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Early warning system for loss of diversity in European livestock breeds

Abstract

Towards the end of the previous century the increasing erosion of biological diversity in livestock was recognized by the animal breeders as an area which needs monitoring and conservation measures. For that purpose various national, regional and global infrastructures was put in place by governmental and non-governmental organizations like European Association for Animal Production (EAAP), Food and Agriculture Organization (FAO) of the United Nations and Rare Breeds International, etc. These organizations have developed a number of methods for estimation the risk status of the breed. However, the different systems use different parameters and thresholds and are hard to compare. Several attempts for uniform European criterion have been made, but still no consensus has been reached. In this study we continue the work of the Animal Genetic Resources group of EAAP towards the uniform criterion based on the effective population size, the expected number of breeding females and the global population. Our main contribution is the novel approach in handling the parameter global population, allowing its external parameterization. The criterion was applied to 21 pig breeds from 8 European countries and the results show clear not at risk status of the big international breeds.

Key Words: degree of endangerment, farm animals, biodiversity

Zusammenfassung

Titel der Arbeit: **Frühwarnsystem vor dem Verlust an genetischer Diversität bei den europäischen Haustierarten**

Gegen Ende des letzten Jahrhunderts wurde der zunehmende Verlust der biologischen Diversität der Haustierarten von den Tierzüchtern als Anlass dafür genommen, Erfassungs- und Konservierungsprogramme einzuführen. Für diese Aufgaben wurden verschiedene nationale, regionale und globale Infrastrukturen von Regierungs- und Nichtregierungsorganisationen wie u.a. der Europäischen Vereinigung für Tierzucht (EVT), der Welternährungsorganisation der Vereinten Nationen (FAO) und Rare Breeds International aufgebaut. Diese Organisationen haben eine Reihe von Methoden entwickelt, um den Gefährdungsstatus einer Rasse zu schätzen. Die verschiedenen Ansätze beruhen auf unterschiedlichen Parametern und Schwellenwerten und sind deshalb schwierig zu vergleichen. Es wurden mehrere Versuche unternommen, für die Europäische Union einheitliche Kriterien zu definieren, jedoch wurde bisher kein Konsens erreicht. In der vorliegenden Studie setzen wir die Arbeit der Arbeitsgruppe Tiergenetische Ressourcen der EVT fort, um ein einheitliches Kriterium für den Gefährdungsstatus einer Rasse zu definieren, was auf der effektiven Populationsgröße, der erwarteten Anzahl von weiblichen Zuchttieren und der globalen Gesamtgröße einer Rasse basiert. Unser Beitrag besteht in dem neuartigen Ansatz, die globale Populationsgröße für den Gefährdungsstatus mit einzubeziehen. Das neu entwickelte Kriterium wurde für 21 Schweinerassen aus 8 europäischen Ländern angewandt. Die Ergebnisse zeigen klar, dass die großen international verwendeten Schweinerassen nicht in ihrem Bestand gefährdet sind.

Schlüsselwörter: Gefährdungsstatus, Nutztiere, Biodiversität

Introduction

In the last 12000 years around 40 livestock species were domesticated resulting in a 6000 to 7000 genetically distinct breeds (SCHERF, 2000). These breeds have been developed and adopted to various production environments and have their importance as a sources of food, element of the rural culture (GANDINI and VILLA, 2003) or a

tool for ecosystems management (GORDON et al., 1990). The preservation of the farm-animal diversity is an insurance against changes in the market demands or production environment circumstances (OLDENBROEK, 1999). With the introduction of new technologies and the increasing demand for high production in the last century, a number of well-marketed breeds have spread all over the world, moving aside the indigenous ones and increasing the danger of their extinction (HALL and RUANE, 1993). As the extinction rates are bigger than the rates of creation of new breeds, a proper estimation of the breeds' status of endangerment is required. During the years various systems for categorization of the endangered breeds of livestock on a national (RUANE, 2000) and international level (AVON, 1992; LOFTUS and SCHERF, 1993; SIMON and BUCHENAUER, 1993; ALDERSON, 2003; REIST-MARTI et al., 2003) have been developed. These systems use different parameters and thresholds, which makes their comparison difficult. An attempt was made by GANDINI et al. (2004) towards a uniform European criterion based on the data collected in the European Association for Animal Production (EAAP) database (EAAP-AGDB).

The aim of this study was to develop a well-defined automatically calculable criterion for classifying the livestock breeds according to degree of endangerment (DE) of their loss along the proposal presented by GANDINI et al. (2004). This criterion should take into account the species specificity, state of the global population and genetic concepts. Special attention is paid to the problem of transboundary breeds. These breeds are present in more than one country and a genetic material is usually exchanged between the populations in the various countries. The currently existing criteria treat the population in each country as a separate breed, thus e.g. listing the Dexter cattle in Germany as critically endangered (SCHERF, 2000). There is a big Dexter population in the United Kingdom (UK) and in the past even some of the German farmers have registered their animals in UK. We propose a method and software tools to cope with various classifications of genetically similar breeds in estimating the degree of endangerment, which is missing in the most of the currently used criteria.

Material and Methods

The criterion is intended to be used mainly within the European farm animal biodiversity information system (FABISnet) (ROSATI et al., 2006) and it is based on the data collected in this network. The criterion has four classes of endangerment - "critical", "endangered", "not at risk" and "unknown", which are calculated on two levels - national and supranational (for transboundary breeds and groups of genetically similar breeds). The available data, the components of the criterion and the procedures for calculation on the various levels are described in this section.

Data

In the databases of this network more than 5720 domesticated breeds or 'country populations' from 28 species in Europe are registered (data from May 2006). On regular intervals data for the population size and structure is supposed to be collected for each breed. These data include number of breeding males and females, overall population size and trend, status of registration, number of herds, average herd size, usage of artificial insemination and presence of conservation programmes. The data used in our work was taken from the European regional database in year 2006 and

represent 3687 breeds from cattle, pig, sheep, goat, horse and ass species. The number of breeds and available population data are shown in Table 1.

Table 1

Data taken from EFABIS database in May 2006 (Verwendete Daten aus der EFABIS Datenbank im Mai 2006)

Species	Number of breeds	Number of population records
Cattle	958	2319
Pig	509	1005
Sheep	1105	2437
Goat	314	737
Horse	750	1761
Ass	51	83
Total	3687	8342

In order to apply the criterion on supranational level, 8 Landrace, 3 Duroc, 4 Pietrain, 4 Large White and 2 Hampshire pig breeds were grouped on the basis of the results of the PigBioDiv program (SANCRISTOBAL et al., 2006). In this program the various populations in several European countries were genotyped for 50 microsatellite loci and genetic distances have been estimated. The breeds groups are shown in Table 2.

Table 2

Grouping of 21 pig populations from eight European countries. The groups are: DU- Duroc, HA- Hampshire, LR – Landrace, LW – Large White, PI – Pietrain. In the last column is the breed code from PigBioDiv Project (SANCRISTOBAL et al., 2006) (Gruppierung der 21 Schweinepopulationen aus 8 europäischen Ländern. Die Gruppen sind: DU- Duroc, HA- Hampshire, LR – Landrace, LW – Large White, PI – Pietrain. In der letzten Spalte wird der Rassencode des PigBioDiv Projekts (SANCRISTOBAL et al., 2006) angegeben)

Most common name	Transboundary name	Country	Group	PigBioDiv code
Duroc	Duroc	United Kingdom	DU	GBDU02
Duroc	Duroc	Italy	DU	ITDU01
Duroc	Duroc	Germany	DU	DEDU03
Hampshire	Hampshire	United Kingdom	HA	GBHA01
Hampshire	Hampshire	Germany	HA	DEHA02
British Landrace	British Landrace	United Kingdom	LR	GBLR10
Dansk Landrace	Danish Landrace	Denmark	LR	DKLR04
Deutsche Landrasse	German Landrace	Germany	LR	DELR14
DL-1970		Denmark	LR	DKLR05
Landrace	French Landrace	France	LR	FRLR01
Landrace Italiana	Italian Landrace	Italy	LR	ITLR03
Maatiaissika	Finnish Landrace	Finland	LR	FILR06
Norsk Landrace	Norwegian Landrace	Norway	LR	NOLR08
Large White	Large White	United Kingdom	LW	GBLW05
Large White	Large White	Germany	LW	DELW02
Large White	Large White	France	LW	FRLW01
Large White	Large White	Italy	LW	ITLW03
Pietrain	Pietrain	Germany	PI	DEPI03
Pietrain	Pietrain	Belgium	PI	BEPI01
Pietrain	Pietrain	United Kingdom	PI	GBPI04
Piétrain	Pietrain	France	PI	FRPI02

Criterion for estimating the degree of endangerment (DE) on national level

The criterion is based on demographic and genetic components. For each of these components a class of endangerment is estimated. The final class estimating the DE of the breed is the “worst” of the demographic and genetic classes.

Demographic component: GANDINI et al. (2004) proposed as a first component of assessing DE of a breed the time to reach critical female population size. This time is

calculated as $t = \frac{(\log N_x - \log N_0)}{\log r}$, where N_0 and N_x are the population size in the initial moment and the projected size, and r is the proportional growth rate. The rate of

growth can be estimated as $r = \sqrt[t]{\frac{N_2}{N_1}}$, where N_1 and N_2 are the number of females in

the population in years Y_1 and Y_2 respectively, and $t=Y_2-Y_1$. This proposal is well suited to assess DE of a single breed in a national context. However, its application may produce misleading results in estimating the DE in context of a group of genetically similar breeds from various countries. This will be illustrated by the following example: Let us have a transboundary breed in two countries – C_1 and C_2 . In C_1 let us assume a population size of $N_1^1 = 5000$ and $N_2^1 = 5000$ in year 2000 and 2001 respectively. The population sizes in country C_2 in the same years are $N_1^2 = 5000$ and $N_2^2 = 1000$. If we sum up both populations we will have population size in year 2000: $N_1=10000$ and in 2001: $N_2=6000$. The rate of growth of the whole population is $r = \frac{3}{5}$

and the time to reach population size of 100 will be $t = \left(\frac{\log 100 - \log 6000}{\log \frac{3}{5}} \right) \approx 8$ years.

But if we look at the population in country C_1 , we will notice that it is stable ($r_1=1$) and therefore the total population size will never go under 5000. This discrepancy shows that such simplistic approach can be misleading in case of breeds present in more than one country.

To keep the demographic part of the criterion simple and uniform for the cases of autochton and transboundary breeds, we propose to calculate the population size after two generation intervals (GI) from the last census and compare it with the critical values. The calculation is done with the formula $N_{\text{exp}} = N_0 r^{2GI}$, where GI is the generation interval for the species. For estimation of the growth rate we use the most recently recorded population size (no more than one GI back from the year for which we want to estimate DE) and the earliest population size available in the interval one to three GI from the most recent one. Thus, we keep to some extent with the idea of time, needed to react to the negative trend. The proposition of GANDINI et al. (2004) gives us the exact time we have for reaction and with this approach the results can be used directly to schedule any changes in the breeding programs. In the new criterion we presume that the minimum time for reaction is two GI and therefore consider breeds endangered if they require immediate intervention preventing them falling under critical value in the near future.

We have used the same thresholds as the ones used by the Food and Agriculture Organization (FAO) of the United Nations (SCHERF, 2000), with the intention to keep uniformity with their world-wide criterion. We consider the following classes of endangerment:

1. not at risk – $N^{2GI,f} > 1000$, where $N^{2GI,f}$ is the expected number of breeding females after 2 generation intervals
2. endangered – $100 < N^{2GI,f} \leq 1000$
3. critical - $N^{2GI,f} \leq 100$

If there are not enough data to estimate $N^{2GI,f}$, we use the value “unknown”.

Genetic component: Here we use as a parameter the effective population size N_e , a factor which reflects the increase of inbreeding. The effective population size assuming no selection is calculated by the Wright formula $N_e = \frac{4N_m N_f}{N_m + N_f}$ (FALCONER and MACKAY, 1996), where N_m and N_f are the number of breeding males and females, respectively. As noted in (GANDINI *et al.*, 2004) the effective population size explain for mass selection, since the presence of unselected populations is not very likely in Europe. Therefore, we calculate the effective population size assuming mass selection in a simplified way as $N_e(sel) = \frac{7}{10} N_e$ following the model described in (SANTIAGO and CABALLERO, 1995). To be coherent with the EAAP criterion, we have used the same thresholds as described by SIMON (1999). These thresholds are based on the maximum acceptable inbreeding $F-50$ after 50 years of conservation. We have transformed the five classes used by EAAP into three:

1. not at risk - $F-50 \leq 10\%$
2. endangered - $10\% < F-50 \leq 40\%$
3. critical - $40\% < F-50$

These thresholds for $F-50$ are converted for N_e through the rate of inbreeding ΔF . This is done using the formula $F_t = 1 - (1 - \Delta F)^t$ (FALCONER and MACKAY, 1996), where F_t is the inbreeding coefficient in generation t . In this formula F_t is replaced with the thresholds for $F-50$ and t with the number of generations in 50 years for the respective species (Table 3) and the equation is solved for ΔF . The result is replaced in the formula $N_e = \frac{1}{2\Delta F}$ (FALCONER and MACKAY, 1996) and the result are the thresholds for N_e . The respective classes per species are shown in Table 3. If there are not enough data to estimate class of endangerment, we used the value “unknown”.

Table 3

Classes of endangerment based on the effective population size N_e . GI is the average generation interval for the species, NG50 is the number of generations for 50 years (Klassen des Gefährdungsstatus auf der Basis der effektiven Populationsgröße N_e . GI entspricht dem durchschnittlichen Generationsintervall für die jeweilige Spezies, NG50 ist die Anzahl der Generationen innerhalb von 50 Jahren)

Species	GI	NG50	Critical(3)	Endangered(2)	Not at risk(1)
Pig	1.5	33	<33	33-156	>156
Sheep/goat	2.5	20	<20	20-94	>94
Cattle	3.5	14	<14	14-66	>66
Horse/ass	4.5	11	<11	11-51	>51

Criterion procedure: The criterion is supposed to be calculated for each breed for a certain year. The estimated DE class should be consider reliable for no more than two generation intervals. The procedure consists of the following steps for the year Y :

Firstly, we find the maximal year Y_2 with available data in the interval $(Y-GI, Y]$, where GI is the species generation interval shown in Table 3. In the best case $Y_2=Y$, but it may happen that the data was reported one or two years earlier (we presume that data is reported at least once each GI). Based on Y_2 we found the minimal year Y_1 in the interval $[Y_2-3GI, Y_2-GI]$ with population data and estimate the growth rate as

$r = e^{\frac{(\log N_f^2 - \log N_f^1)}{t}}$, where $t = Y_2 - Y_1$ and N_f^2 and N_f^1 are the number of breeding females in years Y_2 and Y_1 respectively. The value of the expected female population size after two generation intervals $N_f^{Y_2+2GI}$ was calculated as $N_f^{Y_2+2GI} = N_f^2 r^{2GI}$. The result was compared with the thresholds 100 and 1000 as shown in the demographic part and we obtain class of endangerment C_1 .

The next step is to calculate the effective population size in year Y_2 assuming mass selection: $N_e^2 = \frac{7}{10} \frac{4N_m^2 N_f^2}{N_m^2 + N_f^2}$, where N_m^2 and N_f^2 are the number of breeding males and females in year Y_2 . This value (N_e^2) was compared with the thresholds for the respective breed (Table 3) and as a result we got class of endangerment C_2 .

The final class of DE is the ‘worst’ of the classes C_1 and C_2 .

Criterion for estimating the degree of endangerment (DE) on supranational level

The criterion on supranational level has the same demographic and genetic components as the ones used on national level. However, when the degree of endangerment of a breed is estimated on supranational level the status of the global population should be taken also into account. In case of transboundary breeds, the global population is the sum of the populations in the various countries. If we have grouping of genetically similar breeds, the global population are all animals within the group. To handle this factor we have an additional parameter to the criterion - a list with grouping of the breeds. The list contains the breeds identification and the group, they belong to. With this additional parameter the following procedure is used to calculate the degree of endangerment of a breed from one group for the year Y .

As described before, the idea of the demographic part of the criterion is to estimate the number of breeding females in the population after two generation intervals. However, it was also demonstrated before that if we simply sum up the female population numbers in various countries and apply to the result the national level criterion, we may obtain misleading results. Therefore, we have estimated the expected number of breeding females in each population separately (using the national criterion) and then summed up the results to obtain the expected number of females in the whole breed. Thus, for each breed B_i from the group we calculated:

$$Y_i^2 = \max\{\text{year } y \text{ with data} \mid y \in (Y - GI, Y)\}$$

$$Y_i^1 = \min\{\text{year } y \text{ with data} \mid y \in [Y_i^2 - 3GI, Y_i^2 - GI]\}$$

$$t_i = Y_i^2 - Y_i^1$$

$$r_i = e^{\frac{(\log N_f^{2,i} - \log N_f^{1,i})}{t_i}}$$
, where $N_f^{1,i}$ and $N_f^{2,i}$ are the number of breeding females in year Y_i^1 and Y_i^2 respectively.

$$N_f^{Y_i^2+2GI,i} = N_f^{2,i} r_i^{2GI}$$

The expected number of breeding females in the whole population after two generation intervals was calculated as $N_f^{\text{expected}} = \sum_i N_f^{Y_i^2+2GI,i}$. On the regional level we used the same thresholds as on the national one, i.e. 100 is the upper limit for critically

endangered bred and 1000 – for endangered. In this manner we obtained from the demographic component class of endangerment C_1 .

For the genetic component we summed the number of breeding females and males for each breed in year $Y_2^i : N_f^{Y_2} = \sum_i N_{fi}^{Y_2^i}$ and $N_m^{Y_2} = \sum_i N_{mi}^{Y_2^i}$. Further, we treated $N_f^{Y_2}$ and $N_m^{Y_2}$

as a number of breeding animals from single breed and applied to these numbers the demographic part of the criterion on national level. In this manner we obtained the class of endangerment C_2 . Similar to the single breed case we took the ‘worst’ of the C_1 and C_2 and assigned it to the whole group. In such manner each breed in the group has the same DE class as the others in the group.

One issue that needs attention is the way how breeding females and males numbers are selected. It may happen that the numbers for the various breeds are not taken from the same year. However all years with data should be in the interval $(Y-GI, Y]$. The intervals length is one GI, and we supposed that during such interval of time the population numbers will not change too much. On the other hand, if data for one or more breeds are missing in this time interval, this may influence the results significantly. Therefore, we consider important as part of the results, also the number of breeds from the group, which have been used in the calculation of DE.

Discussion

The criterion proposed here uses a small number of parameters (number of breeding males and females), which have been also used in the FAO and EAAP criteria. Many more parameters can be added, e.g. presence of organization monitoring the breed, number and average size of herds, average age of the farmers, distance between the animals, etc. Although they have an impact on the DE of the breed, this impact is somehow arbitrary. The first attempt for creating a comprehensive system for estimating breeds extinction probabilities was done by REIST-MARTI et al. (2003). This system operates on similar set of data, taken from the Domestic Animal Diversity Information System (DAD-IS) (FAO) and the Domestic Animal Genetic Resources Information System (DAGRIS). It uses 10 parameters, including from total population size and organization of the farmers to political situation in the country and sociocultural importance of the breed. Unfortunately, many of the variables used by REIST-MARTI et al. (2003) require arbitrary assignment of values by a human, which makes them not suitable for automated calculation.

The estimation of the growth rate is also simplified and no regression techniques like the ones used by BENNEWITZ and MEUWISSEN (2005) are applied. This is done mainly due to data insufficiency. We also wanted to keep the calculation procedure comprehensive to a wider group of users as the main intention in using this criterion is to raise attention to the process of breed extinction.

In the demographic part of the criterion we used as a main parameter the number of breeding females. Further parameter in this section could be the number of annually registered female animals. As pointed out by ALDERSON (2003), this number is a more accurate indication of the viability of the population. Unfortunately, these data are not collected in the current databases in the FABISnet, and we cannot include new data in the data collection process.

Table 4

Assessment of endangerment of the European breeds in year 2005 (Schätzung des Gefährdungsstatus der europäischen Rassen- Jahr 2005)

Species/class	Unknown	Not at risk	Endangered	Critical	Total per species
Cattle	639	90	46	27	802
Sheep	812	52	34	36	934
Goat	257	22	5	13	297
Pig	380	4	7	8	399
Horse	456	85	61	66	668
Ass	31	3	8	5	47
Total	2575	256	161	155	3147

The criterion was applied on a national level to 3147 from the 3687 European breeds as the other 540 breeds were extinct. The results for year 2005 (Table 4) raise on the first place concern about the quality of data collected in the database. For 82% of the breeds there are not enough data to estimate status of endangerment. The most worrying is the lack of data for pigs, where 95% of the breeds have status “unknown”. We have to remind that the search for available data is done not only in the target year, but also one GI back. In case of ass breeds, this means a serious lack of data in the time interval 2000-2005. The EAAP and FAO criteria were applied to the same time interval and the results shown in Table 5 confirmed that data are incomplete. The application of the criterion to other years resulted also in a relative big proportion of a breeds with unclear status. This is a strong indication for a need of a special methodology and tools to complete the data collected in the FABISnet and this problem is addressed by DUCHEV and GROENEVELD (2006).

The definition of the uniform criterion suggests that it should list more breeds as endangered than the other two. This is not seen in Table 5 due to the large number of breeds with unknown status. However, these results should be revised, when more data are available.

Table 5

Comparison between the various criteria used in Europe. FAO- criterion used by FAO as defined in (SCHERF, 2000); EAAP – a modified version of EAAP criterion as used in EFABIS (Vergleich der verschiedenen Kriterien für den Gefährdungsstatus in Europa. Das FAO-Kriterium entsprach der Definition von SCHERF (2000); EAAP – ein modifiziertes Kriterium, das in der EFABIS Datenbank verwendet wird)

Class/criteria	FAO	EAAP	The uniform criterion(national level)
Unknown	2476	2537	2575
Not at risk	263	332	256
Endangered	230	278	161
Critical	178	0	155

When applying the criterion on supranational level it is important to notice that there is no uniform grouping of breeds. Such grouping can be done based not only on the genetic distance between breeds, but also on phenotypic traits, sociocultural and environmental role of the breed. The grouping can be done also with a special conservation interest and as stated by RUANE (1999) the genetic distance is not the only important factor. Therefore, different organizations and scientists may have different opinions on the grouping of the breeds. As an example we can use the Pustertaler Sprinzen breed. One grouping can be based on the presence of the same breed in several countries, e.g. the populations in Germany, Austria and Italy. Another grouping can be based on the closer relation of the German Pustertaler to the Pinzgauer

breed as reported by EDWARDS et al. (2000), or we can use the whole Pinzgauer group as defined by EAAP on their web page (EAAP-AGDB).

To illustrate the application of the criterion the results for year 2002 for five pig groups are shown in Table 6, together with the results of the respective breeds on the national level. In the case of the Landrace group data for only two to four out of the eight breeds in the group were available, but even these data were enough to classify the breeds from the group as not endangered. Similar is the situation in Pietrain, where only the German population (6445 females and 4413 males) was beyond the thresholds for being endangered.

Table 6

Assessment of the DE on a supranational level for 21 pig breeds in year 2002. The classes of the demographic and genetic component are shown together with the number of breeds used to estimate the group class. Classes of endangerment: 0 - unknown; 1 - not at risk; 2 - endangered; 3 - critical (Schätzung des Gefährdungsstatus (DE) auf einem übernationalen Niveau für 21 Schweinerassen im Jahre 2002. Zu den Klassen der demographischen und genetischen Komponente wird die Anzahl der Rassen angegeben, die für die Einordnung der Gruppen in Klassen verwendet wurden. Klassen mit dem Gefährdungsstatus: 0 - unbekannt; 1 - nicht gefährdet; 2 - gefährdet; 3 - kritisch gefährdet)

Breed name	Country	Class N_f	Class N_e	Class N_f^{group}	Breeds used	Class N_e^{group}	Breeds used
Hampshire	Germany	3	2	3	1/2	2	1/2
Hampshire	UK	0	0	3	1/2	2	1/2
Duroc	UK	1	0	1	2/3	1	2/3
Duroc	Germany	2	2	1	2/3	1	2/3
Duroc	Italy	0	1	1	2/3	1	2/3
Large White	Germany	0	1	0	0/4	1	2/4
Large White	Italy	0	1	0	0/4	1	2/4
Large White	UK	0	0	0	0/4	1	2/4
Large White	France	0	0	0	0/4	1	2/4
Pietrain	UK	0	0	1	1/4	1	1/4
Pietrain	Belgium	0	0	1	1/4	1	1/4
Pietrain	Germany	1	1	1	1/4	1	1/4
Piétrain	France	0	0	1	1/4	1	1/4
British Landrace	UK	1	0	1	2/8	1	4/8
Dansk Landrace	Denmark	0	0	1	2/8	1	4/8
Deutsche Landrasse	Germany	1	1	1	2/8	1	4/8
DL-1970	Denmark	0	0	1	2/8	1	4/8
Landrace	France	0	1	1	2/8	1	4/8
Landrace Italiana	Italy	0	1	1	2/8	1	4/8
Maatiaissika	Finland	0	0	1	2/8	1	4/8
Norsk Landrace	Norway	0	2	1	2/8	1	4/8

In the Duroc group data only from Germany and UK were available. As a single breed the German Duroc population is classified as endangered by our system and by FAO criterion. On the other hand the status of the Duroc group is clearly “not endangered”, which is the real status of this international commercial breed.

On the opposite side as data is the Hampshire group. Here only the German population has recorded data which allows estimation of the risk status. As an individual breed the German Hampshire is critically endangered and this is also the status of the group. The problem here was that the estimation of the group class N_f was based on only one out of two breeds, which makes the results unreliable.

Therefore, the reliability of the group status estimation should be always presented as a part of the results. This can be the number of breeds used in the calculation and the total number of breeds or the percentage of the used breeds. The former has some

advantages, as some additional conclusions about the DE can be made from the size of the group. Moreover, in case of incomplete data we strongly suggest that the results of the particular classes are shown together with the final status. This will allow the end-users to critically evaluate the reliability of the results and thus contribute for more objective interpretation.

Conclusion

The proposed criterion is based on a minimum number of parameters that are already in the data collection scheme of FABISnet. However, the data incompleteness in the databases of this network, will prevent the regular usage of this criterion at the present moment, but it is a step towards common criterion in Europe. The major effort at this point of time should be targeted for completing the data. This will allow more complex techniques to be applied in the future for the estimation of the degree of endangerment of breed extinction.

The criterion has a novel approach to the status of endangerment of the breeds on a supranational level. It allows various grouping of populations of transboundary and international breeds and genetically similar breeds. The results in a single and group context, presented together with their reliability, provide more objective information about the degree of endangerment.

Availability

The criterion was implemented as OpenSource software module and is available from the authors.

References

- ALDERSON, L.:
Criteria for the recognition and prioritisation of breeds of special genetic importance. *AGRI* **33** (2003), 1-9
- AVON, L.:
Survey about small breeds of cattle, sheep and goats. Dep. Genet. et Controle des Perf., Paris., (1992)
- BENNEWITZ, J.; MEUWISSEN, T.H.E.:
Estimation of Extinction Probabilities of Five German Cattle Breeds by Population Viability Analysis. *J. Dairy Sci.* **88** (2005), 2949-2961
- DAGRIS:
International Livestock Research Institute (ILRI). Domestic Animals Genetic Resources Information System, <http://dagris.ilri.cgiar.org/>.
- DUCHEV, Z.I.; GROENEVELD, E.:
Improving the monitoring of animal genetic resources on National and International level. *Arch. Tierz., Dummerstorf* **49** (2006) 6, 532-544
- EAAP:
European Farm Animal Biodiversity Information System (EFABIS), <http://efabis.tzv.fal.de>, (2006)
- EAAP-AGDB:
Animal Genetic Data Bank, <http://www.tiho-hannover.de/einricht/zucht/eaap/index.htm>, TiHo, Hannover, Germany, (2004)
- EDWARDS, C.J.; DOLF, D.; LOOFT, C.; LOFTUS, R.T.; BRADLEY, D.G.:
Relationships between the endangered Pustertaler-Sprinzen and three related European cattle breeds as analysed with 20 microsatellite loci. *Animal Genetics*, **31** (2000), 329-332
- FALCONER, D.S.; MACKAY, T.F.C.:
Introduction to Quantitative Genetics. Longman, Essex, U.K., 4th ed., (1996)
- FAO:
Domestic Animals Diversity Information System (DAD-IS 2.0), <http://www.fao.org/dad-is/>
- GANDINI, G.C.; OLLIVIER, L.; DANELL, B.; DISTL, O.; GEORGODIS, A.; GROENEVELD, E.; MARTYNIUK, E.; VAN ARENDONK, J.A.M.; WOOLLIAMS, J.A.:

- Criteria to assess the degree of endangerment of livestock breeds in Europe. *Livest. Prod. Sci.* **91** (2004), 173–182
- GANDINI, G.C.; VILLA, E.:
Analysis of the cultural value of local livestock breeds: a methodology. *J. Anim. Breeding and Genetics*, **120** (2003), 1–11
- GORDON, J.I.; DUNCAN, P.; GRILLAS, P.; LECOMTE, T.:
The use of domestic herbivores in the conservation of the biological richness of european wetlands. *Bulletin d'Ecologie*, **21** (1990), 49–60
- HALL, S.J.G.; RUANE, J.:
Livestock breeds and their conservation: a global overview. *Cons. Biology*, **7** (1993), 815–825
- LOFTUS, R.; SCHERF, B.D. (Eds.):
World Watch List for Domestic Animal Diversity. FAO, Rome, (1993)
- OLDENBROEK, J.K. (Ed.):
Genebanks and the conservation of farm animal genetic resources. ID-DLO, Lelystad, The Netherlands, (1999)
- REIST-MARTI, S.B.; SIMIANER, H.; GIBSON, J.; HANOTTE, O.; REGE, J.E.O.:
Weitzman's approach and conservation of breed diversity: an application to african cattle breeds. *Cons. Biology*, **17** (2003), 1299–1311
- ROSATI, A.; GROENEVELD, E.; DUCHEV, Z.I.; IMIALEK, M.; SOLTYS, L.; WIECZOREK, M.; DISTL, O.; GANDINI, G.; JASZCZYNSKA, M.; SCHERF, B.:
EFABIS - the European farm animal biodiversity information system. In 8th WCGALP, Belo Horizonte, Brazil, August 13 to 18, (2006)
- RUANE, J.:
A critical review of the value of genetic distance studies in conservation of animal genetic resources. *J. Anim. Breeding and Genetics*, **116** (1999), 317–323
- RUANE, J.:
A framework for prioritizing domestic animal breeds for conservation purposes at the national level: A norwegian case study. *Cons. Biology*, **14** (2000), 1385–1393
- SANCRISTOBAL, M.; CHEVALET, C.; HALEY, C.S.; JOOSTEN, R.; RATTINK, A.P.; HARLIZIUS, B.; GROENEN, M.A.M.; AMIGUES, Y.; BOSCHER, M.Y.; RUSSELL, G.; LAW, A.; DAVOLI, R.; RUSSO, V.; DESAUTES, C.; ALDERSON, L.; FIMLAND, E.; BAGGA, M.; DELGADO, J.V.; VEGA-PLA, J.L.; MARTINEZ, A.M.; RAMOS, M.; GLODEK, P.; MEYER, J.N.; GANDINI, G.C.; MATASSINO, D.; PLASTOW, G.S.; SIGGENS, K.W.; LAVAL, G.; ARCHIBALD, A.L.; MILAN, D.; HAMMOND, K.; CARDELLINO, R.:
Genetic diversity within and between european pig breeds using microsatellite markers. *Animal Genetics*, **37** (2006), 189–198
- SANTIAGO, E.; CABALLERO, A.:
Effective size of populations under selection. *Genetics*, **139** (1995), 1013–1030
- SCHERF, B.D. (Ed.):
World Watch List for domestic animal diversity. FAO, Rome, Italy, (2000)
- SIMON, D.L.:
European approaches to conservation of farm animal genetic resources. *AGRI*, **25** (1999), 79–99
- SIMON, D.L.; BUCHENAUER, D.:
Genetic diversity of European livestock breeds. Wageningen: Wageningen Pers, 581 p, European Association for Animal Production (EAAP) Publ. 66, (1993)

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