

Inter and intra genetic variability in sire lines of the Czech endangered draft horse breed

Luboš Vostrý^{1,2*}, Hana Vostrá-Vydrová², Barbora Hofmanová¹, Zdeňka Veselá², Jitka Schmidová^{1,2}

¹Czech University of Life Sciences Prague, Praha 6-Suchdol, Czech Republic

²Institute of Animal Science, Praha-Uhřetěves, Czech Republic

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The main objective of the study was to determine the genetic diversity in sire lines of two Czech endangered breeds (populations in the context of a currently conducted conservation program) – Silesian Noriker (SN) and Czech-Moravia Belgian (CMB) and one open breed – Noriker (N). A total of 2,202 animals of 24 lines were considered. Pedigree analyses were carried out for the whole population registered in the studbooks of analyzed breeds. Differences among the sire lines were evaluated using genetic distances and cluster analysis. One gene cluster comprised CMB sire lines, while the third cluster included the sire lines of the N breed. In the second cluster were combined sire lines from the SN and N breeds. The minor genetic differences between sire lines of the SN and N were observed in the second cluster. These results showed that a revision of the breeding strategy is suggested especially between SN and N breed.

Keywords: genetic diversity, sire lines, genetic structure, conservation

1 Introduction

The Silesian Noriker (SN), Czech-Moravian Belgian (CMB) draught horse breeds, along with the Old Kladruber and Hutsul horse, belong to a group of endangered horse breeds recognized as Genetic Resources in the Czech Republic (CR). The CMB horses have a medium square frame and mature earlier than other typical draught breeds. The SN horses have a longer than average frame and are a late maturing individuals. Another draught breed maintained on a large scale in the CR territory is the Noriker (N). To a large extent, the SN and CMB breeds have been geographically separated. The SN, N and CMB breeds were registered as separate breeds until the 1960s, but because of their decreasing numbers, all animals were merged into a single registry, the Czech draught horse – synthetic breed. At this time, stallions and mares were used across the breeds. However, in 1989, draught horses in the CR were reassigned into the original three populations (SN, N and CMB) based on morphological analysis. During this period, although the analyzed breeds were separated, these animals were maintained as open populations and “crossbreeding” was conducted between them. After 1996 and 1999, the populations of SN and CMB horses were certified as rare and endangered breeds (Genetic Resources), and their studbooks were closed. Although Silesian Noriker stallions were still used for breeding with Noriker mares,

their offspring, with more than 50% of the SN breed’s genes, were included in the studbook, and these animals have been regularly included in the SN breed (until 2013). In a previous paper (Vostrá-Vydrová et al., 2016) we analyzed the genealogical information in order to ascertain the genetic variability within and gene flow among three draught horse breeds. All the results showed that the small genetic differences between the analyzed breeds were found, likely reflecting the high frequency of migration between breeds.

The objective of this study was to determine the genetic difference in sire lines of the three Czech draught horse – the Silesian Noriker, the Noriker and the Czech-Moravia Belgian, based on genealogical information.

2 Material and methods

A total of 27,022 pedigree records of registered individuals in studbooks dating from 1900 to 31st June 2013 were provided from the Association of Horse Breeders Unions of the Czech Republic. Pedigree analyses were performed using one reference population containing animals potentially contributing to the next generations. The reference population was defined as the entire active population of individuals (stallions and mares) born in the years of 1996–2010 and included 2,202 animals of 24 sire lines. In the analyses were included only sire lines which included more than 10 animals. The sire lines of

*Corresponding Author: Luboš Vostrý, Czech University of Life Sciences Prague, Kamýcká 129, 165 21, Praha 6-Suchdol, Czech Republic, e-mail: vostry@af.czu.cz

Table 1 Name and year of birth (in the brackets) of line founder for Silesian Norik, Norik and Czech-Moravia Belgian

Breeds		
SN	N	CMB
419 Bravo (1914)	Amor T. (1888)	426 Aglaé (1920)
2262 Gothenschertz (1940)	Direkt (1974)	51 Bayard De Herédia (1920)
2526 Höllriegel (1939)	Malmut (1973)	396 Bourgogne de Monti (1920)
2934 Hubert Nero IX (1964)	50 Norbert (1887)	428 Branibor (1922)
1542 Nero Diamant VI (1941)	Randolf	50 Corale(1909)
1747 Neuwirt Diamant IX (1952)	500 Vogl. Vulkan XI (1958)	9 Marquis de Vraimont
2500 Ritz Vulkan VIII (1943)		26 Miroš (1923)
1350 Streiter Vulkan (1939)		3998 Pandor (1960)
		113 Successeur de Bonef (1926)

draught breeds, including the year of birth of the line founder, are described in Table 1.

The genetic diversity between breeds was evaluated based on genealogical information, using average coancestry coefficient within and between sire lines. According to Caballero and Toro (2000), the average coancestry coefficient (f_g) was estimated using the formula:

$$f_g = \frac{\sum_{i=1}^n \sum_{j=1}^n a_{ij}}{2n^2}$$

where:

a_{ij} represents the elements of the relatedness matrix (**A**) and n is the number of individuals in the pedigree. The elements of the relatedness matrix were estimated using a tabular method (Falconer and Mackay, 1996), based on VanRaden's method (1992) and the average genetic distance (Nei, 1978) according to Caballero and Toro (2002). The average coancestry coefficients and average genetic distance were standardized according to the sample size (Bartolomé et al., 2010).

The rate of genetic similarity between sire lines based on the pedigree information was evaluated through the cluster analysis method using the VARCLUS procedure of the SAS software package (SAS, 2005).

3 Results and discussion

Estimated average intra-line and inter-line coancestry coefficients exhibit the fact that the intra-line average coancestry coefficient (Table 2.) ranged from 0.059 (1747 Neuwirt Diamant IX) to 0.145 (50 Norbert), while the average inter-line coancestry coefficient ranged from 0.005 (500 Vogl. Vulkan XI vs. 26 Miroš) to 0.052 (2934 Hubert Nero IX vs. 2526 Höllriegel).

Standard inter-line genetic distances (D) according to Nei (1978) are listed in Table 2. The lowest value of

average genetic distances according to Nei (1978) was found between the line 2262 Gothenschertz and line 1747 Neuwirt Diamant IX (0.029) and the highest value of genetic distance was estimated between the Randolf and 50 Corale (0.122).

The higher average coancestry coefficients indicate a higher affinity of subjects within the lines. Generally low inter-line values were found between sire lines of CMB vs. SN and N. Conversely, higher average inter-line coancestry coefficients were found within the analyzed breeds. This can be explained by the fact that when designing breeding plans, mating involve individuals within the breeds, while breeding between draft horse breeds occurs not so frequently. A cluster analysis chart (Figure 1) was compiled using the average inter-line coancestry coefficients shown in Table 2. Following genealogical information, sire lines were divided into three basic clusters according to breeds. In the major cluster, animals from CMB sire lines were the most similar, since almost all the animals of these lines were grouped close together, especially animals of sire lines 419 Bravo, 51 Bayard De Herédia and 113 Successeur de Bonef. Although the observation was not based on the statistical inference, the CMB can be perceived as relatively homogeneous. Other sire lines formed two clusters according to breeds. As presented in Figure 1, the first cluster of 4 sire lines was found for the N breed. The consecutive mare of this line is located relatively close to this cluster. However, two sire lines of N considerably stood out from the rest. These two sire lines of N are combined with sire lines of SN in the second cluster.

The high similarity between these lines is also due to the fact that Silesian Noriker stallions were still used for breeding with Noriker mares, their offspring, with more than 50% of the SN breed's genes, were included in the studbook, and these animals have been regularly included in the SN breed. Second cluster showed minor

Table 2 The value of average inter-lines coancestry on diagonal, average intra-lines coancestry (above diagonal) and genetic distances between subpopulations (Di Nei, 1978) below diagonal

	CMB1	CMB2	CMB3	CMB4	CMB5	CMB6	CMB7	CMB8	CMB9	N1	N2	N3	N4	N5	N6	SN1	SN2	SN3	SN4	SN5	SN6	SN7	SN8	
CMB1	0.060	0.048	0.035	0.044	0.037	0.050	0.039	0.041	0.051	0.007	0.009	0.008	0.013	0.008	0.006	0.012	0.011	0.008	0.010	0.010	0.010	0.010	0.012	0.012
CMB2	0.025	0.077	0.036	0.045	0.041	0.046	0.036	0.038	0.049	0.008	0.009	0.009	0.013	0.008	0.007	0.012	0.011	0.009	0.010	0.010	0.010	0.014	0.012	0.012
CMB3	0.050	0.057	0.117	0.043	0.027	0.033	0.023	0.041	0.033	0.013	0.015	0.014	0.019	0.012	0.010	0.020	0.018	0.014	0.019	0.018	0.017	0.022	0.019	0.019
CMB4	0.031	0.038	0.052	0.083	0.035	0.043	0.030	0.038	0.045	0.009	0.012	0.010	0.015	0.009	0.008	0.015	0.013	0.010	0.012	0.012	0.012	0.016	0.014	0.014
CMB5	0.064	0.068	0.095	0.076	0.141	0.041	0.046	0.029	0.051	0.006	0.008	0.008	0.012	0.007	0.005	0.010	0.010	0.007	0.008	0.009	0.008	0.011	0.010	0.010
CMB6	0.025	0.037	0.063	0.043	0.071	0.084	0.039	0.041	0.049	0.008	0.009	0.009	0.014	0.008	0.006	0.013	0.012	0.009	0.010	0.011	0.010	0.014	0.012	0.012
CMB7	0.052	0.063	0.088	0.071	0.081	0.063	0.143	0.031	0.038	0.006	0.008	0.009	0.011	0.009	0.005	0.011	0.011	0.009	0.009	0.009	0.009	0.012	0.011	0.011
CMB8	0.039	0.049	0.059	0.052	0.087	0.050	0.075	0.115	0.039	0.011	0.012	0.012	0.017	0.011	0.009	0.017	0.016	0.013	0.015	0.016	0.015	0.018	0.016	0.016
CMB9	0.025	0.034	0.064	0.041	0.062	0.037	0.065	0.052	0.085	0.007	0.009	0.009	0.012	0.009	0.006	0.012	0.011	0.008	0.010	0.010	0.009	0.013	0.012	0.012
N1	0.077	0.084	0.092	0.085	0.115	0.087	0.104	0.089	0.089	0.127	0.037	0.021	0.037	0.015	0.017	0.019	0.023	0.021	0.023	0.018	0.023	0.023	0.020	0.020
N2	0.073	0.081	0.087	0.081	0.111	0.084	0.101	0.085	0.085	0.065	0.116	0.023	0.036	0.016	0.025	0.023	0.025	0.022	0.025	0.020	0.025	0.027	0.023	0.023
N3	0.074	0.081	0.088	0.082	0.111	0.084	0.100	0.085	0.085	0.081	0.077	0.104	0.027	0.023	0.016	0.026	0.031	0.033	0.030	0.027	0.033	0.022	0.029	0.029
N4	0.072	0.080	0.086	0.080	0.110	0.082	0.100	0.083	0.084	0.068	0.066	0.076	0.145	0.018	0.017	0.025	0.027	0.028	0.029	0.025	0.032	0.025	0.037	0.037
N5	0.084	0.092	0.101	0.093	0.122	0.095	0.110	0.097	0.095	0.097	0.094	0.087	0.094	0.134	0.014	0.032	0.036	0.036	0.029	0.031	0.030	0.023	0.028	0.028
N6	0.059	0.067	0.076	0.068	0.097	0.070	0.087	0.072	0.071	0.068	0.058	0.067	0.069	0.080	0.066	0.017	0.019	0.019	0.019	0.018	0.021	0.015	0.018	0.018
SN1	0.077	0.085	0.090	0.085	0.116	0.088	0.105	0.088	0.089	0.090	0.084	0.081	0.085	0.086	0.074	0.115	0.045	0.047	0.043	0.047	0.039	0.032	0.040	0.040
SN2	0.058	0.066	0.072	0.066	0.096	0.069	0.085	0.069	0.069	0.067	0.062	0.056	0.063	0.061	0.052	0.050	0.070	0.051	0.042	0.040	0.040	0.029	0.039	0.039
SN3	0.082	0.089	0.096	0.091	0.120	0.092	0.108	0.093	0.094	0.089	0.086	0.075	0.083	0.082	0.073	0.068	0.044	0.126	0.052	0.048	0.050	0.028	0.049	0.049
SN4	0.062	0.069	0.073	0.070	0.101	0.073	0.090	0.072	0.074	0.069	0.065	0.060	0.064	0.071	0.055	0.055	0.034	0.046	0.078	0.042	0.041	0.030	0.036	0.036
SN5	0.074	0.082	0.087	0.082	0.113	0.085	0.101	0.084	0.086	0.086	0.082	0.075	0.080	0.081	0.068	0.063	0.049	0.062	0.050	0.105	0.044	0.029	0.041	0.041
SN6	0.054	0.062	0.067	0.062	0.093	0.065	0.081	0.064	0.066	0.060	0.056	0.048	0.052	0.062	0.044	0.050	0.029	0.040	0.030	0.040	0.059	0.028	0.040	0.040
SN7	0.059	0.066	0.071	0.066	0.098	0.069	0.088	0.070	0.071	0.070	0.064	0.069	0.068	0.078	0.058	0.066	0.048	0.070	0.050	0.064	0.044	0.081	0.028	0.028
SN8	0.069	0.077	0.083	0.077	0.108	0.080	0.097	0.081	0.081	0.081	0.076	0.070	0.065	0.081	0.065	0.067	0.047	0.058	0.053	0.061	0.040	0.061	0.098	0.098

CMB1 – 419 Bravo, CMB2 – 51 Bayard De Herédia, CMB3 – 396 Bourgogne de Monti, CMB4 – 428 Branibor, CMB5 – 50 Corale, CMB6 – 9 Marquis de Vraimon, CMB7 – 26 Miroš, CMB8 – 3998 Pandor, CMB9 – 113 Successeur de Bonef, N1 – Amor T., N2 – Direkt, N3 – Malmut, N4 – 50 Norbert, N5 – Randoif, N6 – 500 Vogl, Vulkan XI, SN1 – 419 Bravo, SN2 – 2262 Gothenschertz, SN3 – 2526 Höllriegel, SN4 – 2934 Hubert Nero IX, SN5 – 1542 Nero Diamant VI, SN6 – 1747 Neuwirt Diamant IX, SN7 – 2500 Ritz Vulkan VIII, SN8 – 1350 Streiter Vulkan

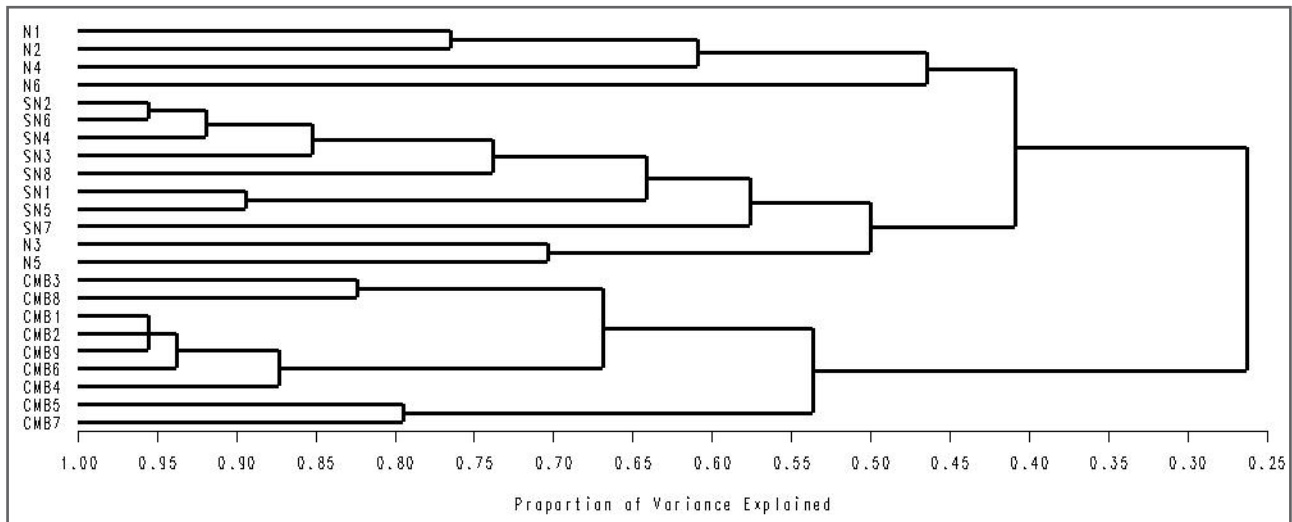


Figure 1 Cluster analysis constructed from the average inter and intra-line coancestry coefficients
 CMB1 – 419 Bravo, CMB2 – 51 Bayard De Herédia, CMB3 – 396 Bourgogne de Monti, CMB4 – 428 Branibor, CMB5 – 50 Corale, CMB6 – 9 Marquis de Vraimon, CMB7 – 26 Miroš, CMB8 – 3998 Pandor, CMB9 – 113 Successeur de Bonef, N1 – Amor T., N2 – Direkt, N3 – Malmut, N4 – 50 Norbert, N5 – Randolf, N6 – 500 Vogl. Vulkan XI, SN1 – 419 Bravo, SN2 – 2262 Gothenscherz, SN3 – 2526 Höllriegel, SN4 – 2934 Hubert Nero IX, SN5 – 1542 Nero Diamant VI, SN6 – 1747 Neuwirt Diamant IX, SN7 – 2500 Ritz Vulkan VIII, SN8 – 1350 Streiter Vulkany

dissimilarity distances existed for sire lines of SN and sire lines N3 and N5 of N. Low genetic distance between sire lines within individual breeds has been caused by alternative mating plan, which is used for the control of inbreeding using rotating mating between the lines within individual breed.

These results correspond with results obtained by Vostrý et al. (2011), who studied intra-line and inter-line genetic diversity in sire lines of the Old Kladruber horses or by Zábek et al. (2005), who comparing a small population of the Biłgoraj horse with common horse breeds.

This method was previously used by Přebyl et al. (1997) to determine the similarity among individuals of the Old Kladruber horse.

4 Conclusions

Good genetic management and optimized breeding decisions might be feasible to maintain a safe level of genetic diversity. Generally, the analyzed populations exhibited satisfactory genetic diversity. On the other hand, some of the analysed sire lines are not considerably genetically differentiated. Hence, a revision of the breeding strategy is suggested especially between Silesian Noriker and Noriker breed.

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