

**THE MOST SIGNIFICANT ANCESTORS  
IN LIPIZZAN HORSE BREED****M. Čačić, I. Čurik****Summary**

The beginning of creation of Lipizzan horse breed took place in 1580 in Lipica stud farm, and later spread on the area of states of former Austrian-Hungarian monarchy. In these states, national and private stud farms were aroused, so as national and private breedings. Due to small population size and closed breeding through centuries, national stud farms were forced to exchange genetic material, primarily the stallions. Consequently, different stallions influenced in different breeds and in whole Lipizzan breed. Research of pedigree with method of the most important ancestor contribution shows that in Croatian Lipizzan breed, despite of tradition longer than 3 centuries, only one stallion is contributing genetically to the today population.

Key words: Lipizzan horse, significant ancestors, genetic variability, Croatia.

**Introduction**

Lipizzan horse is a result of long, strict and system selection, which is why he became one of the world's most famous breeds. Lipizzan breed is small in number (10766 heads; LIF, 2012) and is breeding in „closed“ stud book. Croatian breeding of Lipizzan horses is the largest in the world and counts 2166 heads (CAA, 2014), and is the only national breed that consist two types of Lipizzan (two breeding goals), „*driving type*“ in Đakovo stud farm and in private breeding, and „*classic type*“ in Lipik stud farm, and they must both be preserved in future by well designed and reliably managed national breeding strategy (Čačić et al., 2012).

Zechner et al. (2002) analyzing pedigree data of Lipizzan horses confirmed genetic relation between breeding of eight national stud farms as a result of exchange of horses. In that study, they also analyze effective number of significant ancestor that measures balance of their genetic contribution in relation to current population (reference population) and effective number that evaluates contribution of significant ancestor independently on their being founders of population or not. They determine that in Lipizzan breed there are 10 the most significant ancestors which contribute more than 50% in gene pool of actual Lipizzan population (Table 1.). All 10 significant ancestor were born in 19th century. In the Đakovo stud farm the domination of only three stallions and all of them were foreign, but were born in 20th century and they contribute to genetic variability in stud farm even 40,34%.

In this study, in relation to Zechner et al. (2002), we included Croatian stud farm Lipik, and Croatian private breeding as well as stud farm Vučijak (Bosnia and Herzegovina). That is the reason why twice as large pedigree (7419 horses) in comparison to Zechner et al (2002) (3867 horses). Stud farm Lipik is specific in history, war suffering and absence from Croatia for full 16 years (1991.-2007.). Including of private breeding is important because it is the largest worlds subpopulation of Lipizzan horses, while on the other hand, Bosnian stud farm Vučijak is direct genetic successor of the „old“ stud farm Lipik (1938.-1956.) (Čačić, 2011b) and indirect of stud farm Stančić ergele Stančić (1919.-1938.) (Čačić, 2011b; Čačić, 2011a) where the basis of today's Lipizzan breeding in the Republic of Croatia were set up.

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### Material and methods

In research, as basic database of pedigree data, electronic database created while implementing Copernicus project (Nr. IC15CT96–0904): “*Biotechnical methods in maintenance of genetic diversity of Lipizzan breed*”, was used, in which are completed pedigrees of Lipizzan breeds of European National Stud Farms (Table 2.) and Croatian private breed. Basic database was completed with data of Lipizzan horses in stud books of private breeders (Čačić and Tadić, 2006) and stud farms Lipik (Čačić, 2010) and Vučijak (Stojanović et al., 2006). Whole database of Lipizzan pedigree counted 7419 horses, while the reference population (REFPOP) was 3854 units born from 1988 till 2008. Within REFPOP by time periods of 11 years (generation interval 11,5 years; Čačić and Čurik, 2014) three reference subpopulations were determined by year of birth: Refpop84 (1973.-1984.) (n = 704), Refpop96 (1985.-1996.) (n = 1236) and Refpop08 (1997.-2008.) (n = 1914). Program package ENDOG v.4.8. (Gutiérrez i Goyache, 2005) was used in analysis and method “the most important ancestor contribution”.

### Results and discussion

Table 1. shows the most significant ancestors which explain 50% of genetic variability by subpopulations.

Table 1. – SIGNIFICANT ANCESTORS THAT TOGETHER CONTRIBUTE 50% OF GENETIC VARIABILITY IN REFERENCE POPULATIONS OF LIPIZZAN BREED  
 Tablica 1. – ZNAČAJNIJI PRECI (ANCESTORI) KOJI ZAJEDNO DOPRINOSE 50% GENETSKE VARIJABILNOSTI U REFERENTNIM POPULACIJAMA LIPICANSKE PASMINE

Founder name (place, year of birth)	gender	Zechner et al. (2002) Frequency in %	This research, frequency in %			
			Reference populations			
			REFPOP	Refpop84	Refpop96	Refpop08
Favory Ratisbona II (L.1829)	sire	10,74	10,11	10,09	10,12	10,12
Favory Onerosa (L.1819)	sire	8,67	8,42	8,42	8,46	8,40
Neapolitano Aquileya (L.1820)	sire	6,73	6,93	6,94	6,94	-
Maestoso Erga XXXVI (L.1838)	sire	6,31	6,08	6,07	6,13	5,38
Favory Sezana (L.1872)	sire	-	5,26	-	5,26	-
Siglavy Alea (L.1846)	sire	4,52	4,66	-	4,73	-
Conversano Erga (L.1848)	sire	4,77	3,94	4,61	3,99	4,28
Slavina II (L.1847)	dam	3,78	3,92	3,72	3,96	-
Gazlan OX (desert breed.1840)	sire	4,88	3,71	4,36	3,70	4,54
Alea (L.1837)	dam	-	-	5,06	-	6,42
Siglavy Toscana (L.1830)	sire	-	-	3,89	-	-
5314 Favory XX-7 (Sz.1960)	sire	-	-	-	-	7,46
Neapolitano Valdamora (L.1839)	sire	-	-	-	-	5,62
Pluto Alea (L.1853)	sire	4,68	-	-	-	-
Groczana II (L.1817)	dam	3,54	-	-	-	-
Contribution to gene variability, %		58,62	53,04	53,17	53,29	52,21

In reference population and subpopulations there is altogether 13 significant ancestors, 11 sires and 2 dams. The most significant ancestors in all of them is Favory II (L.1829), who in all reference subpopulation contributes to explanation alone with more than 10% of genetic variability. In all reference subpopulation, significant ancestor sires are Favory Onerosa (L.1819), Maestoso Erga XXXVI (L.1838), Conversano Erga (L.1848) and Gazlan OX (desert breed.1840), while the rest of ancestors that explain 50% of genetic variability shows up in one to two reference subpopulations. In this study, one ancestor more was needed (9) in the group of ancestors who contribute 50% of genetic variability of the breed in relation to Zechner et al. 2002 (8). Sire Pluto Alea (L.1853) and dam Groczana II (L.1817) were not confirmed as significant ancestors. Watching through three subpopulation, it is observed that certain significant ancestors do not show up in all three reference subpopulation, which is result of using different sires in certain time period.

Table 2. shows the most significant ancestor of European Lipizzan breed by the estimated frequency of gene proportion in Lipizzan breed. Out of ancestors that were significant in all three Croatian breeds and in other breeds, is only sire 1116 Conversano Gaetana IV (Lip.1947), who is also the most significant ancestor in Lipica Stud Farm, and consequently in Lipik Stud farm. In these stud farms also is significant proportion of gene frequency of sire 513 Neapolitano Batosta XXI (Kut.1956).

Zechner et al. (2002) as the most significant ancestors in Đakovo stud farm determine sires 5103 Maestoso X Mahonia (Topolcianky, 1982) (17,27%), 5314 Favory XX-7 (Szilvasvarad, 1960) (13,30%) and Pluto Navarra-90 (Piber, 1972) (9,77%), born on the second half of 20th century. This study confirms that, but different value of estimated gene frequency was determined. The largest contribution to the genetic variability in Đakovo stud farm is of sire 5314 Favory XX-7 (Sz.1960), and consequently in private breed too, while in both breeds the second place takes 5103 Maestoso X Mahonia (Top.1982) which is the opposite of the results of Zechner et al. (2002). These three sires in Croatian breed did not have absolutely the largest direct progeny groups, but comparing to other sires through history, in breeding, there was and still is a large number of their offspring. Although Zechner et al. (2002) determine the lowest inbreeding coefficient in Đakovo stud farm, the result will be its rapid increase due large number of direct and further offspring of these three sires which are mating between themselves. Identical situation was determined by Vaez Torshizi et al. (1998) in Australian breed of Thoroughbred. Furthermore, at the beginning of ninties of past century, when Patriotic war in Croatia began, and even before that, intensity of selection work in Lipizzan breed and in whole horse breeding was significantly decreased. Strict criteria of selection is missing, as well as planned breeding implementation and planned distribution of sires in private breeding. All that has a result of action of too large number of sires in breeding, small progeny groups per sire, and large morphological diversity in Đakovo Stud Farm and in private breeding, and the same morphological diversity is significantly showing in private breeding, as a result of different condition of housing and rearing, poor selection (sire choosing) and buying low quality heads excluded from Đakovo stud farm (Čačić, 2011).

Table 2. – ANCESTORS WHO ALLTOGETHER CONTRIBUTE 50 % OF GENETIC VARIABILITY OF LIPIZZAN BREED BY SUBPOPULATIONS (S-SIRE, D-DAM)  
 Tablica 2. – PRECI KOJI ZAJEDNO DOPRINOSE 50 % GENETSKE VARIJABILNOSTI LIPICANSKE PASMINE PREMA SUBOPULACIJAMA (S – PASTUH; D – KOBILA)

Founder name (place, year of birth)	Gender	Subpopulation, %									
		Lipik Croatia)	Pakovo Croatia)	Croatian private breed	Učijak (Bosnia and Herzegovina)	Lipica (Slovenia)	Piber Austria)	Monterotondo (Italia)	Szilvásvárad Hungary)	Topolčianky Slovakia)	Fagaras Romania)
1116 Conversano Gaetana IV (Lip.1947)	S	13,78	4,84	5,95	-	12,94	-	-	-	-	-
513 Neapolitano Batosta XXI (Kut.1956)	S	11,91	-	-	-	9,33	-	-	-	-	-
13 Dubovina (Lipica, 1939)	D	8,25	-	-	-	-	-	-	-	-	-
Maestoso Mascula (L.1974)	S	6,49	-	-	-	-	11,05	-	-	-	-
432 Siglavy Monterosa (L.1907)	S	5,74	-	-	-	-	5,52	-	-	-	-
Favory Sezana (L.1872)	S	5,09	-	-	-	4,74	8,48	-	-	-	-
5314 Favory XX-7 (Sz.1960)	S	-	12,02	11,84	-	-	-	-	-	-	-
5103 Maestoso X Mahonia (Top.1982)	S	-	8,65	5,87	-	-	-	-	-	-	-
Pluto Navarra-90 (P.1972)	S	-	8,64	8,14	-	-	-	-	-	-	-
Favory Ratisbona II (Lipica, 1829)	S	-	5,96	6,73	-	6,42	-	-	9,55	10,49	4,83
Tulipan IX-39 (Fag.1966)	S	-	5,14	-	-	-	-	-	-	-	-
29 Conversano Bravissima XI (Đ.1962)	S	-	-	9,73	-	-	-	-	-	-	-
125 Siglavy Toplica XIV (Đ.1972)	S	-	-	5,78	-	-	-	-	-	-	-
228 Siglavy Bregava XVI (V.1963)	S	-	-	-	11,99	-	-	-	-	-	-
188 Favory Sana I (V.1960)	S	-	-	-	11,10	-	-	-	-	-	-
415 Pluto Ilova I (V.1979)	S	-	-	-	9,81	-	-	-	-	-	-
305 Conversano Dubovina (L.1958)	S	-	-	-	8,82	-	-	-	-	-	-
475 Neapolitano Bachstelze (St.1926)	S	-	-	-	5,42	-	-	-	-	-	-
389 Bregava XXV (V.1975)	D	-	-	-	1,01	-	-	-	-	-	-
Maestoso Erga XXXVI (L.1838)	S	-	-	-	-	5,52	-	4,85	4,17	-	-
Maestoso Bonavoja-45 (P.1967)	S	-	-	-	-	4,74	-	-	-	-	-
Conversano Virtuosa (L.1879)	S	-	-	-	-	-	10,01	-	-	-	-
Neapolitano Capriola (L.1905)	S	-	-	-	-	-	7,54	-	-	-	-
12 Pluto II Materia (L.1912)	S	-	-	-	-	-	5,90	-	-	-	-
Alea (L.1837)	D	-	-	-	-	4,65	-	-	-	-	-
Conversano Austria (L.1911)	S	-	-	-	-	-	-	13,16	-	-	-
Favory Strana (Mont.1948)	S	-	-	-	-	-	-	12,26	-	-	-
Pluto Bonadea (L.1941)	S	-	-	-	-	-	-	10,01	-	-	-
Neapolitano Alba (Mont.1952)	S	-	-	-	-	-	-	7,92	-	-	-
Maestoso Mirabella (Mont.1972)	S	-	-	-	-	-	-	7,10	-	-	-
Favory Onerosa (L.1819)	S	-	-	-	-	-	-	-	7,61	8,44	-
Neapolitano Aquileya (L.1820)	S	-	-	-	-	-	-	-	6,17	5,92	-
1572 Conversano Strana (Lip.1944)	S	-	-	-	-	-	-	-	-	7,69	-
Neapolitano IX Batosta (Top.1974)	S	-	-	-	-	-	-	-	-	6,74	-
Favory X Theodorosta (Top.1977)	S	-	-	-	-	-	-	-	-	5,19	-
Neaplitano VIII Saragossa (Top.1964)	S	-	-	-	-	-	-	-	-	4,84	-
Favory XVIII (Bab.1933)	S	-	-	-	-	-	-	-	11,87	-	-
Conversano XII (Fag.1906)	S	-	-	-	-	-	-	-	5,39	-	-
Maestoso XXI (Bab.1922)	S	-	-	-	-	-	-	-	3,79	-	-
Tulipan III (Sz.1972)	S	-	-	-	-	-	-	-	3,33	-	-
Favory XXIV (Fag.1953)	S	-	-	-	-	-	-	-	-	-	10,66
Conversano XVIII (Fag.1949)	S	-	-	-	-	-	-	-	-	-	10,15
Siglavy Capriola VI (Fag.1952)	S	-	-	-	-	-	-	-	-	-	7,64
Conversano XIII (Fag.1910)	S	-	-	-	-	-	-	-	-	-	6,97
Maestoso XIX (Fag.1924)	S	-	-	-	-	-	-	-	-	-	6,66
Maestoso XXXV (Fag.1967)	S	-	-	-	-	-	-	-	-	-	5,41
Contribution in gene pool (u %)		51,26	52,84	54,05	52,14	50,28	53,16	50,44	52,56	53,48	52,32

Study also confirms large genetic contribution of foreign sires in Đakovo stud farm. In six ancestors that contribute to genetic pool with 50%, not one sire from custom breeding is found (Table 2.). Given that Đakovo stud farm is the center of selection and distribution of young Lipizzan sires for five past decades, similar situation was determined in private breeding as well. The only exception is that in seven significant ancestor which explain 50% of variability, we found two sires of Croatian breeding, 29 Conversano Bravissima XI (Đ.1962) and 125 Siglavy Toplica XIV (Đ.1972). In Topol'cianky stud farm, the most significant ancestor of Croatian breeding is sire 1572 Conversano Stana IV (Lip.1944) who is founder of Croatian branch of Conversano line in Slovakian breeding, but that sires has no significance in Croatian or any other national breeding.

### *Conclusion*

Large number of research results of Zechner et al. (2002) was confirmed in this study, but with including in analysis the larger number of units to whole Lipizzan pedigree, there are certain differences which are to a lesser extent result of completing Lipizzan pedigree with later born heads in eight researched stud farms, and largely the result of including three more Lipizzan breedings into analysis. Researched parameters will certainly be different when the analysis is extended to include other national breedings. In this study, it is determined that beside sire 1116 Conversano Gaetana IV (Lip.1947), no other ancestor bred in Croatia has significant contribution to the whole gene pool of current Croatian population. From the standing point of only Croatian line Tulipan, for Croatian breeding there is only one significant sire of Tulipan line, and he is not bred in Croatia, but in romanian stud farm Fagaras (Tulipan IX-39, Fag.1966). Although Lipizzan horses are being bred in Đakovo stud farm from 1806., not one sire bred in stud farm had a significant mark on Lipizzan breeding in general. Possible explanation is also a fact that in Đakovo stud farm at the beginning of 20th century breeding of Lipizzan horses has significantly weakened, and firm breeding basis is set up again by bringing dams and sires after disbanding „old“ stud farms Lipik and Kutjevo (1956.-1957.), who are bred in Stančić stud farm or were their offspring. It is concluded that in stud farm Đakovo breeding, as a center of national breeding in the last four decades, the importance of preserving Croatian type of Lipizzan horses was not given, but the breeding work was mostly relied on sire selection in foreign stud farms. Significant genetic contribution of foreign sires to Croatian population was confirmed by Zechner et al. (2002) and by this study. That is possible explanation of large morphological diversity in Croatian breeding determined by Čačić (2011). Unconsolidated genetic basis is the largest obstacle to breeding values prediction and reaching the breeding goal, because chosen breeding heads are not able to transfer their desirable characteristics to their offspring.

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## NAJZNAČAJNIJI PRECI U LIPICANSKOJ PASMINI

### Sažetak

Početak stvaranja lipicanske pasmine je 1580. godina u ergeli Lipica, a kasnije se širila na prostoru država bivše Austro-ugarske monarhije. U istim državama nastajale su državne i privatne ergele te privatni nacionalni uzgoji. Zbog male veličine populacije i zatvorenog uzgoja kroz stoljeća, državne ergele su bile prinuđene razmjenjivati genetski materijal, prvenstveno pastuhe. Posljedično, različiti pastusi su utjecali u različitim uzgojima i cjelokupnoj lipicanskoj pasmini. Istraživanje rodovnika metodom doprinosa najznačajnijih predaka pokazuje da je u hrvatskom uzgoju, unatoč tradiciji uzgoja dužoj od tri stoljeća, samo jedan uzgojeni pastuh doprinosi genetskoj varijabilnosti današnje populacije.

Ključne riječi: lipicanac, značajni preci, genetska varijabilnost, Hrvatska.

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