

## Not all inbreeding is depressing

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Inbreeding decreases animal performance (inbreeding depression), but not all inbreeding is expected to be equally harmful. Inbreeding on recent ancestors is expected to be more harmful than inbreeding on more ancient ancestors, because of purging. Purging is the removal of deleterious recessive alleles over time by selection. We investigated the effects of recent and ancient inbreeding on yield, fertility and udder health of 38,792 Holstein Friesian first-parity cows, using linear mixed models. Pedigree data were used to compute traditional inbreeding (F<sub>PED</sub>) and genotype data were used to identify regions of homozygosity (ROH) and compute ROH-based inbreeding (F<sub>ROH</sub>). Inbreeding depression was apparent, e.g. a 1% increase in F<sub>ROH</sub> was associated with a decrease in 305-d milk yield of 36.3 kg (SE=2.4), an increase in calving interval of 0.48 days (SE=0.15) and an increase in mean somatic cell score in day 150 to 400 of 0.86 units (SE=0.28). Distinguishing recent from ancient inbreeding gave mixed results. For example, only very long ROHs (which indicate recent inbreeding) significantly increased calving interval, whereas both long and short ROH decreased protein yield. When F<sub>PED</sub> was split into new and ancestral components, based on whether alleles were identical by descent for the first time or not, there was clear evidence of purging. For example, a 1% increase in new inbreeding was associated with a 2.2 kg (SE=0.4) decrease in protein yield, compared to a 0.9 kg (SE=0.8) increase for ancestral inbreeding. The mixed results may be partly due to difficulties in estimating ancient inbreeding. Distant ancestors are less well registered, and short ROHs may be less reliable than long ROHs. Furthermore, purging may have acted on some, but not all alleles. To conclude, there is purging in the population, but purging effects are only partly reflected by the difference in inbreeding depression due to recent and ancient inbreeding.