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Genetic relationships and trait comparisons between and within lines of local dual purpose cattle

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Background

- The old dual purpose black and white cattle (DSN) belong to the lowland breeds
- Origin: northern Germany & the Netherlands
- Exchange of breeding animals (until 19th century) between Dutch and German herds
 - similar phenotypic and genotypic traits
- Widely distributed in Germany in 1930ies
- 50% of DSN cattle are kept in pasture based farms today
 - ↳ good health, robustness, good fertility, adequate development potential with high forage and dry matter intake capacity



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Aims of the Study

- Line comparisons between DSN and HF regarding functional traits (FPR, SCS)
- Thorough analysis of genetic structure of DSN population
- Genetic evaluations of functional traits, with detailed consideration of environmental effects regarding GxE interactions (multiple trait model)



Distribution of DSN Cattle Herds across Germany

- Testday records, Pedigree
- Calving years: 2010-2015
- 46 Farms: - Holstein-Friesian (3599)
- DSN (3688)



Legend

- <10% DSN
- ▲ 10-50% DSN
- 50-75% DSN
- △ >75% DSN
- Administrative borders
- Large scale dairy production systems
- Small scale family systems
- Intensive grass based production systems



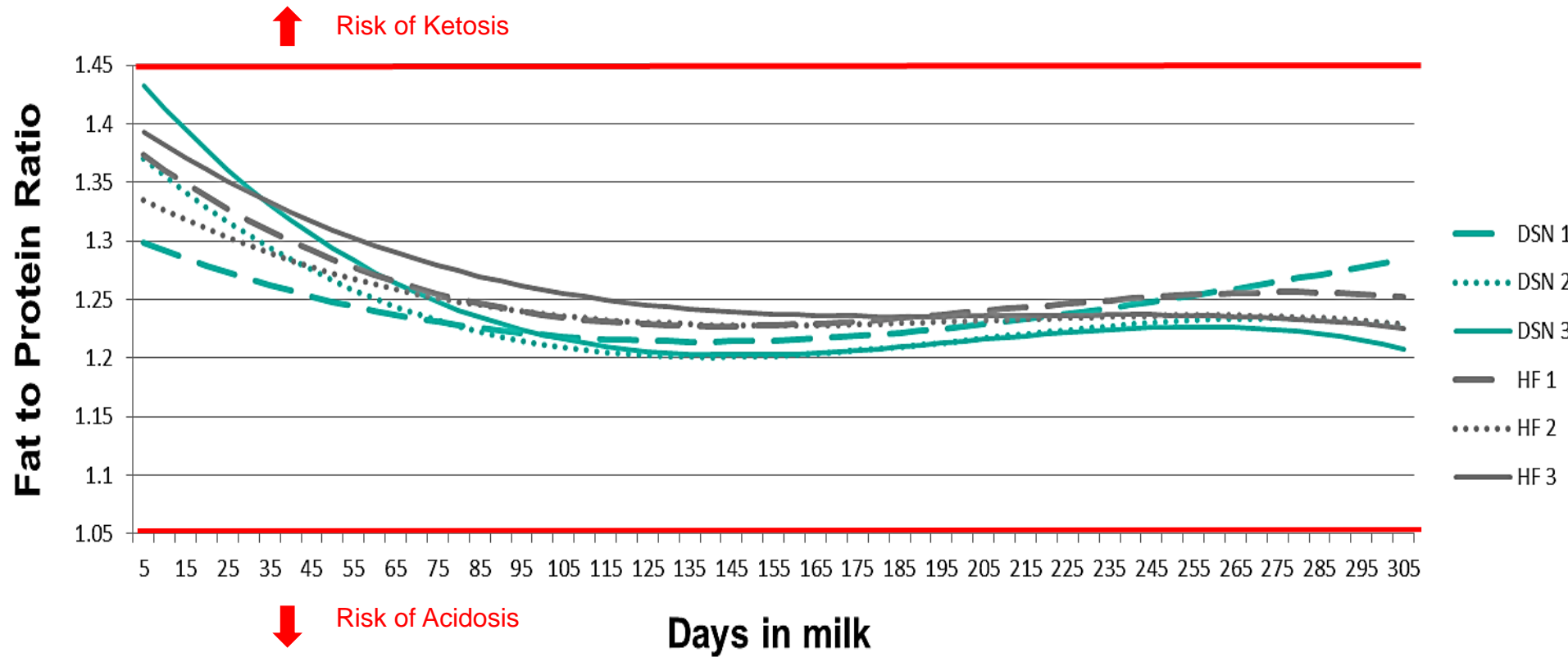
Line Comparisons of HF and DSN for Functional Traits

$$Y_{ijklmn} = \mu + FM_i + YS_j + G^*Lact_k + A_l + \sum_{m=1}^3 \beta z_m + e_{ijklmn}$$

| | | |
|--------------------------|---|---|
| Y_{ijklmn} | = | Vector of observation (FPR, SCS) |
| μ | = | Overall mean of population |
| FM_i | = | Fixed effect of farm and month |
| YS_j | = | Fixed effect of year and season (3 month) of test day records |
| G^*Lact_k | = | Fixed effect of genotype (HF, DSN) and parity (1 st , 2 nd , 3 rd) |
| A_l | = | Random cow effect |
| $\sum_{m=1}^3 \beta z_m$ | = | Regression coefficients (²) for days in milk; (z) covariates describing lactation curve (Legendre polynomials 3rd order) |
| e_{ijklmn} | = | Random error |

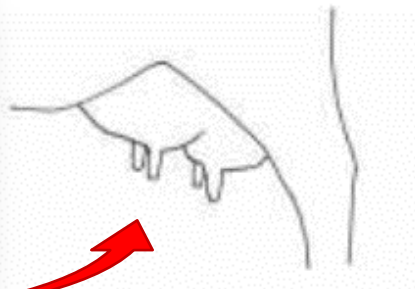
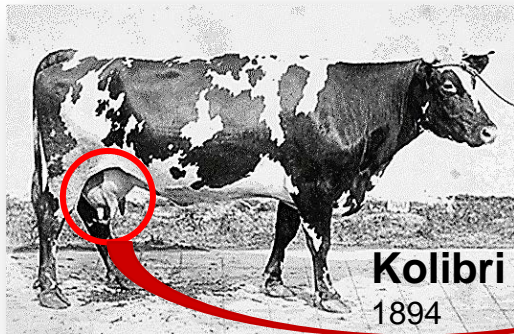
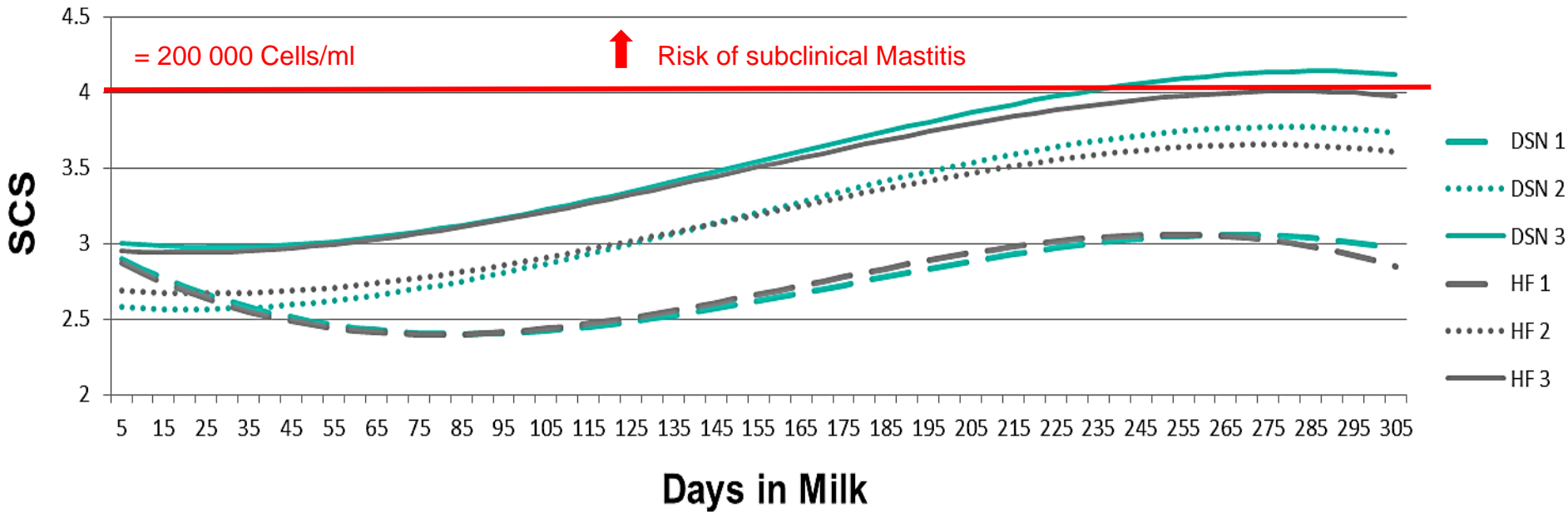
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Least Square Means: Fat to Protein Ratio (FPR)



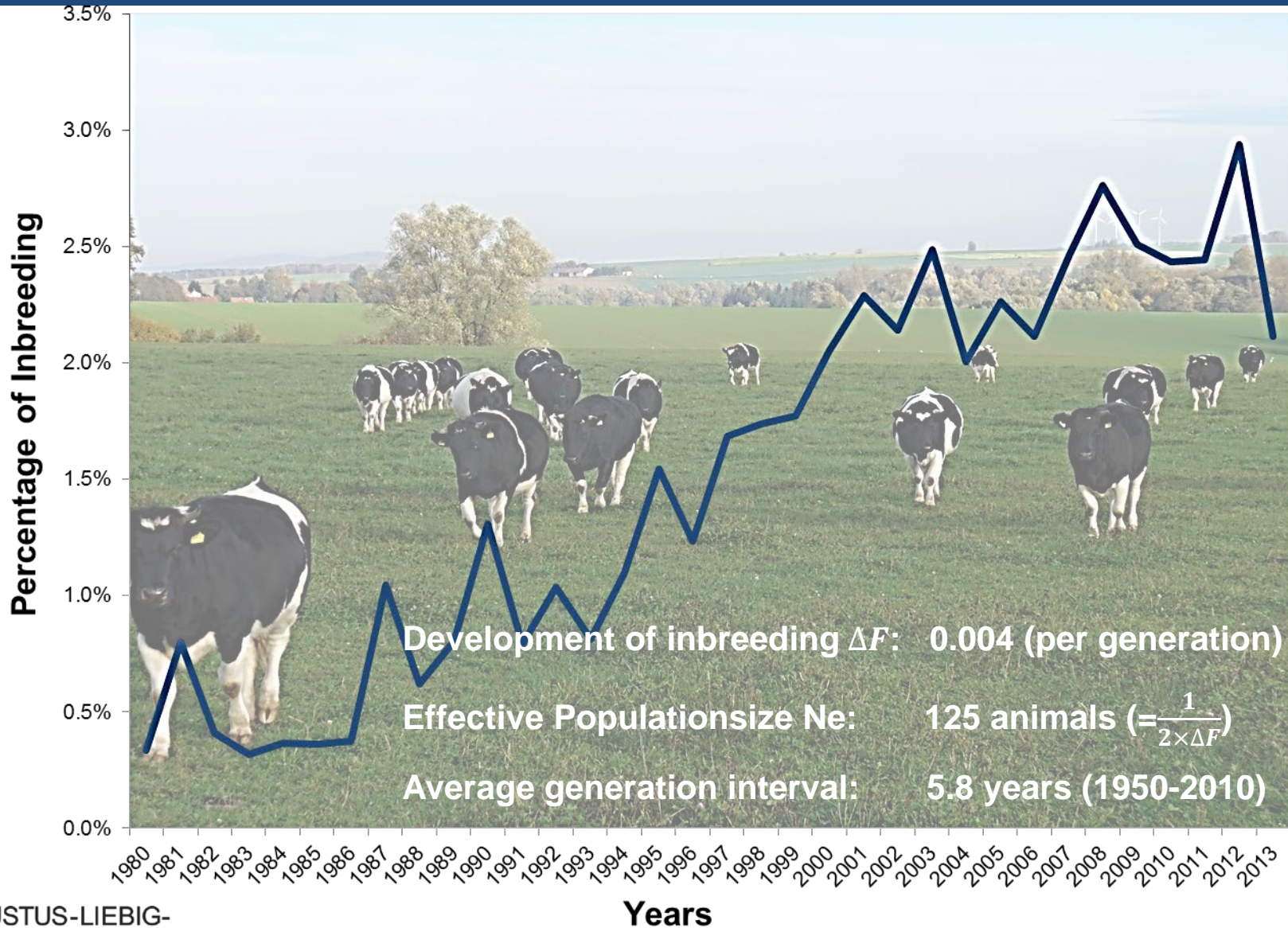
Fat to Protein Ratio (SE d 0.01) for 3 lactations for DSN and HF cattle

Least Square Means: Somatic Cell Score (SCS)



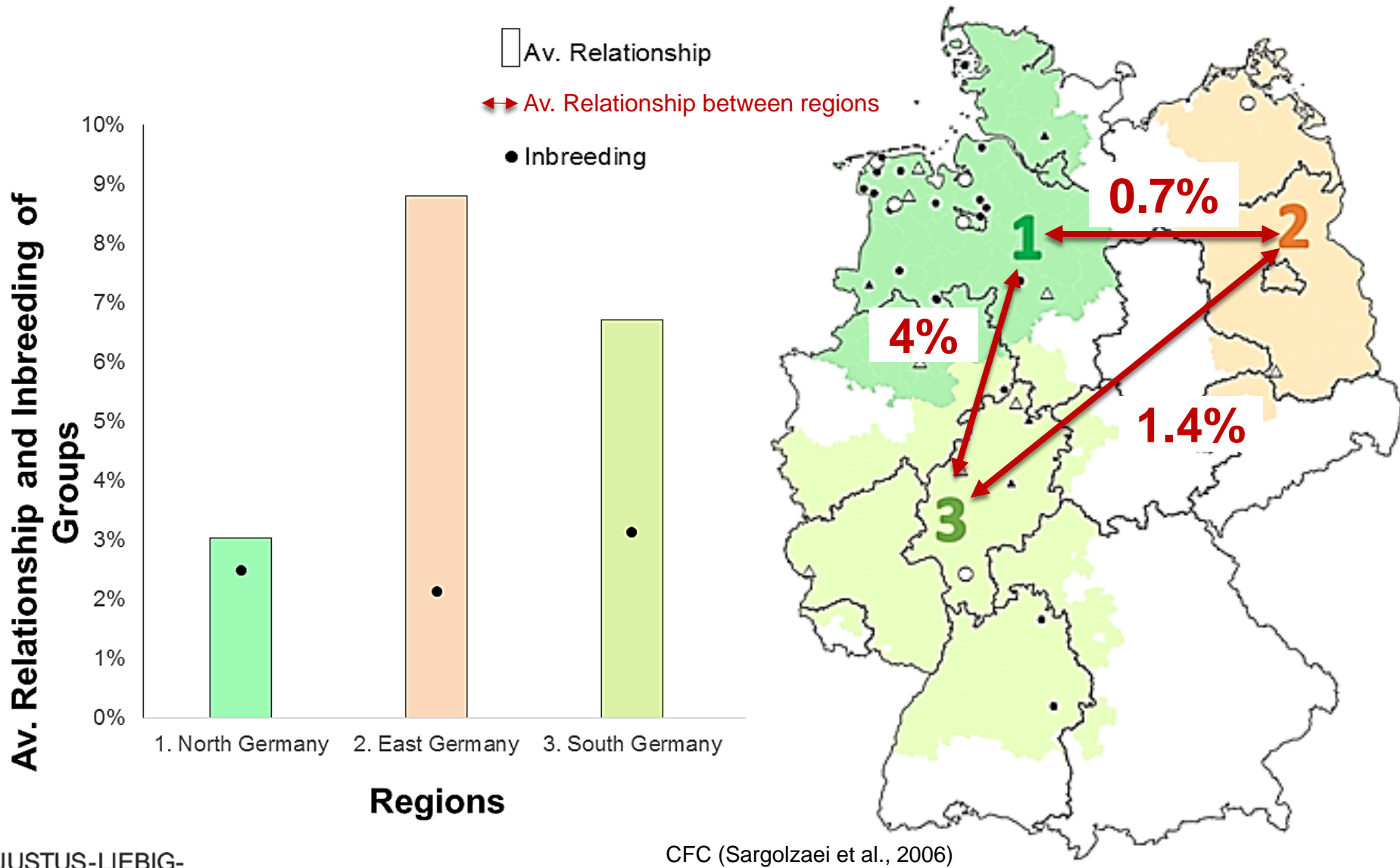
Somatic Cell Score
(SE d 0.05) over 3 lactations
for DSN and HF cattle

Development of Inbreeding and Effective Population Size of DSN



2.13

Average Relationship and Inbreeding Coefficients of Regions

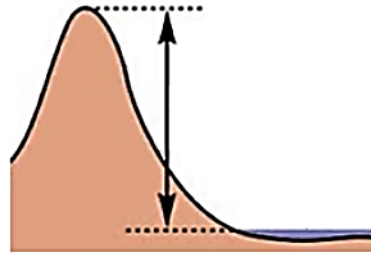


CFC (Sargolzaei et al., 2006)

Environmental Herd Parameters according to Weigel and Rekaya (2000)

Altitude of farm

- <60m over NN= Group 1
- >60m over NN= Group 2



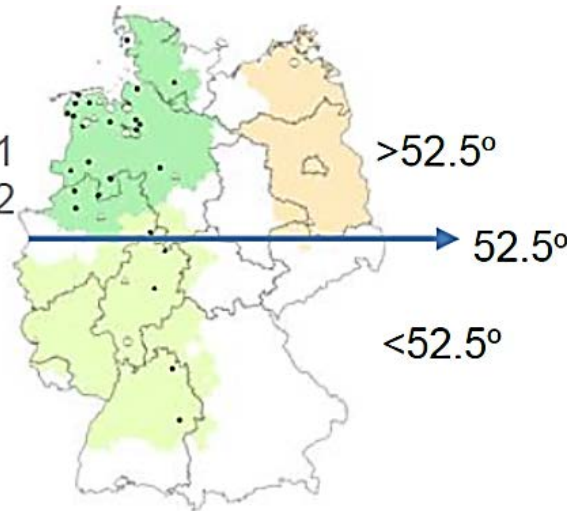
Ø DSN percentage per herd

- <25%= Group 1
- >25%= Group 2



Latitude of farm

- <52.5°= Group 1
- >52.5°= Group 2



Ø Somatic cell count of herd

- <200 000/ml= Group 1
- >200 000/ml= Group 2



Ø Milk yield of herd

- <30 kg= Group 1
- >30 kg= Group 2



Herd size

- <250 animals/ herd= Group 1
- >250 animals/ herd= Group 2



Ø Calving age of herd

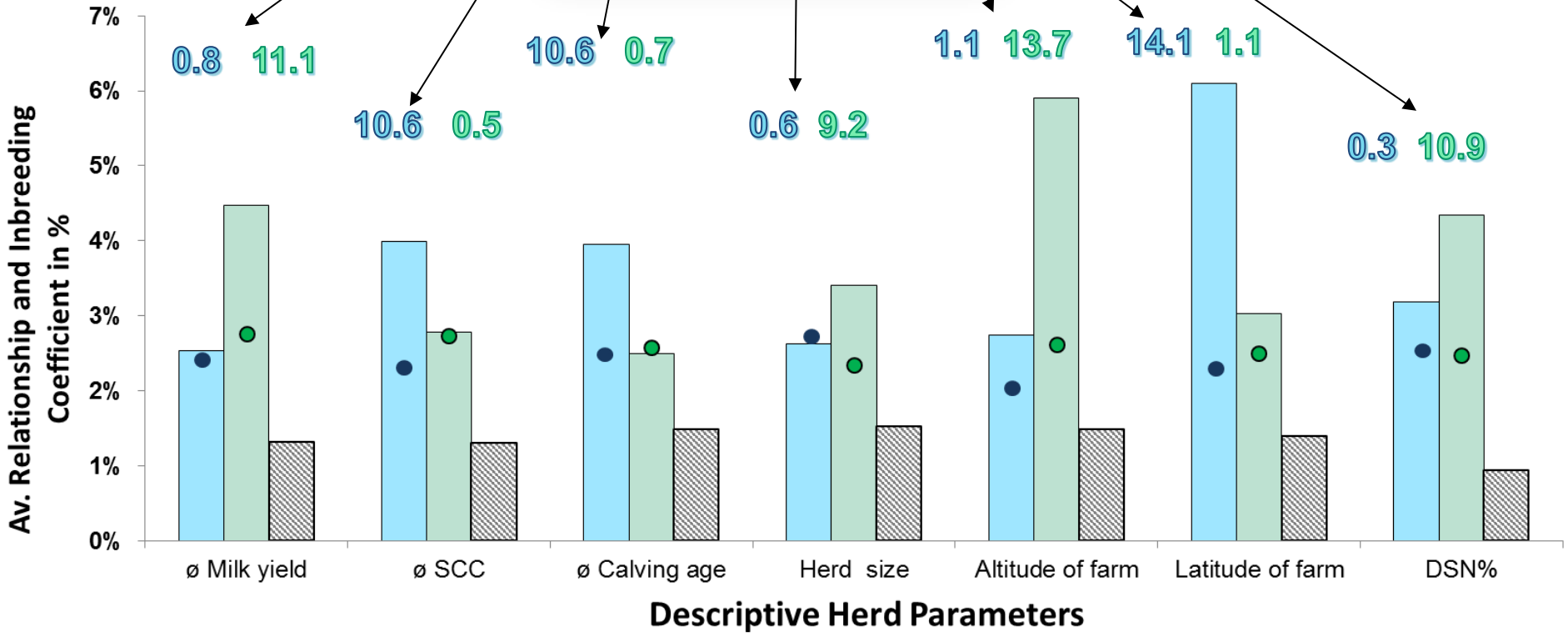
- <38 Month= Group 1
- >38 Month= Group 2

Average Relationship and Inbreeding Coefficients between Herd Parameters

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- Av. Relationship within Gr. 1
- Av. Relationship within Gr. 2
- ▨ Av. Relationship between Gr. 1 & 2
- Inbreeding of Gr. 2
- Inbreeding of Gr. 1



Bivariate Model for Genetic Parameters of Production and Functional traits

Bivariate model for all trait combinations:

$$Y_{ijklmno} = \mu + G_i + YS_j + F_k + Lact_l + T_m + Ca_n + e_{ijklmno}$$

| | | |
|---------------|---|--|
| Y_{ijklmn} | = | Vector of observation (SCC) |
| μ | = | Overall mean of population |
| G_i | = | Fixed effect of genotype (DSN, HF) |
| YS_j | = | Fixed effect of year and season (3 month) of test day records |
| F_k | = | Fixed effect of farm |
| $Lact_l$ | = | Fixed effect of lactation (1 st , 2 nd , 3 rd) |
| T_m | = | Additive genetic effect of animal |
| Ca_n | = | Calving age (covariable) |
| $e_{ijklmno}$ | = | Random error |

DMU (Madsen & Jensen, 2000)

Genetic Parameters of SCC within Herd Parameters

Additive genetic- (\tilde{N}_a^2), residual- (\tilde{N}_e^2) variances and heritabilities (h^2) for average herd SCC

| Herd parameter | ϑ_a^2 | | ϑ_e^2 | | h^2 | |
|------------------|-----------------|---------|-----------------|---------|---------|---------|
| | Group 1 | Group 2 | Group 1 | Group 2 | Group 1 | Group 2 |
| Ø Milk | 0.31 | 0.33 | 2.92 | 2.59 | 0.10 | 0.14 |
| Ø SCC | 0.47 | 0.26 | 2.40 | 3.14 | 0.16 | 0.08 |
| Herd size | 0.27 | 0.48 | 2.98 | 2.52 | 0.08 | 0.16 |
| Ø Calving age | 0.51 | 0.25 | 2.54 | 2.98 | 0.17 | 0.08 |
| Altitude of farm | 0.33 | 0.38 | 2.85 | 2.68 | 0.10 | 0.12 |
| Latitude of farm | 0.33 | 0.36 | 2.74 | 2.79 | 0.11 | 0.12 |
| DSN% | 0.24 | 0.53 | 2.96 | 2.54 | 0.08 | 0.17 |

SE for heritabilities d 0.02

Superior environment

Better expression of true genetic potential

Analysis of Genotype by Environment Interactions

Genetic correlations (r_g) between groups within average herd parameters

| Herd parameters | Traits | | | | |
|------------------|---------|-------|-----------|------|------|
| | Milk-kg | Fat-% | Protein-% | SCC | FPR |
| Ø Milk | 0.99 | 0.87 | 1 | 0.91 | 1 |
| Ø SCC | 1 | 0.93 | 0.97 | 0.90 | 0.73 |
| Herd size | 0.96 | 0.39 | 0.81 | 0.71 | 0.67 |
| Ø Calving age | 0.98 | 1 | 1 | 0.68 | 0.68 |
| Altitude of farm | 0.90 | 1 | 1 | 0.33 | 0.94 |
| Latitude of farm | 0.84 | 1 | 1 | 0.53 | 0.92 |
| DSN% | 0.52 | 1 | 0.73 | 0.13 | 0.81 |

$r_g < 0.8 \rightarrow$ **GxE interaction**
(Robertson, 1959)

Conclusion

- The balanced test design did not reveal differences for phenotypic line comparisons in terms of functional traits (FPR, SCS)
- Distinct relationships between different DSN herds apparent
- Genetic parameters are within the range of HF



Better heritabilities and genetic variances of farms with greater herd sizes or higher production output

- GxE interactions for SCC and FPR



Application of alternative models (RRM, multiple-trait herd cluster model) useful

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Thank you for your attention!



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Genetic Parameters of FPR within Herd Parameters

Additive genetic- (\tilde{N}_a^2), residual- (\tilde{N}_e^2) variances and heritabilities (h^2) for average herd FPR

| Herd parameter Group | ϑ_a^2 | | ϑ_e^2 | | h^2 | |
|-------------------------|-----------------|---------|-----------------|---------|---------|---------|
| | Group 1 | Group 2 | Group 1 | Group 2 | Group 1 | Group 2 |
| Ø Milk | 0.006 | 0.008 | 0.042 | 0.038 | 0.13 | 0.17 |
| Ø SCC | 0.007 | 0.008 | 0.036 | 0.044 | 0.16 | 0.14 |
| Herd size | 0.006 | 0.008 | 0.043 | 0.038 | 0.13 | 0.17 |
| Ø Calving age | 0.009 | 0.011 | 0.025 | 0.036 | 0.27 | 0.24 |
| Altitude of farm | 0.008 | 0.006 | 0.041 | 0.039 | 0.16 | 0.14 |
| Latitude of farm | 0.006 | 0.008 | 0.039 | 0.042 | 0.14 | 0.16 |
| DSN% | 0.008 | 0.006 | 0.039 | 0.041 | 0.17 | 0.14 |

SE for heritabilities d 0.02

Line Comparisons F-Test

- FPR**

| Effect | NumDF | DenDF | FValue | ProbF |
|--------------------|-------|----------|--------|--------|
| ys | 60 | 1,80E+05 | 8,48 | <.0001 |
| bmy | 5863 | 1,80E+05 | 9,07 | <.0001 |
| breed*lanr_tt | 5 | 1,80E+05 | 54,41 | <.0001 |
| lg1(breed*lanr_tt) | 6 | 1,80E+05 | 341,41 | <.0001 |
| lg2(breed*lanr_tt) | 6 | 1,80E+05 | 709,19 | <.0001 |
| lg3(breed*lanr_tt) | 6 | 1,80E+05 | 150,66 | <.0001 |

- SCS**

| Effect | NumDF | DenDF | FValue | ProbF |
|-----------------|-------|----------|---------|--------|
| ys | 60 | 1,80E+05 | 37,15 | <.0001 |
| bm | 451 | 1,80E+05 | 17,37 | <.0001 |
| breed*lanr_tt | 5 | 1,80E+05 | 1715,27 | <.0001 |
| lg1(breed*lanr_ | 6 | 1,80E+05 | 1415,37 | <.0001 |
| lg2(breed*lanr_ | 6 | 1,80E+05 | 37,92 | <.0001 |
| lg3(breed*lanr_ | 6 | 1,80E+05 | 117,25 | <.0001 |