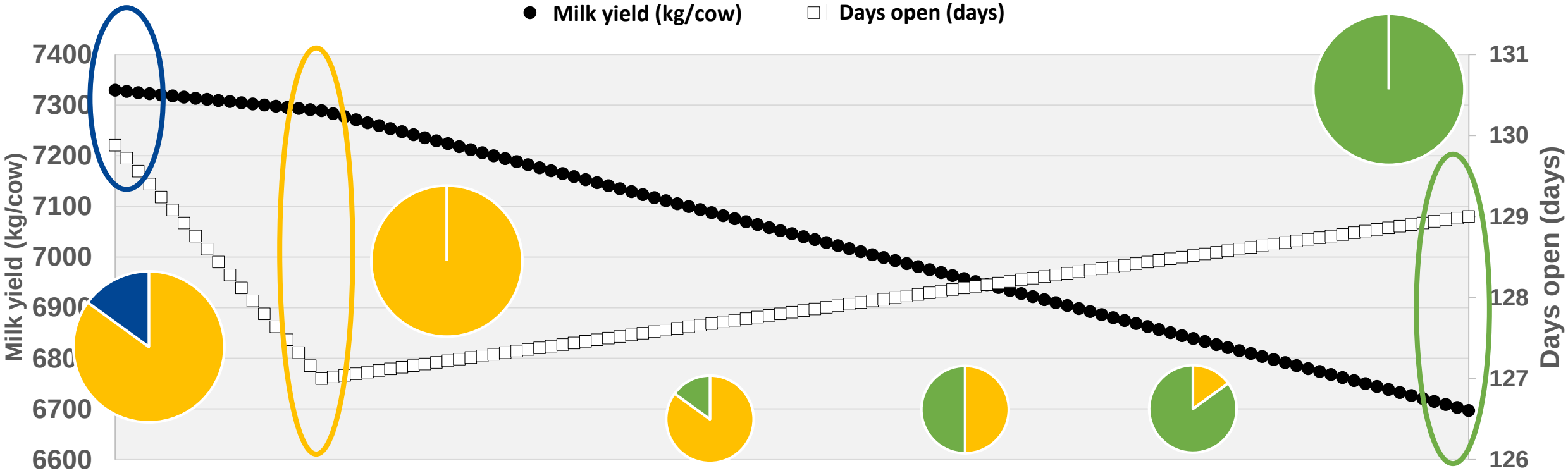


# Results : which combinations of genetic classes optimise herd mean performances?



# Results : trade-offs between performances



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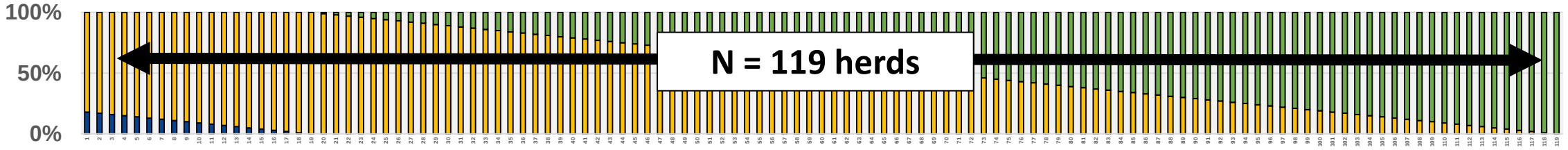
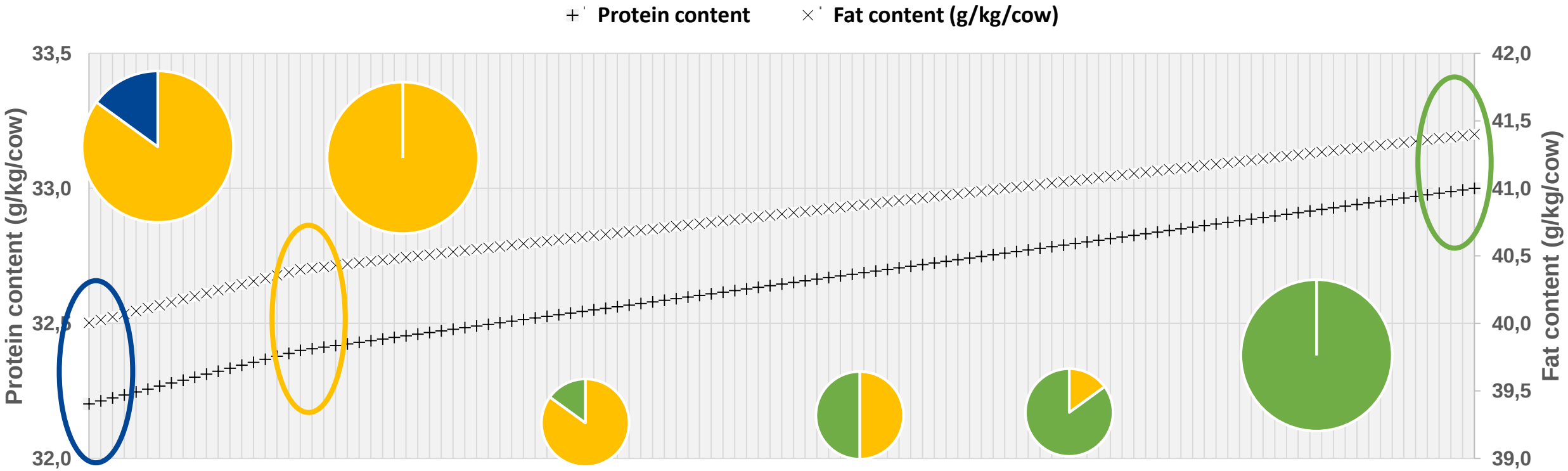
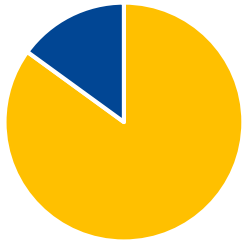
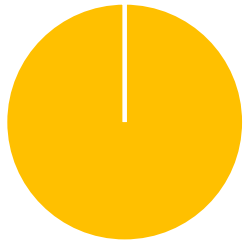
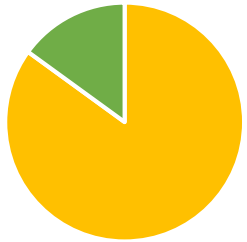
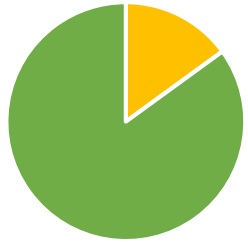
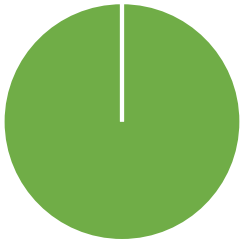


# Results : trade-offs between performances

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

# Thank you for your attention

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