

# Application of random regression models for Gaussian and binary traits to estimate genetic parameters in low input dairy cattle herds



*T. Yin<sup>1</sup>, B. Bapst<sup>2</sup>, H. Simianer<sup>1</sup>, S. König<sup>3</sup>*

<sup>1</sup> Department of Animal Sciences  
Animal Breeding and Genetics Group  
Georg-August-University Göttingen, Germany

<sup>2</sup> Schweizer Braunviehzuchtverband

<sup>3</sup> Department of Animal Breeding  
University of Kassel, Germany





# Background

---

- Low input dairy herds
  - Production traits
  - Reproduction traits
  - Functional traits
- Aim
  - Variance and covariance components
  - Apply different types of random regression models
- Prerequisite
  - Breeding programs
  - Simulation

# Original data

---



- Official records:
  - Brown Swiss
  - low input farms in Switzerland
  - Production traits:
    - 36,877 records
    - 1,293 cows
  - Reproduction traits:
    - 9,982 records 1,434 cows
    - 5,296 records 1,427 cows
  - Pedigree file:
    - 3,542,563 animals
    - Birth year: 1908-2009





# Data

- Traits and programs

Trait complex	Full Name	Abbreviation
Production	Milk yield	<b>MY</b> (in kg)
	Fat%	<b>Fat%</b>
	Protein%	<b>Pro%</b>
	Lactose%	<b>Lac%</b>
	Somatic cell score	<b>SCS</b>
	Milk urea nitrogen	<b>MUN</b> (in mg/dl)
Reproduction	Age at first calving	<b>AFC</b> (in d)
	Calving to 1 <sup>st</sup> service	<b>CTFS</b> (in d)
	Days open	<b>DO</b> (in d)
	Gestation length	<b>GL</b> (in d)
	Calving interval	<b>CI</b> (in d)
	No. insemination	<b>NI</b>
	Calving ease	<b>CE</b> (scale 1-4)
	Still-birth	<b>SB</b> (0 or 1)
	Conception rate	<b>CR</b> (0 or 1)

VCE6 (Groeneveld, E., K. Milena and M.Norbert, 2008)

THRGIBBS1F90 (Misztal et al., 2002)



# Methods

---

- Random regression animal model-1 and 2 (VCE, )

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wp} + \mathbf{e},$$

- Covariates
  - Production traits: DIM, 5-365
  - Fertility traits: parity, 1-8 (Schaeffer, 2004)
- Legendre polynomials
- Effects
  - Production traits: HTD, parity
  - Reproduction traits: herd, age, CY, CS, IY, IN, rS



# Methods

---

- Random regression sire model-3 (Tusruta et al. 2009)

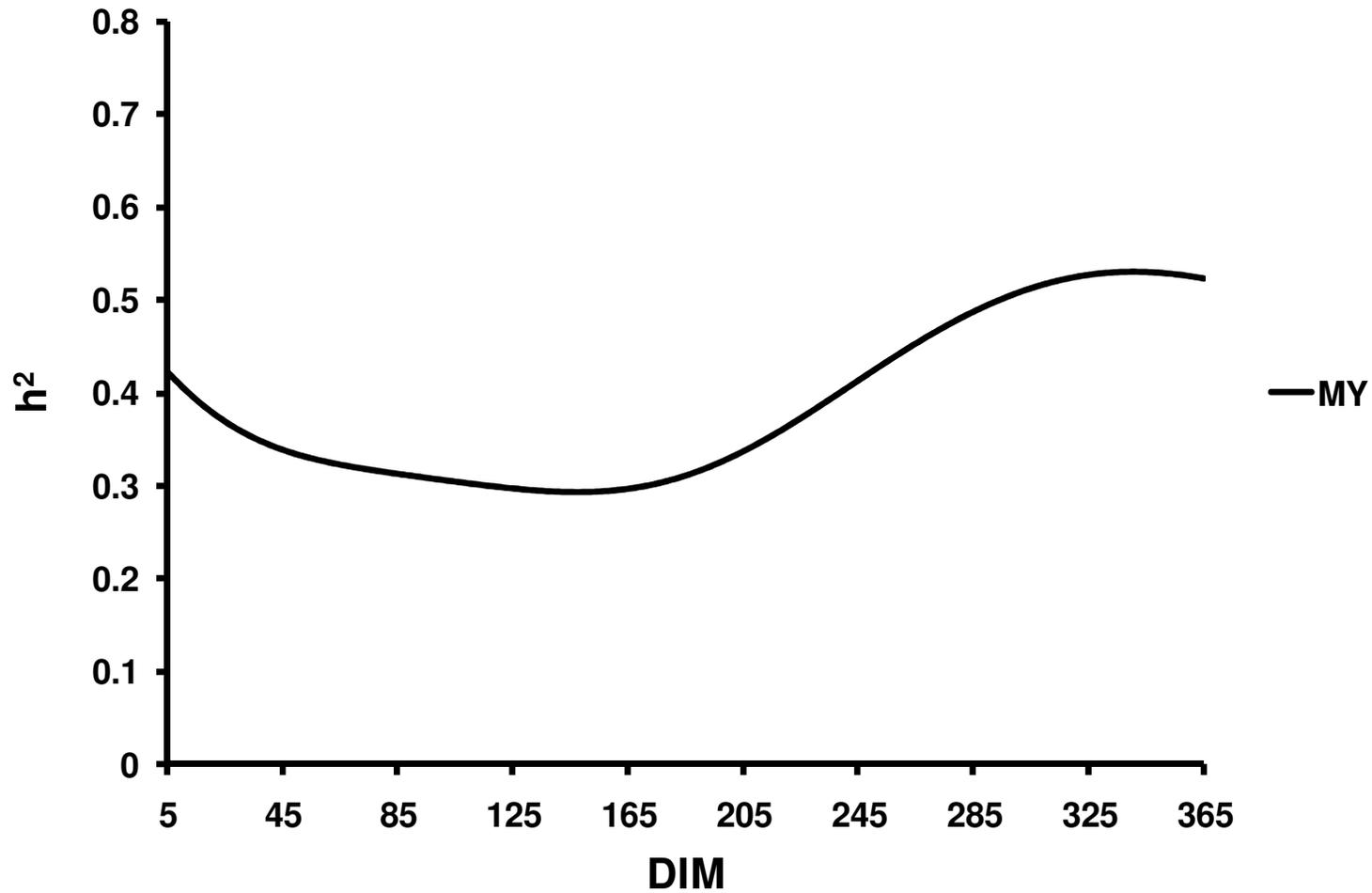
$$\begin{bmatrix} \mathbf{1} \\ \mathbf{y} \end{bmatrix} = \begin{bmatrix} \mathbf{Xb} + \mathbf{Ws} + \mathbf{Z}_1\mathbf{u} + \mathbf{Z}_2\mathbf{p} + \mathbf{e} \\ \mathbf{Xb} + \mathbf{Z}_1\mathbf{u} + \mathbf{Z}_2\mathbf{p} + \mathbf{e} \end{bmatrix}$$

- Covariates: DIM 20-220
- Legendre polynomials
- Fix effects:
  - Herd, insemination year and season



# Results

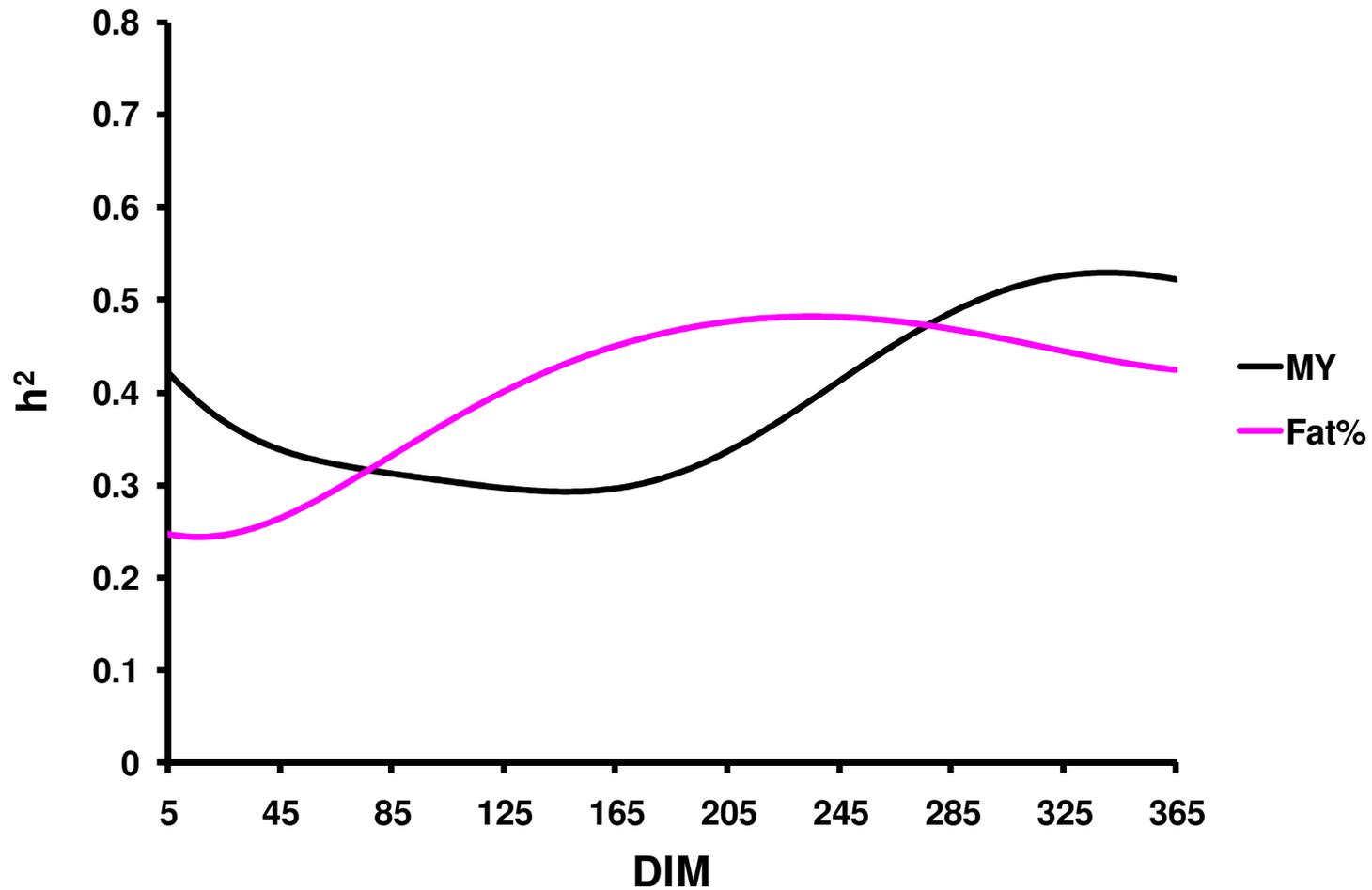
- Heritabilities of production traits from model-1 (DIM)





# Results

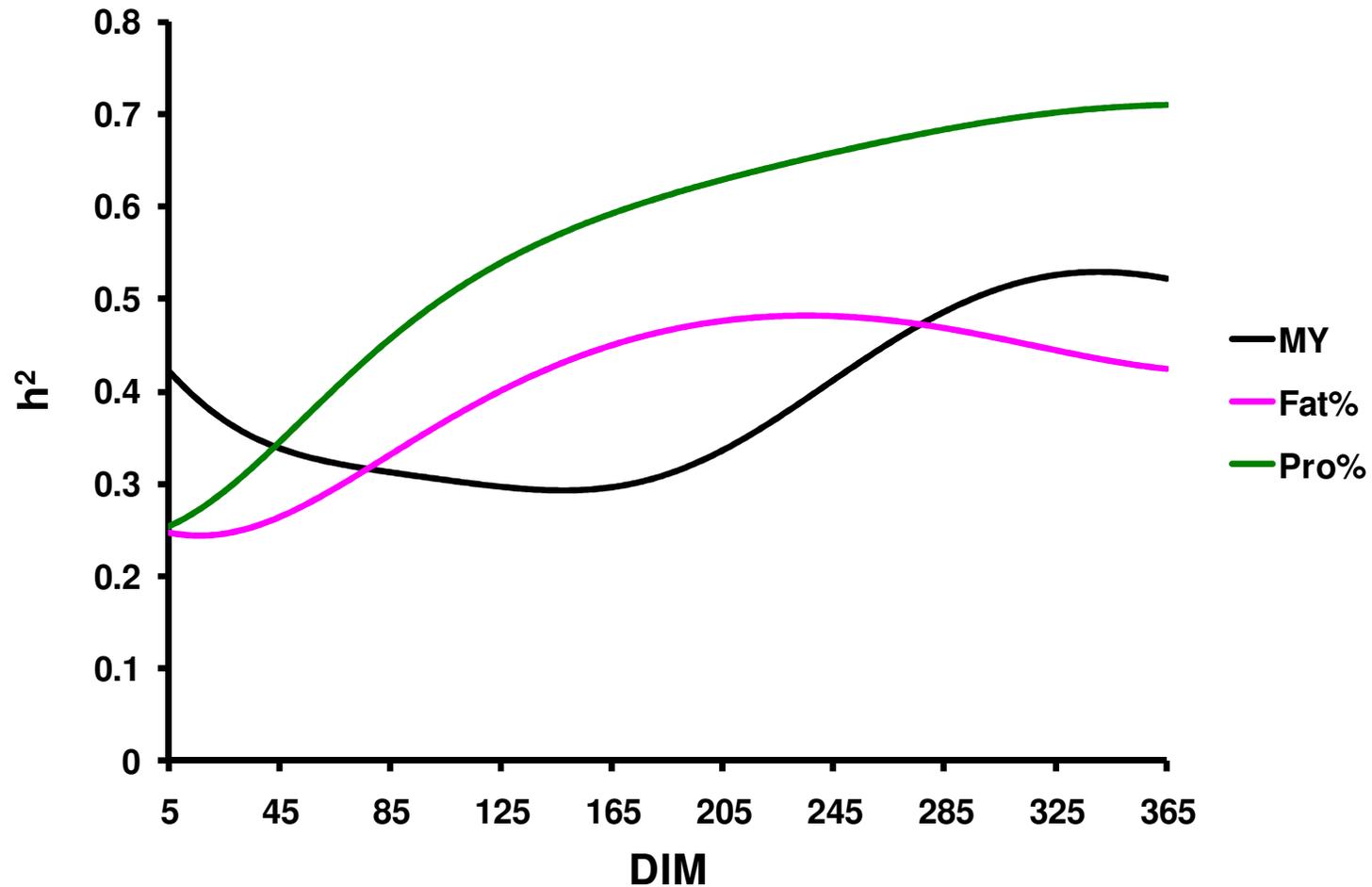
- Heritabilities of production traits from model-1 (DIM)



# Results



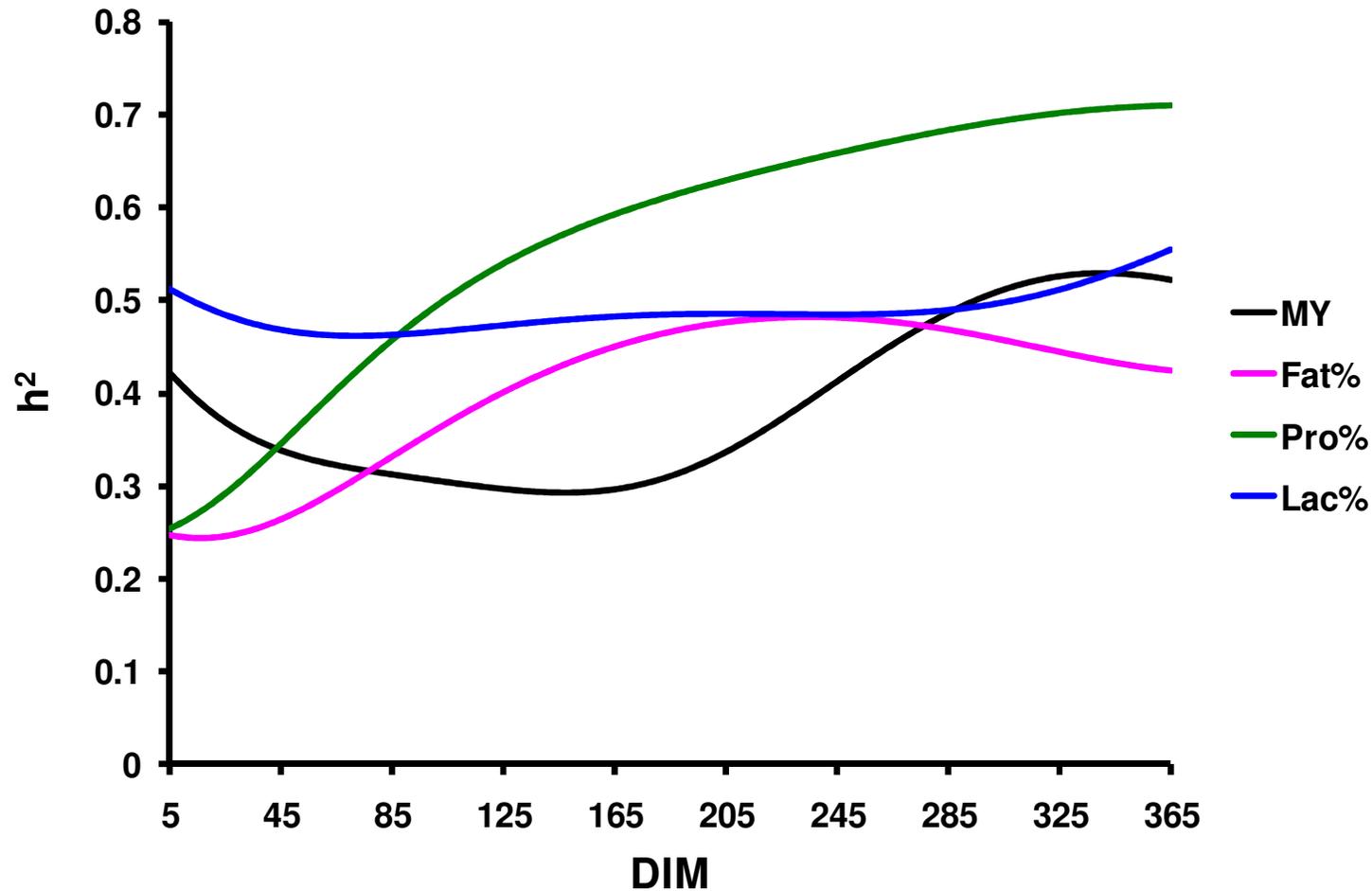
- Heritabilities of production traits from model-1 (DIM)





# Results

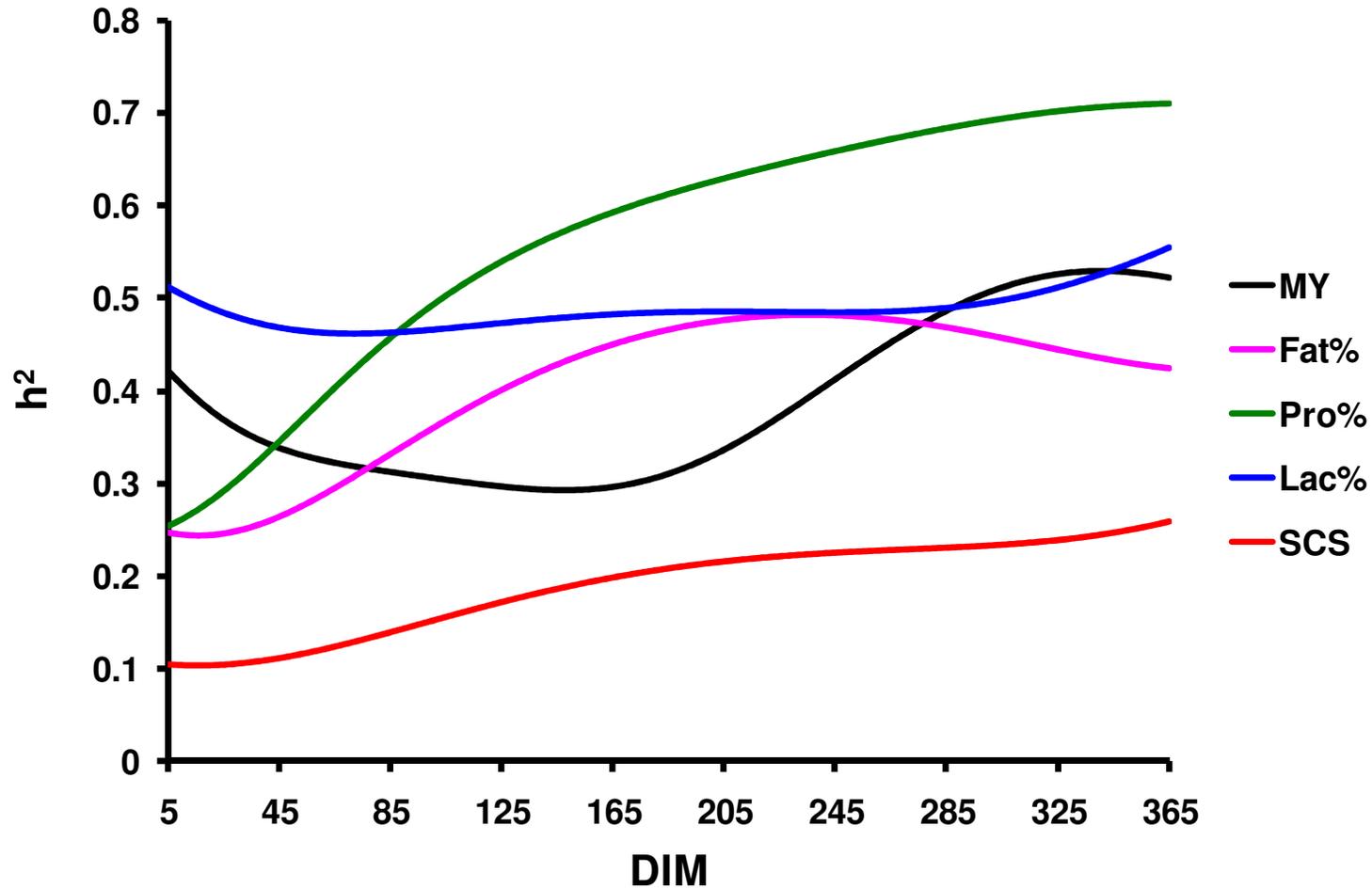
- Heritabilities of production traits from model-1 (DIM)



# Results



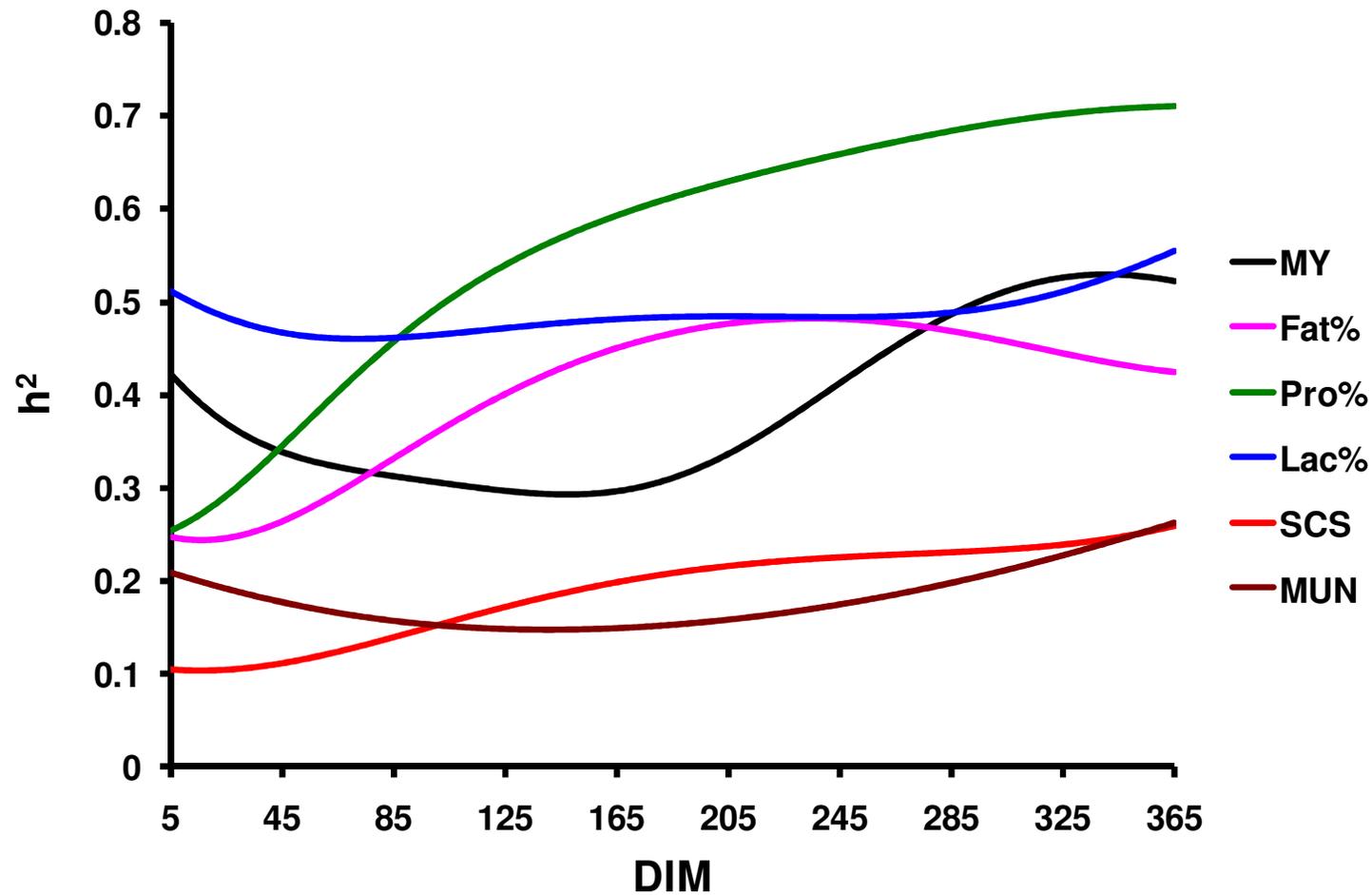
- Heritabilities of production traits from model-1 (DIM)





# Results

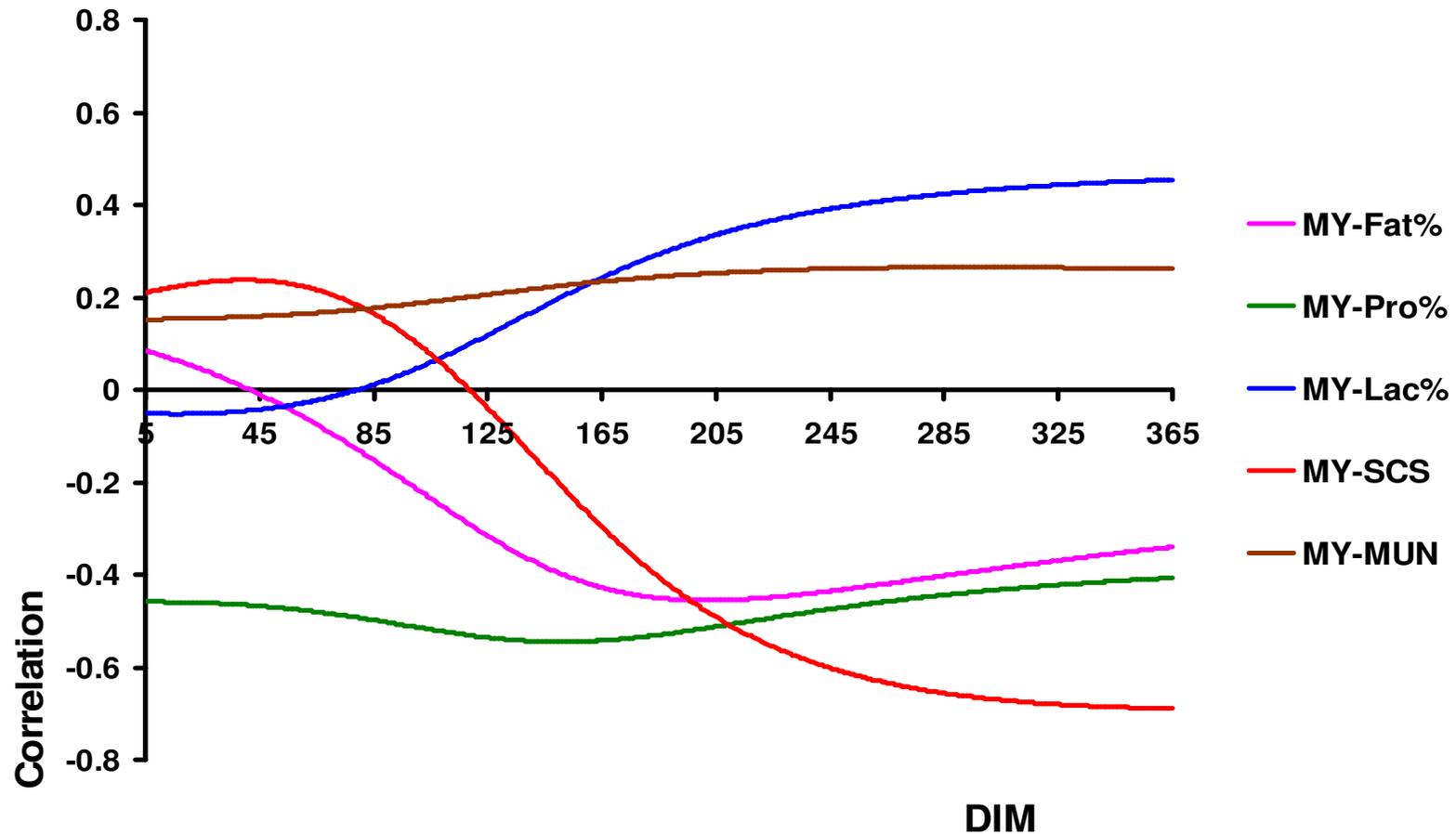
- Heritabilities of production traits from model-1 (DIM)



# Results



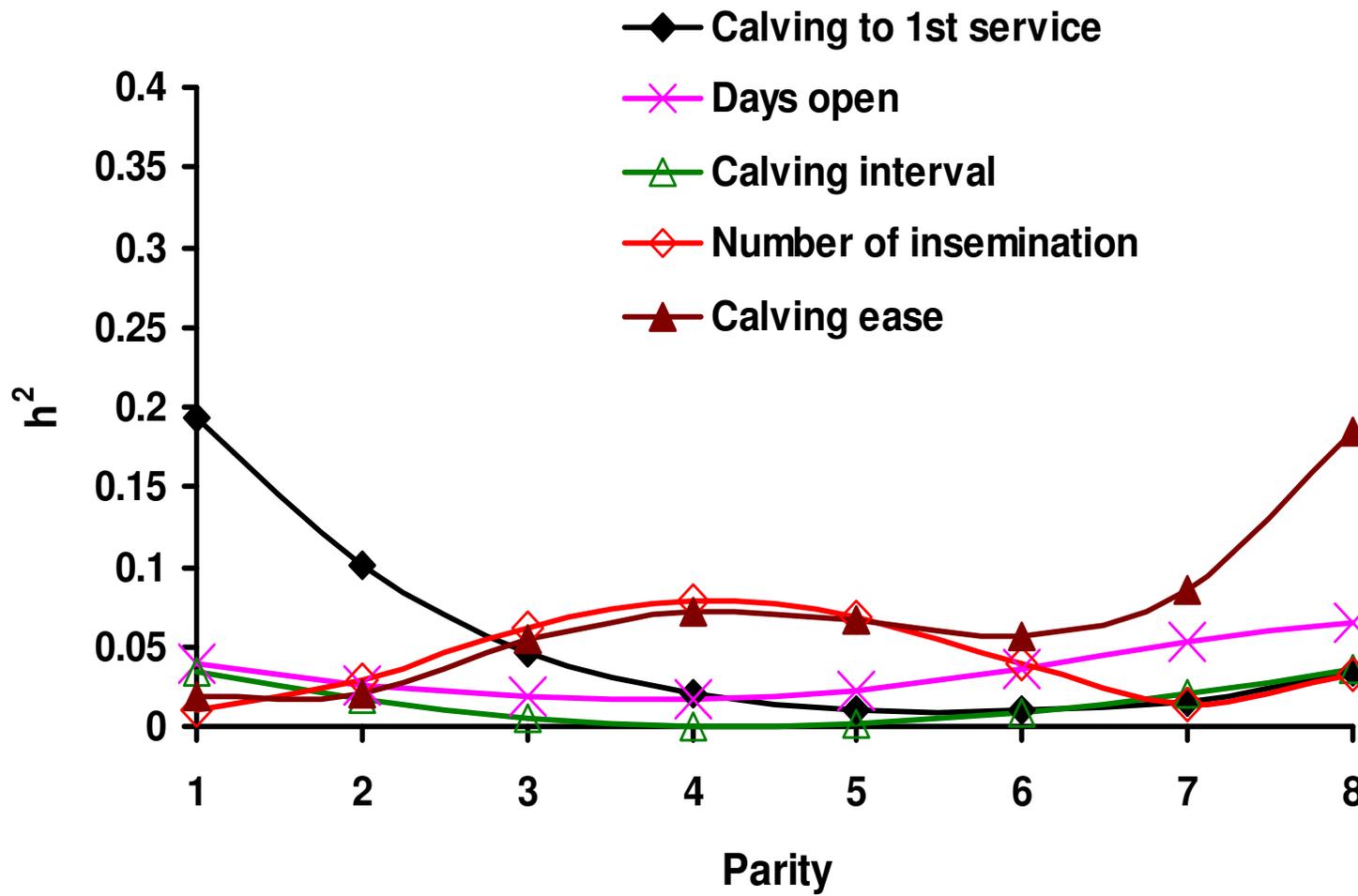
- Genetic correlation from model-1 (DIM)





# Results

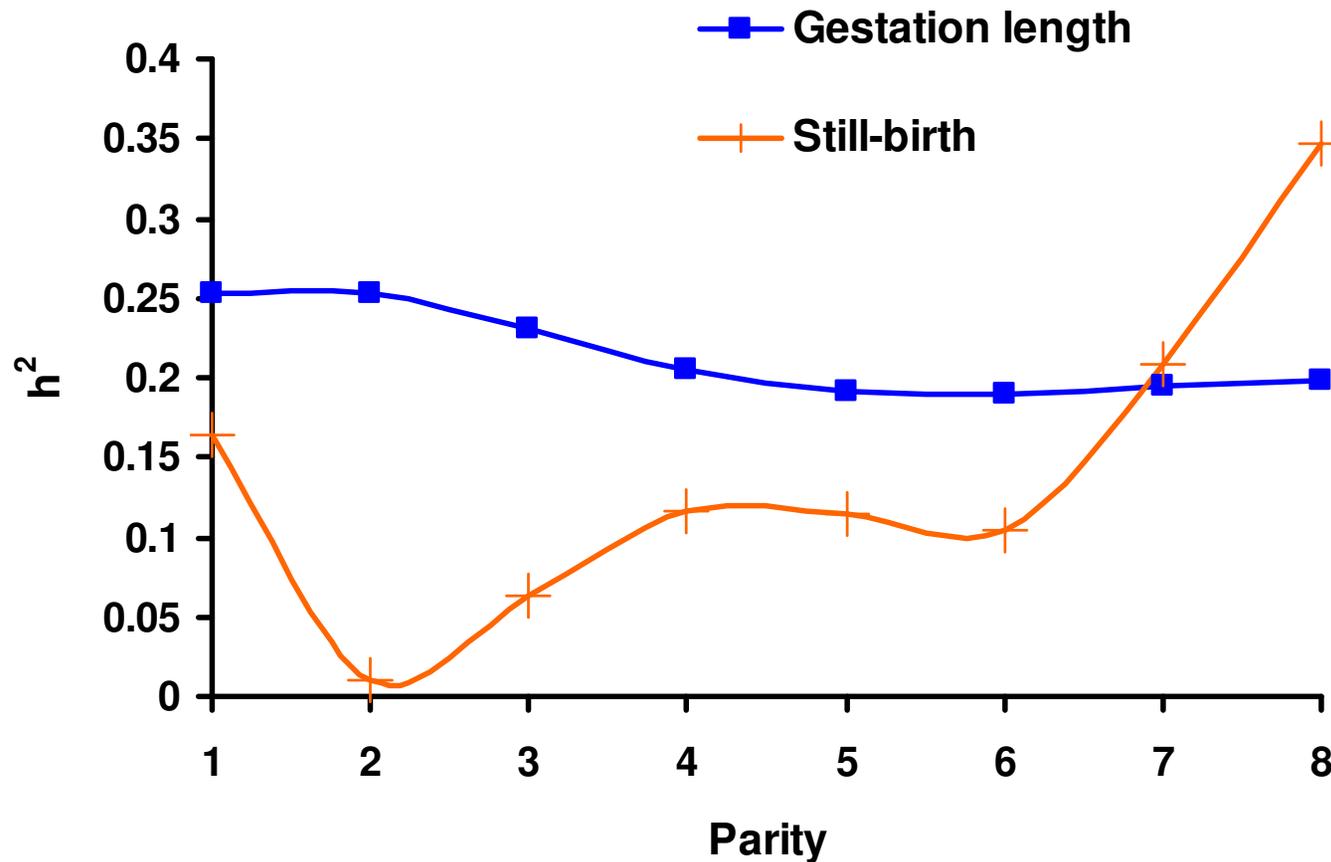
- Heritabilities of reproduction traits from model-2 (parity)





# Results

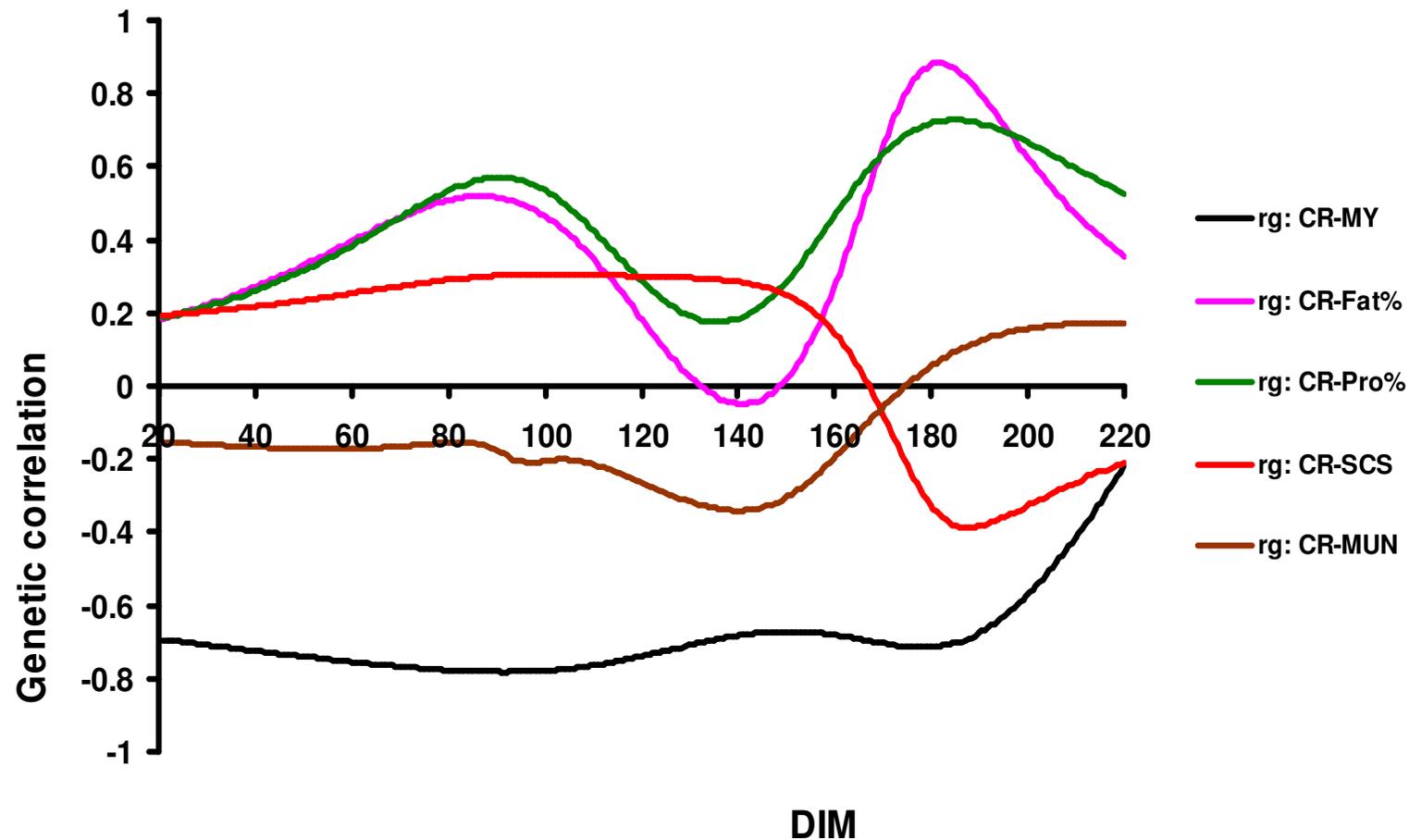
- Heritabilities of reproduction traits from model-2 (parity)





# Results

- Daily relationships between conception rate (CR) and five Gaussian traits from model-3





# Discussion

---

- Daily heritabilities of MY, Fat%, Pro%, Lac%, SCS and MUN followed the same pattern as found for high input production systems
- A positive correlation between MY and Fat%
  - possibilities of the mobilization of body fat reserves
- A positive correlation between MY and MUN implies
  - more energy goes to milk
  - an energy shortage for protein production
  - increased levels of MUN



# Discussion

---

- Heritabilities of female reproduction traits were generally low, but
  - heritabilities of gestation length 0.21-0.25
  - heritabilities of calving to 1<sup>st</sup> service > days open and number insemination
- Genetic antagonism was found between CR and MY, and between CR and MUN
- Simulate daily observations of cows
- Set up suitable breeding programs

# Acknowledgment

---



Gratefully acknowledge co-funding from the European Commission, under the Seventh Framework Programme for Research and Technological Development, for the Collaborative Project LowInputBreeds (Grant agreement No 222623). However, the views expressed by the authors do not necessarily reflect the views of the European Commission, nor do they in any way anticipate the Commission's future policy in this area.





---

# Thank you for your attention !

