

## THE ESTIMATION OF GENETIC DISTANCE BETWEEN GERMAN CATTLE BREEDS

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### *Introduction*

The preservation of genetic diversity in animals is necessary for future breeding options. Microsatellites have been proven as a powerful tool in phylogenetic studies (Bowcock et al., 1994). The estimation of genetic distances based on allele frequencies of microsatellite markers will help to quantify the differences between closely related cattle breeds.

### *Material and Methods*

Included in this study were the endangered breeds Angler (ANG), Original German Brown (OBV), Shorthorn (SH) and Original Black Pied (East DSR, West DSB). Also the standard breeds Holstein-Friesians (HF), German Brown (Württemberg BW, Allgäu BA), German Red Pied (dairy type RH, dual purpose RDN) and German Yellows (GV) were included. For each breed representative samples (20-50 animals) of animals born between 1989-1993 were chosen according to the frequencies of the fathers offspring (Table 1).

Table 1. - NUMBER OF ANIMALS AVAILABLE BORN BETWEEN 1989 - 1993, NUMBER OF FATHERS, NUMBER OF ANIMALS SAMPLED AND NUMBER OF FATHERS REPRESENTED IN THE SAMPLE OF EACH BREED

Breed	DSD	DSR	OBV	SH	ANG	GV	BA	BW	HF	RH	RDN
Female animals		79	890	100	400						
All bulls					325	80	279	151	995	1387	4475
No. of fathers	18	58	22	24	25	20	66	29	123	208	588
Animals sampled	20	25	25	25	50	50	25	25	50	50	50
Fathers represented	18	17	18	19	21	20	23	20	33	42	45

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The microsatellites (Table 2) were chosen according to a list of the FAO and an agreement of the EC Biodiversity Project in Utrecht 1996 for microsatellites which are to be used in studies of genetic diversity. Typing was performed with A.L.F. DNA Sequencer or by silverstaining. The length of the alleles was determined with the Fragment-Manager Vers. 1.2 of RLFpScan software. Genetic distances and trees were calculated according to NETs D and  $D_A$  using the DISPAN-software.

Table 2. - MICROSATELLITE MARKERS AND THE SIZE RANGE IN BASEPAIRS

Microsatellite		Size In bp	Microsatellite		Size In bp
CSSM19	D1S10	142-158	ETH152	D5S1	196-210
MM8	D3	134-148	HEL10	D19S7	99-115
HEL9	D8S1	156-176	ETH3	D19S2	109-127
ETH225	D9S1	140-154	BM3517	D20S13	99-123
CSRM60	D10S5	94-106	HEL5	D21S15	148-166
ILSTS005	D10S25	180-182	HAUT24	D22S26	110-128
BMC1222	D13S13	262-302	HAUT27	D26S21	140-156
CSSM66	D14S31	176-200	BL25	D28S8	171-185
INRA035	D16S11	103-121	BM4005	D29S3	103-129
ETH185	D17S1	220-240			

### Results and Discussion

The estimation of genetic distances (Table 3) shows the largest distance for both measurements between the Shorthorn breed and the German Brown breeds BA (0.476/0.304) BW (0.443/0.294) and German Yellow GV (0.394/0.262). The Angler breed shows large distances to BA (0.346/0.248) and BW (0.372/0.248) as well. A very close relationship is observed between Holstein Friesians and German Red Pied, especially the RH-Population (0.063/0.066). The relation is even closer than between both German Brown populations BA and BW (0.148/0.150). The measurements for the Original Black Pied samples show the lowest distances to the Red Pied and the Holstein-Friesian breeds.

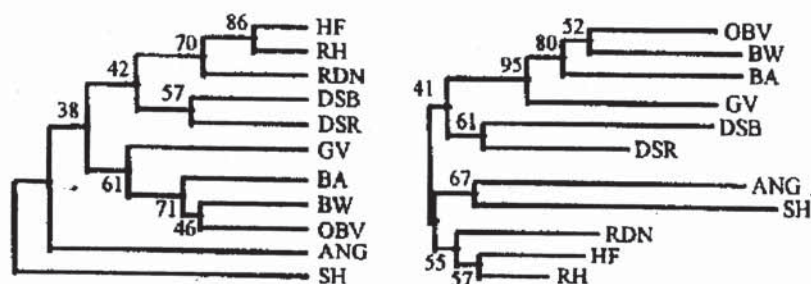
From these data phylogenetic trees were calculated (Fig. 1). They show that within the breeds studied two groups of closely related breeds could be identified. The first group, including the German Brown samples and the German Yellow breed, agrees with earlier results by GRAML, R. et al. 1986. The second group includes the Holsteins and the two Red Pied Populations. A clear adjustment of the Original Black Pied samples was not possible so far, which is indicated by the low bootstrap value of 41. Only the Angler and Shorthorn breeds build independent groups.

Table 3. - NEI'S STANDARD GENETIC DISTANCE D (BELOW DIAGONAL) AND NEI'S GENETIC DISTANCE  $D_A$  (ABOVE DIAGONAL) BETWEEN 11 CATTLE BREEDS CALCULATED FROM 19 MICROSATELLITE MARKERS

	ANG	DSB	HF	OBV	RDN	RH	SH	BA	BW	DSR	GV
ANG		0.240	0.180	0.217	0.189	0.176	0.228	0.248	0.248	0.201	0.236
DSB	0.283		0.173	0.192	0.178	0.177	0.231	0.225	0.227	0.150	0.217
HF	0.283	0.272		0.156	0.114	0.067	0.181	0.203	0.201	0.141	0.165
OBV	0.269	0.226	0.208		0.177	0.162	0.276	0.162	0.123	0.185	0.158
RDN	0.243	0.168	0.150	0.244		0.080	0.199	0.183	0.191	0.154	0.170
RH	0.263	0.247	0.064	0.213	0.119		0.179	0.183	0.189	0.113	0.153
SH	0.300	0.287	0.256	0.359	0.262	0.218		0.304	0.294	0.208	0.262
BA	0.346	0.275	0.308	0.164	0.264	0.273	0.476		0.150	0.205	0.169
BW	0.372	0.263	0.324	0.137	0.293	0.280	0.443	0.148		0.204	0.177
DSR	0.228	0.145	0.193	0.193	0.190	0.137	0.270	0.249	0.226		0.185
GV	0.337	0.281	0.255	0.188	0.249	0.254	0.394	0.208	0.235	0.202	

The standard error of the estimation ranges between 0.018 and 0.1175. These relatively high values indicate that it is necessary to include additional microsatellites in this investigation to increase the accuracy of the estimation (Nei, Takezaki 1996).

Figure 1. - LEFT: UPGMA TREE REDATING THE 11 POPULATIONS EXAMINED, USING NEI'S STANDARD GENETIC DISTANCE. THE NUMBERS AT THE NODES ARE BOOTSTRAP VALUES FOR 1000 BOOTSTRAP RESAMPLINGS OF THE 19 LOCI RIGHT: NEIGHBOR-JOINING-TREE REDATING THE 11 POPULATIONS EXAMINED, USING NEI'S GENETIC DISTANCE  $D_A$



*Conclusion*

The trees reflect the known history of the closely related breeds. The breeds Shorthorn and Angler can be identified as outgroupbreeds, so the development of preservation programs is useful. The adjustment of the Original Black Pied is not clear jet. Additional markers will be typed to increase the accuracy of the estimations.

Neither the distance values between the Holsteins and the dairy Red Pied nor the similar breeding goals let it appear reasonable to keep these breeds separately. This study will be helpful for decisions on preservation of breeds in special conservation programs by *in vivo* and *in vitro* conservation.

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#### PROCJENA GENETSKE UDALJENOSTI MEĐU NJEMAČKIM PASMINAMA GOVEDA

##### Sažetak

Za budući izbor uzgoja potrebno je očuvanje genetske raznolikosti u životinja. U filogenetskim proučavanjima mikrosateliti su dokazani kao snažno sredstvo. (Bowcock et al. 1994.) Procjena genetskih udaljenosti što se temelji na učestalosti alela mikrosatelitskih markera pomoći će u procjeni veličine razlika između usko povezanih pasmina stoke.

Pasmina Shorthorn i Angler mogu se identificirati kao sporedne pasmine, pa je stoga razvoj programa očuvanja vrlo koristan. Prilagođenje pasmine Original Black Pied još nije jasno. Odredit će se dodatni markeri kako bi se povećala točnost procjene.

Niti vrijednosti udaljenosti između Holsteina i mliječnog Red Pied niti slični uzgojni ciljevi čini se da nisu razuman razlog da se ove pasmine drže odijeljeno.

Ovaj će rad biti od pomoći u odlučivanju o očuvanju pasmina u posebnim programima očuvanja konzervacijom *in vivo* i *in vitro*.

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