



Heritability of semen traits in German Warmblood stallions



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ABSTRACT

The objectives of the present study were to evaluate genetic parameters for semen quality traits of 241 fertile German Warmblood stallions regularly employed in artificial insemination (AI). Stallions were owned by the National Studs Celle and Warendorf in Germany. Semen traits analyzed were gel-free volume, sperm concentration, total number of sperm, progressive motility and total number of progressively motile sperm. Semen protocols from a total of 63,972 ejaculates were collected between the years 2001 and 2014 for the present analysis. A multivariate linear animal model was employed for estimation of additive genetic and permanent environmental variances among stallions and breeding values (EBVs) for semen traits. Heritabilities estimated for all German Warmblood stallions were highest for gel-free volume ($h^2 = 0.28$) and lowest for total number of progressively motile sperm ($h^2 = 0.13$). The additive genetic correlation among gel-free volume and sperm concentration was highly negative ($r_g = -0.76$). Average reliabilities of EBVs were at 0.37–0.68 for the 241 stallions with own records. The inter-stallion variance explained between 33 and 61% of the trait variance, underlining the major impact of the individual stallion on semen quality traits analyzed here. Recording of semen traits from stallions employed in AI may be recommended because EBVs achieve sufficient accuracies to improve semen quality in future generations. Due to favorable genetic correlations, sperm concentration, total number of sperm and total number of progressively motile sperm may be increased simultaneously.

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1. Introduction

There is considerable variation in semen quality among stallions (Rousset et al., 1986; Parlevliet et al., 1994; Van Eldik et al., 2006; Labitzke et al., 2013, 2014). Probable reasons for this are consistent stallion specific and genetic effects (Pickett et al., 1976; Pattie and Dowsett, 1982; Rousset et al., 1986; Parlevliet et al., 1994; Van Eldik et al., 2006; Ducro et al., 2011; Labitzke et al., 2014). The inter-individual variation seems to be much larger

than the variation among breeds (Brito, 2007). Several studies confirmed the stallion accounting for a significant proportion of the variance in semen quality. Evaluating data of 30 Hanoverian stallions, Labitzke et al. (2013) demonstrated the large degree of inter-stallion variability accounting for 49–85% of the variance in semen quality traits. In a French study including 80 stallions of the breeds Thoroughbred, French Trotter, Selle Francaise and Breton draught horse, Rousset et al. (1986) found that 37–69% of the variance was due to stallions. Pattie and Dowsett (1982) estimated repeatabilities at 26–48% for semen quality traits of 168 stallions. Gottschalk et al. (2015) showed that stal-

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Table 1Means (\bar{x}), standard deviation (SD), minimum (Min) and maximum (Max) for raw data of semen traits from 241 German Warmblood stallions.

Trait	\bar{x}	SD	Min	Max
Gel-free volume (ml)	37.9	18.1	2	290
Sperm concentration ($\times 10^6$ /ml)	213.1	88.9	1	695
Progressive motility (%)	60.8	9.8	1	95
Total number of sperm ($\times 10^9$)	7.3	3.0	0.6	36.0
Total number of progressively motile sperm ($\times 10^9$)	4.5	2.0	0.3	21.9

lions accounted for 55–65% of the total variance in semen traits of 106 Hanoverian Warmblood stallions.

For an improvement of semen quality through selective breeding it is important to know whether the trait is heritable. Several studies suggested that an improvement in semen quality might be achieved by means of targeted selection. Genetic analyses of semen traits were performed for Dutch Warmblood horses (Parlevliet et al., 1994), Shetland Ponies (Van Eldik et al., 2006) and Friesian horses (Ducro et al., 2011) based on data from breeding soundness examinations prior to studbook registration. In contrast to these Dutch studies, semen data for genetic analyses in Hanoverian Warmblood horses were collected from stallions regularly employed in artificial insemination (AI) (Labitzke et al., 2014). Comparing semen quality among paternal half-sibs, Parlevliet et al. (1994) determined a significant sire effect for gel-free volume, progressive motility and sperm concentration in 66 maiden Dutch Warmblood stallions. A study on 285 Shetland Pony stallions revealed high heritabilities for ejaculate volume ($h^2 = 0.57$) and progressive motility ($h^2 = 0.46$) with the remaining semen traits showing low to moderate estimates (Van Eldik et al., 2006). Ducro et al. (2011) investigated data from 1146 Friesian stallions. Heritability estimates were moderate for gel-free volume ($h^2 = 0.16$) and progressive motility ($h^2 = 0.27$), while higher heritabilities were found for percentages of normal sperm cells ($h^2 = 0.52$) and abnormal acrosomes ($h^2 = 0.60$). In a study on 30 Hanoverian stallions, Labitzke et al. (2014) identified high heritabilities for gel-free volume ($h^2 = 0.43$) and moderate estimates for total number of sperm ($h^2 = 0.29$) and progressive motility ($h^2 = 0.20$).

In Friesian stallions, sperm motility showed a positive genetic correlation to gel-free volume, sperm concentration and sperm morphology, indicating that selection on progressive motility may improve these parameters (Ducro et al., 2011). A highly positive genetic correlation was found among gel-free volume and total number of sperm in Hanoverian stallions, whereas gel-free volume and sperm concentration showed a highly negative genetic correlation (Labitzke et al., 2014).

The objective of the current study was to estimate permanent environmental and genetic variances for semen quality traits of 241 fertile German Warmblood stallions routinely employed in AI. Permanent environmental and genetic variation could be distinguished as recording extended over 14 consecutive years and included 63,972 fresh semen reports. Estimated breeding values (EBVs) and their reliabilities should show whether breeders may have the option to improve semen quality in stallions through breeding measures.

2. Materials and methods

2.1. Stallions

Semen traits were recorded between 2001 and 2014 for 241 stallions routinely used in AI on the Lower Saxon National Stud Celle and the North Rhine-Westphalian National Stud Warendorf. The present study only included stallions approved for AI and with a conception rate of at least 70% in >9 mares bred from a stallion (Klug, 2002). Therefore, all stallions under study were considered as fertile. Stallions were housed in boxes on straw without contact to mares and fed hay and oats three times daily at both national studs. Water was freely available. Stallions were 3–30 years old and were registered by five different German Warmblood horse breeding associations including Hanoverian, Holsteiner, Oldenburger, Rhinelander and Westphalian. Stallions from the different horse breeding organizations were connected through their pedigrees with common ancestors and exchange of stallions.

2.2. Evaluation of semen traits

Semen samples were collected once daily on six consecutive days every week in the months February to August using a phantom and an artificial vagina (Hanover model). Prior to evaluation of semen traits, semen was passed through a sterile filter to remove the gel portion of the ejaculate. Afterwards, gel-free volume, sperm concentration, total number of sperm (TNS), progressive motility and total number of progressively motile sperm (TNM) were evaluated. The sperm concentration, presented as millions per ml (10^6 /ml), was assessed by means of photometry using a SpermaCue photometer (Minitube, Tiefenbach, Germany). For calculation of the TNS ($\times 10^9$), gel-free volume and sperm concentration were multiplied. After dilution to a concentration of 25×10^6 /ml, progressive motility was determined by experienced observers through subjective visual estimation using a phase-contrast microscope with a stage heater at 200–400X magnification (Olympus CH-II, Olympus Optical, Hamburg, Germany). All semen parameters were documented immediately after fresh semen examination at the respective national stud. A total of 63,972 fresh semen reports were used for analyses. Means, standard deviations, minima and maxima of semen traits from 241 fertile German Warmblood stallions are presented in Table 1.

2.3. Statistical analyses

Mixed linear models were employed to analyze the fixed effects of year, month and stud as well as the ran-

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