

Partitioning of Genetic Trends by Origin in Croatian Simmental Cattle

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Summary

The objective of this study was to partition genetic trend for milk (protein yield) and meat (net daily gain) traits by the origin of selection in Croatian Simmental cattle. In order to evaluate overall genetic trend, breeding values were averaged by the year of birth and origin. Origin was defined as a country where animal was initially registered. Overall genetic trend for protein yield was positive. The relative effect of three origins on the overall genetic trend for protein yield was 43.5% for Germany, 33.9% for Croatia, and 22.1% for Austria at the end of analysed period. Genetic trend for net daily gain was also positive. The Croatian and German partitions had large contribution to the overall genetic trend, while small partition was attributed to the Austrian origin. At the end of analysed period, the relative effect of these three origins on the overall genetic trend for net daily gain was 57.0% for Croatia, 38.5% for Germany, and 4.5% for Austria. Selection work originated from Austria, Croatia, and Germany had effect on genetic trend in Croatia. Other origins did not contribute notably to the overall genetic trend of both traits.

Key words

genetic trends, origin, protein yield, net daily gain, Simmental cattle

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Aim

The basis for selection is the identification of superior individuals and their widespread use within the population. Nowadays, the selection of superior individuals is based on breeding values as inferred via genetic evaluation process employing pedigree based mixed models (Henderson, 1973; Mrode, 2005). Genetic evaluation includes collected phenotypes (e.g. production data) and pedigrees, which provide genetic information about the relationship among animals in evaluation. Genetic trend can be observed in population and often summarized by the average breeding value per birth year of individuals. Intensive selection in dairy cattle in some countries has led to a considerable genetic gain and strong international competition. On a global level, there is a lot of exchange (mainly semen) among some countries, while some countries would like to leverage on foreign progress by widespread import. In recent years, there has been considerable import of semen and heifers (especially from Austria and Germany) to Croatian cattle population. Therefore, the objective of this study was to partition the genetic trend in Croatian Simmental cattle for the protein yield and net daily gain according to the origin of selection.

Material and methods

In Croatia, genetic evaluation for milk and meat traits is based on the animal model methodology. All data was collected from the central database of Croatian Agricultural Agency. Milk production data included 1,750,136 test-day records of 101,475 cows for the period between January 2003 and February 2011 (Table 1). Lactation protein yield (kg) records were used from this trait group. Meat production data included commercial abattoir records on 121,029 young bulls of age between one and two years for the short period between January 2006 and February 2011. Net daily gain (g/day) records were taken from meat trait group. For each trait, pedigree data was prepared separately including all animals with records and their relatives tracing back for three generations. Larger number of animals was involved in the pedigree for meat (303,348) compared to milk trait (170,610). Routine genetic evaluation was performed following Špehar (2010) for protein yield and Špehar et al. (2007) for net daily gain.

Origin of each animal was defined as a country where animal was officially registered. The definition implies that the decision to keep (select) an animal for production and possibly also for reproduction is considered as a selection work performed by the country (origin) of registration. As expected the largest number of animals was of Croatian origin (Table 1). Countries with a considerable number of imported animals were from Austria and Germany. For milk traits, a group of imported heifers (526) was tracked to Czech Republic. Pedigree data included more animal of foreign origin. There were also pedigree records on animals from the United States of America, Canada, and The Netherlands. These animals were grouped together as one origin as they represent animals of Red Holstein breed. A small number of animals in the pedigree were of other origins.

Following the idea of Garcia-Cortes et al. (2008) we partitioned inferred breeding values \hat{a} by the origin (country of registration) of animals using:

Table 1. Number of animals with phenotype and pedigree data in genetic evaluation by trait and origin of registration

Group	Trait / Origin	No. of animals	
		Phenotype data	Pedigree data
Milk	Protein yield (kg)	101,475	170,610
	Austria	1,917	10,469
	Croatia	98,292	152,684
	Czech Republic	526	526
	Germany	740	6,755
	UCN (USA, Canada, The Netherlands)	—	137
	Other	—	139
	Meat	Net daily gain (g/day)	121,029
Meat	Austria	—	5,232
	Croatia	121,029	294,111
	Czech Republic	—	—
	Germany	—	3,606
	UCN (USA, Canada, The Netherlands)	—	193
	Other	—	206

$$\hat{a} = TP_1T^{-1}\hat{a} + TP_2T^{-1}\hat{a} + \dots + TP_kT^{-1}\hat{a},$$

where matrix T traces the flow of genes from one generation to the other, i.e., it describes the expected genetic contribution of genes identical by descent between each individual and all its ancestors, while P_i matrix is the “indicator” or “path” matrix for the i -th origin that selects a partition of animals’ breeding value attributed to selection work performed by the i -th origin.

The application of method of Garcia-Cortes et al. (2008) in our study can be described upon the following arguments. Animal carrying “foreign” genes can either have good or bad performance in particular country. Information regarding potential performance of animal prior to production is the average breeding value of parents (parent average), which in the case of foreign parents represents foreign selection work as expressed on national level. However, decision to select such an animal is performed by a national level. The difference between realized performance in production and prior knowledge (parent average) gives us an estimate of the so called Mendelian sampling deviation (either negative or positive), which can be attributed to national selection work. Since both parent average and Mendelian sampling terms determine the breeding value of individual animal we can use partitioning according to the origin as shown by Garcia-Cortes et al. (2008) to monitor the contributions of different origins on national genetic trend.

Partitions of all breeding values were summarized with averages by the year of birth, which in turn provides partitioning of the overall genetic trends by the origin of selection work. Relative contribution of each origin was evaluated for the last analysed year of birth. As genetic evaluation data involves rather short period of collected phenotypes (from 2003 and 2006 onwards for milk and meat traits, respectively), we performed two partitioning analyses by setting the base population at the year 1995 and 2000. Base population was set by removing all ancestors of animals born in the year 1995 (or 2000), while breeding values of retained animals were as obtained from genetic evaluation.

Results and discussion

Overall genetic trend for protein yield is positive as expected given the economic importance, which naturally implies active national selection for this trait as well as import (Figure 1). Among all the analysed origins Czech Republic, UCN (USA, Canada, and The Netherlands - representing mainly animals of Red Holstein genes) and other countries did not have any particular effect on the overall genetic trend, which can be attributed to a small number of animals from these origins. In addition to this, phenotype data for these origins was available only for a small group of imported heifers from Czech Republic, which lead to the shrinkage of their contributions to the prior mean of breeding values in pedigree based mixed model, i.e., to zero. Selection work from other three origins (Austria, Croatia, and Germany) had evident effect on genetic trend in Croatia. However, there was a large difference between two analyses, where base population was set to the year 1995 or 2000. In the case of the first analysis (base population set at the year of birth 1995), we can notice increase after the year 2000 for all three origins. The average level of partition for Croatia was much lower at the beginning, but reached the same level as partitions for Germany

for the Croatian partition for a period before the year 2000 are puzzling (negative trend), but could be attributed to the fact that phenotype data was available only after the year 2003 and by moving further back into the past shrinkage of breeding value to zero was stronger due to the lack of phenotype information. In order to avoid this, we performed another analysis by setting base population at the year of birth 2000. This led to a more favourable trend for Croatian partition (Figure 1, Table 2), but largely due to the fact that by setting base population at a certain point in time we neglect that a share of genes in a locally registered animal might not be of a local origin. These results clearly show that the method of Garcia-Cortes et al. (2008) gives partitioning that is always relative to some base population. In the case of our data, the first analysis with base population set at the year of birth 1995 is preferred, though with a remark about shrinkage in the period before the year 2000.

Genetic trend for net daily gain was also positive (Figure 2). The first analysis (base population set at the year of birth 1995) showed large two partitions of genetic trend attributed to Croatian and German origin, a small partition for Austrian origin, while other origins did not contribute a lot to the overall genetic trend.

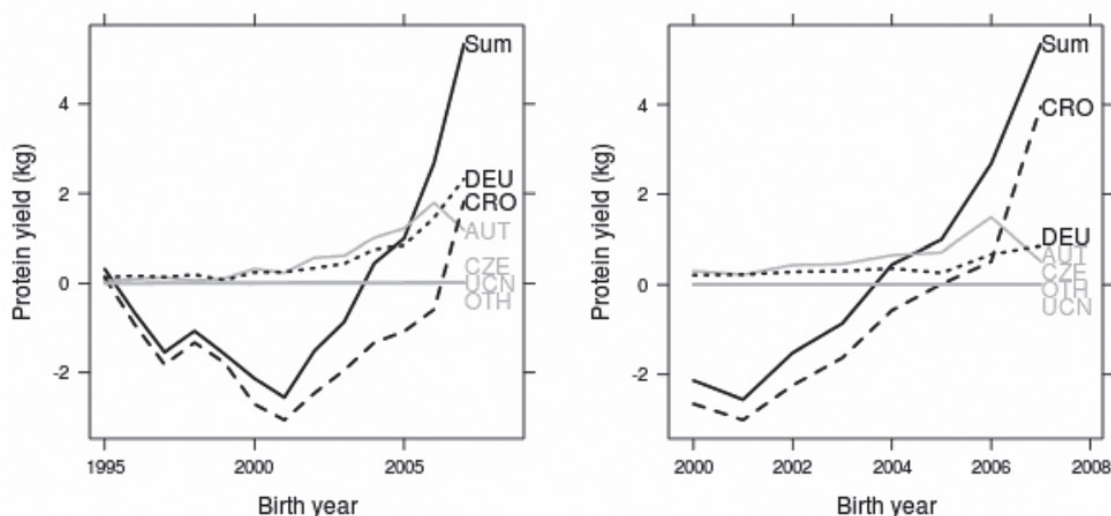


Figure 1. Partition of genetic trend for protein yield (kg/lactation) by origin with base population set at 1995 (left) or 2000 (right) (Sum – overall genetic trend; AUT – Austria; CRO – Croatia; CZE – Czech Republic; DEU – Germany; UCN – United States of America + Canada + The Netherlands; OTH – Other)

and Austria, which shows that selection at a national level is positive. The source of information for partitioning for these three origins was available both from phenotype and pedigree data, though for the Austrian and German origin majority of information came through pedigree (Table 1). At the end of analysed period the relative effect of these three origins on the overall genetic trend was 43.5% for Germany, 33.9% for Croatia, and 22.1% for Austria (Table 2). This agrees with the fact that Croatia had a substantial import of cattle, especially heifers, from Austria and Germany during the 90's of the last century, while a large proportion of semen is imported each year. Results

Table 2. Relative partitioning of genetic trend for protein yield in the year of birth 2007 by origin and base population definition

Origin	Base population	
	1995	2000
Austria	22.1	9.7
Croatia	33.9	73.9
Czech Republic	0.3	0.3
Germany	43.5	16.1
USA, Canada, The Netherlands	0.2	0.0
Other	0.0	0.0

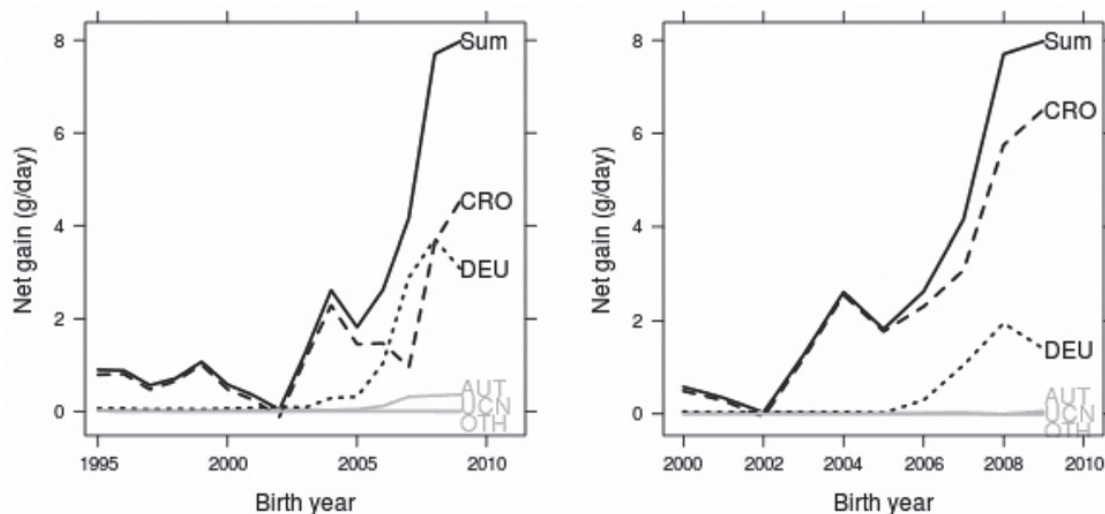


Figure 2. Partition of genetic trend for net daily gain (g/day) by origin with base population set at 1995 (left) or 2000 (right) (Sum – overall genetic trend; AUT – Austria; CRO – Croatia; DEU – Germany; UCN – United States of America + Canada + The Netherlands; OTH - Other)

Table 3. Relative partitioning of genetic trend for net daily gain in the year of birth 2007 by origin and base population definition

Origin	Base population	
	1995	2000
Austria	4.5	0.8
Croatia	57.0	81.7
Germany	38.5	17.5
USA, Canada, The Netherlands	0.0	0.1
Other	-0.0	-0.1

The source of information for the Croatian partition was available both from phenotype and pedigree data, while for the Austrian and German origin information came only through pedigree data (Table 1). At the end of analysed period, the relative effect of these three origins on the overall genetic trend was 57.0% for Croatia, 38.5% for Germany, and 4.5% for Austria (Table 3). These results again agree with the import dynamics in Croatia, but also shows that imported genetics from Austria did not have large impact (positive or negative) on the overall genetic trend for net daily gain in Croatia. The importance of base population definition was also clearly seen in this trait as setting base population to the year 2000 increased the relative effect of Croatian partition from 57.0% to 81.7% (Figure 2, Table 3).

Conclusions

Overall genetic trends were positive for protein yield and net daily gain in the analysed period. Partitions of the overall genetic trend by the origin confirmed a large influence of Austrian and German origin, while other origins did not have sizeable influences. Austrian origin did not have considerable effect for the net daily gain, while German origin had significant effect for both analysed traits. The relative effect of Croatian partition was 33.9% for protein yield and 57% for net daily gain. These results show that countries can achieve some additional genetic progress even when there is an abundant import of live animals and semen. However, a question is if genetic gain in such situations is attained mainly due to the proliferation of imported genetics or due to the own selection decisions carried on the national level.

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