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Combining survival analysis and a linear animal model to estimate genetic parameters for social effects on survival in layers

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Mortality due to cannibalism in layers is a difficult trait to improve genetically, because censoring is high (animals still alive at the end of study period) and mortality depends on both the individual itself and behaviour of its cage mates. To estimate genetic parameters for social effects on survival time, we compared a two-step approach (2STEP) that combines survival analysis and a linear animal model including social effects (LAM) with LAM applied directly to observed survival time. LAM, therefore, ignored censoring. Survival data of three purebred White Leghorn layer lines from Institut de Sélection Animale B.V., a Hendrix Genetics company, were used in this study. In total, 16,780 hens with intact beaks were kept in four-bird cages. Cross validation was used to compare 2STEP with LAM. Using 2STEP, total heritable variance, including both direct and social genetic effects, expressed as proportion of phenotypic variance, ranged from 32% to 64%. Though this was substantially larger than heritability with LAM (6% to 19%), those values cannot be compared directly. Cross validation showed that 2STEP and LAM performed equally well in predicting records that were set to missing, and gave approximately the same response to selection when animals were selected based on predicted records. Further investigation showed that this occurred because all records were censored at the same survival time point. When censoring was at different time points, 2STEP was superior to LAM. Cross validation showed that selection based on both direct and social genetic effects, using either 2STEP or LAM, gave largest response to selection. It can be concluded that 2STEP is useful to estimate genetic parameters for social effects on survival time in layers when individuals are censored at different time points