

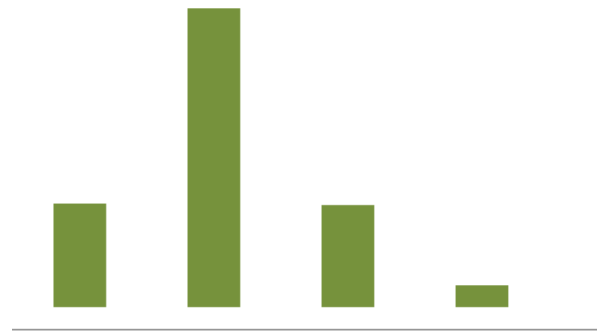
# Genetic Heteroscedastic Models for Sheep Litter Size



**Samira FATHALLAH**

**Loys BODIN, Ingrid DAVID**

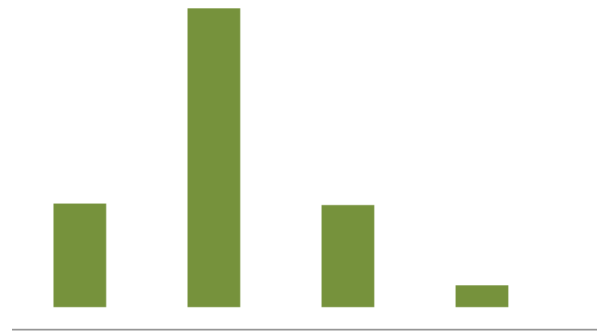




## Litter size in sheep

TP=1, 2,3,...n  
Discrete variable





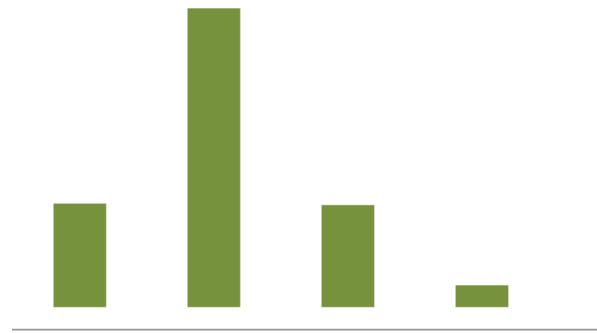
### Litter size in sheep

TP=1, 2,3,...n  
Discrete variable

Heteroscedastic - continuous



Classical canalization model



**Litter size in sheep**

TP=1, 2,3,...n  
Discrete variable

Heteroscedastic - continuous



Classical canalization model

Homoscedastic - discrete



Classical threshold model

# Classical canalization model

Continuous trait

$$y = \mu + u + f(\eta, v) \varepsilon$$



mean



variability

$$\varepsilon \sim N(0, 1)$$

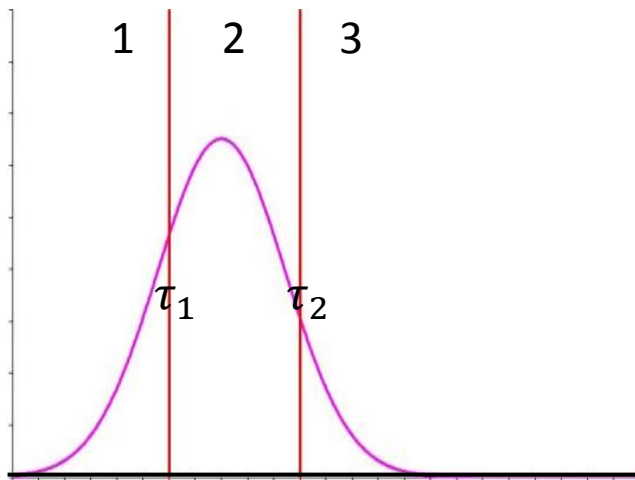
$$\begin{pmatrix} u \\ v \end{pmatrix} \sim N \left( \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_u^2 & \sigma_{uv} \\ \sigma_{uv} & \sigma_v^2 \end{pmatrix} \otimes A \right)$$

$f$ : link function  
(Exponential, Square R., Linear)



# Classical threshold model

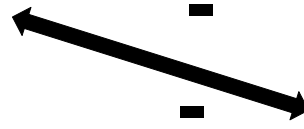
Discrete trait



Liability  $l|u \sim N(\mu + u, 1)$

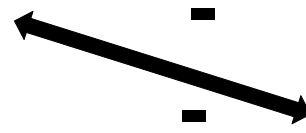
Set of thresholds  $t = (\tau_1, \dots, \tau_{n-1})$

**Heteroscedastic**  
**Homoscedastic**



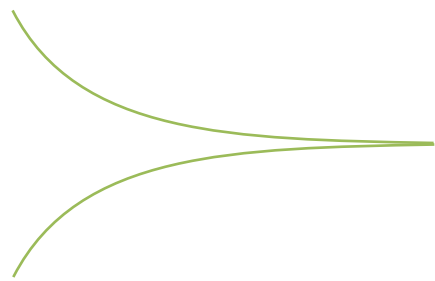
**Continue**  
**Discrete**

**Heteroscedastic**  
Homoscedastic



**Continue**  
**Discrete**

$$y = \mu + u + f(\eta, v) \varepsilon$$



$$\text{Liability } l | u \sim N(\mu + u, f^2(\eta, v))$$

$$t = (\tau_1, \dots, \tau_{n-1})$$

Liability  $l | u \sim N(\mu + u, 1)$

$$t = (\tau_1, \dots, \tau_{n-1})$$

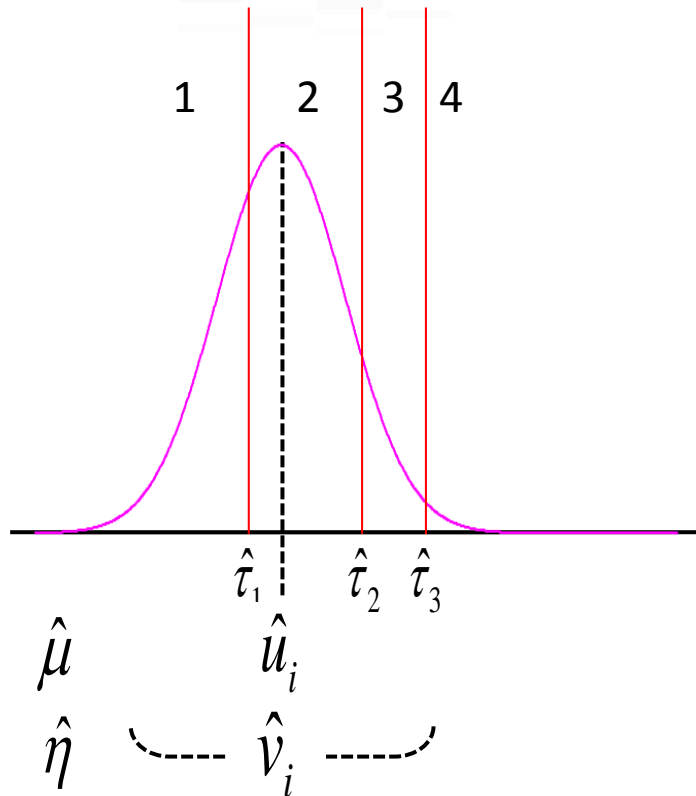




# Heteroscedastic threshold model

Underlying scale

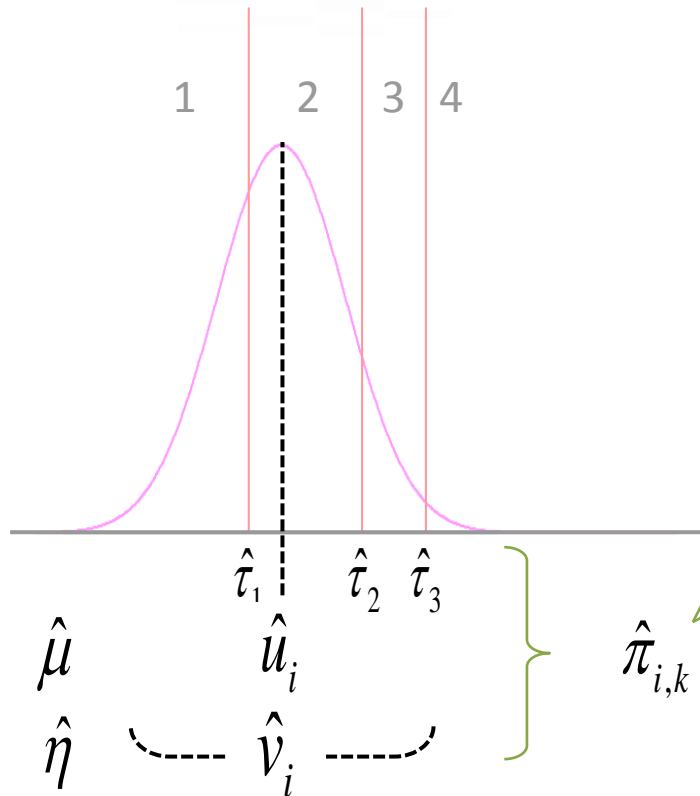
Observed scale



# Heteroscedastic threshold model

Underlying scale

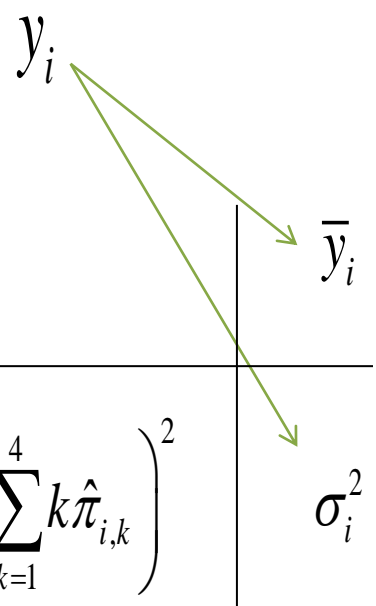
Observed scale



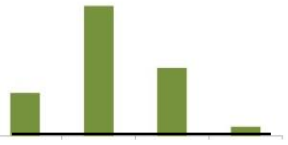
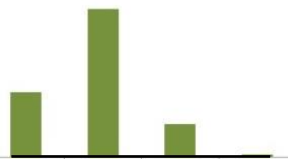
$$\bar{y}_i = \sum_{k=1}^4 k \hat{\pi}_{i,k}$$


---


$$\hat{\sigma}_i^2 = \sum_{k=1}^4 k^2 \hat{\pi}_{i,k} - \left( \sum_{k=1}^4 k \hat{\pi}_{i,k} \right)^2$$



# Data

Breed	Prolificacy	Distribution				Nb of obs
		1	2	3	4	
Romane	2.06					72 623
Rouge de l'Ouest	1.86					99 384
Suffolk	1.62					30 328

# Genetic parameters on the underlying scale

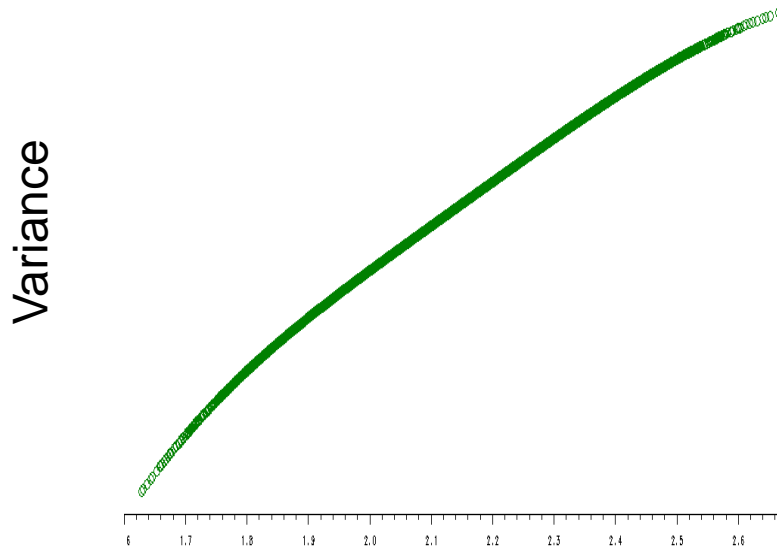
Breed	$\sigma_u^2$	$\sigma_v^2$	$\rho$
Romane	0.069	0.020	-0.40
Rouge de l'Ouest	0.100	0.022	-0.26
Suffolk	0.079	0.008	-0.46



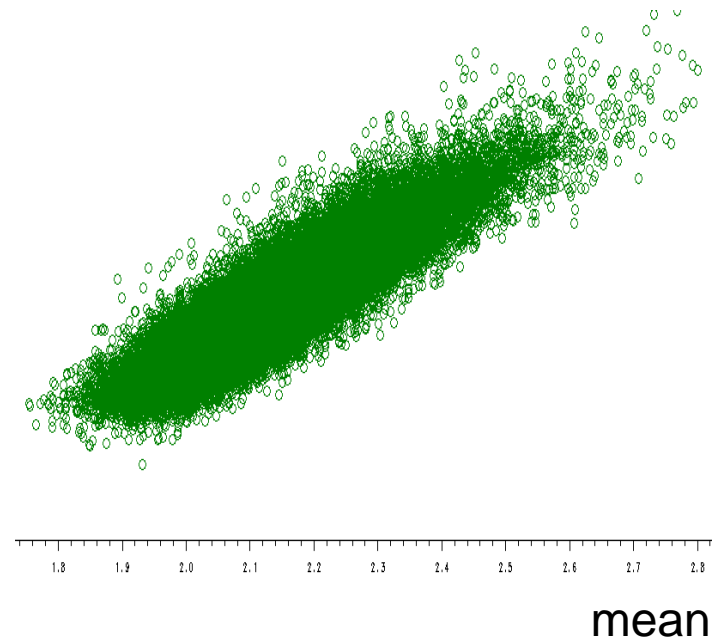
# Genetic values on the observable scale

Exemple: Romane breed

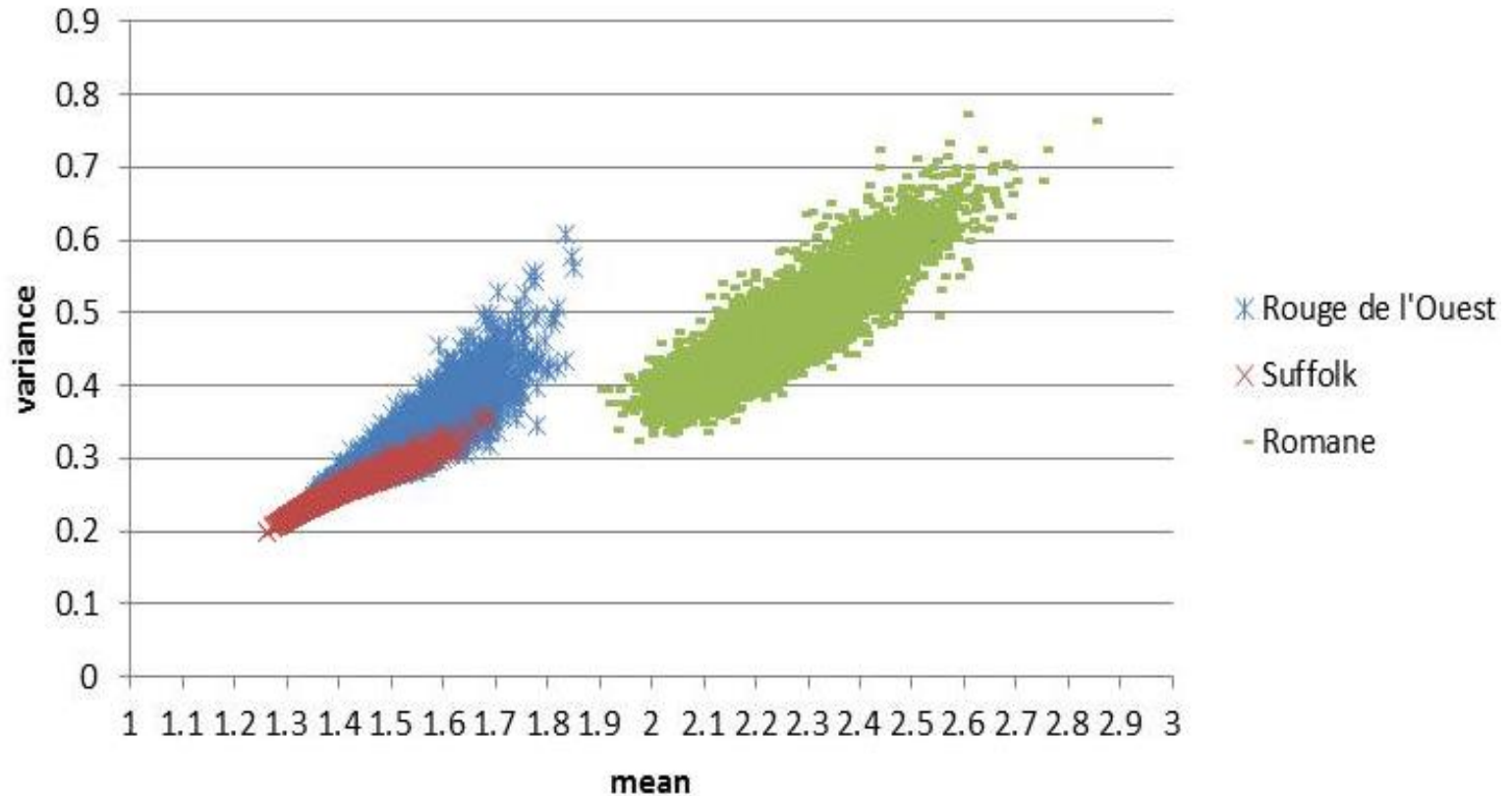
homoscedastic  
Threshold model



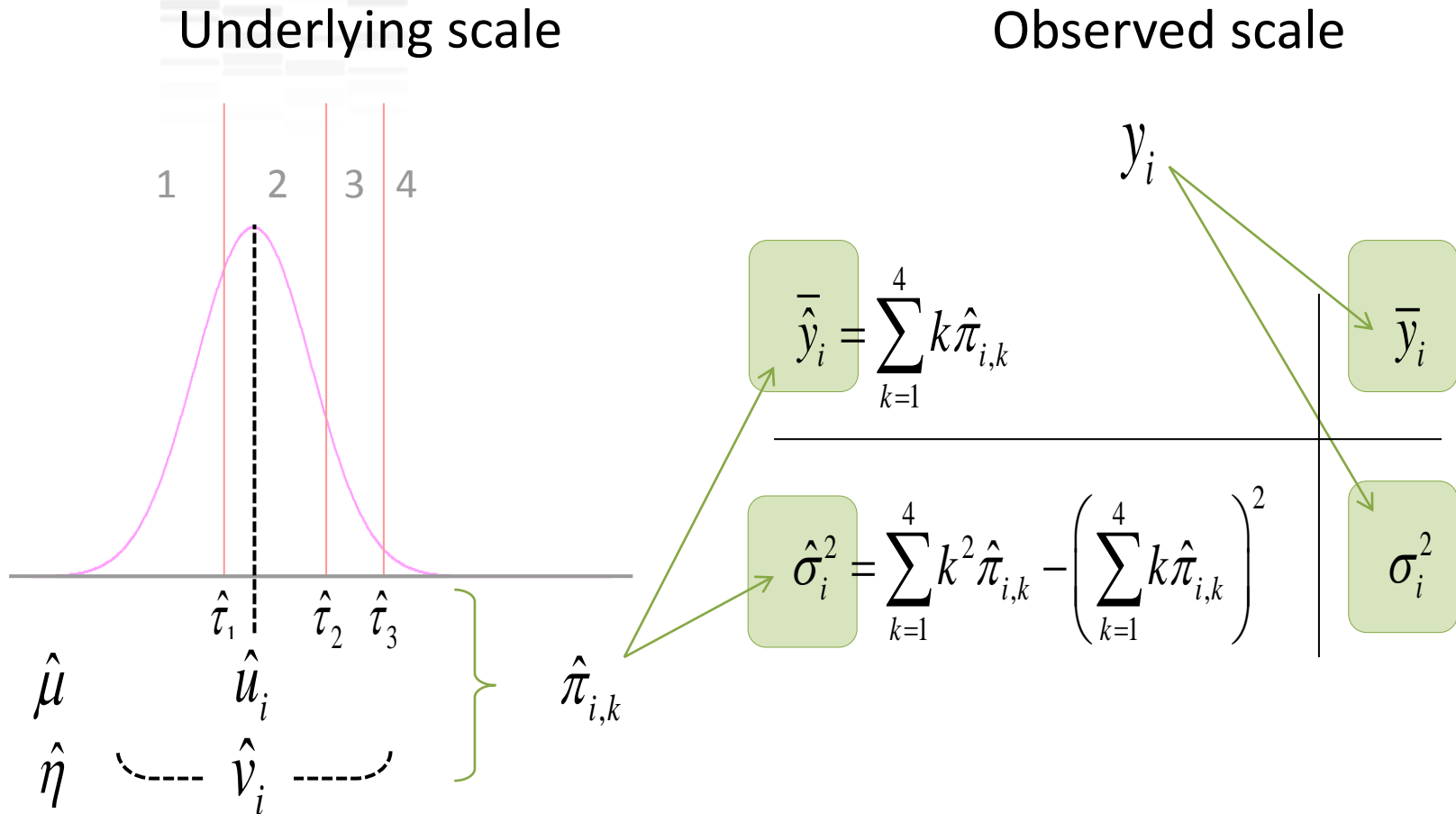
heteroscedastic  
Threshold model



# Genetic values on the observable scale



# Goodness of fit on the observable scale



# Goodness of fit on the observable scale

Breed	Prol	Model scedasticity	$\rho_{y_i, \bar{y}_i}^-$	$\rho_{\sigma_i^2, \hat{\sigma}_i^2}$
Romane	2.06	Hetero Homo	<b>0.79</b> (0.78)	<b>0.61</b> (0.21)
Rouge de l'Ouest	1.86	Hetero Homo	<b>0.77</b> (0.78)	<b>0.50</b> (0.16)
Suffolk	1.62	Hetero Homo	<b>0.84</b> (0.84)	<b>0.38</b> (0.24)





# Goodness of fit on the observable scale

Breed	Prol	Model scedasticity	$\rho_{y_i, \bar{y}_i}$	$\rho_{\sigma_i^2, \hat{\sigma}_i^2}$
Romane	2.06	Hetero Homo	<b>0.79</b> (0.78)	<b>0.61</b> (0.21)
Rouge de l'Ouest	1.86	Hetero Homo	<b>0.77</b> (0.78)	<b>0.50</b> (0.16)
Suffolk	1.62	Hetero Homo	<b>0.84</b> (0.84)	<b>0.38</b> (0.24)



# Goodness of fit on the observable scale

Breed	Prol	Model scedasticity	$\rho_{y_i, \bar{y}_i}^-$	$\rho_{\sigma_i^2, \hat{\sigma}_i^2}$
Romane	2.06	Hetero Homo	<b>0.79</b> (0.78)	<b>0.61</b> (0.21)
Rouge de l'Ouest	1.86	Hetero Homo	<b>0.77</b> (0.78)	<b>0.50</b> (0.16)
Suffolk	1.62	Hetero Homo	<b>0.84</b> (0.84)	<b>0.38</b> (0.24)



# Conclusion

- ▶ **Modeling the variance of liability of a threshold model is a simple way for modeling the environmental sensitivity of sheep litter size**
- ▶  **$\sigma_v^2$  is not zero  $\rightarrow$  genetic origin in variance heterogeneity**
- ▶ **the correlation between  $u$  and  $v$  is negative for the three breed**
- ▶ **Canalization of sheep litter size should be possible**

# Conclusion

- Modelling the variance of liability of a threshold model is a simple way for modelling the environmental sensitivity of litter size in sheep.
- $\sigma_v^2$  is not zero  $\rightarrow$  genetic origin in variance heterogeneity
- The correlation between the  $u$  and  $v$  is negative for the three breeds
- Canalization of sheep litter size should be possible

