

## Influence Of Specialisation On Connectedness And Genetic Parameters In The Dutch Warmblood Horse Population

G. Rovere<sup>\*†</sup>, P. Madsen<sup>†</sup>, E. Norberg<sup>†</sup>, J.A.M. VanArendonk<sup>\*</sup> and B.J. Ducro<sup>\*</sup>

<sup>\*</sup> Animal Breeding and Genomics Centre, Wageningen University, <sup>†</sup> Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University

**ABSTRACT:** During the last decades, a process of specialisation into show jumping (JH) and dressage (DH) has been taking place in the Dutch Warmblood studbook (KWPN). The objectives of this paper were to describe the evolution of the connectedness between JH and DH over the last 15 years and to analyse the change in genetic parameters for some traits in JH and DH. The genetic connectedness between JH and DH, measured as stallions in common, genetic similarity and coefficient of relationship, has been weakening during this period. The specialisation process in JH and DH is expressed in lack of genetic connectedness and in lower genetic correlations between traits measured by JH and DH.

**Keywords:** genetic similarity; show-jumping horse; dressage horse

### Introduction

Historically, sport horses performed in both disciplines dressage and show jumping. Nowadays, competing at advanced level implies an intense preparation and specific training of the horses, with the consequence that they can participate in only one of the disciplines. Consequently, individual breeders have started to breed horses for one of the two disciplines. This breeding practice within the Dutch Warmblood studbook (KWPN) has resulted in an increasing specialisation of horses in either show-jumping (JH) or dressage (DH). A recent analysis revealed that both groups of horse are still genetically linked to a certain extent (Rovere et al. (2012)). However, the genetic parameters of the traits in both sub-lines might have changed as a result of selection under different breeding goals. The objectives of this study were: 1) to describe the evolution of the connectedness between JH and DH during the last 15 years when the process of specialisation started; and 2) to analyse the change of the genetic parameters of a sample of traits with different importance in the selection of JH and DH.

### Materials and Methods

**Data.** A dataset comprising the studbook inspections from the period 1989 through 2012, and a pedigree file was provided by KWPN. The horses in the data file were assigned to one of two groups: Show-Jumping horses (JH) or Dressage horses (DH). Each horse received an overall evaluation as a JH or DH in its studbook inspection. The JH and DH populations comprised 23,800 and

18,125 horses, respectively, and they were born between 1995 and 2009. Animals from both groups were traced back as far as possible to construct a common pedigree file comprising 96,869 animals. The index of pedigree completeness (MacCluer et al. (1983)) for 5 generations (*CI5*) was on average 0.96 for JH and 0.97 for DH and was highest for the later year of birth. Horses born in 1995 had an average *CI5* of 0.93 in JH and DH while horses were born in 2009 had a *CI5* of 0.98 in JH and 0.99 in DH. The generation interval for the animals traced was 9.96 years for JH and 9.37 years for DH. For genetic parameter estimation, we used the data from first inspection of JH and DH (41,925 records) and the common pedigree file constructed.

**Genetic connectedness.** Genetic connectedness between JH and DH refers to the genetic links that exist between both subpopulations. Several studies on genetic connectedness in sport horses have been performed with the aim to evaluate the feasibility of common genetic evaluations of two or more populations (Furre et al. (2013), Ruhlmann et al. (2009), Thorén Hellsten et al. (2008)). In these studies, number of stallions in common (*SC*) and Genetic Similarity (*GS*) (Rekaya et al. (1999)) were used to measure connectedness between two populations. We calculated *SC* as the number of stallions with progenies in JH and DH, and *GS* as the ratio between the number of progenies of *SC* in JH and DH and the total number of progenies of all stallions. The contribution of JH and DH to the *GS* was calculated following Thorén Hellsten et al. (2008). The coefficient of relationship between two animals (*r*) is the correlation coefficient between their additive breeding values (Falconer and Mackay (1996)). If the specialisation process affected the connectedness between JH and DH over time, it should be reflected in a change in the average relationship per year of birth within and between the JH and DH subpopulations. The indirect method of Colleau (2002), implemented in the software package CFC (Sargolzaei et al. (2006)), was used to compute *r* among animals.

**Genetic parameter estimation.** A detailed description of the traits considered in the studbook inspections and their genetic parameters is given by Ducro et al. (2007). In the present study we chose to analyse height, an objective measure of the stature of the animals at the level of the withers, three subjective traits (conformation, walk and trot) and three descriptive traits related to trot (length of stride, elasticity and impulsion).

The traits were analysed for the whole population and then as different traits in JH and DH. Heritabilities of each trait were estimated for the total period and for each of the three periods defined according classes of year of birth: 1995-1999, 2000-2005 and 2005-2009. Genetic correlations between the traits defined were estimated for the total period and for the three periods.

Genetic parameters of the traits analysed were estimated using the model:

$$y_{ijklmn} = \mu + pd_i + cy_j + age_k + sex_l + pt_m + a_n + e_{ijklmn}$$

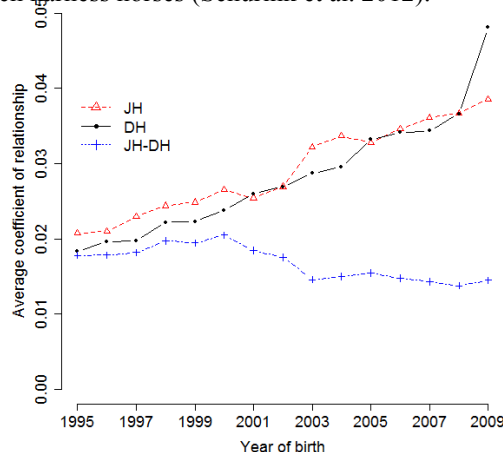
where:  $y_{ijklmn}$  is the height in cm or the observed score for each subjective and descriptive trait;  $\mu$  is the population mean;  $pd_i$  is the fixed effect of interaction of event place and date (1406);  $cy_j$  is the fixed effect of interaction of classifier and year (217);  $age_k$  is the fixed effect of age (2yr, 3yr, 4yr, 5yr,  $\geq 6$ yr);  $sex_l$  the fixed effect of sex (mares, stallions, geldings);  $pt_m$  is the fixed effect of the proportion of thoroughbred ( $>1/8, 1/8, 2/8, 3/8, \geq 4/8$ );  $a_n$  is the random effect of the  $n^{th}$  animal  $\sim N(0, A\sigma_a^2)$ ;  $e_{ijklmn}$  is the random residual term  $\sim N(0, I\sigma_e^2)$ .

Genetic correlations were estimated with bivariate analyses using the DMU software (Madsen and Jensen (2013)).

## Results and Discussion

**Genetic connectedness.** In total 1,495 different stallions were used and 599 (40 %) had offspring in both JH and DH. The number of SC used in both subpopulations decreased strongly from 191 (76%) in 1995 to 8 (2.7%) in 2009. The GS between JH and DH was on average 0.83 and the contribution to GS was 57.9% from JH and 42.1% from DH. The GS decreased strongly from  $\sim 0.9$  in the cohorts born in the 90's to  $\sim 0.10$  in the cohorts born after 2005, but the subpopulations contribute equally to the GS. The largest values of GS found in the literature were  $\sim 0.30$ , e.g. 0.27 between KWPN and Holstein stud-book, 0.29 between Danish and Swedish Warmblood horse populations (Thorén Hellsten et al. 2008). Similar results are presented by Furre et al. (2013) and Ruhlmann et al. (2009) considering Warmblood horse populations from different countries, and by Schöpke et al. (2013) in the German sport horse population. Figure 1 shows the trend of average  $r$  by year of birth of the horses. The cohorts born in 1995 presented similar level of relatedness within and between groups. From the cohort of horses born in 2000,  $r$  had a dissimilar trend, increasing among animals within JH and DH, and diminishing between JH and DH. The mean and standard deviation of  $r$  between JH and DH horses decreased from the cohort born in 1995 to the ones born in 2009 indicating that  $r$  between JH and DH is homogenously decreasing along the last 15 years (Table 1). Despite this decreasing trend of  $r$  over the time, the level of connectedness is larger than the relatedness between lines in Spanish Sport Horses (Bartolomé et al.,

(2011)), but smaller compared to the average relatedness among animals belonging to small populations like the Dutch harness horses (Schurink et al. 2012).



**Figure 1.** Evolution of the average coefficient of relationship within JH subpopulation (JH), DH subpopulation (DH) and between both subpopulations (JH-DH) according year of birth of horses

**Table 1.** Descriptive statistics of coefficient of relationship ( $r$ ) between horses in JH, DH and between both groups (JH-DH) for cohorts born in 1995 and 2009.

Cohort	Group	1 <sup>st</sup> Q <sup>1</sup>	Mean	3 <sup>rd</sup> Q <sup>2</sup>	SD <sup>3</sup>
1995	JH	0.004	0.021	0.023	0.04
	DH	0.004	0.019	0.019	0.03
	JH-DH	0.004	0.018	0.019	0.03
2009	JH	0.017	0.038	0.044	0.04
	DH	0.012	0.050	0.071	0.06
	JH-DH	0.008	0.014	0.018	0.01

<sup>1</sup>1<sup>st</sup> Quartile, <sup>2</sup>3<sup>rd</sup> Quartile, <sup>3</sup> Standard deviation

**Genetic parameters.** Table 2 shows the results from the univariate analyses for the whole population and the total period. Height showed the highest heritability while the heritabilities for the other traits were between 0.25 and 0.38. Similar results were obtained by Ducro et al. (2007) for the same traits and population. For traits like conformation, walk and trot, literature reviewed presented heritabilities that ranged between 0.25 and 0.30 in both Swedish Warmblood horses (Viklund et al. (2008)) and German sport horses (Schöpke et al. (2013)). When the univariate analyses were performed by group (e.g. each trait defined in both JH and DH) similar results were obtained. For some traits we found differences in phenotypic means in favour of one of the groups, which could be the result of different emphasis in the selection. However, this is not reflected in different genetic parameters. The biggest difference in heritability between JH and DH was for height (0.54 vs. 0.64), because of a bigger estimate of additive variance in DH. Table 4 shows the results of bivariate analyses of traits defined by group of horse for the whole period studied and for the different sub-periods considered. For all traits, the genetic correlations between JH and DH for the whole period were close to one, suggesting that the traits are the same for both groups. When the genetic correlations were estimated in different sub-

periods of time, the genetic correlations decreased for all traits in more recent years. For the Swedish Warmblood horse population, Viklund et al. (2008) found genetic correlations from 0.60 to 0.93 for type (similar to Conformation), walk and trot, measured in different period of time, suggesting different criterion used in the evaluation of the traits in different periods. However, our results show a decreasing trend of the genetic correlations in all traits analysed, even for height, which is independent of the change of criteria used in the inspections, suggesting that these changes are more related to the progressive lack of genetic connectedness between JH and DH.

**Table 2. Number of records (n), phenotypic mean (standard error) and heritability ( $h^2$ )(standard error) from univariate analyses with all horses.**

Trait	N	Mean (s.d)	$h^2$ (s.e.)
Height	36612	166 (3.42)	0.64 (0.02)
Conformation	41369	67.3 (5.9)	0.31 (0.01)
Walk	24414	67.0 (6.8)	0.25 (0.02)
Trot	24424	67.5 (7.7)	0.38 (0.02)
Trot: length stride	41252	18.7 (5.8)	0.32 (0.01)
Trot: elasticity	41269	20.4 (6.2)	0.29 (0.01)
Trot: impulsion	41265	20.7 (6.3)	0.28 (0.01)

**Table 3. Phenotypic mean (standard error) and heritability ( $h^2$ ) from univariate analyses by group of horse (JH, DH).**

Trait	Mean JH	Mean DH	$h^2$ JH	$h^2$ DH
Height	166 (3.3)	166 (3.5)	0.51	0.61
Conformation	67.4 (5.6)	67.2 (6.4)	0.29	0.28
Walk	65.6 (6.0)	68.5 (7.3)	0.22	0.25
Trot	65.5 (6.9)	69.8 (8.0)	0.39	0.36
Trot: length stride	19.6 (5.5)	17.4 (5.9)	0.27	0.28
Trot: elasticity	21.0 (5.8)	19.7 (6.6)	0.26	0.25
Trot: impulsion	21.1 (5.9)	20.1 (6.7)	0.24	0.27

All standard error of  $h^2$ JH and  $h^2$ DH ranged 0.02-0.03

**Table 4. Number of records analysed by group (nJH and nDH) in each period of time, and genetic correlation (GC) and standard error (s.e) between traits defined as JH and DH.**

Trait	Period <sup>1</sup>	nJH	nDH	GC (s.e.)
Height	All	19852	16695	0.99 (0.01)
	1	6632	4740	1.00 (0.04)
	2	6905	5817	1.00 (0.04)
	3	6315	6138	0.80 (0.17)
Conformation	All	23421	17948	0.98 (0.02)
	1	8392	5426	0.95 (0.04)
	2	8735	6395	0.95 (0.05)
	3	6294	6127	0.93 (0.13)
Walk	All	12972	11442	0.97 (0.05)
	1	-	not recorded	
	2	6686	5324	0.99 (0.06)
	3	6286	6118	0.86 (0.20)
Trot	All	12980	11444	1.00 (0.03)
	1	-	not recorded	
	2	6688	5324	1.00 (0.03)
	3	6292	6120	0.90 (0.14)

Trot: length stride	All	23388	17864	1.00 (0.01)
	1	8392	5422	1.00 (0.03)
	2	8704	6330	0.89 (0.06)
	3	6292	6112	0.89 (0.17)
Trot: Elasticity	All	23403	17866	0.99 (0.02)
	1	8393	5422	1.00 (0.04)
	2	8714	6332	0.93 (0.06)
	3	6296	6112	0.81 (0.17)
Trot: Impulsion	All	23401	17864	1.00 (0.04)
	1	8393	5421	0.97 (0.04)
	2	8714	6332	0.95 (0.05)
	3	6294	6111	0.72 (0.20)

<sup>1</sup>Period: All=1998-2012; 1=1998-2002; 2=2003-2007; 3=2008-2012

## Conclusions

The specialisation process in the Dutch Warmblood riding horse population affects the genetic connectedness between JH and DH. The lack of genetic connectedness is expressed also in lower genetic correlations between traits measured by JH and DH. The consolidation of two subpopulations with less genetic links should be considered in further studies on breeding strategies applied to the Dutch Warmblood horse population.

## Acknowledgements

Gabriel Rovere benefited from a joint grant from Royal Dutch Warmblood Studbook (KWPN) and Aarhus University, within the framework of the Erasmus-Mundus joint doctorate "EGS-ABG".

## Literature Cited

- Bartolomé E, Cervantes I, Valera M, Gutiérrez JP. 2011. *Livest. Sci.* 142:70–79.
- Colleau, J.J. (2002). *Genet. Sel. Evol.* 34:409-421.
- Ducro, B.J, Koenen, E.P.C., van Tartwijk J.M.F.M. et al. (2007). *Livest. Sci.* 107:227-234.
- Furre S., Viklund Å., Heringstad B. et al (2013). *Acta Agr. Scand. A-An.*1-8.
- MacCluer J.W., Boyce A.J., Dyke B. et al. (1983). *J. Hered.*74:394-399.
- Madsen, P., and Jensen, J.A. (2013). DMU. Version: 6, Release: 5.2
- Rekaya, R., Weigel, K.A. and Gianola, D. (1999). *Proc. 50<sup>th</sup> Annual Meeting, EAAP.*
- Rovere, G., Madsen, P., Ducro, B. et al. (2012). *Proc. 63<sup>rd</sup> Annual Meeting, EAAP*
- Ruhlmann C, Bruns E, Fraehr E. et al. (2009). *Livest. Sci.* 120:75-86.
- Sargolzaei, M., Iwaisaki, H. and Colleau, J.J.. (2006). *Proc. 8<sup>th</sup> WCGALP. Communication 27-28 (CD).*
- Schöpke K., Wensch-Dorendorf M., Swalve H.H. (2013). *Arch.Tierzucht* 56.
- Schurink A., Arts D.J.G. and Ducro B.J. (2012). *Livest. Sci.* 143:270-277.
- Thorén Hellsten E., Jorjani H., Philipsson J. (2008). *Livest. Sci.* 118:147-156.
- Viklund Å., Thorén Hellsten E., Näsholm A. et al. (2008). *Animal*.2:1832-1841.

