



Including caseine α s1 major gene effect on genetic and genomic evaluations of French dairy goats

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Including $\alpha s1$ casein gene effect on genomic evaluations of French dairy goats

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Why adding major gene in genomic evaluations?

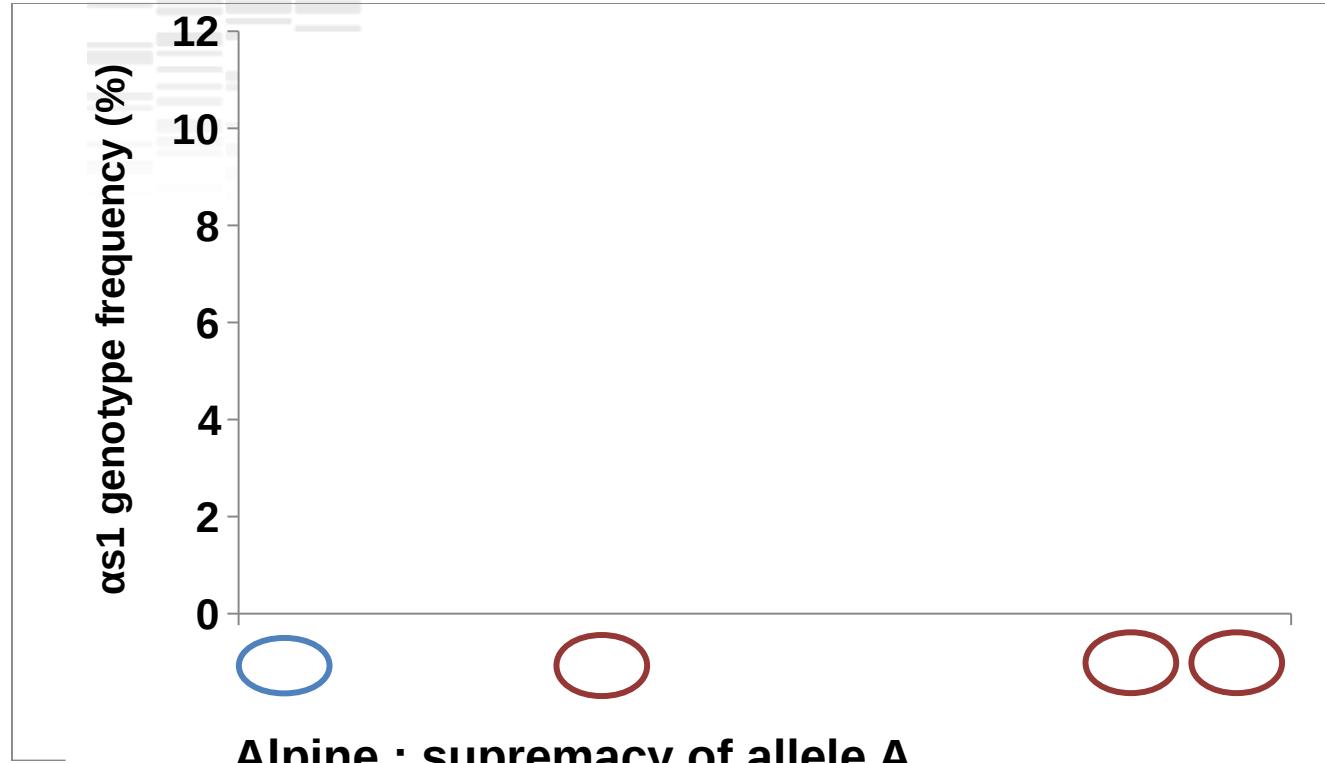
- **α s1 casein major gene in dairy goat**
- **genomic selection : all SNP = equal part of variance**

French dairy cattle 1: Adding QTL in genomic evaluation □ accuracy +3% to +12 %

Goats with α s1 casein genotypes:

-  **3 861 bucks** → 823 with 50k genotypes } Alpine + Saanen
-  **2 949 dams of bucks**

Breed differences in α s1 casein allele frequencies



Alpine : supremacy of allele A

Saanen : supremacy of genotypes AE, CO and EE

α s1 casein: a major gene for dairy goat

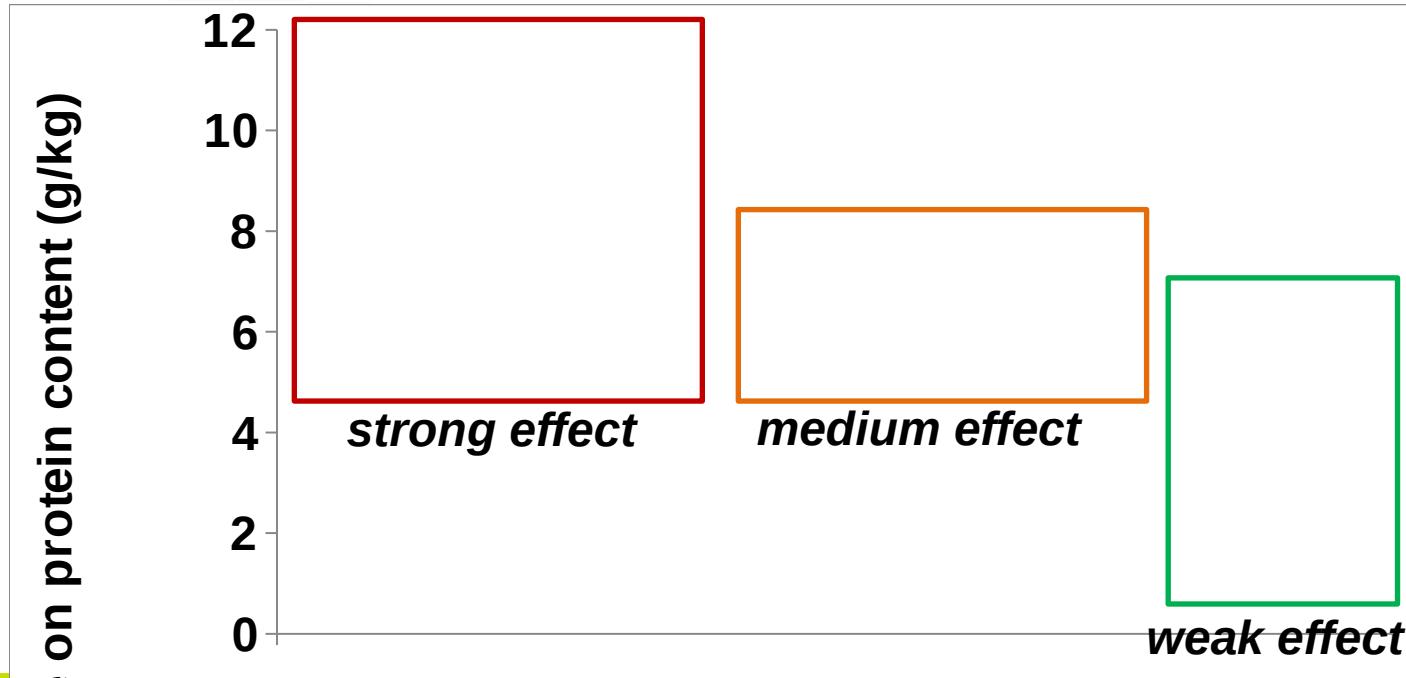
Genetic Model used: $y = Zu + Tw + e$

with y : DYD, u : polygenic part, w : α s1 casein genotype random effect

Part of genetic variance (%) explained by α s1 casein genotype:

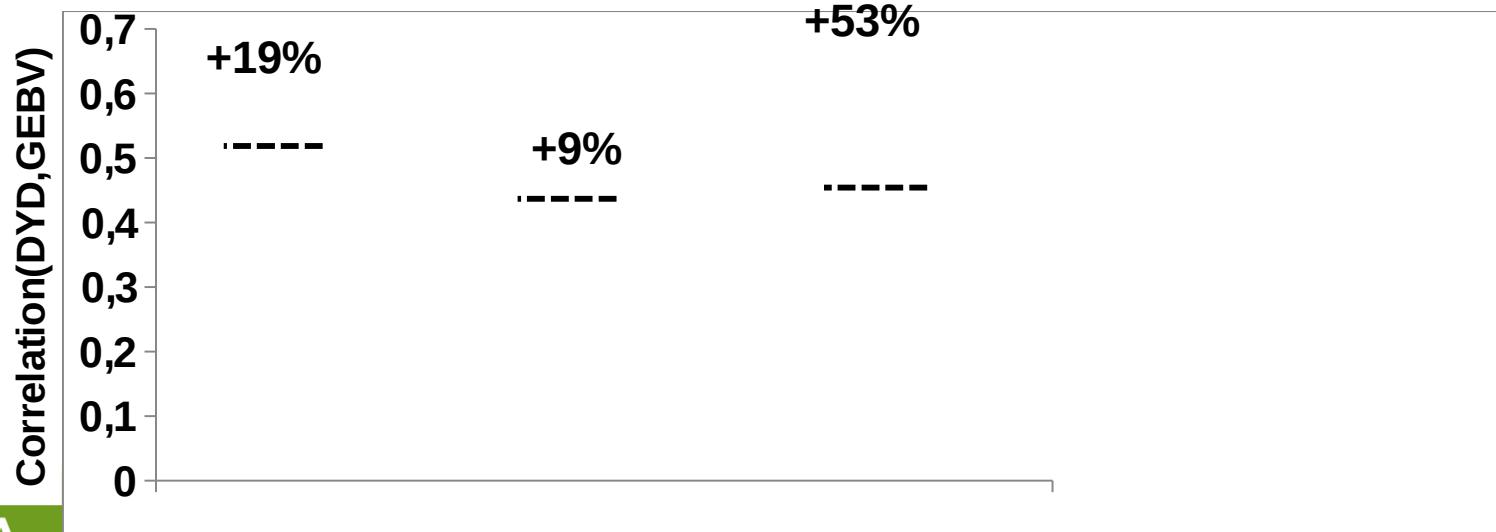
| | Multi-breed | Alpine | Saanen |
|-----------------|-------------|--------|--------|
| Milk yield | 9 | 12 | 7 |
| Fat content | 20 | 24 | 17 |
| Protein content | 41 | 43 | 38 |

Three classes of $\alpha s1$ casein genotypes (strong, medium and weak effects)



How to integrate α s1 casein genotype in genomic evaluations?

- 1. Based on male phenotypes (DYD) and genotypes
 - fixed ≈ random effect
 - no significant effect on milk yield and fat content



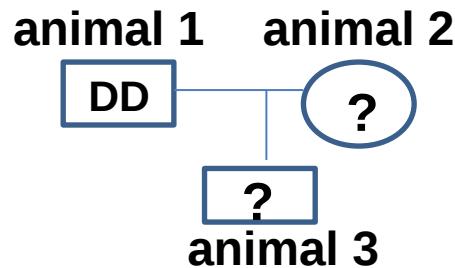
How to integrate α s1 casein genotype in genomic evaluations?

2. Based on female phenotypes (genotyped or not)

2.1 Predict genotype for females using peeling iterative method

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

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



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 |

How to integrate $\alpha s1$ casein genotype in genomic evaluations?

2.1 Predict genotype for females using peeling iterative method2

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)

How to integrate $\alpha s1$ casein genotype in genomic evaluations?

2. Based on females phenotypes

2.2 Predict genotype for females using gene content

multiple trait model using simultaneously pedigree, known genotypes and phenotypes

$$\left\{ \begin{array}{l} \text{fixed effect} \quad \text{genomic effect} \quad \text{permanent environment} \\ \mathbf{y} = \mathbf{X}_g \boldsymbol{\beta}_g + \mathbf{Z}_g \mathbf{u}_g + \mathbf{W}_g \mathbf{P}_g + \mathbf{e}_g \text{ model for genetic evaluation of phenotype} \\ \\ \mathbf{y}_A = \boldsymbol{\mu}_1 + \mathbf{Z}_1 \mathbf{u}_1 + \mathbf{e}_1 \\ \mathbf{y}_B = \boldsymbol{\mu}_2 + \mathbf{Z}_2 \mathbf{u}_2 + \mathbf{e}_2 \\ \mathbf{y}_C = \boldsymbol{\mu}_3 + \mathbf{Z}_3 \mathbf{u}_3 + \mathbf{e}_3 \\ \mathbf{y}_E = \boldsymbol{\mu}_4 + \mathbf{Z}_4 \mathbf{u}_4 + \mathbf{e}_4 \\ \mathbf{y}_F = \boldsymbol{\mu}_5 + \mathbf{Z}_5 \mathbf{u}_5 + \mathbf{e}_5 \\ \mathbf{y}_O = \boldsymbol{\mu}_6 + \underbrace{\mathbf{Z}_6 \mathbf{u}_6}_{\text{polygenic}} + \mathbf{e}_6 \\ \end{array} \right.$$

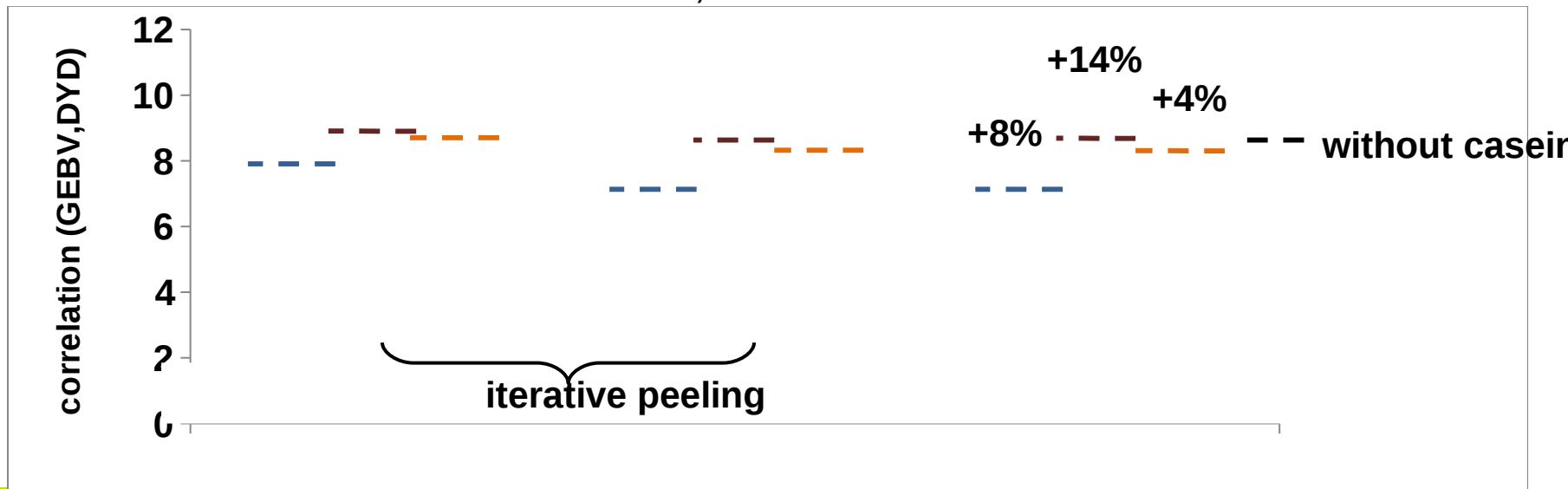
model for gene contents of each allele (y_A, \dots, y_O)
number of copie of allele (0,1 or 2))

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

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 α s1 casein genotype in genomic evaluation improved prediction of breeding values

α s1 casein major gene : 40% of genetic variance of protein content

genomic evaluation

Based on male performances :

- fixed effect \approx 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 α s1 casein effect improved breeding values prediction



Appendix

Design of cross validation

