



Parameter Estimation for Fertility Traits of Dairy Cattle Using a Multiple Trait Model

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Overview

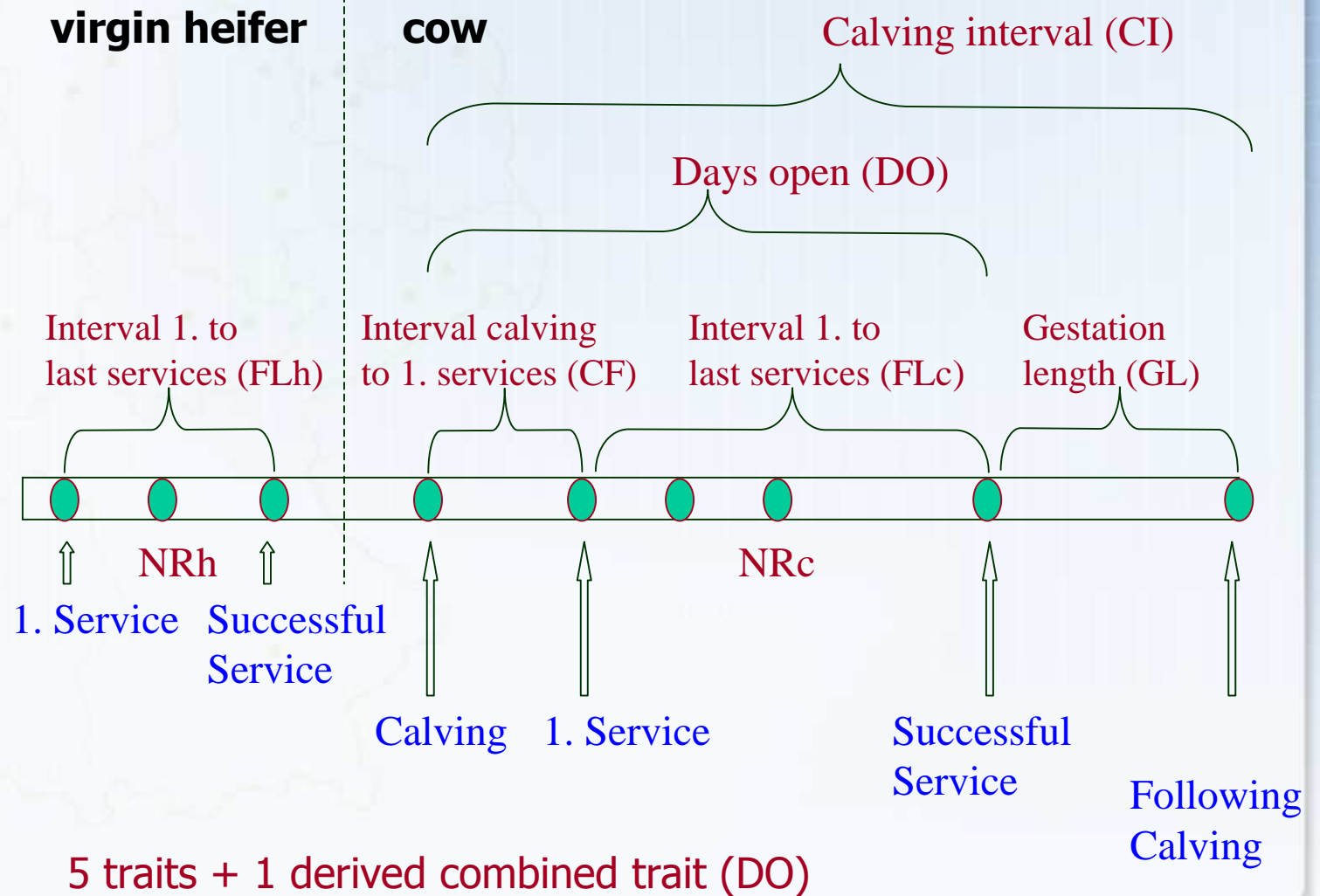
- The new fertility model
- Data selection for parameter estimation
- Parameter estimates
- Results and discussion

The new fertility model



- Current single trait maternal effect model for NR90
 - Correlated paternal genetic effect
- A multi-trait model (Sep 2006 to Jun 2007)
 - Age at first insemination (AF)
 - Interval calving to first insemination (CF)
 - Non-Return Rate 56 days for virgin heifer (NRh) & cow (NRc)
 - Days open (DO)
 - Calving interval (CI)
- The new, updated fertility model since July 2007
 - AF removed
 - Component fertility traits instead of combined trait DO
 - FL: interval first to last inseminations
 - $DO = CF + FL$, no longer CI

Relations among the fertility traits



The genetic evaluation model



- Trait =
 - herd-year (HY)
 - + parity x age_class x month_insemination (PAM)
 - + type_bull x owner_AI_stud x user_AI_stud (BOU)
 - + random maternal genetic effect of female animal (a)
 - + random permanent environmental effect of cow (p)
 - + fixed effect of service sire (F)
 - + random year effect within service sire (t)
 - + residual
- * NR56 traits ** cow fertility traits
- } **male fertility**

Selection of insemination records



- Breeds: Holstein B&W and R&W
- Insemination ranged from 1999 to 2005
 - Slight difference between cows and virgin heifers
 - Shorter time span for animal model than sire model
- Selection on trait level: only valid trait values (min/max)
- Selection on lactation level
 - Only sequential missing trait patterns allowed
- Selection on animal level
 - Virgin heifer records present
- Selection on herd level
 - 10 cows or 5 virgin heifers per herd-year
- Selection on service sire level
 - 100 inseminations

The selected data sets



- Large datasets but within the limitations of computing resources
- Parameter estimation with sire model
 - 305,000 heifer and 282,000 cow inseminations
 - 2400 sires of females and service sires
 - 4700 animals in pedigree
- Parameter estimation with animal model
 - 60,000 heifer and 42,000 cow inseminations
 - 360,000 animals in Pedigree
 - Only applied to single trait analyses

Results: Paternal genetic effect for NR56



- Parameter estimates for heifer and cow NR56 traits
 - Heritability c.a. 0.2%
 - Genetic correlation with maternal genetic effect
 - -0.70 for heifer NR56
 - -0.31 for cow NR56
- Correlated with maternal genetic effect
 - Very low heritability estimates found worldwide
 - Only included in the current German model
 - International harmonisation
- The paternal genetic effect makes parameter estimation and genetic evaluations significantly more difficult
- Therefore, the effect was no longer considered in further parameter estimation



Genetic parameter estimates: h^2 and r_G

Trait	FLh	NRh	CF	NRc	FLc	DO
FLh	.014	-.53	.17	-.25	.48	.36
NRh		.012	-.02	.63	-.15	-.09
CF			.039	.05	.37	.89
NRc				.015	-.39	-.16
FLc					.010	.76
DO						.026

Discussion: Selection of fertility traits



- CF has a part-whole relationship with DO or CI
- Analysing CF with DO or CI in a model double counts phenotypic information of CF
- The double counting exists also for FLc and DO/CI.
- Including DO/CI with CF causes
 - Inflated heritability estimates
 - Higher proof variances
 - Less impact on genetic correlation estimates
- Using component traits CF and FLc is a better alternative (Jamrozik et al. 2005)

Summary



- Paternal genetic effects will no longer be modelled
- Low heritability estimates for the fertility traits 1-4%
- High genetic correlations among time interval traits
 - FLh, FLc, CF, and DO
- Moderate genetic correlations of the same traits between virgin heifer and cow (NR, FL)
- Nearly zero correlations between CF and NR
- Low to moderate residual / p.e. correlations
- Reasonably high genetic variances for NR56 traits
- Model with component traits for routine evaluations



Thank you !