A PART OF GENETIC HISTORY IN HORSES: IMPORTANT ANCESTORS OF GIDRAN HORSE FROM TULUCESTI STUDFARM

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Abstract

Study of important ancestors give us information about breeding methodic in analized population (origins, selection on ascendants) and also about possibilities of breed evolution (small number of ancestors, maintaining the genetic similarity with remarkable ancestors or the preference for descendants of certain individuals, may lead to inbreeding and genetic drift).In pedigrees of Gidran horse, from Tulucesti studfarm, was identified 104 male ancestors. It was ordered by three criteria: the kinship with sire stallions, the relationship with brood mares, and with the population, as a whole (reproductive nucleus, stallions and mares) at that time. The results highlight the fact that the kinship share of male ascendants in the population is between 0% and 19.46%. Eight stallions have a higher genetic resemblance to the population, ranging from 15.84% to 19.46%. The relatively small differences between sire stallions reveal concerns for maintaining a large number of males, necessary to avoid inbreeding and to ensure a normal population evolution under reproductive isolation.

Key words: Gidran, Tulucesti, ancestors, relationship, stallion.

INTRODUCTION

The Gidran horse is an anglo-arabian population, that has been formed in parallel in Mezohegyes and Radautistud farms (Marginean, 2012). Due to the small size of population, it became one of the preserved breeds. These kind of researches could facilitate conservation efforts for preserving the genetic diversity of the Gidran horse (Sziszkosz et al., 2016).

This study is just a part of an ample research regarding the genetic history of most important Romanian horse breeds. We must say that we had this opportunity because of a good collaboration with National Autthority for Forestry, with the support of specialists from Horse Breeding Department. This study of important ancestors, in Gidran horse, give us information about breeding methodic in analized population (origins, selection on ascendants) and also about possibilities of breed evolution (small number of ancestors, maintaining the genetic similarity with remarkable ancestors or the preference for descendants of certain individuals, may lead to inbreeding and genetic drift).

MATERIALS AND METHODS

In pedigrees of Gidran population, from Tulucesti studfarm, it was identified 104 sire stallions.They were odered through three chriterias: relatedness with sire stallions, with brood mares (mother mares), and with overall population at the time of research (Table 1a and 1b). Method used was „The numerator relationship matrix" elaborated by Henderson and Cuningham in 1976, presented for the first time in Romania by Grosu in 1997.

RESULTS AND DISCUSSIONS

The results highlight the fact that the share of male ascendants in the population is between 0% and 19.46%. Eight stallions have a higher genetic resemblance to the population, ranging from 15.84% to 19.46%. The relatively small differences between the sires reveal the preoccupations for maintaining a large number of males, necessary to avoid inbreeding and to ensure a normal evolution of the population, under conditions of reproductive isolation (Figure 1). Our desire was to identify the stallions that are relatedness at least 15% with

population. So, in the population's pedigree of the Gidran from Tuluceşti studfarm, we identified, with maximum certainty, 8 such ancestors.

Table 1a. Genetic relationship of male ascendants with sire stallions, brood mares and with overallpopulation

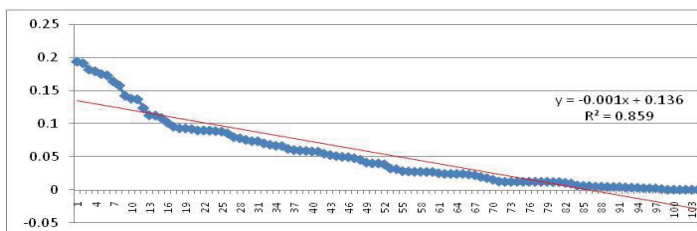| INDIVIDUALS	CODE	Ra	$S_{\bar{x}}$	Ri	$S_{\bar{x}}$	R pop	$S_{\bar{x}}$
G K	1	0.0273	0.0093	0.0273	0.0022	0.0273	0.0022
SACHMAT	4	0.0273	0.0093	0.0273	0.0022	0.0273	0.0022
SOUVENORDER	6	0.0137	0.0067	0.0113	0.0016	0.0116	0.0016
PERIS	8	0.0137	0.0067	0.0113	0.0016	0.0116	0.0016
G 46	10	0.0530	0.0063	0.0380	0.0031	0.0400	0.0029
G 60	12	0.1060	0.0126	0.0760	0.0062	0.0800	0.0059
G IX	15	0.1094	0.0106	0.0872	0.0071	0.0901	0.0064
G 53	18	0.0532	0.0050	0.0363	0.0028	0.0386	0.0027
TABOR	21	0.0176	0.0067	0.0117	0.0018	0.0125	0.0018
OLEANDER	23	0.0176	0.0067	0.0117	0.0018	0.012	0.0018
RAUFBOLDT	25	0.0352	0.0133	0.0234	0.0036	0.0250	0.0036
RAZBEG	27	0.0703	0.0267	0.0469	0.0073	0.0500	0.0072
G XI	30	0.0618	0.0117	0.0430	0.0044	0.0455	0.0042
G XIII	31	0.0901	0.0103	0.0713	0.0060	0.0738	0.0054
G XV	33	0.0773	0.0121	0.0567	0.0053	0.0595	0.0050
G XIX	34	0.1251	0.0233	0.0871	0.0084	0.0922	0.0081
K VI	37	0.0410	0.0128	0.0262	0.0024	0.0282	0.0027
K VIII	39	0.0674	0.0149	0.0485	0.0048	0.0510	0.0046
K XIX	40	0.0513	0.0102	0.0397	0.0049	0.0412	0.0044
G VIII	41	0.0117	0.0068	0.0103	0.0019	0.0105	0.0019
G VI	46	0.0547	0.0186	0.0545	0.0044	0.0546	0.0044
G XIV	48	0.1094	0.0372	0.1091	0.0088	0.1091	0.0087
G 54	52	0.0000	0.0000	0.0027	0.0011	0.0023	0.0010
G L	55	0.0234	0.0070	0.0139	0.0022	0.0152	0.0021
G X	61	0.0000	0.0000	0.0074	0.0026	0.0064	0.0023
G XII	64	0.1233	0.0269	0.0797	0.0092	0.0855	0.0090
G IV	68	0.0486	0.0168	0.0246	0.0024	0.0278	0.0032
G XVII	69	0.0989	0.0196	0.0884	0.0087	0.0898	0.0079
H VII	70	0.0000	0.0000	0.0313	0.0047	0.0271	0.0046
HADIK	77	0.0352	0.0133	0.0306	0.0051	0.0313	0.0047
G 52	82	0.0098	0.0074	0.0026	0.0001	0.0035	0.0013
G 53'	84	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SB I 5	85	0.0078	0.0078	0.0021	0.0001	0.0029	0.0013
G VII	92	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WIZZER	93	0.0273	0.0133	0.0225	0.0032	0.0232	0.0032
H IV	95	0.0000	0.0000	0.0198	0.0025	0.0120	0.0023
G III	101	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
K G I	104	0.1193	0.0192	0.0843	0.0066	0.0890	0.0065
K X	111	0.0352	0.0174	0.0169	0.0020	0.0194	0.0029
M V	122	0.0000	0.0000	0.0138	0.0025	0.0120	0.0023
M VI	123	0.0000	0.0000	0.0138	0.0025	0.0120	0.0023
GAZAL V	125	0.0000	0.0000	0.0138	0.0025	0.0120	0.0023
N PERKUN	129	0.0000	0.0000	0.0138	0.0025	0.0120	0.0023
S XXVIII	131	0.0000	0.0000	0.0138	0.0025	0.0120	0.0023
N IV	134	0.0000	0.0000	0.0138	0.0025	0.0120	0.0023
S XVIII	140	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
G LIII	142	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
G 49	143	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Figure 1. Genetic relationship of male ascendants with population

Table 1b. Genetic relationship of male ascendants with sire stallions, brood mares and with overallpopulation

INDIVIDUALS	CODE	Ra	$S_{\bar{x}}$	Ri	$S_{\bar{x}}$	R pop	$S_{\bar{x}}$
PRINCE ORANGE II	144	0.0000	0.0000	0.0024	0.0017	0.0021	0.0014
ARKINA	146	0.0000	0.0000	0.0048	0.0033	0.0042	0.0029
MANPAEOD	148	0.0000	0.0000	0.0024	0.0017	0.0021	0.0014
FIRDAUSSI	150	0.0000	0.0000	0.0054	0.0030	0.0047	0.0026
FANTASTIC	153	0.0000	0.0000	0.0063	0.0036	0.0055	0.0031
CORDON ROUGE	155	0.0000	0.0000	0.0036	0.0020	0.0031	0.0017
M IX	160	0.0000	0.0000	0.0276	0.0050	0.0240	0.0047
H IX	163	0.0000	0.0000	0.0276	0.0050	0.0240	0.0047
M VIII	166	0.0000	0.0000	0.0276	0.0050	0.0240	0.0047
PETRUS	173	0.0000	0.0000	0.0012	0.0012	0.0010	0.0010
G XVIII	177	0.0734	0.0220	0.0583	0.0082	0.0603	0.0076
G XXI	179	0.1227	0.0287	0.0887	0.0087	0.0932	0.0085
G XXII	180	0.1480	0.0505	0.0673	0.0094	0.0781	0.0113
G XXV	181	0.0612	0.0189	0.0514	0.0058	0.0527	0.0055
G XXVII	183	0.1383	0.0455	0.1088	0.0150	0.1128	0.0142
G XXIX	196	0.0948	0.0381	0.0704	0.0112	0.0737	0.0108
G XXIV	202	0.1367	0.0546	0.1221	0.0117	0.1241	0.0120
K XIII	203	0.0454	0.0189	0.0243	0.0024	0.0271	0.0033
RIVOL	207	0.0000	0.0000	0.0048	0.0033	0.0042	0.0029
MANTALORZ	209	0.0000	0.0000	0.0048	0.0033	0.0042	0.0029
EPIGOR	211	0.0000	0.0000	0.0054	0.0034	0.0047	0.0029
M XIII	213	0.0000	0.0000	0.0553	0.0100	0.0479	0.0093
H XVI	215	0.0000	0.0000	0.0571	0.0098	0.0495	0.0092
G XXIII	217	0.1167	0.0521	0.0610	0.0072	0.0684	0.0094
RG I	224	0.1424	0.0340	0.1086	0.0159	0.1131	0.0145
G XXX	226	0.0885	0.0291	0.0676	0.0069	0.0704	0.0070
G XXVIII	229	0.0905	0.0171	0.1037	0.0141	0.1019	0.0124
G XXXI	231	0.2201	0.0531	0.1563	0.0173	0.1648	0.0167
G XXXII	232	0.2120	0.1075	0.0751	0.0114	0.0933	0.0182
G XXXIV	235	0.0692	0.0228	0.0562	0.0082	0.0579	0.0076
G XXVI	248	0.0802	0.0138	0.0643	0.0076	0.0664	0.0068
M XI	251	0.0000	0.0000	0.0276	0.0050	0.0240	0.0047
GAL	252	0.0000	0.0000	0.0108	0.0075	0.0094	0.0065
SATELIT	254	0.0352	0.0133	0.0316	0.0071	0.0321	0.0063
M XVIII	257	0.0000	0.0000	0.1106	0.0200	0.0958	0.0186
G XXXV	260	0.0808	0.0232	0.0647	0.0113	0.0668	0.0102
COPIL	263	0.0000	0.0000	0.0068	0.0050	0.0059	0.0044
G K I	265	0.0596	0.0096	0.0589	0.0094	0.0590	0.0082
G XXXVI	272	0.0982	0.0226	0.0888	0.0088	0.0900	0.0081
G XXXIX	274	0.2400	0.1040	0.1636	0.0251	0.1737	0.0253
G XXV 38	276	0.0762	0.0079	0.0554	0.0061	0.0582	0.0055
G XXVIII	279	0.0905	0.0171	0.0881	0.0085	0.0884	0.0076
GR I	285	0.1784	0.0652	0.1310	0.0249	0.1374	0.0230
NANDOR	288	0.0000	0.0000	0.0204	0.0138	0.0177	0.0120
G XXXVII	290	0.0689	0.0066	0.0768	0.0137	0.0758	0.0119
M XXII	292	0.0000	0.0000	0.2216	0.0400	0.1921	0.0373
G XXXVIII	295	0.1997	0.1108	0.1800	0.0297	0.1826	0.0288
NAUM	297	0.0176	0.0067	0.0228	0.0096	0.0221	0.0083
G XL	303	0.1913	0.1120	0.1301	0.0196	0.1383	0.0218
GRUIA	318	0.0088	0.0033	0.0449	0.0270	0.0401	0.0234
G XLIV	322	0.1309	0.0254	0.2019	0.0295	0.1946	0.0268
G XLV	324	0.1678	0.0550	0.1772	0.0343	0.1759	0.0304
G XLII	326	0.1109	0.0350	0.1881	0.0361	0.1801	0.0328
G XLVI	330	0.2141	0.1061	0.1498	0.0237	0.1584	0.0243
G XLIII	340	0.0791	0.0214	0.0602	0.0062	0.0621	0.0059
G XLVII	341	0.1399	0.0136	0.1430	0.0148	0.1427	0.0133

Note
Ra = average relatedness with sire stallions;
Ri = average relatedness with broodmares;
R pop. = average relatedness with population.

Table 2. Important ancestors in Gidranpopulational pedigree

Ancestor's name	Code	Relatedness with:		
		Sire stallions	Broodmares	Population
G XLVI	330	0.2141	0.1498	0.1584
G XXXI	231	0.2201	0.1563	0.1648
G XXXIX	274	0.2400	0.1636	0.1737
G XLV	324	0.1678	0.1772	0.1759
G XLII*	326	0.1109	0.1881	0.1801
G XXXVIII	295	0.1997	0.1800	0.1826
M XXII	292	0.0000	0.2216	0.1921
G XLIV*	322	0.1309	0.2019	0.1946

* Active in the current reproductive nucleus
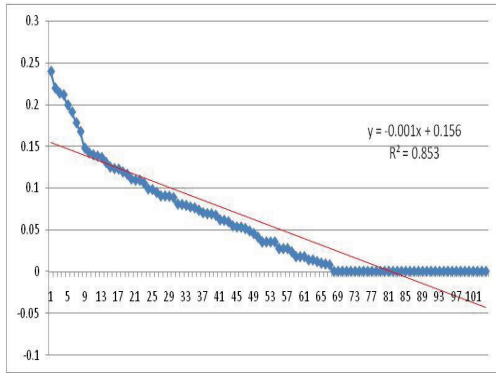
Figure 2. Genetic relationshipof males ascendant with sire stallions from current reproductive nucleus

In terms of reproductive isolation, homozygosity has the meaning of maintaining greater genetic similarity with valuable reproducers (Popa, 2009). In the Gidran population from Tuluceşti studfarm, it was considered the presence of the descendants from as many stallions as possible, thus maintaining genetic diversity and creating a field of action for selection. There are, however, 8 male ascendants, whose descendants were selected mainly for the basic flock.

Regarding the relationship of male ascendants with current sire stallions, were determined values ranging from 0% to 24%. 37 male offspring of the population have the relatedness coefficient equal with 0, at the time of analysis, of which more than 30 are immigrants (one part is in the ascendancy of the mares, the other is not genetically persistent in the population). At the other end of the series of relatedness coefficients, between the male ascendants and the actual sire stallions (ordered according to the coefficients values), there are 4 stallions with a strong accentuated relationship with the sire stallions: G XXXII (21.20%), G XLVI 21.41%), G XXXI (22.01%) and G XXXIX (24%) - Figure 2. These stallions have a greater participation in the establishment of the population's genetic found, being present in a significant proportion in the pedigrees of the current sire stallions.

Regarding the relatedness of the 104 male ascendants with the current stock of broodmares, from the graph shown in figure 3, it is noted the existence of coefficients of relatedness between 0% and 22.16%. Only 6 males from the population's ascendancy have a null value of the relatedness coefficient with the broodmares at the time of the analysis. 4 male ascendants have a stronger relationship with the mare herd, which also determines the high values of the population with the whole population: M XXII (22.16%), G XLIV (20.19%), G XLII (18.81%) and G XXXVIII (18%).
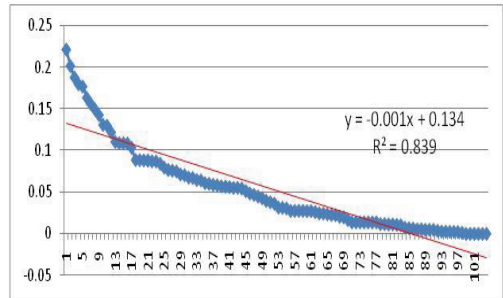

Figure 3. Genetic relationship of males ascendants with current broodmares

CONCLUSIONS

Great resemblance to the population of important ancestors is explained firstly by the adoption of a working model specific to the desire to maintain genetic resemblance with remarkable ancestors.

According to this model, the population is not maintained as a whole, but the mating plan allows the pairing of coupleswhich presents in the pedigrees common ascendants.

The values of the population of these important ancestors are determined by their presence in the pedigrees of both, stallions and mares, with some equilibrium (certainly undisturbed).

ACKNOWLEDGEMENTS

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