



Changes on Female Fertility Aggregate Index in Italian Holstein Dairy Cattle

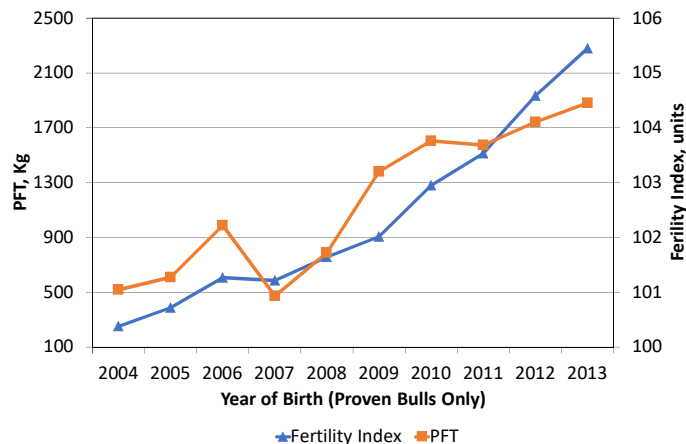
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Genetic Evaluation of Female Fertility?

- Accounted in both national selection indexes **PFT (10% emphasis)** and **IES (18% emphasis)**
- Aggregate index:** Interval from calving to first insemination (**DTFS**), non-return rate at 56 d after first insemination (**NR56**), calving interval (**CI**), equivalent mature milk yield (**MY**), and angularity (**ANG**)
- Breeding objective:** Increase conception rate (**CR**) at first insemination

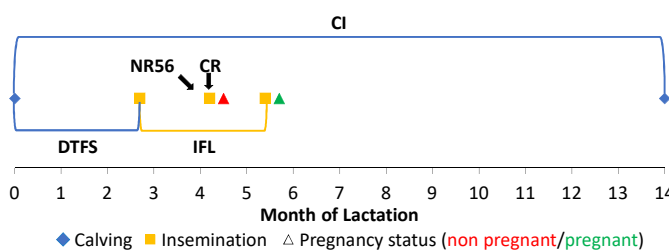


Aims

To replace i) EBV of ANG with body condition score (**BCS**) and ii) EBV of CI with interval from first to last insemination (**IFL**) in the aggregate fertility index

Materials and Methods

- 5,466,546 cows with information on insemination, calving, and pregnancy status (available from 2015)
- 1,111,111 cows with **BCS** (available from 2007)



- IFL** is available **earlier** and on **more animals**
- BCS** predicts **more accurately** cow fertility
- r_g ANG; **BCS weaker** over time

- (Co)variance components** estimated on **6 subsets randomly selected** of approx. 15,000 cows each
- Fixed effects:** herd-year-season of calving (**DTFS, NR56, IFL, MY, CR**), age|year of calving (**DTFS, NR56, IFL, CR**), month of calving (**DTFS, IFL, CR**), month of insemination (**NR56**), herd-year-season of linear scoring (**BCS**), age|stage of lactation (**BCS**), year of calving (**BCS**)
- Random effects:** animal additive genetic, residual

Results and Conclusion

- Genetic variability** for fertility-related traits ranged between 0.10 (**NR56**) to 0.24 (**IFL**)
- BCS** and **MY** had the lowest genetic variability (0.06 and 0.08, respectively)
- Selection index methodology** employed to derive **appropriate weights** for aggregate fertility index
- Response to selection** of **CR** is expected to increase by **5.6%** after one selection round using information on **BCS** and **IFL**

	BCS	IFL	DTFS	NR56	MY	CR
BCS	0.188	-0.04	-0.12	-0.01	-0.01	0.02
IFL	-0.26	0.042	0.01	-0.27	0.08	-0.64
DTFS	-0.44	0.44	0.076	0.07	-0.03	0.03
NR56	0.01	-0.68	0.25	0.013	-0.10	0.64
MY	-0.31	0.41	0.41	-0.05	0.292	-0.07
CR	0.28	-0.89	-0.30	0.77	-0.29	0.019

Heritability on diagonal; genetic correlations from bivariate analysis below diagonal; phenotypic correlations above diagonal.