

STUDY OF IMPORTANT ANCESTORS IN ROMANIAN HUCUL HORSE POPULATION FROM LUCINA STUDEFARM

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Abstract

Study of remarkable ancestors offer information about breeding methods in analyzed population (origins, ascendants selection) and the future evolutive possibilities of this (small number of ancestors, maintaining of genetic similarity with remarkable ascendants or preferring of descendants from some individuals, may contribute to inbreeding and genetic drift). The results put in front that the share of genetic relationship between sire stallions with population is between 0% and 24.45%. A number of 8 stallions have a genetic similarity with population bigger than that (20.20% - 24.45%). Small differences between sire stallions reveal the concerns for maintaining a big number of males necessary for avoiding inbreeding and also to ensure a normal population evolution.

Key words: Hucul, inbreeding, genetic drift, ancestors

INTRODUCTION

Study of remarkable ancestors offer information about breeding methods in analyzed population (origins, ascendants selection) and the future evolutive possibilities of this (small number of ancestors, maintaining of genetic similarity with remarkable ascendants or preferring of descendants from some individuals, may contribute to inbreeding and genetic drift).

MATERIAL AND METHODS

Material is represented by all possible genealogical information from farm register. The numerator relationship matrix was the applied method for this study (Henderson & Cunningham, 1976) [1].

RESULTS AND DISCUSSIONS

In Romanian Hucul horse population pedigrees we identified 69 male ascendants. They was ordered by three criteria: genetic relationship with sire stallion, with brood mares and with hole population (brood mares and sire stallions) when analysis (table 1a and 1b).

The results put in front that the share of genetic relationship between sire stallions with population is between 0% and 24.45%. A number of 8 stallions have a genetic similarity with population bigger than that (20.20% - 24.45%).

Small differences between sire stallions reveal the concerns for maintaining a big number of males necessary for avoiding inbreeding and also to ensure a normal population evolution – figure 1. Regarding genetic relationship of male ascendants with current sire stallions we find values between 0% and 33.62%. A single male ascendant presents a null value of genetic relationship coefficient in present moment (Hroby II). At the other end of genetic relationship coefficient values, between male ascendants and current sire stallions (ranged by coefficient values), we find three stallions who have a stronger genetic relationship: Oușor X (33.62%), Oușor IX (32.19%) and Goral XXI (31.32%) – figure no. 2. This stallions have a significant participation on population genetic resources establish (due to significant number of males retained for reproduction), without being important ascendants (they don't have a similar situation with hole population).

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Regarding genetic relationship between 69 male ascendants with current brood mares livestock, analyzing figure no. 3, we saw a linear tendencies for genetic relationship

coefficients without being able to highlight male ascendants with a higher proportion of common genes with current broodmares livestock.

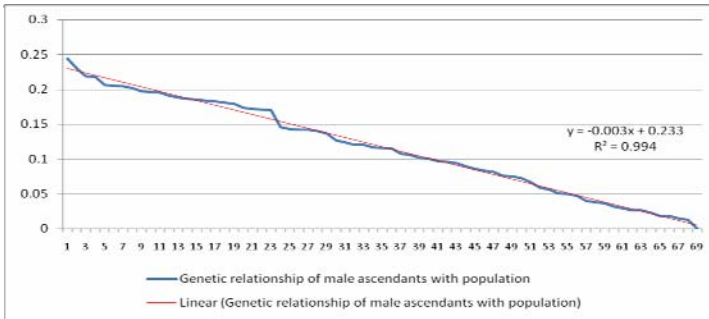


Figure 1 Genetic relationship of male ascendants with population

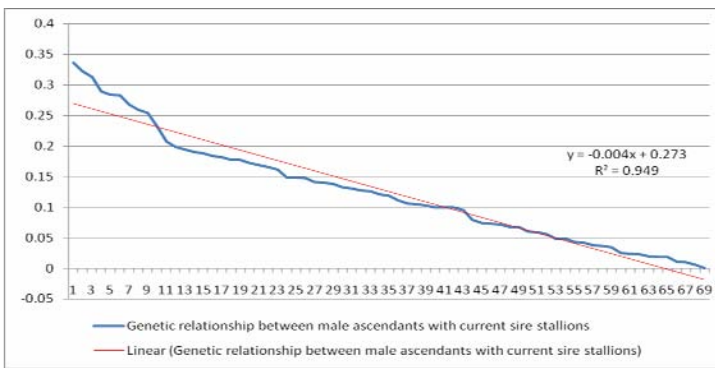


Figure 2 Genetic relationship between male ascendants with current sire stallions

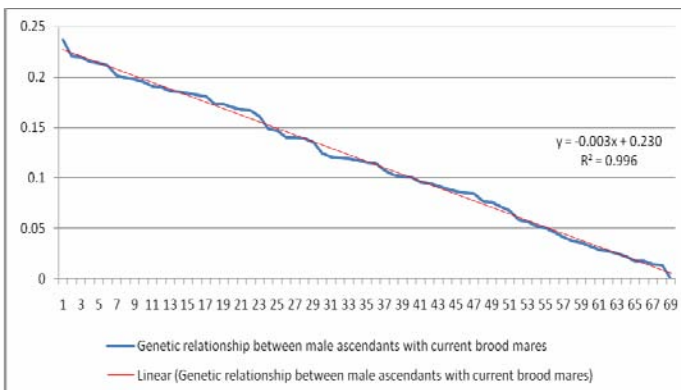


Figure 3 Genetic relationship between male ascendants with current brood mares

Table 1 Average genetic relationship between male ascendants and reproductive nucleus (Sire stallions and brood mares) and with population

INDIVIDUAL	Ra	S_{f}	Ri	S_{f}	R pop	S_{f}
G I	0.1189	0.0072	0.1154	0.0017	0.1154	0.0016
G II	0.0594	0.0036	0.0586	0.0004	0.0585	0.0004
G III	0.1775	0.0130	0.1700	0.0023	0.1707	0.0024
G IV	0.0996	0.0066	0.1082	0.0013	0.1075	0.0013
G IX	0.1486	0.0181	0.1249	0.0037	0.1269	0.0038
G V	0.2068	0.0198	0.1811	0.0034	0.1834	0.0036
G VI	0.1201	0.0125	0.1208	0.0030	0.1208	0.0029
G X	0.1268	0.0088	0.1199	0.0044	0.1205	0.0041
G XIII	0.1413	0.0355	0.1030	0.0076	0.1063	0.0076
G XIV	0.1770	0.0415	0.1194	0.0055	0.1244	0.0063
G XIX	0.2592	0.0579	0.1906	0.0111	0.1965	0.0113
G XV	0.1259	0.0070	0.1145	0.003	0.1155	0.0028
G XVI	0.2676	0.0660	0.1958	0.0139	0.2020	0.0140
G XX	0.2836	0.1273	0.1612	0.0115	0.1718	0.0151
G XXI	0.3132	0.1269	0.1671	0.0071	0.1797	0.0129
H I	0.0240	0.0028	0.0321	0.0011	0.0314	0.0011
H II	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
H III	0.0184	0.0019	0.0180	0.0002	0.0180	0.0002
H IV	0.0187	0.0047	0.0295	0.0014	0.0286	0.0014
H V	0.0413	0.0032	0.0507	0.0017	0.0499	0.0016
H VII	0.0093	0.0024	0.0148	0.0019	0.0143	0.0018
H VIII	0.1041	0.0058	0.1177	0.0032	0.1165	0.0030
H X	0.0227	0.0093	0.0417	0.0026	0.0400	0.0026
H XI	0.0587	0.0049	0.0675	0.0030	0.0668	0.0028
H XII	0.0485	0.0108	0.0851	0.0043	0.0819	0.0042
H XIII	0.0248	0.0173	0.0227	0.0018	0.0229	0.0022
H XIV	0.0721	0.0103	0.0848	0.0043	0.0837	0.004
H XIX	0.1475	0.0283	0.1839	0.0088	0.1808	0.0084
H XVI	0.0789	0.0205	0.1483	0.0088	0.1423	0.0085
H XVII	0.0994	0.0194	0.1019	0.0064	0.1017	0.0066
H XX	0.1403	0.0319	0.1405	0.0111	0.1405	0.0104
H XXI	0.1302	0.0139	0.2142	0.0150	0.2069	0.014
H XXII	0.1901	0.0627	0.1391	0.0094	0.1435	0.0101
H XXIII	0.1379	0.0125	0.2118	0.0137	0.2055	0.0128
H XXIV	0.2896	0.1258	0.1731	0.0127	0.1831	0.0158
O	0.0480	0.0088	0.0374	0.0019	0.0383	0.0019
O I	0.0340	0.1113	0.0257	0.0019	0.0264	0.002
O II	0.1105	0.0114	0.0925	0.0033	0.0940	0.0032
O III	0.0552	0.0057	0.0462	0.0016	0.0470	0.0016
O IV	0.1985	0.0243	0.1855	0.0059	0.1866	0.0058
O IX	0.3219	0.1365	0.2372	0.0213	0.2445	0.0225
O V	0.0993	0.0121	0.1009	0.0047	0.1008	0.0044
O VI	0.1655	0.0278	0.1404	0.0063	0.1426	0.0062
O VII	0.2328	0.0629	0.2021	0.0103	0.2048	0.0107
O X	0.3362	0.1324	0.2201	0.0156	0.2301	0.0182

Note:

Ra = average genetic relationship with sire stallions;
 Ri = average genetic relationship with brood mares
 R pop. = average genetic relationship with population.

Table 1b Average genetic relationship between male ascendants and reproductive nucleus (sire stallions and brood mares) and with population

INDIVID	COD	Ra	S_T	Ri	S_T	R pop	S_T
Pi	108	0.0368	0.0038	0.0359	0.0014	0.0360	0.0013
Pi I	109	0.0184	0.0019	0.0180	0.0002	0.0180	0.0003
Pi II	111	0.0737	0.0076	0.0718	0.0028	0.0720	0.0026
Pi III	121	0.1487	0.0059	0.1358	0.0024	0.1370	0.0023
Pi IV	124	0.1947	0.0162	0.1677	0.0039	0.1700	0.0039
Pi IX	136	0.1691	0.0124	0.1996	0.0104	0.1970	0.0096
Pi V	131	0.1027	0.0168	0.0963	0.0037	0.0968	0.0037
Pi VI	133	0.1813	0.0105	0.1729	0.0039	0.1736	0.0037
Pi VII	169	0.0953	0.0184	0.0891	0.0039	0.0897	0.0039
Pi VIII	135	0.1834	0.0330	0.1861	0.0091	0.1859	0.0087
Pi X	214	0.1883	0.0596	0.2207	0.0168	0.2179	0.0161
Pi XI	274	0.2539	0.1288	0.2157	0.0156	0.2190	0.0177
Pr	137	0.0056	0.0043	0.0138	0.0013	0.0131	0.0013
Pr I	140	0.0112	0.0087	0.0277	0.0027	0.0262	0.0026
Pr II	145	0.0369	0.0073	0.0523	0.0025	0.0510	0.0024
Pr III	147	0.0430	0.0069	0.0569	0.0031	0.0557	0.0029
Pr IV	148	0.0715	0.0104	0.0869	0.0051	0.0856	0.0048
Pr IX	210	0.1616	0.0309	0.1912	0.0132	0.1887	0.0124
Pr V	149	0.1054	0.0117	0.0950	0.0028	0.0959	0.0027
Pr VI	154	0.0670	0.0080	0.0762	0.0039	0.0754	0.0036
Pr VII	176	0.1323	0.0184	0.1470	0.0069	0.1458	0.0065
Pr VIII	196	0.0674	0.0065	0.0768	0.0033	0.0760	0.0030
Pr X	249	0.1715	0.0656	0.1983	0.0174	0.1960	0.0167
Pr XI	330	0.2833	0.1279	0.1829	0.0088	0.1915	0.0134

Note:

Ra = average genetic relationship with sire stallions;
 Ri = average genetic relationship with brood mares
 R pop. = average genetic relationship with population.

CONCLUSIONS

In situation of a population in which is applied a directional selection, it has a certain evolution way by maintaining genetic similarity with at least two ancestors.

In case of Romanian Hucul horse population from Lucina stud farm, figure no. 1 reveals linear tendencies of genetic relationship coefficients between male ascendants and population. Thus, it is not noted a significant tendency of population genetic similarity with any male ascendant. In other words, in this population, genetic similarity with remarkable ascendants was not intended to increase. For Romanian Hucul horse from Lucina stud farm, absence of this trend and maintain relatively small differences between reproductive individuals, is a better matter for avoiding inbreeding (effective big number of males) and that is the reason for

normal evolution of population. Also, revealed situation from figure no. 1, indicate compliance with specific mating system from horse studs for avoiding inbreeding.

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