# Including αs1 casein gene effect on genomic evaluations of French dairy goats

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# αs1 casein: a major gene for dairy goat

- αs1 casein major gene in dairy goat
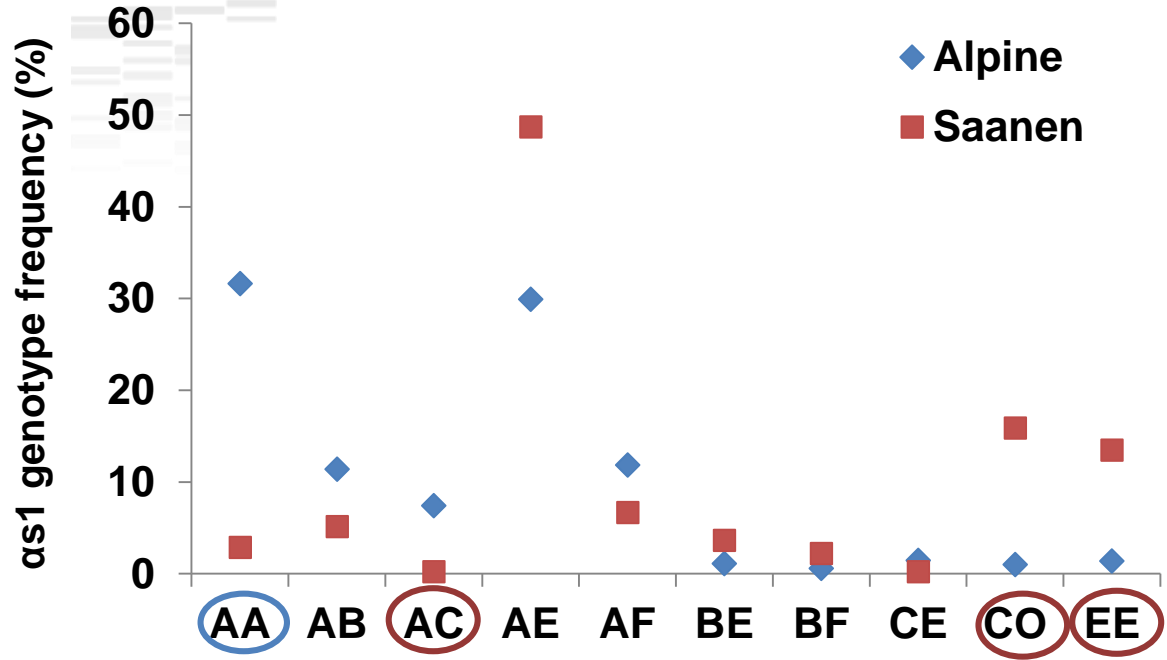- genomic selection : all SNP = equal part of variance

**French dairy cattle [1]:**
**Adding QTL in genomic evaluation ➔ accuracy +3% to +12 %**

**Goats with αs1 casein genotypes:**


- **3 861 bucks ⟶ 823 with 50k genotypes**


- **2 949 dams of bucks**

**Alpine + Saanen**

[1] **Boichard et al., 2012, *Anim Prod Sci*, 52: 115-120**

# Breed differences in αs1 casein allele frequencies



Alpine : supremacy of allele A
Saanen : supremacy of genotypes AE, CO and EE

# αs1 casein: a major gene for dairy goat

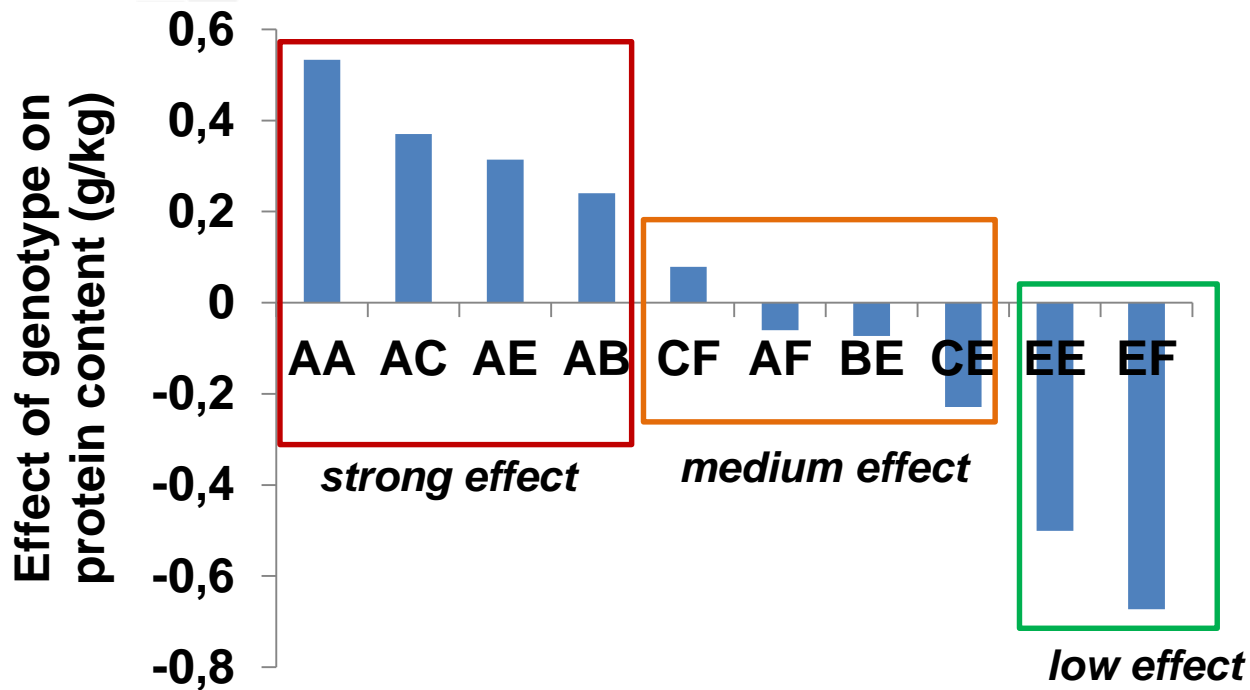**Genetic Model used:** $\mathbf{y} = \mathbf{Zu} + \mathbf{Tw} + \mathbf{e}$

*with y: DYD, u: polygenic part, w: αs1 casein genotype random effect*

**Part of genetic variance (%) explained by αs1 casein genotype:**

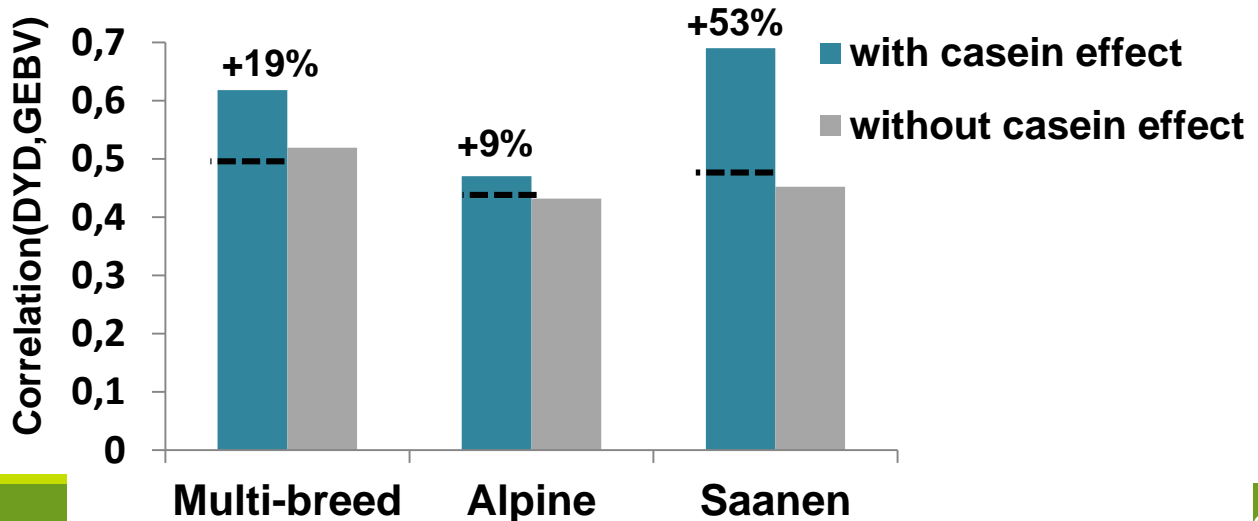|                  | Multi-breed | Alpine | Saanen |
|------------------|-------------|--------|--------|
| **Milk yield**   | 9           | 12     | 7      |
| **Fat content**  | 20          | 24     | 17     |
| **Protein content** | 41       | 43     | 38     |

# Three classes of αs1 casein genotypes (strong, medium and low effects on protein content)



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# How to integrate αs1 casein genotype in genomic evaluations?

**1. Based on males phenotypes (DYD) and genotypes**

- **fixed ≈ random effect**
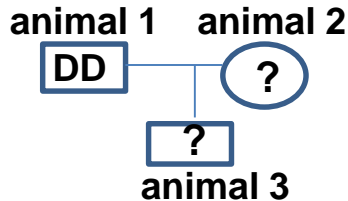- **no significant effect on milk yield and fat content**

# How to integrate αs1 casein genotype in genomic evaluations?

## 2. Based on female phenotypes (genotyped or not)

### 2.1 Predict genotype for females using peeling iterative method[2]

**Example (biallelic marker):**  **frequencies in population (%):**

| D | d |
|---|---|
| 58,5 | 41,5 |

**animal 1    animal 2**

DD — ?

? animal 3

**Probability for genotype of animal 2:**
➔ *Frequencies in population (%)*

| DD | Dd | dd |
|----|----|----|
| 32 | 53 | 15 |

**Probability for genotype of animal 3 (%):**

| DD | Dd | dd |
|------|------|---|
| 58,5 | 41,5 | 0 |

[2] Vitezica et al., 2005, *Genet Sel Evol*, 37: 403-415

# How to integrate αs1 casein genotype in genomic evaluations?

**2.1  Predict genotype for females using peeling iterative method[2]**
  ➔ **probabilities for each 19 possible genotypes**

|            | AA   | AB   | AC | AE   | AF   | AO   | BB   | BC   | BE   | …  | FF |
|------------|------|------|----|------|------|------|------|------|------|----|----|
| **Female 1** | 0,10 | 0,05 | 0  | 0,05 | 0,25 | 0,05 | 0,15 | 0,10 | 0    |    | 0  |
| …          |      |      |    |      |      |      |      |      |      |    |    |
| **Female n** | 0    | 0,15 | 0  | 0    | 0    | 0,25 | 0    | 0,35 | 0,20 |    |    |

**Including probabilities in genomic evaluation:**

1) **Random probabilities : each combination of 19 probabilities = level of random effect**
2) **3 groups of probabilities : 3 fixed effects (strong, medium and weak effects)**

**[2] Vitezica et al., 2005, *Genet Sel Evol*, 37: 403-415**

# How to integrate αs1 casein genotype in genomic evaluations?
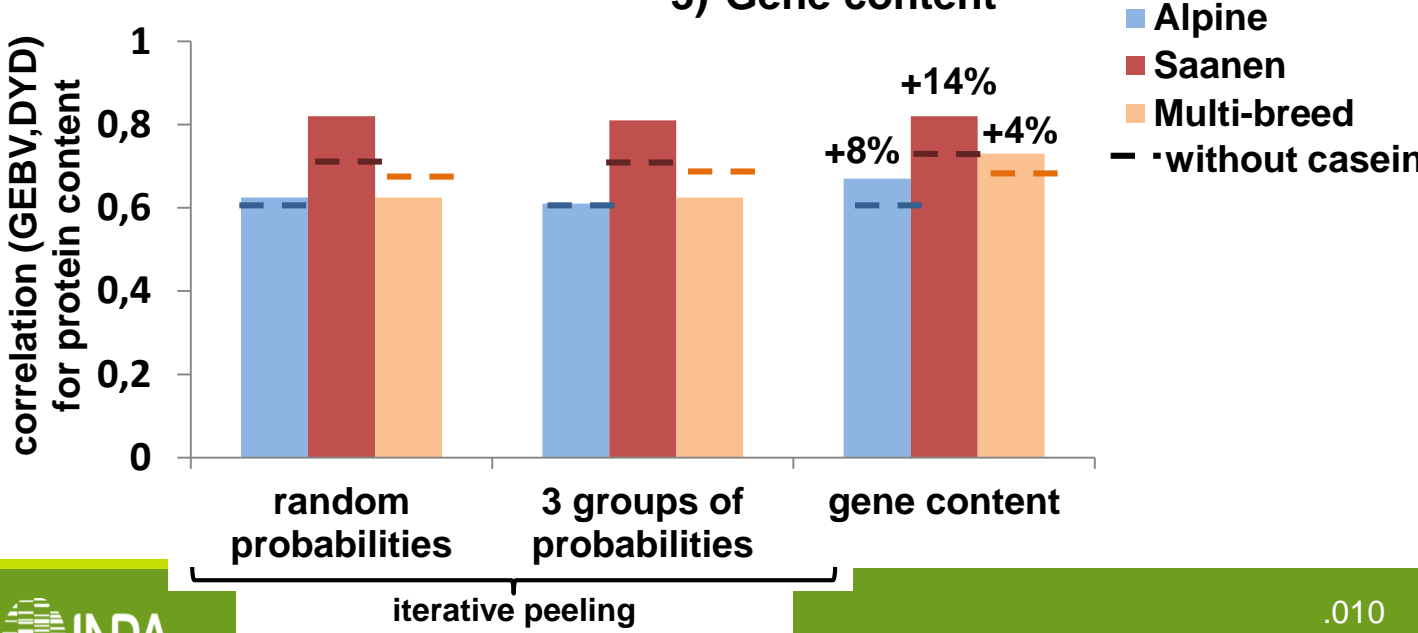
## 2. Based on females phenotypes
### 2.2 Predict genotype for females using gene content[3,4] approach:
multiple trait model using simultaneously pedigree, known genotypes and phenotypes

$$\mathbf{y} = \mathbf{X}_g \boldsymbol{\beta}_g + \mathbf{Z}_g \mathbf{u}_g + \mathbf{W}_g \mathbf{p}_g + \mathbf{e}_g$$

**Protein content** — **fixed effect** ($\mathbf{X}_g\boldsymbol{\beta}_g$), **genomic effect** ($\mathbf{Z}_g\mathbf{u}_g$), **permanent environment** ($\mathbf{W}_g\mathbf{p}_g$) — model for genetic evaluation of phenotype

$$\mathbf{y}_A = \boldsymbol{\mu}_1 + \mathbf{Z}_1\mathbf{u}_1 + \mathbf{e}_1$$
$$\mathbf{y}_B = \boldsymbol{\mu}_2 + \mathbf{Z}_2\mathbf{u}_2 + \mathbf{e}_2$$
$$\mathbf{y}_C = \boldsymbol{\mu}_3 + \mathbf{Z}_3\mathbf{u}_3 + \mathbf{e}_3$$
$$\mathbf{y}_E = \boldsymbol{\mu}_4 + \mathbf{Z}_4\mathbf{u}_4 + \mathbf{e}_4$$
$$\mathbf{y}_F = \boldsymbol{\mu}_5 + \mathbf{Z}_5\mathbf{u}_5 + \mathbf{e}_5$$
$$\mathbf{y}_O = \boldsymbol{\mu}_6 + \mathbf{Z}_6\mathbf{u}_6 + \mathbf{e}_6$$

**Gene content** — **polygenic**

model for gene contents of each allele ($\mathbf{y}_A , \ldots , \mathbf{y}_O$ : number of copie of allele (0,1 or 2))

$$\mathbf{u}_i \sim N(\mathbf{0}, \mathbf{A}\sigma_{u_i}^2)$$

[3] Gengler et al., 2008, *J Dairy Sci*, 91: 1652-1659
[4] Legarra and Vitezica, EAAP 2015 session 50

# Using gene content approach improved GEBV prediction

## 2. Based on females phenotypes

Three models used :   iterative peeling
1) Random probabilities
2) 3 groups of probabilities
3) Gene content

# Include αs1 casein genotype in genomic evaluation improved prediction of breeding values

αs1 casein major gene : 40% of genetic variance of protein content

genomic evaluation

*Based on male performances :*
- **fixed effect ≈ random effect**
- **gain Saanen > gain Alpine > gain multi-breed**

*Based on female performances :*
➔ **Predict genotypes of non genotyped females**
- **gene content >> peeling iterative**
- **gain : 4 to 14% on protein content**

## Include αs1 casein effect improved breeding values prediction

# Appendix

# Design of cross validation



reference population

training set

(425 males born between 1993 and 2005)

DYD in 2008          genotypes

*predicting equation*

validation set

(252 males born between 2006 and 2009)

genotypes          *DYD in 2013*

r² ( DYDobs, GEBV)= prediction reliability

GEBV