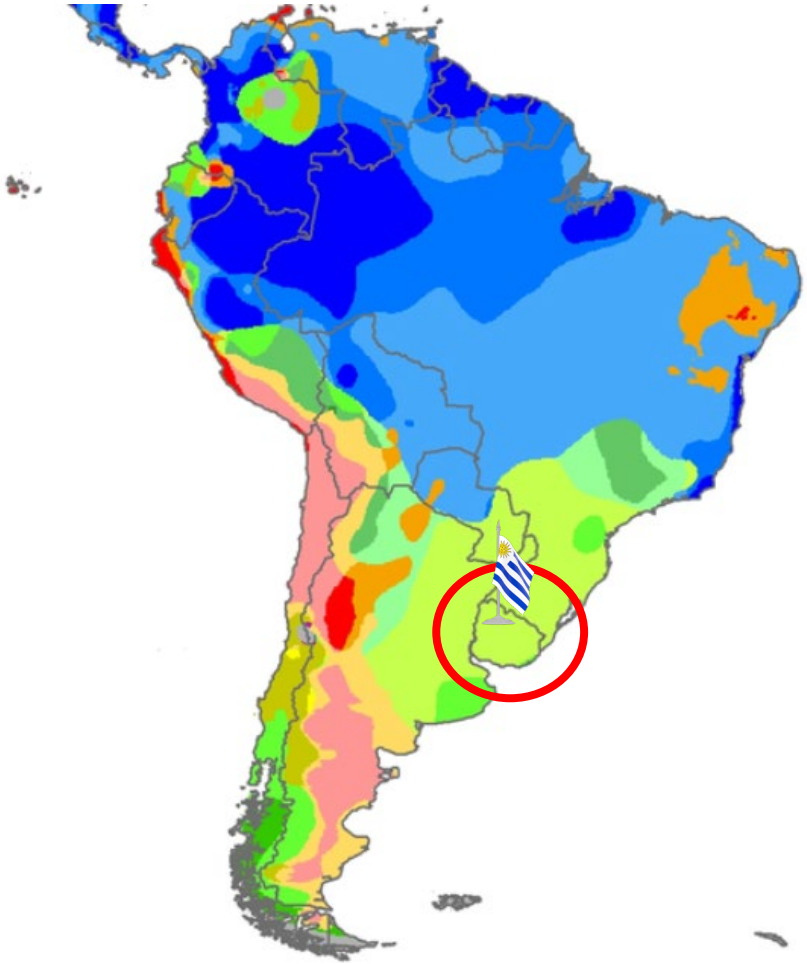
Somatotropic axis of Holstein cows of diverging genetic origin under two pasture-based systems

Benoit I.[1], García-Roche M.[2], Mendoza A.[1]

[1]Programa de Producción de Leche, INIA "La Estanzuela", Uruguay; [1]Departamento de Producción Animal y Pasturas, Facultad de Agronomía, Universidad de la República, Uruguay.

INTRODUCTION



URUGUAY

- Temperate grassland biome
- 70% of the milk produced is for export. (INALE, 2024)
- Mixed systems, combined differents levels of inclusion of the pasture, concentrate and forage reserves in the diet.
  - Low production costs.
  - Weather dependent.
  - Imbalance between supply and demand of nutrients required by the cows.

(Dillon 2006, Chilibroste et al., 2015)

- Search for genotypes adapted to pasture-based system in order to increase the grazing efficiency.
- Genotypes
  - 78% North American Holstein (NAH)
  - 13% New Zealand Holstein (NZH) (INALE 2019)

INTRODUCTION

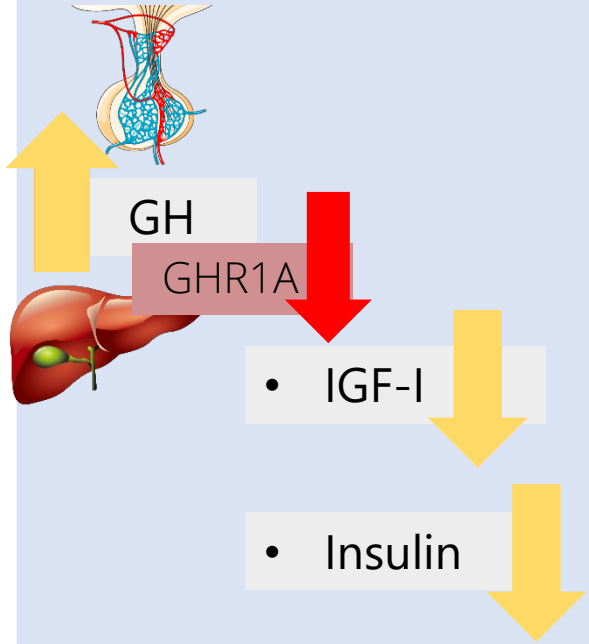
Criteria of selection:

- High individual milk production

- Walking long distances and grazing

INTRODUCTION

Somatotropic axis uncoupling



Radcliff et al., 2003

Promotes catabolic processes like lipolisis and hepatic neoglucogenisis to ensure the glucose flow to the mammary gland for milk production.

DIFFERENCES IN SOMATOTROPIC AXIS UNCOUPLING BETWEEN GENOTYPES

NAH display a larger degree of somatotropic axis uncoupling than NZH.
(Grala et al., 2011; Lucy et al.,2009.)

- Earlier recoupling of the somatotropic axis in NZH associated with higher levels of insulin.

(Grala et al., 2011)

- Previous studies report contradictory effects of feeding supplementation in the recoupling of the somatotropic axis.

(Grala et al., 2011, Lucy et al, 2009)

HYPOTHESIS

We hypothized that NAH cows with more pasture inclusion in the diet would present more severe uncoupling of the somatotropic axis than NAH fed a PMR and NZH in both systems.

GOAL

Study the gene expression of the components of the somatotropic axis in two divergent Holstein genotypes with different levels of pasture inclusion.

MATERIALS AND METHODS
Experimental design

Experimental Station **"Dr. Alberto Boerger"**
INIA La Estanzuela
Semillero, Colonia, Uruguay

N= 48 multiparous
Holstein cows
of diverging genotypes

NAH
640 Kg BW
7500 Kg
yield/lactation

NZH
575 Kg BW
5500 Kg
yield/lactation

MaxP FixP

MaxP FixP

MaxP

- 27% concentrate
- 73% grazed pasture + forage reserves

DM basis

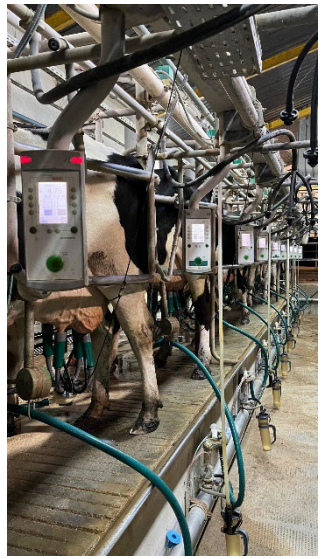
FixP

- 67% TMR (55:45 F:C)
- 33% grazed pasture

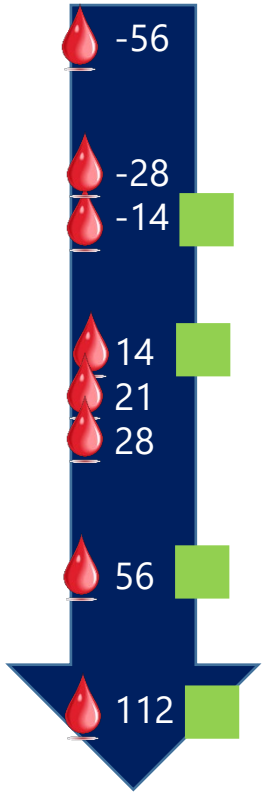
DM basis

Same production goal within genotypes

MATERIALS AND METHODS
Sample collection and analyses



- Milk yield was recorded daily with the GEA´s software.

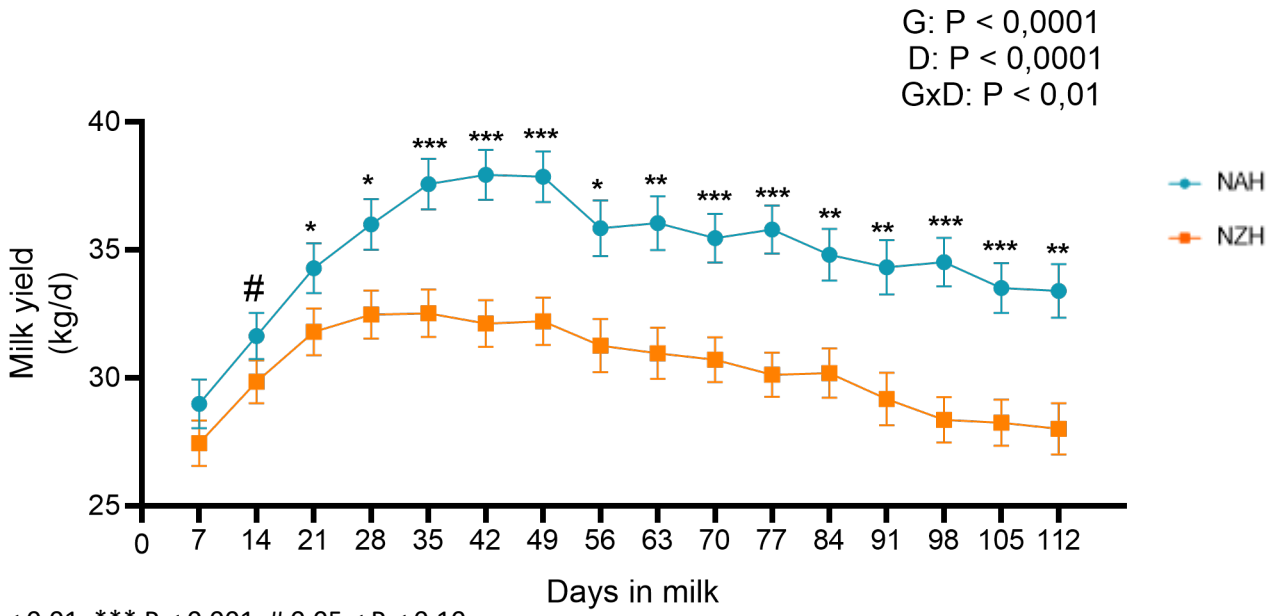


- Serum samples
  - Insulin and IGF-I were measured with commercial kits
- Liver biopsies
  - mRNA abundance of IGF-I receptor (IGFI-R) and growth hormone receptor 1A (GHR1A) were studied using real time PCR.

Data were analyzed using a mixed model with repeated measures that included genetic origin (G), days postpartum (D), feeding strategies(FS) and their interactions as fixed effects.

RESULTS

	NA-H		NZ-H			*P value*				
	FixP	MaxP	FixP	MaxP	*SEM*	*G*	*FS*	*G*FS*	*G*D*	*FS*D*
Milk yield, (Kg/d)	33.82	35.92	30.81	29.87	1.07	<0.0001	0.60	0.14	<0.01	0.84

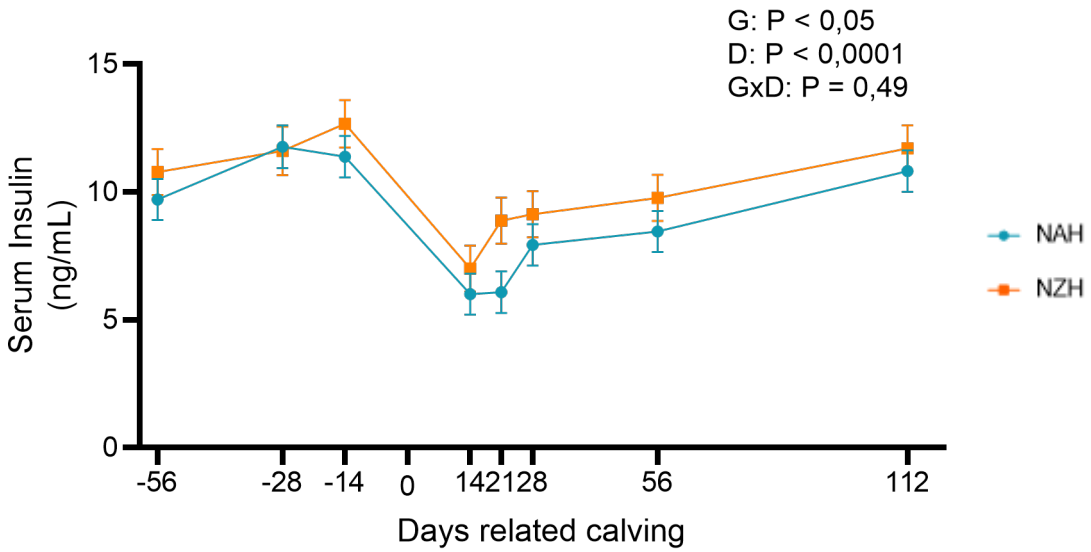


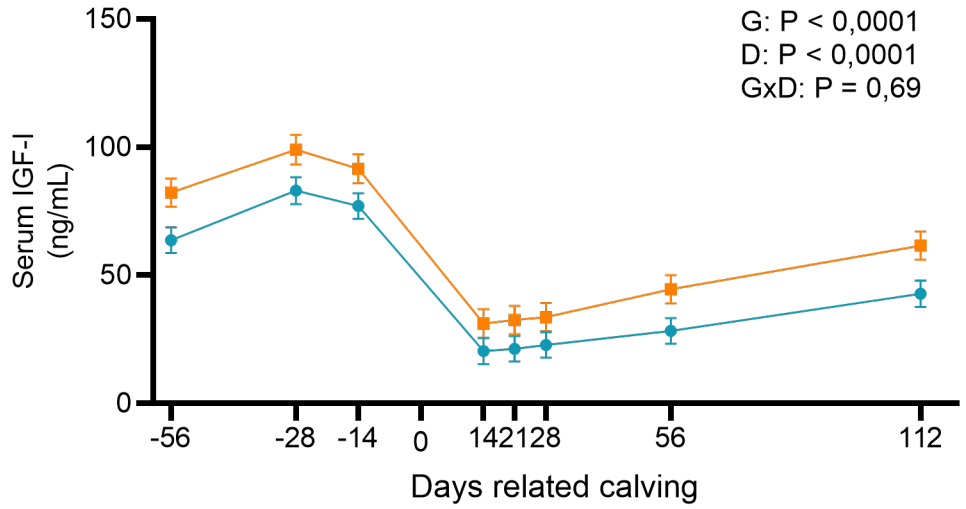
*P < 0.05; **P < 0.01; *** P < 0.001; # 0.05 < P < 0.10

These results are in agreements with previous reports
(Roche et al., 2006; Horan et al., 2005a).

RESULTS

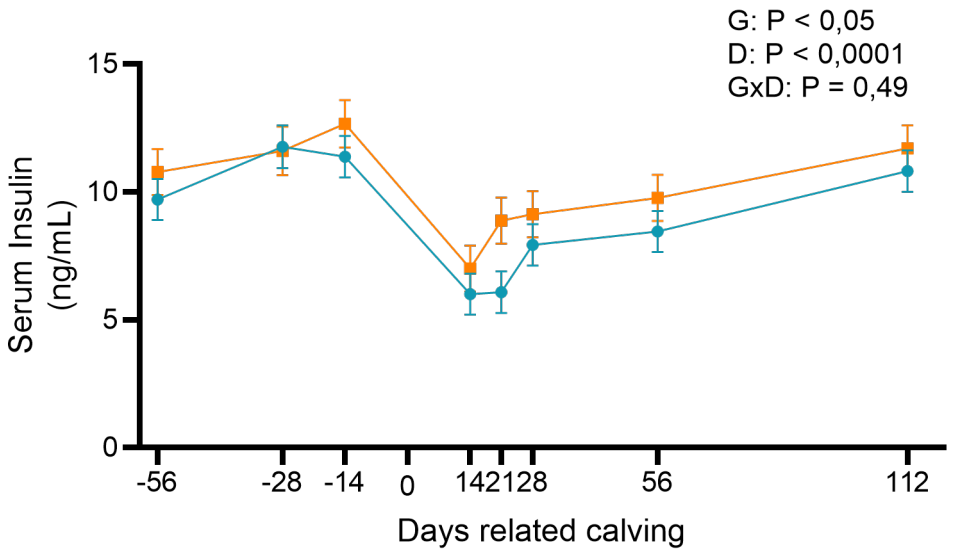
	NA-H		NZ-H			*P value*				
	FixP	MaxP	FixP	MaxP	*SEM*	*G*	*FS*	*G*FS*	*G*D*	*FS*D*
Insulin, ng/mL	11.29	11.09	12.92	11.89	1.05	<0.05	0.23	0.49	0.46	0.72
IGF-I, ng/mL	43.50^{b}	46.36^{b}	62.32^{a}	56.82^{a}	3.85	<0.0001	0.75	<0.05	0.69	0.83

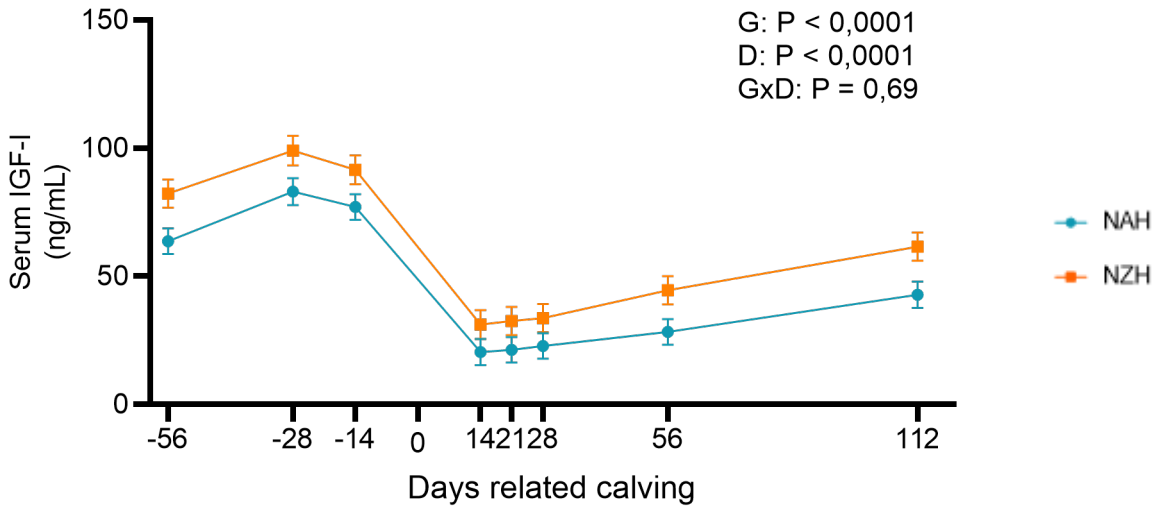




RESULTS

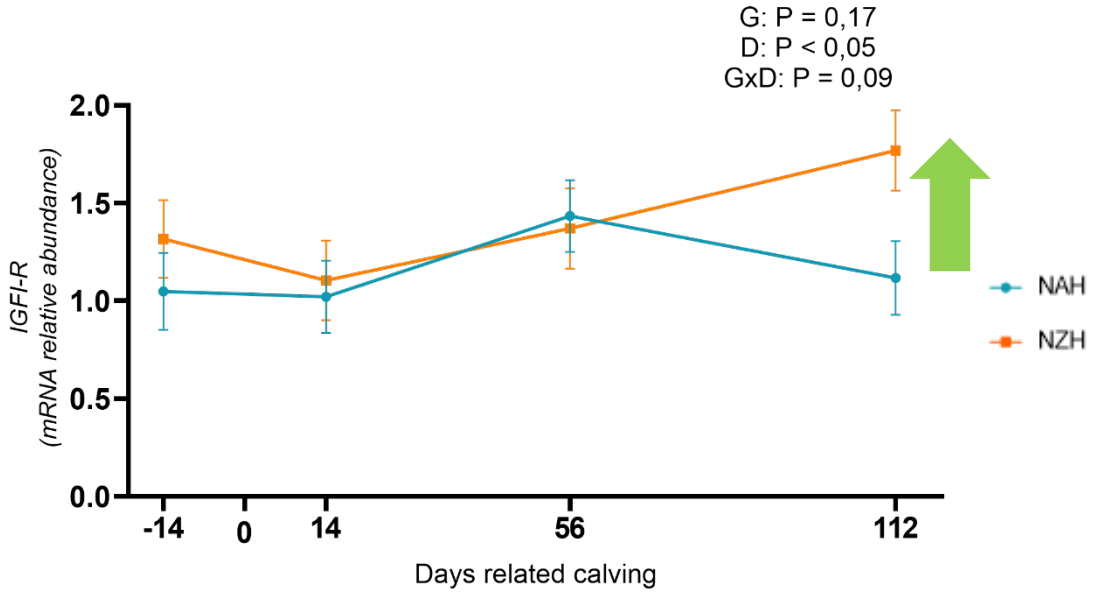
Similar curves of both hormones have been reported by Radcliff et al., 2003, showing coordinated changes of insulin and IGF-I, and reflect the dependence of IGF-I on insulin in postpartum dairy cows. (Butler et al., 2003).

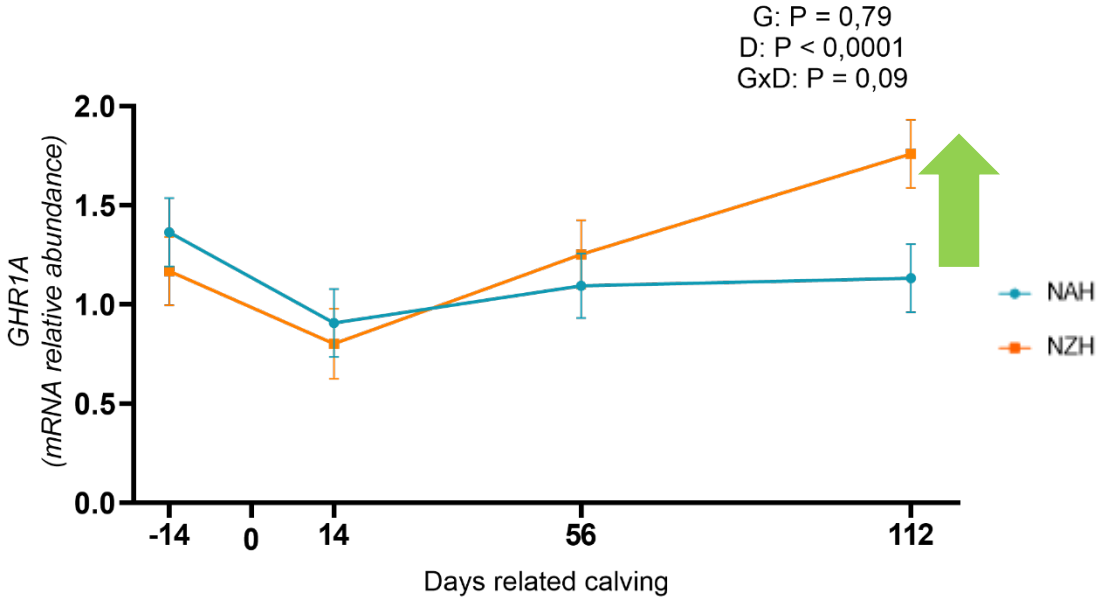




RESULTS

	NAH		NZH			*P value*				
	FixP	MaxP	FixP	MaxP	*SEM*	*G*	*FS*	*G*FS*	*G*D*	*FS*D*
IGFI-R, mRNA	0.85	1.46	1.27	1.51	0.19	0.18	0.08	0.56	0.09	0.91
GHR1A, mRNA	0.97	1.28	1.36	1.13	0.14	0.79	0.94	0.11	0.09	0.42





RESULTS

- By mid-lactation (112 DPP) the highest levels of insulin coincided with the highest levels of *GHR1A* and *IGFI-R* transcripts, as well as increased serum IGF-I levels, revealing the recoupling of the somatotropic axis at this moment.

- The recoupling of the somatotropic axis was different between genotypes, as NZH cows showed a tendency to express 1.6 fold higher *GHR1A* and *IGFIR* transcripts than NAH.

CONCLUSIONS

- Cows of both genotypes experienced uncoupling of the somatotropic axis during early lactation.
- There was a tendency for NZH cows to experience recoupling before NAH cows.
- There was no effect of the level of inclusion of pasture in the diet on the uncoupling of the somatotropic axis.

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