Proceedings of 27th Annual Meeting of DAGENE

Danubian Animal Genetic Resources

Volume 1 (2016)

DAGENE
International Association for the Conservation
of Animal Breeds in the Danube Region
1078 Budapest, István street 2.
Hungary

Danubian Animal Genetic Resources
Volume 1 (2016)

“*Innovative approaches in biotechnology and genetic engineering applied in rare breed preservation*”

Proceedings of 27th Annual Meeting of DAGENE
in Hilgertshausen, Schwaiganger and Glentleiten, Germany
from 22nd to 24th of April 2016

DAGENE
International Association for the Conservation
of Animal Breeds in the Danube Region
1078 Budapest, István street 2.
Hungary

Danubian Animal Genetic Resources

Volume 1 (2016)

Editorial office: DAGENE - International Association for the Conservation of Animal Breeds in the Danube Region, 1078 Budapest, István u. 2. office@dagene.eu - www.dagene.eu

Publisher: DAGENE - International Association for the Conservation of Animal Breeds in the Danube Region, 1078 Budapest, István u. 2. office@dagene.eu - www.dagene.eu
Person responsible for publishing: Pál HAJAS president of DAGENE

Printed by A/3 Printing and Publishing Ltd., Péter MOHAI

HU ISSN: 2498-5910

This journal, founded 2016 is the official leaflet of the Annual Scientific Conference of DAGENE, as well as the publication medium for the yearly activity of DAGENE members.

Our journal is freely distributed in hard copy among the members of DAGENE and cooperating associations, however it is available from website www.dagene.eu.

Supporting and advertising are possible at the office.

CONTENT
PROGRAM OF ANNUAL MEETING

The date of 27th Annual Meeting of DAGENE is from **22nd to 24th of April 2016** (three days).

Place of Conference at the location of Agrobiogen GmbH. Here you will find the proper address with GPS coordinates: **Thalmannsdorf 25**, 86567 Hilgertshausen-Tandern, Germany, degrees of latitude: 48.435206 and longitude: 11.385151.

The program is the followings:

22.04.2016:
arrival (14.00), a guided visit to Agrobiogen GmbH (from about 15.30)

23.04.2016:
from 9.00: greetings and Jubilee Book handover, In Memoriam *Prof. Kalle Maijala*; then Conference ("*Innovative approaches in biotechnology and genetic engineering applied in rare breed preservation*") with scientific poster & paper presentations.

page

9.15: SESSION I – Chair of the Session is Prof. DDr. Drs. h.c. Gottfried Brem (Germany):

10.30: *Coffee break*

10.45: <u>SESSION II</u> – Chair of the Session is Prof. Dr. Dr. Hans Hinrich Sambraus (Germany):

12.30: *Lunch with traditional German food and beer,* after that leaving to Schwaiganger

from 16.30: a guided visit to „*Haupt- und Landgestüt Schwaiganger*”, where German horse breeds, Murnau-Werdenfelser Cattle as well as sheep breeds (Brillenschafe und Steinschafe) will be presented by our host leader Mr. Hasso Höck.

24.04.2016:
from 9.00: optional visit to the *Glentleiten Open Air Museum* the largest of its kind in Southern Bavaria. DAGENE members are kindly invited by working group of Braunes, Schwarzes und Geschecktes Bergschaf (http://www.braunesbergschaf.de/start.html) on the "*Day of Historical Domestic Animals*".

from 11.30: farewell

Was ist eine alte und gefährdete Rasse?

SAMBRAUS, Hans Hinrich

Waldtruderinger Straße 17 a, D - 81827 München, Bundesrepublik Deutschland

Abstract

Es geht um die Kombination der Begriffe „Rasse", „gefährdet" und „alt". Über „alt" und „gefährdet" gehen die Vorstellungen etwas auseinander. Was eine „Rasse" ist, ist eine Frage der Definition. Nur wenige Rassen haben ein geschlossenes Zuchtbuch, sind also im Laufe ihrer Zuchtgeschichte ohne Einkreuzungen. Einkreuzungen sollten akzeptiert werden, zumal gerade Restbestände von Rassen kaum frei von Einkreuzungen sind. Wenn eine Rasse allerdings ausgestorben ist, ist das unwiederbringlich. Der Name dieser Rasse darf nie wieder für andere Tiere verwendet werden. Das gilt auch dann, wenn andere Tiere der ausgestorbenen Rasse phänotypisch sehr ähnlich sind. Wäre es anders, dann könnte sich leicht die Überzeugung durchsetzen, der Verlust einer Rasse sei nicht schwerwiegend. Bei Bedarf könne man sie sich ja durch eine Neuschöpfung wieder zurückholen.

Einführung

In zahlreichen Ländern Europas gibt es seit einigen Jahrzehnten Organisationen, die sich um die Erhaltung alter und in ihrem Bestand gefährdete Rassen bemühen. In diesem Satz gibt es drei entscheidende Wörter:

- alt
- gefährdet sowie
- Rasse.

Die folgenden Ausführungen sollen versuchen, diese Begriffe etwas klarer zu definieren.

Material und Methoden

Die vorliegende Arbeit ist nicht das Ergebnis von Experimenten. Sie ist das Resultat jahrzehntelanger Erfahrung mit dem Umgang etlicher Organisationen zur Erhaltung alter Rassen.

Ergebnisse und Diskussion

Darüber, wann eine Rasse alt ist, kann sicher diskutiert werden. Sinnvoll ist, dass es verschiedene Kategorien der Gefährdung gibt, und zwar von lediglich „gefährdet" bis „extrem gefährdet". Lange Zeit galten bei den einzelnen Nutztierarten für die Gefährdung unterschiedliche Werte:

Rinder: Weniger als 1.000 Kühe oder zwischen 1.000 und 5.000 Kühe bei sinkender Zahl oder weniger als 20 nicht mit einander verwandte Stiere.

Schafe und Ziegen: Weniger als 500 Muttertiere oder zwischen 500 und 1.000 Muttertiere bei sinkender Zahl oder weniger als 20 nicht mit einander verwandte Böcke.

Schweine: Weniger als 200 Sauen oder zwischen 200 und 600 Sauen bei sinkender Zahl oder weniger als 20 nicht mit einander verwandte Eber.

Bei der deutschen „Gesellschaft zur Erhaltung alter und gefährdeter Haustierrassen“ (GEH) gilt: „Eine Rasse wird als gefährdet bezeichnet, wenn der Bestand die Mindestzahl von 5.000 Tieren (Pferd, Schwein, Ziege, Esel) beziehungsweise 1.500 Tiere (Schafe) oder 7.500 Individuen (Rinder) unterschreitet.

Zweifellos kann man sich darüber unterhalten, ob zwischen den verschiedenen Nutztierarten unterschiedliche Maßstäbe angelegt werden sollten. Es kommt hinzu, dass verschiedene Länder unterschiedliche Zahlen für die Gefährdung einer Rasse zugrunde legen. Auch die FAO in Rom hat eigene Vorstellungen. Möglichweise ist eine Rasse schon dann in ihrem Bestand gefährdet, wenn sie 10.000 Individuen unterschreitet. Bei den meisten der als gefährdet geltenden Rassen liegt der aktuelle Bestand allerdings weit darunter. Die deutsche „Bundesanstalt für Landwirtschaft und Ernährung“ (BLE) orientiert sich nicht an der Zahl der Individuen, sondern an der „effektiven Populationsgröße“. Bei der Frage nach der Gefährdung sollte man deshalb nicht allzu dogmatisch vorgehen.

Auch für das Attribut „alt“ gelten unterschiedliche Maßstäbe. Häufig gilt eine Rasse dann als alt, wenn sie schon mindestens 70 Jahre existiert. Das deutsche „Ministerium für Ernährung, Landwirtschaft und Forsten“ wertet eine Rasse dann als „alt“, wenn es sie schon mindestens seit Ende des Zweiten Weltkriegs gibt. Voraussetzung ist allerdings, dass für die Rasse ein Zuchtbuch besteht. Auch bei diesem Begriff weichen die Maßstäbe voneinander ab. Man sollte auch hier nicht zu dogmatisch sein.

Für am Problematischsten halte ich den Begriff „Rasse“. Zwar gab es den Begriff „Race“ bei Pferden schon seit dem 18. Jahrhundert und früher, aber damals bedeutete das Wort etwas anderes als später beim Rind und den anderen landwirtschaftlichen Nutztieren. Seit Robert Bakewell gelten Maßstäbe, die auch heute noch weitgehend Gültigkeit haben. Die Individuen einer Rasse haben ein weitgehend einheitliches Aussehen, und sind daher als einer bestimmten Rasse zugehörig erkennbar. Damit ist auch die Leistung eines einzelnen Tieres einigermaßen einschätzbar. Oder umgekehrt: weicht das Erscheinungsbild eines einzelnen Tieres vom Rasse-Typus ab, dann muss mit einer Einkreuzung von Fremdblut gerechnet werden. Die erwartete Leistung dieses Tieres ist fraglich.

Um ein Beispiel zu nennen: Das Ostfriesische Milchschaf hat einen behaarten (also nicht bewollten) Schwanz. Hat der Schwanz aber auch nur einen Ansatz von Wolle, werden Interessenten misstrauisch, weil eine Einkreuzung denkbar ist. Mit einer geringeren Milchleistung muss dann gerechnet werden. Aber diese Zusammenhänge sind Ihnen natürlich zumindest ebenso gut bekannt wie mir. Bemerkenswert ist, dass sich manche Züchter und Organisationen nicht an die allgemein akzeptierte Definition halten.

Bekannt und akzeptiert sind Rassen, die zwei unterschiedliche Farbvarianten umfassen. Ein gutes Beispiel hierfür ist das ungarische Zackelschaf mit den Varianten schwarz und weiß. Es bleiben aber daneben genug andere Details, um ein Individuum dieser Rasse zuzuordnen: z.

B. Hornform, Mischwolle und Ohrlänge. Entsprechendes gilt für das Tux-Zillertaler Rind in Österreich, Groninger Blaarkop in den Niederlanden und weitere Rassen.

Man muss einräumen, dass ein geschlossenes Zuchtbuch – also die Tatsache, dass keinerlei Fremdblut eingekreuzt wurde – die Ausnahme bildet. Beispiele sind Schottisches Hochlandrind und Englisches Vollblut. Bei vielen Rassen wurden aus unterschiedlichen Gründen andere Rassen eingekreuzt. In das Vorderwälder-Rind im Schwarzwald wurde Ayrshire, Red Holstein und Montbeliarde eingekreuzt. In das Weißköpfige Fleischschaf in Deutschland kreuzte man Texelschafe ein. Nie war eine solche Einkreuzung ein Akt der Willkür. Immer gab es hierfür gute Gründe, um die Rasse wieder konkurrenzfähig zu machen. Wäre diese Einkreuzung nicht geschehen, wäre die Rasse vermutlich ausgestorben.

Nicht als Rasse zu akzeptieren ist die Kreuzung verschiedener Rassen von einzelnen Züchtern, um diesem Produkt dann einen bisher nicht gebräuchlichen Namen zu geben. Ich bin mal auf die Rasse „Bergziege“ aufmerksam gemacht worden, die durch die Kreuzung verschiedener Rassen zustande kam. Sie kam allerdings nur in einem einzigen Bestand vor, und das auch nur seit wenigen Jahren. Dieses Produkt ist noch keine Rasse und es ist auch nicht alt (was auch nicht behauptet wurde). Dabei kann die Kreuzung von zwei oder gar drei Rassen im Laufe der Zeit durchaus zu einer neuen Rasse führen. Wir kennen das von Luing. Diese Rasse entstand ab 1947 aus der Kreuzung von Beef-Shorthorn mit Schottischen Hochlandrindern. Entsprechendes gilt für das Uckermärker Rind in der früheren DDR. Diese Rasse entstand 1975 durch Kreuzung von Charolais und Fleckvieh. Sie sind durchaus als Rassen zu bezeichnen. Aber auch wenn sie aus alten Rassen entstanden, sind diese selbst Neuschöpfungen selbst selbstverständlich nicht alt.

Gelegentlich werden vereinzelt vorkommende Individuen, die in jeder Rasse vereinzelt vorkommen, zusammengefasst und zu einer neuen Rasse geformt. Das gilt z. B. für das Schwarze Bergschaf, das aus dem Braunen Bergschaf entstand. Das Schwarze Bergschaf ist inzwischen zweifellos eine *Rasse*, aber keine alte.

In allen Rassen erscheinen als Mutanten gelegentlich Einzeltiere, die in der Färbung vom üblichen Rassebild abweichen. Bekannt ist das „schwarze Schaf“, das in Herden weißer Schafe erscheint und in den deutschsprachigen Ländern im übertragenen Sinn für Personen steht, die vom Üblichen abweichen. In der Ziegenpopulation von Österreich erscheinen seit langer Zeit ab und zu graue bis blaugraue Einzeltiere, die man als Blobe (tirolerisch für „Blau“) bezeichnet. Nirgendwo in der älteren Literatur erscheint „Blobe“ als Rasse, und schon gar nicht als eine mit Zuchtbuch. In der 3. Auflage aus dem Jahr 2000 der „World Watch List for Domestic Animal Diversity“ der FAO (Scherf, 2000) ist die Blobe-Ziege deshalb auch nicht aufgeführt. Seit einiger Zeit sammelt ein einzelner Züchter diese blobefarbenen Einzeltiere. Der Bestand umfasste vor zwei Jahren weniger als zehn Tiere. Eigentlich würde man sagen, daraus kann mal eine Rasse werden. Aber Blobe gilt als Rasse, und zwar sogar als eine alte. Das ist nicht zu akzeptieren.

In den 80er Jahren des vergangenen Jahrhunderts fand in Stoneleigh Park/England ein internationaler Kongress über gefährdete Rassen statt. Man war sich einig, dass der Name einer Rasse, die ausgestorben ist, nie wieder verwendet werden darf. Dieser Grundsatz wurde allerdings mehrfach nicht beachtet. So gab es früher in der Schweiz die Rinderrasse „Bündtner Grauvieh“. Die Rasse war klein und zierlich. Seit Anfang des 20. Jahrhunderts wird diese Rasse in der Literatur nicht mehr erwähnt. Nachforschungen nach Restbeständen waren ergebnislos; die Rasse war offensichtlich ausgestorben. In Österreich und Südtirol gibt es gleichfalls eine Grauviehrasse. Wie bei allen Rassen besteht bei den Individuen diese Rasse eine gewisse Schwankungsbreite in der Größe. Die Schweizer holten sich besonders kleine Tiere, und bezeichneten sie fortan als Bündtner Grauvieh. Es mag phänotypisch eine große Ähnlichkeit der kleinen Tiroler Grauvieh-Rinder mit dem ausgestorbenen Bündtner Grauvieh vorhanden sein. Aber ausgestorben ist ausgestorben. Die erneute Verwendung des Namens ist Etikettenschwindel.

Ein weiteres Beispiel: Beim schwarz-weißen Angler Sattelschwein in Nord-Deutschland gab es gelegentlich rot-weiße Individuen. Diese Tiere wurden in der Nachkriegszeit zu einer Rasse zusammengefasst. In den 60er Jahren des vergangenen Jahrhunderts war dieses Rotbunte Schwein sogar Herdbuchrasse. Wenig später war die Rasse ausgestorben. Um 1980 kamen schwäbisch-hällisch-blütige Schweine (im Grunde Kreuzungstiere) aus dem Bodenseegebiet in den Schwarzwald. Rotbunte Individuen dieser Kreuzung wurden 1984 auf der Internationalen Grünen Woche in Berlin ausgestellt. Von dort kamen die Tiere über Zwischenstationen nach Nord-Deutschland. Inzwischen wurde der Name gewechselt und schließlich fanden sie unter unterschiedlichen Namen – aber immer im Zusammenhang mit dem ursprünglichen Namen der ausgestorbenen Rasse „Rotbuntes Schwein“ – einige Verbreitung. Das ist nicht akzeptabel. Die Verantwortlichen wissen um die fehlerhafte Darstellung. Die jetzigen Schweine gleichen nicht einmal phänotypisch dem früheren Rotbunten Schwein. Nur die Ferkel sind rotbunt. Die erwachsenen Tiere sind meist saufarben.

Früher gab es im Osten von Bayern das Oberpfälzer Rotvieh. Diese Rasse starb nach dem zweiten Weltkrieg aus. Vor einigen Jahrzehnten wollte man in der Oberpfalz im Landschaftsschutz Rinder einsetzen. Man kaufte im übrigen Deutschland und auch im Ausland rote Rinder ein, und nennt sie heute wieder Oberpfälzer Rotvieh. Auf den Einwand, dass dies ein nicht zulässiges Vorgehen sei, wurde geantwortet, wenn die Rinder einen anderen Namen bekämen, würden sie in der Oberpfalz nicht anerkannt werden.

Um ein besonders markantes Beispiel aus der übrigen Tierwelt zu erwähnen: Der Ur oder Auerochse starb bekanntlich im 17. Jahrhundert aus. Durch Kreuzung verschiedener Hausrinderrassen schufen die Brüder Heinz und Ludwig Heck in den 20er Jahren des vergangenen Jahrhunderts eine Rinderform, die dem Auerochsen in einigen Aspekten ähnelt. Lange Zeit wurde das Ergebnis als „Versuch einer Rückzüchtung des Auerochsen“ bezeichnet. Heute werden die Tiere häufig nach ihren „Schöpfern“ als „Heck-Rinder“ bezeichnet. Vor einigen Jahren wurde dennoch ein „Verein zur Förderung des „Auerochsen“ e. V.“ gegründet. Die Tiere werden also als „Auerochsen“ (mit Anführungsstrichen) bezeichnet. Allerdings werden die Anführungsstriche gewöhnlich weggelassen. Ohnehin wird häufig der Eindruck erweckt, der Auerochse sei wieder auferstanden. Das ist keineswegs der Fall. Was jetzt vorliegt ist eine weitere Rinderrasse mit etlichen Merkmalen des Auerochsen.

Beschluss und Empfehlung

Bei den Restbeständen vieler gefährdeter alter Rassen muss davon ausgegangen werden, dass Einkreuzungen fremder Rassen vorgenommen wurden. Deshalb muss man die gefährdete Rasse nicht aufgeben. Durch geschickte Auswahl rassetypischer Tiere kann man den ursprünglichen Zustand wieder herstellen. Ein gutes Beispiel sind die Ennstaler Bergschecken in Österreich. Ende der 80er Jahre des 20. Jahrhunderts gab es kein einziges reinrassiges Tier dieser Rasse mehr, aber es gab etliche Kreuzungstiere. Durch geschickte Auswahl rassetypischer Tiere konnte inzwischen wieder ein beachtlicher Bestand aufgebaut werden. Gleiches gilt in Deutschland für das Ansbach-Triesdorfer Rind, von dem es heute wieder eine beachtliche Zahl von Tieren gibt. Anders ist es mit ausgestorbenen Rassen, von denen nicht einmal Kreuzungstiere vorhanden sind. Was weg ist bleibt weg. Dieser Grundsatz ist kein sinnentleerter Dogmatismus. Rassenamen erneut zu verwenden schadet der Idee der Erhaltung alter Rassen. Wenn es *so* leicht ist, eine ausgestorbene Rasse wieder zu beleben, dann kann man sich die Mühe der Erhaltung sparen, werden viele denken. Bei Bedarf kann man die gewünschte Rasse ja erneut schaffen.

Literatur

FRISCH, W. (2010): Der Auerochs, Verlag Ilka Frisch, Starnberg

SAMBRAUS, H.H. (1986): Bedrohte Nutztierrassen in den deutschsprachigen Ländern. Teil I: Allgemeines, Tierärztl. Prax. 14, 297-307.

SAMBRAUS, H.H. (2010): Gefährdete Nutztierrassen. 3. Auflage, Eugen Ulmer Verlag, Stuttgart

SCHERF, B.D. (2000): World Watch List, FAO, Rom

The practice of the *ex situ* gene preservation at the Veterinary Faculty of Budapest

SEREGI, János[1] – GÁSPÁRDY, András[1] – GÁL, János[1] – MAROSÁN, Miklós[1] –
FARKAS, Róbert[1] – KOVÁCS, Ágnes[1] – SÓTONYI, Péter[1] –
MEZŐSZENTGYÖRGYI, Dávid[2]

[1]Szent István University, Faculty of Veterinary Science, 1078 Budapest, István street 2., Hungary
[2]Herman Ottó Institute, 1223 Budapest, Park u. 2., Hungary

Abstract

The „Dagene Genebank" and the „Janisch Miklós Zoo" are located next to each other in the Dóra farm at Üllő. The Dagene Genebank was established at the Üllő Dóra farm in 1990. The main purpose was to present the Hungarian native domestic animals to the veterinary students and visitors. The Genebank had a serious role in the life of Üllő Dóra farm and Research Institute of the Veterinary University Budapest. After the changes in the function of the Institute the state of the Genebank was declined. By 2011-12 the number of animals was decreased. The restoration works started in October of 2015 with the aim to have a sufficient gene pool of the Hungarian native domestic animals, and to realize the field trips of the Animal Breeding education.

This antecedent explained the intention that besides the gene bank the „Janisch Miklós Zoo" should be established as well in 2015, where the students can get to know the national game animals, hunting methods and wildlife management technologies.

These two facilities can be really helpful in the practical education of various departments: the name giver's „basis" Department of Parasitology and Zoology, the Department of Animal Breeding and Genetics and the Department of Exotic Animal and Wildlife Medicine.

Introduction

The preserved domestic animals are the part of our national treasure

The animal species and breeds showed in the following pictures are the vital part of the Hungarian animal breeding culture. Our country can be proud, because we can present a compelling list of domestic animal species and breeds related to the lifestyle. They will be displayed with their main characteristics and typical pictures from the leading Grey Cattle to the pigeons and fishes, which are giving a fame to our country with their appearance and traditional tastiness.

Preservation of the national gene-reserve animals

According to our goal in the education we must have a complete native gene pool and cooperative partners; the presented animals have to produce embryo and semen for further storage.

The facility could join to the production of bio-products by keeping the local cattle, swine, sheep and chicken breeds. This field is to be strengthened by the cooperation with DAGENE, accepting visitors and locate new domestic and wild animal species to Üllő. Furthermore we are planning to form and prepare new products.
The animals are kept extensive and semi-extensive, fitting to the landscape, with a small playground.

Education

The Dagene Genebank could offer a practical help to these subjects:

- Animal Breeding
- Nutrition
- Pharmacology
- Parasitology
- Reproduction
- Surgery
- Topographic and applied anatomy
- Food hygiene

The tasks of the Janisch Miklós Zoo

The Research Institute of the Veterinary University started to establish a zoo with the aim of supporting education and research projects in1990, at the time of the opening the Dagene Genebank. This initiative was supported by the freshly established “Dóra Sándor” educational and researcher hunting society. But the functioning of this society was prohibited by multiple reasons, so in 1993 it became the “Dóra Hunting Society” without any educational or research purposes.

These antecedents explained the expectations that the students should meet a proper collection of the local game population, and acquire the necessary knowledge for a veterinarian in the field of hunting technologies.

The name giver’s „basis” was the Department of Parasitology and Zoology. Nowadays the educational tasks would include the Department of Animal Breeding and Genetics and the Department of Exotic Animal and Wildlife Medicine.
There is a wildlife management course at the Veterinary Faculty of Szent István University, as well.
The special courses are the followings:

- Wildlife zoology
- Wildlife ecology
- Fundamentals of hunting
- Game breeding and nutrition
- Game management
- Hunting guns and ballistics
- Trophy evaluation and management
- Wildlife health
- Zoo and Wild Animal Medicine

In the Janisch Miklós Zoo the students can acquire and practice

1. the breeding of different game animal species
2. specific health care, parasitology and zoology knowledge, game nutrition, pasture management
3. thesis students can accomplish their research in Üllő

Presenting the traditional species and breeds

The **Hungarian Grey Cattle** (Figure 1) is one of the native Hungarian, by law protected domestic animals. It is a late maturing, medium-sized cattle of solid constitution developed by our ancestors in the Carpathian-basin. It has a hardy and solid body conformation, and it has a striding movement. Colour ranges from the shade of silvery grey to dark crane grey. The front of the bulls is darker, so called "sooty". Bulls have characteristic blackened eye-patch. Horns are typically long and curved initiating from a broad horn-base and take various forms. They are white with a black tip. Calves are reddish coloured until the age of 3 or 4 months.

Figure 1. Hungarian Grey Cattle bull

The **Mangalica Pig**: The Hungarian National Association of Mangalica Breeders was established in 1927 with the aim of improving the breed. The Mangalica is a typical lard pig developed in the Carpathian-basin at the beginning of the 19th century. There are three different varieties of it: blonde (Figure 2), swallow-bellied and red. In all three varieties the body is covered by curly, spirally upward winding hair that is shed in the summer, when the animals become smooth-haired. The hair colour of blonde Mangalica ranges from grey to yellow, the skin is pigmented greyish-black, while natural body orifices, the end of the snout, teats and nails are black. There is a lighter patch on the base of ear (Wellmann patch). Ears are dropping ahead, eyes are brown and the tuft of the tail is always black. It has a fine, but firm bone structure. The swallow-bellied Mangalica was developed in the South of Hungary by crossing with the Srem pig. Basically it is black, but there is a gently upwardly stretching yellowish-white colour of the throat and the underbelly, just like the tail, but the tuft is always black. Red Mangalica has evolved from the crossing of the red "Szalontai" pig and the blonde Mangalica. Traditionally it was bred in the eastern region of the Hungarian Great Plain. It has a lighter shade of brownish-red hair. Other external traits of the variety are the same as that of the blonde Mangalica.

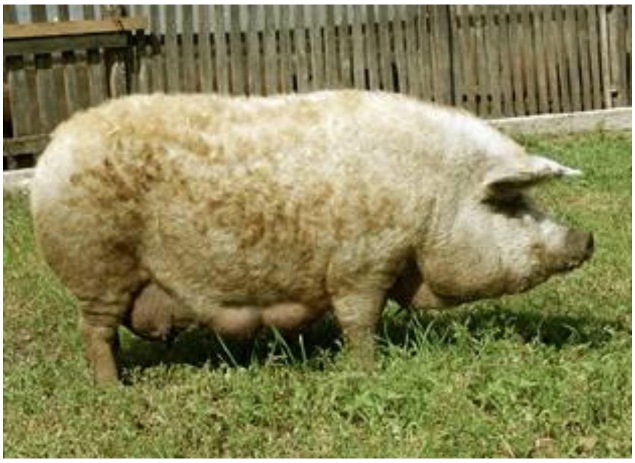


Figure 2. Blonde Mangalica sow

The **Hungarian Racka Sheep** (Figure 3) or Hortobagyer Sheep is an old Hungarian sheep breed, which is believed to be with the Hungarian people since the Settlement. It is a hardy, multi-purpose breed used for milking, wool and meat. Their wool is long and coarse, and appears in two general types: a cream wool with light brown faces and legs, and a black variation. Ewes weigh around 88 lb (40 kg), and rams 132 lb (60 kg). Two colour varieties of it are known: black and white. Its main characteristic is the V-shaped, erected, twisted horn worn by both sexes. It is a triple-purpose (meat, milk and wool) breed, but it could not compete with the higher and better quality production of modern breeds, therefore its national stock enjoys a protected gene reserve status. It is typical in both colour varieties that the head and the end of feet are covered by short, shiny hair. In the white variety this is yellowish-brown, in the black variety it is shiny black. Ears are set horizontally, the head is tapering and the eyes are bright. Fleece of the white variety is yellowish-white, while that of the black variety is black. The wool staples form clusters, the fibres are wavy and 30 to 40 cm long. It has a lively temperament. We keep stocks of the breed for demonstration purpose.

Figure 3. Racka Sheep

Conclusion

The modern animal breeding has effective techniques to select the gene pool of the domestic animals, which is proven to be useful from the point of view of the present and future of mankind. At the same time we have to avoid the loosing of old and seemingly useless genes, so the genetic poorness of the animals.

Hungary was among the first countries in the world to save the endangered breeds. In our country the intensive breeds couldn't entirely displace the traditional breeds. Luckily the native Hungarian breeds are saved, on the base of culture historical and economical feelings, and on the other hand based on rational and scientific arguments. The old breeds are still existing with small population numbers in endangered position. The official gene preservation aimed only to maintain the headcount. Nowadays using the modern biotechnology the multiplication of rare valuable genotypes, the scientific evaluation of gene frequency and the estimation of distance between genotypes can happen as well. The Veterinary Faculty of the Szent István University wants to take part in this noble task on scientific and practical fields.

References (basic in the field)

ASSOCIATION OF HUNGARIAN GREY CATTLE BREEDERS': http://www.szurkemarha.hu/

DEBRECEN UNIVERSITY: http://www.agr.unideb.hu/

GAÁL, L. (1966): A magyar állattenyésztés múltja. Akadémiai Kiadó, Budapest

HORTOBÁGYI NONPROFIT LTD.: http://www.hortobagy.eu/

HUNGARIAN ASSOCIATION OF SHEEP AND GOAT BREEDERS': http://mjksz.hu/

HUNGARIAN NATIONAL ASSOCIATION OF MANGALICA BREEDERS: http://www.mangalicatenyesztok.hu/

MIHÓK, S. (2006): Génmegőrzés. Hagyományos háziállatfajták genetikai és gazdasági értékének tudományos feltárása. NKTH, Debrecen

SEREGI, J (ed.) (2014): Adatok a környezetkímélő, öko-jellegű állattenyésztés hazai bevezetésének és működésének feltételeihez. MNVH Budapest

TŐZSÉR, J. – BEDŐ, S (eds.) (2003): Történelmi állatfajtáink enciklopédiája, Mezőgazda Kiadó, Budapest

WILD PARK BUDAKESZI: http://www.vadaspark-budakeszi.hu/haziallatok

Actual animal genetic resources in Slovakia

CHRENEK, Peter[1] – MAKAREVICH, Alexander[1] – BULLA, Josef[12]

[1]Research Institute for Animal Production, NAFC, Nitra, Slovak Republic
[2]Slovak University of Agriculture, Nitra, Slovak Republic

Abstract

Availability of the animal genetic resources has an impact on the present and also future life quality and important effect on the food safety. Ratification of the Convention on the Biodiversity oblige Slovak Republic to protect biodiversity, to guarantee sustainable use of its components and fair and equal access to benefit sharing from genetic resources.

Embryo freezing enables genetic material cryoconservation of males as well as females and represent a big opportunity for the preservation of population heterozygosis and integrity. However it is more complex and economic demanding procedure than the spermatozoa freezing. Perspective chance how to preserve endangered animal species (breeds) appears to be the use of stem cells. Of course, before their use the cells have to be collect, cultivate *in vitro* for the purpose of their proliferation, evaluated in the terms of originality and quality for the subsequent freezing.

In the time when Slovak agriculture and mainly the animal production permanently year by year achieve decrease in the farm animal number it is necessary to be aware of the fact that the farm animal breeding has not only production function, but also out of production functions which supply culturally country cultivation, countryside development etc. In the last fifty years there was a significant decrease in the animal number in SR and in some species the origin, autochthonous breed completely disappeared.

The situation with animal genetic resources in Slovak Republic is not satisfactory, due to the fact that DNA samples and semen doses stored are only from the cattle breeds (Slovak Pinzgauer Cattle, Slovak Spotted), sheep breeds (original Valachian Sheep) and rabbit breeds (Nitra Rabbit and Zobor Rabbit). From the last update statuses of animal breeds in the Slovak Republic, which took place at the end of 2011 it is obvious that 3 breeds of cattle and two breeds of pig are subjected to extinction.

Type traits of Istrian Pramenka in Slovenia compared to Istrian Sheep in Croatia

SIMČIČ, Mojca[1] – KAIĆ, Ana[2] – BOJKOVSKI, Danijela[1]

[1]University of Ljubljana, Biotechnical Faculty, Department of Animal Science, SI-1000 Ljubljana; Jamnikarjeva 101, Slovenia
[2]University of Zagreb, Faculty of Agriculture, Department of Animal Science and Technology, 10000 Zagreb; Svetošimunska 25, Croatia

Abstract

The aim of the study was to compare type traits of Istrian Pramenka in Slovenia with Istrian Sheep in Croatia. Altogether, 102 ewes of Istrian Pramenka in Slovenia were measured, where 64 of them were adult. Type traits were analysed by the means procedure of the SAS/STAT software. Results shown, that adult ewes of Istrian Pramenka in Slovenia achieved lower body weight and wither height compared to ewes of Istrian Sheep from Croatia. On the other hand, Slovenian Istrian Pramenka ewes had higher body length, chest depth and chest width compared to Croatian Istrian Sheep ewes. Chest girth and cannon bone circumference were lower in Slovenian Istrian Pramenka compared to Croatian Istrian sheep. The majority of Slovenian Istrian Pramenka ewes had white wool colour with black dots. Large difference in the percentage of completely white wool ewes in Slovenian Istrian Pramenka compared to Croatian Istrian Sheep was found.

Introduction

The population of Istrian sheep was developed on a large area of the Istrian Peninsula and neighbourhood Karst region. Today, the name of the breed comes from the Istrian Peninsula. In Slovenia, the breed was known also as Karst Sheep (kraška ovca, Carsolina), Littoral Sheep (primorska ovca) or Sheep with coarse wool. The breed is the result of local sheep population improved with rams of Italian breeds in the majority (MIOČ et al., 2012; BOJKOVSKI et al., 2014).

In the past, Istrian Sheep presented one population where the transhumance breeding technology was used. In the last decades, new political borders were established and transhumance grazing is prohibited. Istrian sheep is nowadays fragmented in three separated and reproductively almost isolated populations in Slovenia, Croatia and Italy (ŠALAMON et al., 2015). In Slovenia, the breed is known as Istrian Pramenka (istrska pramenka) with the population size of 1020 animals (KOMPAN et al., 2016). In Croatia, the breed is called Istrian Sheep (Istarska ovca) with 2743 breeding animals (MULC et al., 2014). A population is present in Italy as well under the name Istriana or Carsolina with about 1000 animals (ŠALAMON et al., 2015).

The breeding technology is based on the grazing Istrian and Karst pastures during vegetation period, which are almost dry during summer time. The breed is mainly used for cheese production in all three countries, known under the name Istrian or Karst sheep cheese. In the

196 days of lactation, ewes of Istrian Pramenka from Slovenia produced 157 kg of milk with 7.3% of fat and 5.7% protein content (ZAJC et al., 2015). In the 195 days of lactation, ewes of Istrian Sheep from Croatia produced 205 kg of milk with 7.24% of fat and 9.19% protein content (MULC et al., 2014).

Although type traits of Croatian Istrian Sheep were recorded and analysed (MIKULEC et al., 2007), there was no comparison with the Slovenian Istrian Pramenka. According to this fact, the aim of the study was to record and to analyse type traits of Istrian Pramenka from Slovenia and to compare with Istrian Sheep from Croatia.

Material and methods

In total, 102 ewes of Slovenian Istrian Pramenka were measured during the autumn in the year 2007, when animals were in very good body condition after finished grazing season. All ewes were located in three farms in the Coastal-Karst statistical region in Slovenia. There were 29 to 39 ewes reared per farm.

Very basic recording equipment was used such as Lydtin stick, tape and calibrated scale. The following measurements were taken with the Lydtin stick for each animal: wither height, croup height, body length (shoulder to pin bone), body length (wither to pin bone), chest width, chest depth and croup width. Chest girth and cannon bone circumference were taken with the tape. Body weight was taken with calibrated scale. In the same time, wool colour was described as follows: white, white with black dots, multi-coloured and black. The colour of the head was described as white or white with black dots. Likewise, the presence of horns was recorded. Data were analysed using means procedure in the statistical package SAS/STAT (SAS Institute Inc., 2001). Descriptive statistic was performed for all ewes included in the study and for adult ewes only. Type traits of ewes above 3.5 years (n = 64) which were considered as adults were compared to literature data for type traits of Istrian Pramenka from Croatia.

Results and discussion

All Slovenian Istrian Pramenka ewes included in the study were in average 4.45 ± 2.17 years old, where the youngest has 1.65 years and the oldest 10.94 years (Table 1). The average wither height and croup height were 69.52 ± 2.79 cm and 68.63 ± 2.79 cm, respectively. Body length was measured twice, from shoulder to pin bone (78.88 ± 2.80 cm) and from wither to pin bone (71.87 ± 3.12 cm). The measures of body length were larger than the ones of wither height and thus indicated a rectangular body frame. The highest variability among ewes was observed in the chest girth (92.15 ± 7.65 cm). Ewes were wider in chest (22.25 ± 2.56 cm) compared to the croup (20.90 ± 1.84 cm). The average measured cannon bone circumference was 7.78 ± 0.42 cm.

Table 1: Descriptive statistics of type traits for all 102 measured Istrian Pramenka ewes in Slovenia

Type traits (n = 102)	Mean	SD	Min	Max
Age (years)	4.45	2.17	1.65	10.94
Body weight (kg)	58.35	9.90	30.70	80.40
Wither height (cm)	69.52	2.79	62.00	77.00
Croup height (cm)	68.63	2.79	63.00	78.00
Body length (shoulder to pin bone, cm)	78.88	2.80	71.00	90.00
Body length (wither to pin bone, cm)	71.87	3.12	61.50	80.00
Chest depth (cm)	32.87	2.51	23.00	38.00
Chest width (cm)	22.25	2.56	17.00	34.00
Croup width (cm)	20.90	1.84	18.00	28.00
Chest girth (cm)	92.15	7.65	71.00	108.00
Cannon bone circumference (cm)	7.78	0.42	6.60	9.00

Legend: SD – standard deviation, Min – minimum, Max - maximum

MIKULEC et al. (2007) found that growing period of Croatian Istrian Sheep finished in the age of three years. Consequently, 64 ewes of Slovenian Istrian Pramenka older than 3.5 years were taken as adult animals (Table 2). The traits that were available from both breeds were compared. Compared to the type traits of Croatian Istrian sheep (MIKULEC et al., 2007), it was found that Slovenian Istrian Pramenka ewes were lighter in body weight for around 6.0 kg and lower in wither height for around 4.0 cm. On the other hand, Slovenian Istrian Pramenka ewes had higher body length, chest depth and chest width compared to Croatian Istrian Sheep ewes. Chest girth and cannon bone circumference were lower in Slovenian Istrian Pramenka compared to Croatian Istrian Sheep (Table 2).

Table 2: The comparison of type traits between Slovenian Istrian Pramenka and Croatian Istrian Sheep

	Istrian pramenka - Slovenia		Istrian sheep – Croatia (MIKULEC et al., 2007)	
	Mean (n = 64)	SD	Mean (n = 451)	SD
Body weight (kg)	61.29	8.80	67.38	9.98
Wither height (cm)	69.62	2.63	73.51	3.64
Body length (shoulder to pin bone; cm)	79.39	2.89	77.33	4.39
Chest depth (cm)	33.59	2.35	32.98	2.70
Chest width (cm)	22.69	2.56	21.71	2.43
Chest girth (cm)	93.80	6.84	96.69	5.41
Cannon bone circumference (cm)	7.85	0.43	9.02	0.51

Legend: SD – standard deviation

The records of the wool and the head colour as well as the presence of horns belonged to all 102 recorded ewes of Slovenian Istrian Pramenka. The majority of ewes had white wool colour with black dots (38%) (Figure 1). There was similar percentage of multi-coloured (24%) and white wool (29%) coloured ewes, while black wool had just 9% of them.

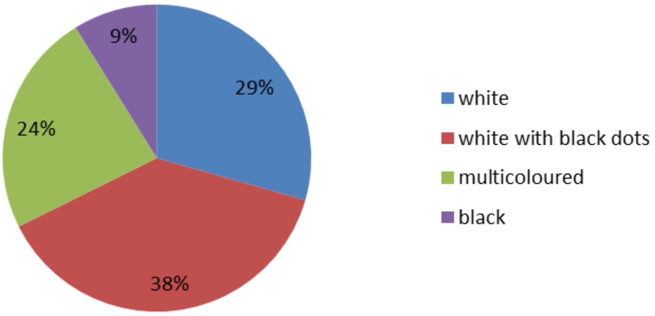
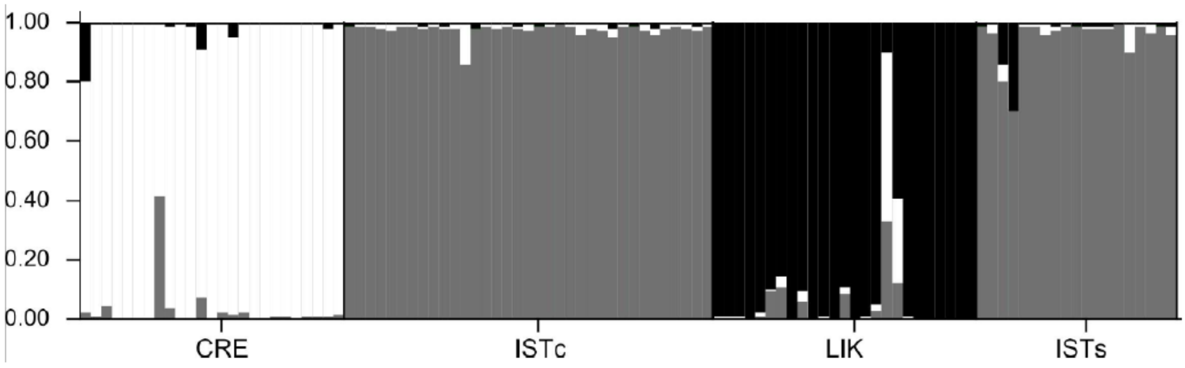


Figure 1: The wool colour of 102 ewes of Slovenian Istrian Pramenka

According to MIKULEC et al. (2007) the wool colour of Istrian Sheep ewes from Croatia is mainly white with black spots (41%) or black with white spots (8%), grey with black spots (13%) and multi-coloured (11%). There were 26% of animals with completely black wool and only 1% with completely white wool colour. Large difference in the percentage of white wool ewes in Slovenian Istrian Pramenka (29%) compared to Croatian Istrian sheep (1%) was observed. Likewise black wool coloured ewes were more widespread in Croatian Istrian Sheep (26%) compared to Slovenian Istrian Pramenka (9%).

The colour of the head was described separately from the colour of the wool. Slovenian Istrian Pramenka ewes had mainly white (67.6%) or white with black dots (32.4%) coloured head. MIKULEC et al. (2007) found that Croatian Istrian Sheep ewes had mainly multicoloured head, followed with black and very rarely completely white head. Horns were present in 37.8% of Slovenian Istrian Pramenka ewes, where others 62.2% were polled. MIKULEC et al. (2007) reported higher percentage of horned ewes (84%) compared to polled ewes (16%) in the Croatian Istrian Sheep.

Although there were found some differences in type traits between both populations in average, ŠALAMON et al. (2015) found no marked genetic divergence between Slovenian Istrian Pramenka and Croatian Istrian Sheep based on the genetic characterisation with 26 microsatellite markers. Both populations showed a close genetic relationship (Figure 2) despite they are included in two different breeding programs in two different countries.



CRE - Cres Island Sheep, LIK - Lika Pramenka Sheep, ISTs - Istrian sheep population from Slovenia, ISTc - Istrian sheep population from Croatia

Figure 2: Graphical presentation of the clustering outcome suggested by the Bayesian analysis performed to assess the structure of the studied populations at *K* = *3* (ŠALAMON et al., 2015)

Conclusion and recommendation

This study was the first type traits characterisation of Slovenian Istrian Pramenka. Likewise, the comparison with type traits of Croatian Istrian Sheep was performed for the first time. According to the measured traits, some differences in the body frame size between both breeds were found. The difference in the number of recorded animals within each breed should be considered. Describing wool and head coat colour found large differences in the percentage between completely white and completely black wool and head coat colour in ewes of both breeds. On the other hand, genetic characterisation based on microsatellite markers shown no genetic divergence between Slovenian Istrian Pramenka and Croatian Istrian Sheep. In the future, genetic characterisation with larger number of markers is recommended. Related breeds, which are reared in the neighbourhood, should be genotyped with larger number of markers to performed more accurate conclusions.

References

BOJKOVSKI, D. – CIVIDINI, A. – ČEPON, M. – HOLCMAN, A. – KOMPAN, D. – KOVAČ, M. – KOMPREJ, A. – ŽAN LOTRIČ, M. – MALOVRH, Š. – POTOČNIK, K. – SIMČIČ, M. – TERČIČ, D. – ZAJC, P. (2014): Slovenske avtohtone in tradicionalne pasme domačih živali. Ljubljana, Ministrstvo za kmetijstvo in okolje, 80 p.

KOMPAN, D. – BOJKOVSKI, D. – CIVIDINI, A. – MALOVRH, Š. – POTOČNIK, K. – SIMČIČ, M. – TERČIČ, D. – ŽAN LOTRIČ, M. (2016): Program varstva biotske raznovrstnosti v slovenski živinoreji: poročilo za leto 2015. Domžale, Biotehniška fakulteta, Oddelek za zootehniko

MIKULEC, D. – PAVIĆ, V. – SUŠIĆ, V. – MIOČ, B. – MIKULEC, K. – BARAĆ, Z. – PRPIĆ, Z. – VNUČEC, I. (2007): Odlike vanjštine različitih kategorija istarskih ovaca. Stočarstvo, 61: 13-22.

MIOČ, B. – PRPIĆ, Z. – BARAĆ, Z. – VNUČEC, I. (2012): Istrska ovca – hrvatska izvorna pasmina. Zagreb, Hrvatski savez uzgajivača ovaca i koza, 115 p.

MULC, D. – JURKOVIĆ, D. – DUVNJAK, G. – SINKOVIĆ, T. – DAUD, J. – LJEŠIĆ, N. – ŠPEHAR, M. – DRAŽIĆ, M. (2015): Ovčarstvo, kozarstvo i male životinje. Godišnje izvješče 2014. Križevci, Hrvatska Poljoprivredna Agencija

SAS Institute Inc. (2001): The SAS System for Windows, Release 8.02. Cary, NC, SAS Institute Inc.

ŠALAMON, D. – GUTIERREZ-GIL, B. – SIMČIČ, M. – KOMPAN, D. – DZIDIĆ, A. (2015): Microsatellite based genetic structure of regional transboundary Istrian sheep breed populations in Croatia and Slovenia. Mljekarstvo, 65, 1: 39-47.

ZAJC, P. – KOMPAN, D. – CIVIDINI, A. – BIRTIČ, D. – BOJKOVSKI, D. – DRAŠLER, D. – JEVŠINEK SKOK, D. – SIMČIČ, M. – ŽAN LOTRIČ, M. (2015): Mlečnost ovc v kontroliranih tropih v Sloveniji v letu 2014. Domžale: Biotehniška fakulteta, Oddelek za zootehniko

Ursprung und Entwicklung des autochthonen Cikta Schafes bis zum Gegenwart in Ungarn

KOVÁCS, Endre[1] – RABE, Anna – ANNUS, Kata[1] – SÁFÁR, László[2] –
GÁSPÁRDY, András[1]

[1] Szent István Universität, Fakultät für Veterinärmedizin, 1078 Budapest, István Str. 2, Ungarn
[2]Verband für Ungarische Schaf- und Ziegenzüchter, 1134 Budapest, Lőportár Str. 16, Ungarn

Zusammenfassung

Die Cikta Schafe gehören in Ungarn zu den autochthonen Schafrassen. Deshalb ist seine Bewahrung eine erstrangige Aufgabe nicht nur für die Tierzüchter, sondern auch für alle umweltbewusste Menschen, die dazu etwas beitragen können. Um diese Rasse in der breiten Öffentlichkeit bekannt zu machen ist es wichtig, alle bekannten Daten über seinen Ursprung und Entwicklung veröffentlichen, damit die Erhaltung und mögliche Verbreitung der Rasse zu fördern. Der lange geglaubte Ursprung der Rasse; als Zaupelschaf durch deutsche Einwanderer in der XVIII. Jahrhundert eingeführt wurde ist nach den heutigen Erkenntnissen nicht zutreffend. Vielmehr handelt sich um eine Rasse, die seine Vorfahren nicht nur von Westen, sondern auch damals in XVII. Jahrhundert von Osten gekommen sind.

Einleitung

Durch die immer größere Interesse an autochthonen Tierarten auch in der Nutztierhaltung in EU und in Ungarn durch das Förderprogramm der EU im Jahre 2010 für die Erhaltung dieser Tierarten auch in Ungarn. Deshalb bemüht sich der ungarische Zuchtverband für Schafe und Ziegen mit großen Informationskampanien die Landbevölkerung von der Zucht für die Cikta zu gewinnen.

Die Cikta Schafe gehören zu dem autochthonen Nutztiere, die in Ungarn als eigene Rasse entstanden, durch die Mitwirkung von Menschen und Natur, war. Diese Rasse verbindet sich sehr eng mit der deutschsprachigen Bevölkerung, die in dem 18. Jahrhundert durch Unterstützung von Königin Maria Theresia in den Komitaten von Tolna und Baranya angesiedelt waren.

Die neusten Forschungsergebnisse zeigen, dass der bisher geglaubten Ursprung von Cikta nicht alleine durch Einführung von deutschen Einsiedlern entstanden sein sollte, sondern auch durch die Völkerwanderung in 17. Jahrhundert von Osten für die Entstehung dieser Rasse eine nicht zu unterschätzende Bedeutung unbedingt zugeschrieben werden sollte. Diese Tatsache ist für uns wichtig, obwohl die Cikta niemals zu führenden ungarischen Schafzuchtrassen gehörte.

Beschreibung des Cikta Schafes

Das mischwollige Zaupelschaf ist Begleiter der Indogermanen gewesen und zwar nördlich der großen Gebirgskette, die sich von den Pyrenäen über die Alpen bis zum Balkan zieht (BOHM, 1878). Seine Herkunft läßt sich auf das neolithische Torfschaf zurückverfolgen (MASON, 1967). In den Gebieten mit günstigen futterbaulichen und klimatischen Verhältnissen wurden die Zaupelschäfe langsam durch wirtschaftlich ertragreichere Rassen verdrängt oder durch fortgesetzte Kreuzung mit diesen veredelt (BOHM, 1878).

Eine Vertretung des hier beschriebenen des Landschafs war der Zaupelschaf, der heute ausgestorben ist, aber von dem im Laufe der Zeit mehrere Rassen (z.B. Steinschaf, Waldschaf, Sumavka, Cikta usw.) entstanden sind. Glücklicherweise haben wir über diesen Rasse vom BOHM (1878) einer ausführlichen Beschreibung. Im Lehrbuch Schafzucht (ausgegeben in Berlin) findet sich auch über die Schafrasse Cikta eine Beschreibung, die ziemlich gut zu bei uns lebenden Cikta Schaf passt. Seine Körpergröße ähnelt zu Merino. Die Widder hatten ein Schultermaß von 58-60 cm, die aus - gewachsenen Mutterschafe von 55-56 cm. Die metrischen Unterschiede kamen durch die verschiedene Haltungen und Aufzüchten der Tiere.
Der Kopf verhältnismäßig klein, der Stirn flach und schmal. Bei den Widder, der Nasensattel gewölbt, bei den weiblichen dagegen recht flach. Die Schnauze ist schmal und spitz. Die Augen sind klein und matt, die Ohren scharf trichterförmig zusammengerollt, schmal und spitz, haben aber keine aufrechte Richtung, sondern stehen in mehr waagerechter Lage von dem Kopf ab. Gehörnt sind in der Regel nur die Widder. Die Horn-fortsetze stehen auf dem Scheitel ziemlich weit voneinander. Auf nicht allzu breiter Basis wenden sich die Hörner sofort nach hinten, krümmen sich nach Art des Merino -hornes nach unten, wieder nach vorn und endigen dann in eine stumpfe Spitze, welche sich wieder nach aufwärts richtet und in der Linie zwischen Auge und Ohr ihr Ende erreicht.
Das Knochengerüst ist fein und schwach, deshalb erscheinen die Beine im Verhältnis zum Rumpf, dünn und schmal. Der Schwanz reicht mit seinem letzten Wirbeln nicht ganz bis zur Ferse. Gesicht, Ohren und Beine diese noch hoch über Knie und Ferse hinauf, sind mit kurzen, straffen, glatt anliegenden Haaren bedeckt, der ganze Rumpf, sowie der Hals vom Scheitel herab und der Schwanz tragen eine ziemlich grobe Mischwolle, bestehend aus langem glänzendem Grannenhaare, reichlich mit etwas feinerem Wollhaare durchsetzt.
Die Farbe ist zum größten Teil ein schmutziges Weiß mitunter aber auch braun uns schwarz. Bei den lilienweißen Tieren findet man oft eine schwarze Schnauze und mehr oder weniger regelmäßige Ringe um die Augen. Die Tiere werden in ihrer Heimat in der Regel jährlich zweimal geschoren. Zu vollem Jahreswuchs erreicht die Wolle eine Länge von 20-24 cm und ist dann, aber nur bei dem gut gepflegten Tieren, das Schurgewicht höchstens 1,5 kg bei guter Wäsche; bei dem geringen Fettschweiße, mit welchem das Haar überzogen ist, und der gutartigen Natur derselben ist eine solche aber sehr leicht zu erreichen.

Die Tiere sind sehr fruchtbar, sie werfen sehr oft Zwillinge und wird bei ihnen gerühmt, dass sie schon in einem Alter von einem Jahr das erste Lamm bringen. Dies ist offenbar ein nicht richtiges Verfahren der Züchter, sie schädigen dadurch unbedingt die körperliche Entwicklung der ganzen Rasse. Soll ein Schaf in einem Alter von 12 Monaten schon ein Lamm bringen, so muss es in einem solchen von 7 Monaten schon gedeckt werden. Es steht dann noch in der ersten körperlichen Entwicklung. Wir sind der festen Überzeugung , dass die Formendverhältnisse der ganzen Rasse sehr bald zu ihrem großen Vorteile verbessern würden, wenn man das Mutterschaf erst gehörig auswachsen und mit vollendeten dritten Jahr das erste Lamm bringen ließe.“

Geschichte des Cikta Schafes

Aus den mittelalterlichen Ausgrabungen in Europa geht es hervor, dass es damals nur ein einziger Schafrasse, der Langschaf in ganzen Europa existierte, wie es BÖKÖNYI (1963), wie folgt, beschrieb: „Der allergrößte der europäischen mittelalterlichen Schafe – wie auch Rinder – gehörten nur zu einzigen Rassen. Diese Rasse war sehr primitiv von Habitus her und die Körpergröße war klein, Diese Eigenschaft ähnelte sehr mit der heutigen, aussterbenden, westeuropäischen Landschaf. Die Widder hatten robuste schraubenartige Hörner mit dreieckiger Durchmesser und zeigten einer gerundeten Form. Die Muttertiere hatten kürze, sogenannten Ziegenhorn oder waren sie hornlos, selten waren sie vierhörnig.“

Verantwortlich war für diese Entwicklung einerseits der gleiche Ursprung, anderseits die Tatsache, dass es im Mittelalter die Rassenzüchtung und Veredelung der Tiere unbekannt waren. Hin und da gab es gewichtigere Tiere, eine bessere Haltung erfuhren hatten. Die brachten auch eine größere Wollenproduktion. Zu diesen kamen aus Ost- und Südosteuropa von den unterschiedlichen ganz fremden Rassen auch.
Vor 200 Jahren wurde noch zwischen Zaupelschaf und Steinschaf nicht unterschieden. In folgenden Gebieten war es verbreitet: ganz Süddeutschland, Teilen Mitteldeutschland bis Belgien, Böhmen, Mähren, Schlesien und Teile von Ungarn sowie Österreich, Schweiz und Norditalien. In den drei letztgenannten Gebieten kam es noch häufig vor (FITZINGER, 1859). Bayern hatte 1863 bei einem Gesamtschafbestand von 2,1 Mio. Tiere immerhin noch einen Anteil von 10,1 % Zaupelschafen. Dieser war allerdings 1912 bereits auf 4,57 % abgesunken. 1939 konnte man das Zaupelschaf nur noch in Ober- und Niederbayerns, Oberschwabens und Böhmens auffinden (GOLF, 1939).
Karl III., Maria Therese und Josef II. hatten ab 1720 deutsche Siedler nach Ungarn gebracht, die dann den Zaupelschaf nach Ungarn in mehrere Etappen eingeführt. Von die Tiere im Laufe der Zeit, etwa nach mehr als hundert Jahre hat sich der heutige Cikta Schaf entwickelt. Diese Tiere hatten eine viel bessere Wollqualität als das einheimische Schaf, sodass die Schaf haltende Grundbesitzer allmählich diese Schafe ihre Zuchten umstellten. Diese Entwicklung bestätigt auch der Aufsatz von Andrásfalvy über die Geschichte von Komitaten Tolna, wonach: „Die Bauern von Gemeinde Decs beklagten sich über die Grundbesitzern, weil ihre Zibben im Jahre 1749 die Trauben-Bergen verwüstet haben. Das Gleiche war zu lesen vom Brief der Kleinbauern im Jahre 1766 aus dem Gegend von Pilis.“ Also die Grundbesitzer hatten keine Schafhaltung, sondern Zibbenhaltung und das sollte ein Hinweis auf die Haltung von Cikta Schafen sein, die einer besseren Qualität von Wolle lieferten. Es konnte kein Merino sein, weil die erst durch Maria Teresa im Jahre 1773 eingeführt wurden.

Diese gut wolligen Schafe waren die mittel-europäische Landschafe, wahrscheinlich die Cikta Zibben auch genannt Schwäbischer Schaf von Tolna und Baranya. Diese Schafe weideten schon auch in den Komitaten Fejér und Zala von 100 bis 1000 Tiere pro Gruppen (BOCZ, 1939).
Es gab noch eine Möglichkeit, um den Cikta Schaf nach Westungarn einzuführen. Dies geschah durch den deutschen Schäfer, die ungarischen Weiden pachteten damals, um ihre Tiere halten zu können. Die wurden als Zibben-Schäfer in der Umgangssprache genannt. Das Wort „Zibben“ wurde schon in 16.-17. Jahrhundert benutzt, zuerst eine Morva Rasse benannt. Der war eine Variante von dem mitteleuropäischen Landschaf. Diese Herden wurden im Norden des Landes von Morva Schäfern von einem hämischen Bauern übernommen. Die Benutzung des Wortes „Zibben“ wurde langsam im ganzen Land üblich. Damit war die Abgrenzung vom Racka- Schaf erreicht.

Mit der Zeit hatte sich der deutsche Zibben überall in Ungarn verbreitet, auch im Großgrundbesitz von Grassalkovich in Gödöllő. Damit wurde das Ungar-Schaf durch den Deutsch-Schaf verdrängt. Der letztere hatte eine bessere Qualität von der Wolle. Die 1770-er Jahren diese Entwicklung wurde in den Schafherden von Großgrundbesitzern abgeschlossen. Erwähnenswert ist ein Fall in der Stadt Kecskemét, wo ein gesellschaftlicher Konflikt

zwischen der Halter deutscher und ungarischer Schafe ausgebrochen war und wurde nach 4 Jahren beendet. In dieser Zeit hatte sich der deutsche Schafbestand so gewaltig vermehrt, dass die Herde von Großbauern pro Hof um die 2500 Tiere gezählt haben. Im Jahre 1775 kamen die Merinos nach Ungarn und damit eine grundlegende Änderung in der Schafzucht, wonach die einheimischen Landschafe mit die Merinos durchgekreuzt wurden.
In XIX. Jahrhundert plötzlich hatte sich die Fachliteratur über die Schafzucht sehr vermehrt, wobei über die Landschafzucht wenig berichtet wurde. In Vordergrund standen die verschiedenen Merino Zuchten und die Empfehlungen zur Veredelung der gegenwärtigen Schafzuchten. Die Benennungen der Rassen waren uneinheitlich und teilweise auch verwirrend. Alle Langschafrassen wurden mit Racka bezeichnet. In den großen landwirtschaftlichen Betrieben wurden nur Merinos gezüchtet und gehalten, wobei die negativen Faktoren der extensiven Haltung stufenweise abgebaut wurden.

Es waren die Kleinbauer, die weiterhin die anspruchslosen Landrasse beibehalten hatten und ins besondere in Westungarn hauptsächlich die Abkömmlingen des Zaupelschafes, der heutigen Cikta Schaf gehalten haben. Überwiegen diese Kleinbauer waren deutschsprachig, die sogenannten Schwaben. Diese Volksgruppe lebte in den Komitaten von Tolna und Baranya und bis zum Ende des II. Weltkrieges waren hier noch in bedeutenden Zahl Cikta Schafbestände (CZUPPON, 1965). Stellt sich die Frage: warum gerade hier? In diesen zwei Komitaten ist die Schafzucht in Hintergrund geraten, weil die Hauptrolle übernahmen die Rinder und die Schweine. Die guten Weiden haben nicht die Schafe, sondern die Rinder gekriegt. Die nassen Wiesen hatte sich der Leberegelbefall durch Fasciola hepatica verbreitet, der den Viehbestand minderte.

Die Tierhaltung wurde auf intensiv umgestellt und die Weiden wurden umgewidmet als zusätzliche Ackerländer (BALÁSHÁZY, 1827). Unter dieser ungünstigen Situation hatten die von Schwaben bewohnten Dörfer die kleine Schafhaltung beibehalten, um ihre Bekleidung aus Wolle weiterhin herstellen zu können. Diese Tiere wurden als Haus- und nicht als Nutztiere gehalten. Als Futter hatten auf der Straßen entlang wachsenden Unkraut und Akazien Büsche, die von den Rindern nicht gefressen wurden. Die wurden auch im Winter nicht verwöhnt, so die empfindlichen Tiere dies nicht überleben konnten. Deshalb diese Rasse, was die Eigenschaften betraf, näher zum Landschaf stand.
Nach dem I. Weltkrieg wurden versucht, die schlechte Schafzuchten durch Kreuzungen – Widder (Racka aus Siebenbürgen und Fries) – zu verbessern. Dies war ergebnislos geblieben. Die großen Schafzüchter hatten mit Kamm Merino Haltung begonnen. Die Klein- und Mittelbauer blieben bei den „deutsche Zibben“, d.h. Cikta Schaf. Für die Verbreitung dieser Rasse zeigte auch die Verordnung dem Landwirtschaftsminister in Jahre 1941 – 155.000 – wonach für die Benutzung der Zuchtwidder auch die Rasse von Cikta erwähnt wurde. Auch die Fachpresse hatte sich mit der Cikta Schafrasse beschäftigt. SCHANDL hatte ein Artikel in 1940 in der ungarischen Zeitschrift für Tierzucht über diese Rasse berichtet und der Cikta Schaf als Schwäbisch Schaf von Tolna und Baranya – Komitaten – benannt. Wo die meiste Tiere gezüchtet und gehalten wurden. Ferner beschrieb er die äußere Merkmale und Verwendung dieser Tiere, und die Rassen, die für die Veredelung vorgesehen waren, mit der Bemerkung, dass nur diese Rasse verdient dieser Maßnahmen auf Grund seiner Anspruchslosigkeit und seine weiße Farbe als sehr gut geeignet.

Die angehenden Entwicklungen des Landes und den größten Teil des Schafbestandes hatte die II. Weltkrieg zunichte gemacht. Die Rückführung der deutschsprachigen Bevölkerung des Landes nach Deutschland hatte die Cikta Züchter vermindert. Trotzdem waren in den Komitaten von Tolna und Baranya die Cikta Rasse führend. Dies bewies die amtliche Mitteilungen über die Zahlen von Schwäbisch Cikta Zibben in dem Komitaten Tolna im Jahre

1947. Die Ursache war es, dass die Schwaben die Hofhaltung von Cikta Schafen wegen ihrer Wolle sehr bevorzugten. Wovon sie verschiedene Kleiderstücke in Hausarbeit herstellten. In der Cikta Zibben dominierten die Eigenschaften von Racka Schafen. Damals zählten in Tolna die Mutterschafe von 26.931 St., und die Widder waren 504 St. Durch die Auswechselung der Landbevölkerung ist das Interesse an Haltung von Cikta Schafe sehr zurückgegangen. Obwohl KONKOLY THEGE in 1948 meinte: Die Züchtung von Cikta Schafe auch in die Zukunft gerechtfertigt, um die Wolle für die Hausarbeiten bereitzustellen. Nur die Zuchtsteuerung und die Blutauffrischung sollte vorgegeben werden .Trotzt dem war die Rasse ab Jahre 1950 durch die Regierung als unerwünscht eingestuft. Wegen der zwanghaften Zuchtvorschriften waren die Cikta Muttertiere durch fremde Rassen gepaart.

Wahrscheinlich die Cikta Rasse wäre ausgestorben, wenn nicht das Interesse an autochthonen Rassen aufgekommen wäre. So nach Racka und Cigaja wurden im Jahr 1974 in der letzten Minuten alle Exemplar der übrig gebliebenen Cikta Schafe zusammengesammelt und in Nagydorog – Bezzegpuszta / Tolna auf dem Landesgut des Schafzuchtanstalt untergebracht. Ab dem nächsten Jahr wurde bei der Nutztierschau auch der Cikta Schaf vorgeführt. Anzahl der Cikta stieg in den achtziger Jahren über die zwei hundert. Nach der Wende im Jahre 1992 kam der Herd in Privatbesitz von Josef Tisch. Nach seinem Tod im 2003 hat seine Familie sukzessive vom Herd distanziert und der wurde schließlich im Jahre 2008-2009 aufgelöst.

Wesentliche Änderung kam im Jahre 2004, wann der Donau-Drau National Park mit 60 Cikta Mutterschaf in Nagydorog die Tierzucht wieder aufgenommen hatten. Auch private Züchter hatten sich mit der Erhaltung die Cikta Rasse befasst. Notgedrungen musste auch nicht Stammbuch geführte Tiere in die Zucht aufnehmen. Der nächste glückliche Zustand kam im Jahre 2010; wann die EU mit einem Programm unterstützte der autochthone Tierrasse unter anderen die Cikta auch. Somit wurde die Verbreitung von Cikta weiter gefördert. Die diente auch, die Einrichtung einer Aufzucht für Zuchtwidder der Cikta. Im Jahre 2015 waren schon neun Stammzüchter von Cikta. Die Zunahme der Stammzüchter ist vorteilhaft, um die Diversität der Rasse zu erhalten und wenn es möglich ist, zu steigern.

Konklusion, weitere Pläne

Im Rahmen der Bewahrung der seltenen Nutztieren ist es vorrangig aufgrund der mitochondrialen DNS Sequenz die genetische Biodiversität der Rasse zu untersuchen, Ferner die Befunde ist mit dem Sequenz der Genbank zu vergleichen. Diese Forschungsergebnisse dienen ferner die Durchführung der Selektion innerhalb der Familien. Diese Arbeit haben wir durch Sammlung von Blutproben in Nagydorog im Herbst 2015 begonnen und werden im nächsten Treffen von Dagene im Jahre 2017 berichten. Es ist auch geplant, die Cikta verwandten Schafen in den Nachbarländern in diese Untersuchung einzubeziehen.

Literaturverzeichnis

BALÁSHÁZY, J. (1827): Gyűjtemény a juh tenyésztéséről.
BOCZ, E. (1939): Néhány szó a tolna-baranyai cikta-juhról. Magyar Állattenyésztés, I. évf. 10. 272.
BOHM, J. (1878): Die Schafzucht. 2. Teil: Die Züchtung des Schafes, Berlin
BÖKÖNYI, J. (1963): A budai Várpalota ásatásának állatcsont anyaga: Bud. Rég. 20:395-425.
CZUPPON, L. (1965): A tolna-baranyai sváb juh nemesítése Ile de France fajtával. Gödöllő
FITZINGER, L. (1859): Über den Rassen des zahmen Schafes, Wien
GOLF, A. (1939): Die geschichtliche Entwicklung der deutschen Schafzucht und –Haltung in rassischer und wirtschaftlicher Richtung. Handbuch der Schafzucht und -haltung, Bd. 1, Wien
KONKOLY THEGE, S. (1948): Állattenyésztésünk fejlesztésének irányai, eszközei és eredményei. Budapest
MASON, I.L. (1967): The sheep breeds of the Mediterranean basin. Commonwealth Agricultural Bureau, Edinburgh
SCHANDL, J. (1940): A tolna-baranyai sváb juh. Magyar Állattenyésztés, II. évf. 1.sz. 9-11.

Challenges of in situ conservation of endangered Zackel sheep type

SAVIĆ, Mila[1] – DIMITRIJEVIĆ, Blagoje[2] – GÁSPÁRDY, András[3] – ZSOLNAI, Attila[4] – BECSKEI, Zsolt[1]

[1]Department of Animal Breeding and Genetics, Faculty of Veterinary Medicine University of Belgrade, Serbia
[2]Clinic for Ruminants and Pigs, Faculty of Veterinary Medicine, University of Belgrade, Serbia
[3]Department of Animal Breeding and Genetics, Faculty of Veterinary Science, Szent István University Budapest, Hungary
[4]Research Institute for Animal Breeding, Nutrition and Meat Science, Herceghalom, Hungary

Abstract

The focus of investigations were the health status and the adaptive characteristics of autochthonous breeds, their ability to cope well with challenging aspects of the production environment including knowledge of the impact of types of livestock keeping on ecosystem functions. The multidisciplinary approach is focused on pasture impact, economic and social factors which are driving livestock-sector trends affecting the management of Zackel sheep genetic resources. As a result of strong support for the maintenance of Zackel sheep populations in their traditional production environments and application of conservation strategies that involve in situ measures, we are facing many challenges. In this sense, we shall point out the problems of the in situ conservation of endangered type Zackel sheep. The gastrointestinal parasitic infections were the main health problem in Lipe sheep populations. The research presented in this paper focused on the influence of intensity and type of parasitic infections to the degree of oxidative stress in endangered Lipe type of Zackel sheep with special attention to the activity of the enzyme superoxide dismutase 1 (SOD 1).

Introduction

The intensification of all aspects of production and the time of The Fourth Industrial Revolution (SCHWAB, 2016) have great sociological impact on changing attitudes and needs of people. Consequently, an imbalance of ecosystems and biodiversity erosion of natural resources are observed. Data analysis of FAO's Domestic Animal Diversity Information System (DADIS) indicates a significant loss of breeds and strains of domestic animals. One of the current problems accelerated by intensive production is global climate change that require fast and effective action plan as defined at 21st Conference of the Parties to the United Nations Framework Convention on Climate Change (COP21). The emergence of the unprecedented floods in the basin of the Sava and Danube rivers and disruption of ecosystems during 2015 year along with other objective parameters are only the part of the threats to animal genetic and plant resources in this part of Europe.

Four decades ago Faculty of Veterinary Medicine (FVM) Belgrade carried out the monitoring of population trends and characterisation of animal genetic resources. Also, FVM Belgrade takes active part in the activities aimed at knowledge transfer in the frame of continual education of veterinarians and extension service regarding animal genetic resources and their production environments.

Conservation management of autochthonous Zackel Sheep breed based on rational utilization contributes in many ways to livelihoods, specific quality of products, food security, rural development, cultural life and environmental management.

Zackel breed is widespread mainly in the mountainous regions of the Balkan Peninsula. Since this is a triple purpose breed, mainly low productive, most strains are under pressure. The most common factors which influence the loss genetic diversity are lack of profitability, competitiveness, indiscriminate cross-breeding mainly with Wurttemberg and Ile de France, introduction and increased use of exotic breeds, production system intensification, and in some cases are loss of pasture or production environment.

In this paper we present challenges for managing animal genetic resources, Lipe sheep endangered type of Zackel Sheep.

Considering that Lipe Sheep is a local breed traditionally reared in Lipe village, monitoring of trends in the size, structure and distribution of breed populations morphology traits, performance as well specific quality product served as a basis for identifying the breeds at risk of extinction and prioritizing conservation activities (BECSKEI, 2012; SAVIĆ et al., 2013; SAVIĆ et al., 2014;) Adaptability to specific environment and health control of population were in the focus of interest.

In clinical pathology of sheep, parasitic infections occupy a significant place and besides health issues, pose a great economic problem in sheep breeding. Sheep are highly susceptible to parasitic infections, even under conditions of very low pasture infections. In this way, sheep support the sustainability and amplification of parasitic fauna intensity in an epizootiological region and may at the same time serve as “indicators” of animal species with the aim of evaluating the presence of parasitic fauna in a specific region.

During the process of the in situ conservation of Lipe Sheep negative consequences of identified parasitic infections on the health status of sheep, unsatisfactory effects of applied antiparasitic therapy and other measures relating to the management of pastures have been observed. The research focused on the influence of extensiveness and intensity of parasitic infections of the degree of oxidative stress in Lipe type of Zackel Sheep with special attention to the activity of the enzyme superoxide dismutase 1 (SOD 1) (DIMITRIJEVIĆ, 2013; DIMITRIJEVIĆ et al., 2013).

Material and methods

The study was performed on a total of 60 sheep (aged 12 to 18 months) of Lipe Zackel which are included in the programme for conserving animal genetic resources in the Republic of Serbia kept under semi intensive conditions in Lipe village (44°38′17″N; 20°59′35″E). Health status was estimated upon results of physical, haematological and biochemical investigation. Distribution and intensity of parasitic infections were assessed using methods of standard parasitological analyses. Within Lipe type, a control group of sheep was established (n=10) negative to parasitic infection. The distribution of parasites in sheep was evaluated using the native smear coprological technique, by sedimentation and flotation methods. The degree of infection intensity per sheep was quantitatively established by the method of McMaster (modified by Zajicek).

The oxidative stress parameters were measured for catalase activity (CAT), the red cell membrane damage by level of malondialdehyde (MDA), while carbonyl and thiol plasma protein group concentrations were used as indicators of the degree of protein oxidative modification. The activity of Cu, Zn - superoxide dismutase (SOD 1) was determined electrophoretically.

Statistical analysis of data was performed using the computer program GraphPad Prism 5.00 (San Diego, CA, USA). The research results are presented with the help of descriptive statistical parameters. Statistical significance of difference in the observed value (p) was determined using ANOVA, Tukey 's test.

Results and discussion

The Lipe Sheep is a milky type of Zackel breed, traditionally reared in village Lipe, in lower Morava valley in Northern Serbia. In 1935, at Sorbona University, Slobodan Pavlović, professor of the Faculty of Veterinary Medicine in Belgrade, in his Doctoral Dissertation has described Lipe sheep as a robust sheep with excellent milk properties for cheese production. At that time, population of Lipe sheep counted about 40 000 animals. Nowadays, Lipe Sheep is an endangered population, registered at the Endangered – Maintained breed list. Lipe Sheep is a triple purpose, late maturing sheep, raised under semi intensive management conditions. Average estimated body weight ranges from 50 to 70 kg. Coat colour is white, with black head and dark legs. Horns are large and spiral, triangularly shaped in rams and ewes are usually polled. Lambing rate is 120%. Average milk yield is 150 kg. The specific characteristics of cheese and cream prepared in a traditional way like famous Lipe cheese were examined. The gastrointestinal parasitic infections were the main health problem in Lipe Sheep populations.

The analysis of extensiveness parasitic infections examined sheep, the epizootic area, determined that is 70 % Lipe type were negative for the presence of parasitic infection. It was established that 7.69% Lipe type is determined simultaneously infected with two types of parasites (*Trichostrongylidae* + *Protostrongylidae*) and (*Trichostrongylidae* + *Strongyloides*) and monoinfection with *Trichostrongylidae*. Intensities of parasitic infections were *Trichostrongylidae* (72±46), *Trichuris* spp (11±3) and *Strongyloides* spp (41±2).

In order to investigate the influence of the intensity of parasitic infection on the parameters of oxidative stress we analyzed the activities of antioxidative defence (SOD 1 and CAT), degree of cell membrane damages, i.e. lipid peroxidation, through the level of MDA and the degree of oxidative modification of proteins via thiol and the concentration of carbonyl groups. It was noticed that the overall activity of the enzyme SOD 1 increases, depending on the presence of parasite species and intensity of the infection in comparison with the control group of sheep. The results of analyses of the activities of oxidative stress parameters are presented in Table 1.

Table 1. Descriptive statistics of oxidative stress parameters

Parameters	CAT (U/gHb)	SOD 1 (P/gHb)	MDA (nM/gHb)	Carbonyl groups (μM/L)	Thiol groups (μM/L)	NO_2 (μ M/L)
Lipe Sheep	28.42	30.74	59.29	8.54	268.4	13.20

SOD (EC 1.15.1.1) represents the first line of defence under conditions of disturbed redox balance, as they prevent the formation of a series of very harmful reactive oxygen and nitrogen species (hydroxyl radicals and peroxynitrites) and the initiation of oxidative chain reactions, which as an outcome are significant damages to biomolecules (lipids, proteins and nucleic acids). The level of oxidative stress in local Lipe type of Zackel sheep is different depending on the species and intensity of parasitic infection. These results showed a large scale of variability of host responses to parasitic infections.

Drivers of change in animal genetic resources management are evident. In the framework of The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture FAO Commission on Genetic Resources for Food and Agriculture Assessments the magnitude of impact and predicted trends in animal genetic resources management were identified. Our results are in accordance with the fact that certain factors have a major impact on animal resources and increasing trends such as: demand for livestock products, economic, livelihood and lifestyle factors, policy factors, technology, climate and changes to grazing land and other natural resources. In the report the impact of diseases on animal genetic resources is low. It also predicts that the impact of the disease on animal genetic resources despite the above changes acting on the ecosystem, pastures and others will not be changed, which is not in accordance with our results.

Conclusion and recommendation

During the long term health monitoring of Zackel Sheep the gastrointestinal parasitic infections were the main health problem and challenge for in situ conservation. Sheep farmers in Lipe village are very interested in saving Lipe sheep, as well as in preserving an ancient treasure, old crafts and customs. Lipe Sheep is a brand supported on traditional festival "Lipe shepherd days". Care for local Lipe sheep with the application of modern approach on the control of well adapted sheep for pasture management gives great chances for in situ conservation of endangered type.

Acknowledgements

This research work was carried out with the support of Ministry of Education, Science and Technology Development.

References

BECSKEI, Zs. (2012): Application of in situ programme for conservation of animal genetic resources, Thesis, Faculty of veterinary medicine, University of Belgrade, pp 54.

DIMITRIJEVIĆ, B. (2013): Investigation the possibilities of using superoxide dismutase 1 isoenziyme forms as biomarkers for determination the intensity of parasitic infections in sheep. PhD Thesis, Faculty of veterinary medicine, University of Belgrade, 2013, pp 204.

DIMITRIJEVIĆ, B. – BOROZAN, S. – JOVIĆ, S. – BACIĆ, D. – KATIĆ-RADIVOJEVIĆ, S. – STOJANOVIĆ, S. – SAVIĆ, M. (2013): The effect of the intensity of parasitic infection with *Strongyloides papillosus* and albendazole therapy on biochemical parametars in sheep blood. Acta veterinaria, 63 (5-6), 581-601.

FAO (2015): The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture. Proccedings of the Global National Coordinator Workshop, Rome, Italy, Food and Agricultural Organisation of the United Nations, pp 606.

SAVIĆ, M. – TRAILOVIĆ, R. – PETRUJKIĆ, B. – BECSKEI, ZS. – DIMITRIJEVIĆ, V. (2013): Determining the value of Vlashko-Vitoroga Zackel sheep for the conservation process. Acta Veterinaria, 2013, 63 (5-6), 621-629.

SAVIĆ, M. – BALTIĆ, M. – BECSKEI, ZS. – DIMITRIJEVIĆ, B. – DIMITRIJEVIĆ, V. – SAVIĆ, Đ. – VEGARA, M. (2014): Evaluation of Zackel lamb meat quality with the aim of increasing the conservation value of the breed. Acta Veterinaria, 2014, 64 (4), 438-446.

SCHWAB, K. (2016): The Fourth Industrial Revolution. The World Economic Forum, pp 173.

Assessment of some health status traits of endangered Balkan goat in order to improve in situ conservation program

BECSKEI, Zsolt[1] – SAVIĆ, Mila[1] – PAVLOVIĆ, Ivan[2] – IVANOVIĆ, Snežana[2] – DIMITRIJEVIĆ, Blagoje[3] – GÁSPÁRDY, András[4] – KÖNYVES, Tibor[5] – RELIĆ, Renata[6]

[1]Department of Animal Breeding and Genetics, Faculty of Veterinary Medicine Univerisy of Belgrade, Serbia
[2] Scintific Veterinary Institute, Belgrade, Serbia
[3]Clinic for Ruminants and Pigs, Faculty of Veterinary Medicine, University of Belgrade, Serbia
[4]Department of Animal Breeding and Genetics, Faculty of Veterinary Science, Szent István University Budapest, Hungary
[5]Department of Animal Science and Nutrition, Faculty of Biofarming Backa Topola, John Naisbitt University Belgrade, Serbia
[6]Institute of Zootechnics, Faculty of Agriculture, University of Belgrade, Serbia

Abstract

Hilly mountain region of Serbia represents a valuable natural resource with high potential in livestock production, especially for sustainable goat and sheep rearing. The Balkan Goat, as a transboundary breed, is on the list of endangered breeds. For decades it has been exposed to pressure from high performance, exotic, meliorate breeds. Nowadays, it is necessary to improve the strategy for advanced characterization and conservation of the Balkan Goat breed. Previous investigations of the genetic structure of this autochthonous, transboundary breed revealed the existence of genetic variability and good adaptive ability to the local, unfavorable environment and extensive conditions. Monitoring of some health traits is necessary for effective planning of advanced breed characterization and conservation. As the most severe health problem in goat production systems are parasitic infections, determination of gastro-intestinal parasites is important for definition of health status. The aim of this study was to assess the prevalence and extensity of gastro-intestinal parasitism of Balkan goat populations in hilly mountain regions of Serbia, where the breed is traditionally reared. The study was conducted in 131 Balkan Goat flocks, kept mainly under extensive production system. The results show that all the tested flocks are infected, while the predominant gastro-intestinal parasites detected were nematodes. Such results are valuable in making strategies for development of integrated approach to achieve the best control of parasitic infections of Balkan Goat flocks. Keeping in mind that one of the main challenges of livestock production are parasitic infections, obtained resultants can also be an important point to determine some advanced characteristics of Balkan Goat, necessary for conservation process. The importance of conservation of Balkan Goat, as an endangered, autochthonous genetic resource is less economical, but mostly cultural, historical and heritage oriented. There is also the aesthetic argument that Balkan goat is an element of nature and landscape protection.

Introduction

An increasing number of studies have emphasized the importance of indigenous goat breeds as an important potential for development of agro-biodiversity in the mountain regions. Preservation of indigenous populations has become increasingly popular in light of the emergence of global climate change and the challenges that await us. Under pressure from newcomer productive breeds, indigenous population are rapidly disappearing, eroding in that way the local biodiversity and natural genetic potential of those resources (HOSTE, 2011; BECSKEI, 2012). Sustainable development of indigenous goat breeds in the mountainous regions in European countries with developed livestock such as Switzerland, Austria and Norway, is the subject of extensive studies (SMAL, 2011). The focus is on the protection and rational use of indigenous goat breeds. It also highlights the importance of biodiversity of pastures where goats are reared. Special attention is given to highlight the value of local products, specific characteristics obtained from goats. All these positive effects are directly contributing to the revival and promotion of the region (MARGUERAT, 2011; BECSKEI, 2012).

The Balkan Goat is an autochthonous breed, reared in mountain regions of the Balkan Peninsula under very modest conditions and poor pasture quality. Micro-evolution of this breed is characterized by its adaptation to severe environmental conditions of mountain climates on the Balkan region. In Serbia, the breed is traditionally reared in Central and South parts of the country (Stara plana, Sjenica and Golija mountains) and it has great potential for sustainable production (SAVIĆ et al., 2011). The Balkan goat population was quite numerous up until World War II, however, its number have been rapidly declining since that time. Between 1950 and 1980 rearing of goats was forbidden by the law (ĆINKULOV et al., 2009). Presently, the number of purebred Balkan goat populations continues to decline, due yet again to depopulation in underdeveloped regions and requiring measures to protect indigenous breeds. Nowadays, Balkan Goat is endangered considering two reasons. Firstly, because of rapid depopulation of underdeveloped regions and secondly, tendency of continual Saanen crossbreeding for improved milk production. The estimate purebred population size is around 1000 animals (FAO, 2015).

The current genetic structure of Balkan Goat breed revealed the existence of genetic variation and good adaptive ability of individuals to the often unfavorable growing conditions (SAVIĆ, 1993; JOVANOVIĆ et al., 2006). Analysis of environmental and genetic factors in growth characteristics, composition and traits of kid carcasses, milk yield, milk composition characteristics and fertility traits of Balkan Goat have been revealed (ŽUJOVIĆ et al., 2012; MEMIŠI et al., 2010; BOGDANOVIĆ et al., 2008). One of the most severe health problems in goat production systems is gastro-intestinal parasitism (PAVLOVIĆ et al., 1995, 2012). For this reason, this study obtained the examination of parasitic fauna of Balkan Goat populations at various regions of Serbia, predominantly in hilly mountain regions, where the breed is traditionally reared.

Material and methods

The prevalence and extensity of gastro-intestinal parasitic infections were assessed in 131 flocks of autochthonous Balkan Goat breed. The tested animals originated from 39 villages of hilly mountain region of Serbia (Stara plana, Sjenica and Golija mountains). The study was carried out both on fecal samples and carcasses. During the survey a total of 731 fecal samples and 72 carcasses were tested. Fecal samples were analyzed using standard coprological technique protocols (EUZEBY, 1981; PAVLOVIĆ and ANĐELIĆ-BUZADŽIĆ, 2010). Parasitical necropsy were done on slaughtered goats at local slaughterhouses in order to determine the adult and larval forms of parasites in the gastro-intestinal tract, trachea and lungs, also in some other parenchymal organs.

The adult and larval forms of the parasites found were fixed in 10% formalin and mounted in lactofenol for later identification. Total differential worm counts were performed on all the alimentary tract and lungs using the technique described by PAVLOVIĆ and ANĐELIĆ-BUZADŽIĆ (2010). Determination of helminths were done by keys given by SOULSBY (1977).

Results and discussion

Gastro-intestinal helminths were detected in all 131 tested goat flocks. Results of coprological examination of fecal samples revealed the presence of eggs of variety helminths. Also, adult forms of parasites were identified in the gut and lungs of tested carcasses. The number of guts and lungs examined in this survey thought small in number, but in combination with results of coprological examination, samples appeared to represent the population adequately.

Both the coprological and parasitic necropsy survey revealed the same parasite species: *Teladorsagia* (*Ostertagia*) *circumcincta*, *Ostertagia trifurcata*, *O. ostertagi*, *Trichostrongylus axei*, *T. colubriformis*, *T. capricola*, *Nematodirus spathiger*, *N. filicollis*, *Haemonchus contortus*, *Marshallagia marshalli*, *Skrjabinema capre*, *Bunostomum trigonocephalum*, *Chabertia ovina*, *Oesophagostomum venulosum*, *Cooperia curticei* and *C. punctata*, as it is shown in Figure 1.

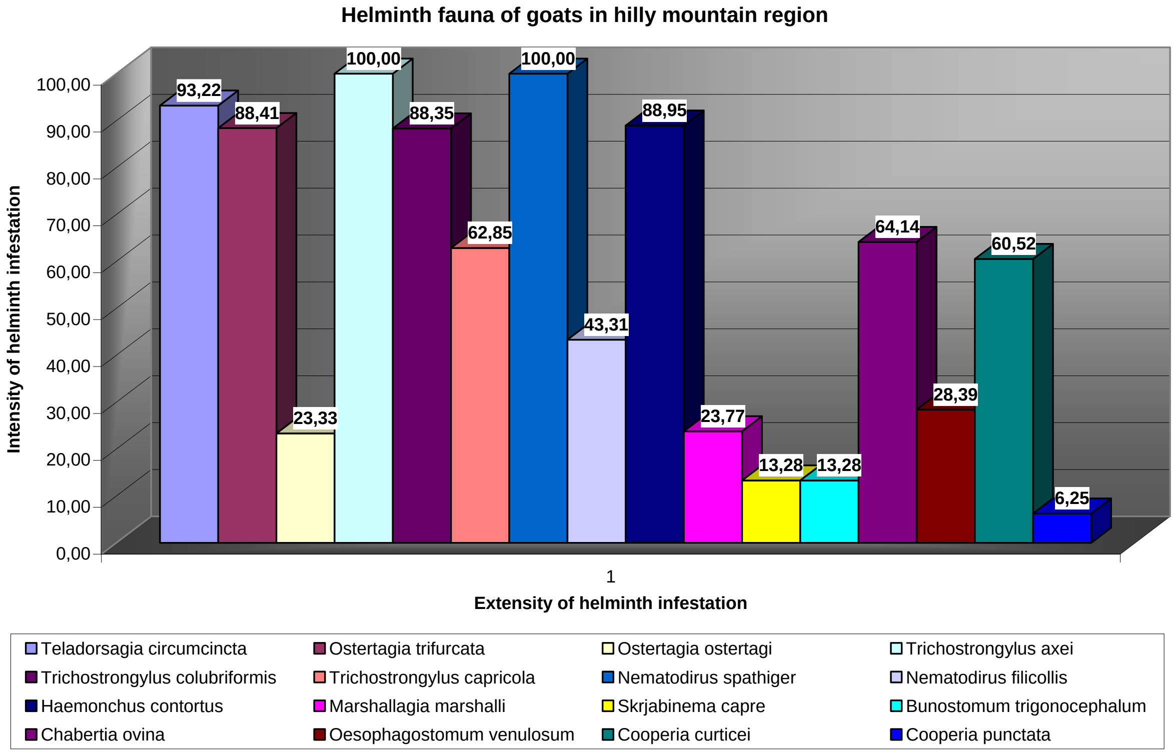


Figure 1. The prevalence of gastrointestinal helminths of Balkan Goats in the hilly mountain region

Comparing this results with similar surveys that have been done at mountain areas of Serbia, on Sjeničko-Pešterski Highland, Dimitrovgrad, Tutin and Zlatar mountain (VUJIĆ et al., 1991), Stara Planina (PAVLOVIĆ et al., 2012), and at Prizren District-Kosovo (PAVLOVIĆ et al., 1995), it can be concluded that dominant nematode species were *Ostertagia*, *Nematodirus* and *Trichostrongylus* (PAVLOVIĆ et al., 2012). Similar results we obtained during examination of goats at Timok District (ILIĆ, 1990; ILIĆ et al., 1991). Similar results were published in other Balkan countries to, such as Romania, Macedonia or Bulgaria (ARDELEANU et al., 2007; GEORGIEVSKI, 1991).

Negative influence of parasitic infections are mainly reflected through weight lost and milk yield decrease (NJAU et al., 1990). Numerous data reports about harmful effects of parasitic infections on goat production performance, and it was undoubtedly shown that there is a need to conduct the measures of anthelmintic treatment (CHARTIER et al., 2000; PAVLOVIĆ et al., 2012; PAVLOVIĆ et al., 2016*)*.

Conclusion and recommendation

Hilly mountain region of Serbia constitute a substantial Natural resources and have great potential for livestock production. In this sense the allocated regions of Stara plana, Sjenica and Golija that have the characteristics of High Nature Value. Sustainable goat production in South Serbia has great potential. Locally adapted breeds can promote sustainable development, reduce production costs, and prevent genetic pollution of a region’s biodiversity.

Previous investigations of the genetic term structure of Balkan Goat breed revealed the existence of genetic variability and good adaptive ability of individuals to the often unfavorable growing conditions. Broader analysis of prevalence of parasitic infections in hilly mountainous areas, where the breed is traditionally reared and is evolutionarily adapted, could significantly contribute to the recent advanced characterization of the breed. It would also provide a good basis for designing breeding programs ensuring good health.

Benefits of the preservation and conservation of transboundary Balkan Goat breed is reflected in the fact that it is well adapted to the local environment, which makes it favorable in alternative, sustainable, low input systems. Although the population size of Balkan Goat in Serbia is small, counting about 1000 animals in total, it represents an important biodiversity resource of our country. The importance of conservation of this animal resource is less economical, but mostly cultural, historical and heritage oriented. There is also the aesthetic argument that Balkan Goat, with its specific long horns and hair, is an element of nature and landscape protection.

Acknowledgements

This research work was carried out with the support of Ministry of Education, Science and Technology Development of Republic of Serbia.

References

ARDELEANU, D. – PIVODA, C. – NEACSU, M. – IDA, A. (2007): Bio-ecological phenomenon of poly-parasitism –actual major problem in breeding of sheep and goats. Lucr. Stii. Zootehnie şi Biotehnologii, 40(2), 309-317.

BECSKEI, Zs. (2012): Application of in situ programme for conservation of animal genetic resources, Thesis, Faculty of veterinary medicine, University of Belgrade, pp 54.

BOGDANOVIĆ, V. – ĐORĐEVIĆ, I. – ĐURĐEVIĆ, I. (2008): Osobine mlečnosti balkanske koze u poluintenzivnim uslovima gajenja, Biotechnology in Animal Husbandry, 24 (1-2), 59-67.

CHARTIER, C. – ETTER, E. – HESTE, H. – PORS, I. – KOCH, C. – DELLAC, B. (2000): Efficacy of copper oxide needles for the control of nematode parasites in dairy goats. Vet. Res. Commun., 24, 389-399.

ĆINKULOV, M. – KRAJINOVIĆ, M. – PIHLER, I. – JOSIPOVIĆ, S. – IVAČKOVIĆ, J. – ŽUJOVIĆ, M. (2009): Carcass yield and slaughter traits of kids from Serbian fawn goat population. Book of Abstract of the 60th Annual Meeting of the European Association for Animal Production, Barcelona, Spain 24-27 August, pp 547.

EUZEBY, J. (1981): Diagnostic experimental de helminthoses animals", ITVC, Paris, France.

FAO (2015): The Second Report on the State of the Worlds Animal Genetic Resources for Food and Agriculture, FAO Commission on Genetic Resources for Food and Agriculture. http://www.fao.org/3/a-i4787e/index.html

GEORGIEVSKI, B. (1991): Rasprostranjenost parazitskih infekcija na području opštine Prilep, BSc thesis, Faculty of Veterinary Medicine in Belgrade.

HOSTE, H. (2011): Improving “Low Input” Sheep Production Systems in Europe. First Low Input Breeds Symposium on Ethical Consideration in Livestock Breeding, Wageningen, Netherlands, March 15-16.

ILIĆ, G. (1990): Parasitic fauna of goats and pathological changes at goat at Timok District. PhD disertation, Faculty of Veterinary Medicine, University in Belgrade (in Serbian, with English abstract).

ILIĆ, G. – JOVANOVIĆ, D. – NEŠIĆ, D. – PAVLOVIĆ, I. (1991): Parasitose in goat and its role in pathology of goat at Timok District in period 1986-1989. Proceeding of I International Summer Conference for Advancement of Sheep and Goat Production, Ohrid, 390-395.

JOVANOVIĆ, S. – SAVIĆ, M. – POPOVIĆ VRANEŠ, A. – BOBOS, S. (2006): The importance of autochthonous Balkan goat in sustainable farming in Serbia. The 57 thAnnual Meeting of the European Association for Animal Production, EAAP Turkey, Book of abstracts No.12 pp 99.

MARGUERAT, C. (2011): Environmental value of animal genetic resources. Book of apstracts of the 62 Annual Meeting of the European Federation of Animal Science No 17, pp 17. Stavanger 29 August -3 September.

MEMIŠI, N. – ŽUJOVIĆ, M. – TOMIĆ, Z. – PETROVIĆ, M.P. (2010): .Influence of lactation order and live weight on milk yield and fertility traits in domestic Balkan goat Biotechnology in Animal Husbandry, 26 (3-4), 179-185.

NJAU, B.C. – SCHOLTENS, R.G. – KASALI, O. (1990): Parasites of sheep at the international livestock centre for Africa debre berhan station, Ethiopia. Preventive Veterinary Medicine, 9 (4), 267-277.

PAVLOVIĆ, I. – KULIŠIĆ, Z. – NEŠIĆ, D. – ROMANIĆ, S. (1995): Endoparasites of sheep and goats in Prizren district. Proceedeing of 3rd International Conference of Sheep and Goats Production, Ohrid, Macedonia, 106-110.

PAVLOVIĆ, I. – ANĐELIĆ-BUZADŽIĆ, G. (2010): Osnovi dijagnostike parazitskih bolesti životinja za studente visoke poljoprivredne škole strukovnih studija U Šapcu studijski program: strukovna veterina. Naučni institut za veterinarstvo Srbije, 1-28.

PAVLOVIĆ, I. – IVANOVIĆ, S. – JOVIČIĆ, D. – ŽUGIĆ, G. – JOVČEVSKI, S. (2012): Gastointestinal helmints of goats breeding at Stara Plana area (Serbia) Book of Abstracts V International Symposium of Livestock Production, 05-07. 9. 2012., Skopje, Macedonia, 144.

PAVLOVIĆ, I. – IVANOVIĆ, S. – DIMITRIĆ, A. – VEGARA, M. – VASIĆ, A. – ŽIVKOVIĆ, S. – MIJATOVIĆ, B. (2016): Tick population in goats and sheep in Šabac, Macedonian Veterinary Review, 39 (1), i-ii.

SAVIĆ, M. (1993): Polimorfizam proteina u krvi Balkanske rase koza. Doktorska disertacija, Veterinarski fakultet, Beograd.

SAVIĆ, M. – JOVANOVIĆ, S. – TRAILOVIĆ, R. – DIMITRIJEVIĆ, V. – DIMITRIJEVIĆ, B. (2011): Autochtonous breeds as livestock potential in sustainabe farming in Serbia. Congress proceedings of the 19th International Congress of Mediterranean Federation of Health and Production of Ruminants, Belgrade, Serbia, 25-28 May, 16-22.

SMALL, R.W. (2011): Potential for conservation of local livestock breeds trough delivery of ecosystem service. In: Book of abstracts of the 62 Annual Meeting of the European Federation of Animal Science, 17, Stavanger, 29 August-3 September, pp 73.

SOULSBY, E.J.L. (1977): Helminths, arthropods and protozoa of domesticated animals, and Cassell Co, London.

VUJIĆ, B. – BOŠKOVIĆ, V. – SAVIĆ, Ž. (1991): Most important parasites species of sheep and goat and its eradication. Proceeding of 1st International Summer Conference for Advancement of Sheep and Goat Production, 375-381.

ŽUJOVIĆ, M. – MEMIŠI, N. – TOMIĆ, Z. – STANIŠIĆ, N. – BIJELIĆ, Z. – MAKSIMOVIĆ, N. – MARINKOV, G. (2012): Relationship of slaughter carcass traits of Balkan goat kids Biotechnology in Animal Husbandry, 28 (2), 263-274.

Incidence and predisposition of the hip dysplasia in Hungarian shepherd dogs

KISS-PETŐ, Tibor[1] – SÆLAND, Heidi[1] – BECSKEI, Zsolt[2] – ANNUS, Kata[1] – GÁSPÁRDY, András[1]

[1]SZIE-ÁOTK, Department for Animal Breeding and Genetics, 1078 Budapest, István u. 2., Hungary
[2]Department of Animal Breeding and Genetics, Faculty of Veterinary Medicine Univerisy of Belgrade, Serbia

Abstract

Dogs with CHD are born with normal hips that later undergo varying degrees of subluxation of the coxofemoral joint. Although the aetiology of CHD is multifactorial, the pathogenesis or stages of change within the affected coxofemoral joint(s) are similar regardless of cause. With the onset of disease, there are progressive structural changes including joint laxity and femoral head subluxation, swelling, stretching, fraying, and eventual rupture of the teres ligament; articular cartilage, eburnation of subchondral bone, DJD and perioarticular ostephyte formation. It is very hard to decide to which extent CHD is multifactorial genetic. If a pedigree chart is taken of the dogs' family and we can see that its brothers and sisters have hip dysplasia; then it is likely that the disease is genetic and that the dog will also be a carrier. However, this is unfortunately not enough to prove if a dog will manifest with hip dysplasia or not. We need to be able to prove that the pattern of inheritance is "non-Mendelian" and that environmental factors might play a role as well. This would require a lot of research and studying though; hundreds and more dogs and their pedigrees should be examined before we can draw a conclusion of the disease being multifactorial or not.

Introduction

Canine hip dysplasia is a polygenetic multifactorial disease, conditioned by environmental factors, and is characterized by instability of the coxofemoral joint, which may lead to secondary degenerative osteoarthritis in terms of calcification (HENRIGSON et al., 1966). This defect can occur in one or both hips. Secondary changes are due to abnormal wear inside the joint and can later result in acetabular bone sclerosis, osteophytosis, thickened femoral neck, capsule fibrosis and subluxation of the femoral neck. Since the joint disease is irreversible, the only way to prevent the manifestation of hip dysplasia in dogs is through gene testing and selective breeding.

By reviewing data from observations on military working dogs in the past, HD accounted for the rejection of approximately 20% of the total number of the dogs evaluated for training (STUNKARD et al., 1969; OLSON 1971; TOWNSEND, 1972).

However there are many studies conducted into other common dog breeds, such as the Labrador (LAVRIJSEN et al., 2014), Golden Retriever (TODHUNTER et al., 2005), the German shepherd (STOCK et al., 2011; WILSON et al., 2012) as well as Bulldogs and Pugs (Orthopaedic Foundation for Animals, 2015), examining the hip dysplasia in the Hungarian Shepherd breeds were not so popular.

The hip joint (articulation coxae) is an spheroidal joint, made up of two bones; the femoral bone and the pelvic bone. The hip joint (Figure 1) is formed by the head of the femur (caput femoris) articulating with the acetabulum of each hipbone (os coxae) (BRAGULLA et al., 2009). The hip joint being a ball-and-socket construction gives rise to a great range of movements; flexion, extension, abduction and adduction (MILLER et al., 1979). Despite the fact that at birth the femoral head and acetabulum are mainly composed of cartilage, the canine hip joint is functional and stable in newborns. The joint capsule, chondro-osseus conformation, the teres ligament (ligament of the head of the femur) and the pelvic musculature are all major contributors to the stability of the hip joint (RISER, 1975, KRONTVEIT, 2011).

There have been many different theories regarding the aetiology and pathogenesis of canine hip dysplasia but “the true cause of canine hip dysplasia still remains unclear” (TOBIAS and JOHNSTON, 2012). At birth, puppies are born with normal hips and they will stay healthy if the congruity between the femoral head and the acetabulum is maintained. However, if the femur and acetabulum is pulled apart for any reason (injury, stress etc.), the development follows an abnormal course that correlates with the incongruity of the joint and hip dysplasia can develop (ALEXANDER, 1992).

Heredity clearly plays an important role in acquiring the disease, but also (over) weight (KEALY et al., 1997), growth rate (LUST et al., 1973, HEDHAMMER et al., 1974) and nutrition has shown to have great impacts on its development. In addition, over-exercise at an early age, can also contribute to the early onset of signs and severity of the disease (MCGAVIN and ZACHARY, 2007). The abnormal development of the hip joint is thought by many to be caused by a delay in the development of muscle mass, combined with rapid growth of the skeleton. These structures are responsible for the congruity between the articular surfaces between the head of the femur and the acetabulum. This is why canine hip dysplasia has been classified as a “biomechanical” disease (RISER and LARSEN, 1974). Hence, the changes in biochemical balance, stress, compression, lubrication and muscle pull, or changes in congruity between the joint components can affect the normal development of the hip (RISER and SHIRER, 1967).

Up until now veterinarians have mostly relied on a phenotypic assessment of the hips of dogs based on radiography. This method of diagnosis has been combined with a clinical examination to make treatment decisions, but is not a reliable method for eliminating affected dogs from a breed. A phenotypically normal dog can carry mutations that influence trait expression. The concept is to find the genes that contribute to hip dysplasia, and to use molecular markers near these contributing genes or the genetic mutations themselves to identify susceptible or resistant dogs. This information is then used in conjunction with radiographic hip screening on a pedigree to derive breeding values that could be applied in breeding programs or registries to reduce the incidence of the trait (ZHU et al., 2009).

The aim of this study is to increase the understanding of factors related to the development of canine hip dysplasia (CHD), the methods of early detection of inherited genes as well as the ways to prevent the disease from developing in future breeding dogs. In this study the various aspects of the Norberg angle in three Hungarian dog breeds: Mudi, Pumi and Puli was examined. In addition to this the incidence, level of hip dysplasia (HD) and the predisposition were analysed in the mentioned breeds in relation to influencing factors like gender, age and kennel.

Material and methods

The data collection was produced and provided by the Hungarian Pet Orthopaedic Association (MKOE, Magyar Kisállat Ortopédiai Egyesület). The sampling material was a large group of privately owned dogs: Mudi (n=64), Pumi (n=72) and Puli (n=193). The individual X-ray images were made by local veterinarians at veterinary clinics throughout Hungary and sent to the MKOE for an evaluation and determination of level of hip dysplasia (HD) according to the Norberg angle analysis.

For the data processing the categories of Norberg angle (after FCI classification system: A ≥102.5°, B ≥97.5° and <102.5°, C ≥92.5° and <97.5°, D ≥87.5° and <92.5° and E <87.5°) as well as the average Norberg angle (individual average of the left and right values) were created and investigated.

For the evaluation of the Norberg angle General Linear Models were used with the following fixed effects: breed, gender and kennel. The year of birth as well as the age at the time of screening was added as covariates into this model. The statistical significance of these effects was estimated by a backward elimination, while taking into account what effects were eligible for removal. As a result, the p-value, as well as the mean and standard error of mean (SEM) will be presented according to breed and category (StatSoft, Inc. 2005).

Results and discussion

Figure 1 shows that the level of hip dysplasia in the individual investigated breeds decreases as the level of severity increases. Figure 2 shows that the incidence of hip dysplasia is highest in category “A Free”, where 23 Pumi, 98 Puli and 41 Mudi dogs were categorized. This equates to 32%, 50.7% and 64% respectively. Dogs grouped as borderline (B) were 15 Pumi, 47 Puli and 14 Mudi, thus 20.8%, 24.3% and 21.8% according to the chart above. This is noticeably half of the dogs in category “A Free”. This decreasing trend of HD incidence continues with 29.2%, 16.5% and 4.7% of the dogs being regarded as mildly (C) affected, 15.3%, 6.2% and 4.7% classified as moderately affected and 2.7%, 2% and 4.7% of the dogs were regarded as severely affected.

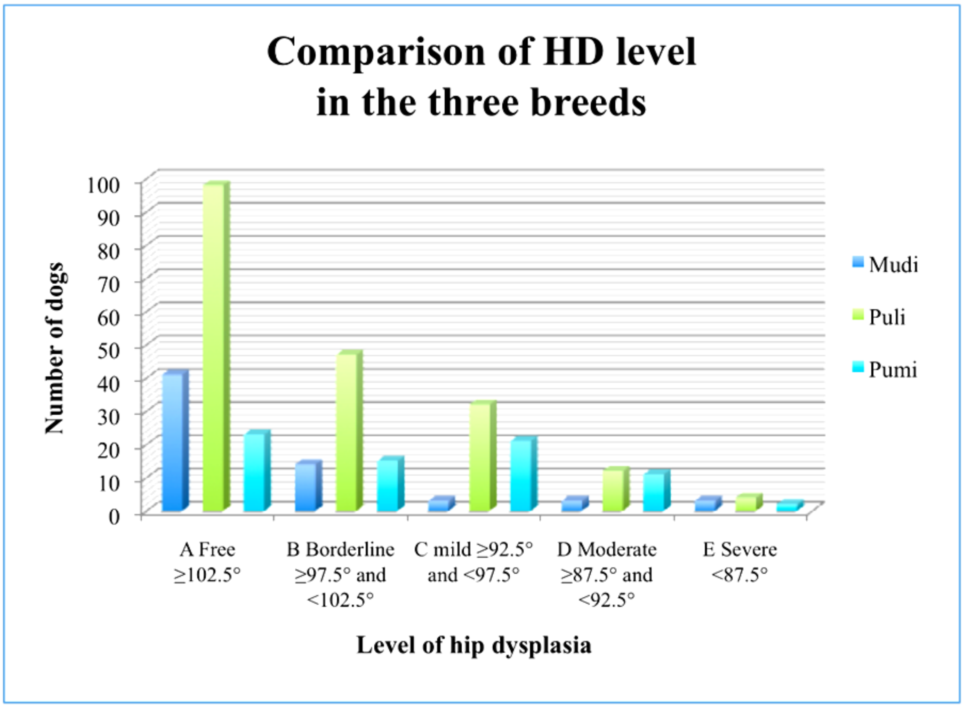


Figure 1. Comparison of the level of hip dysplasia in the different breeds

Among the dogs screened for our research, 181 were females and 148 were males, resulting in a gender distribution of 55% females versus 45% males. Figure 10 indicates that the incidence of hip dysplasia in females and males is highest in category "A Free", in which 87 females and 75 males were categorized from all the three breeds. This shows that 48% of the total number of females and 50.7% of the total number of males were classified as free (A), suggesting that males have slightly lower incidence of HD than females at this stage.

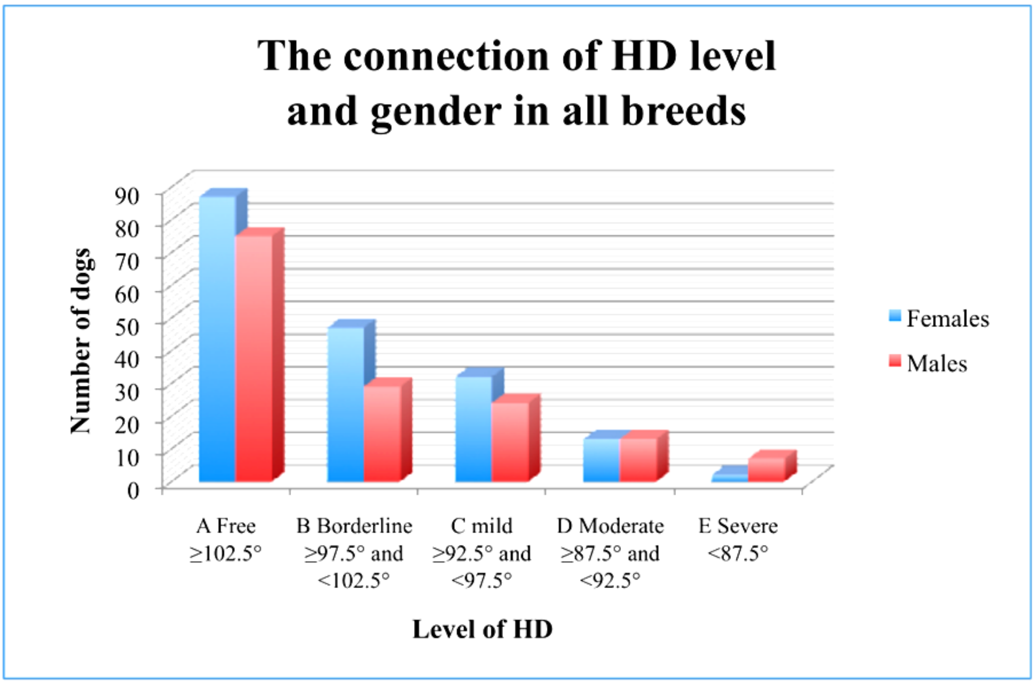


Figure 3. The connection of level of hip dysplasia and gender in all breeds

From the statistical analysis of the average Norberg angle, we found significant effect of the breed (P = 0.019) only. As Table 1 shows the Mudi and the Puli have identical values, however the values for the Pumi differed from them and shows a significant lower and less convenient Norberg angle.

Table 1. Average left and right Norberg angle according to breed (n refers to individuals)

Breed	n.	Norberg angle, °	
		Mean	SEM
Mudi	63	100.5^{b}	0.70
Puli	191	100.4^{b}	0.40
Pumi	56	98.1^{a}	0.74

a,b - different letters show statistically significant difference (Tukey test P<0.05)

According to Table 2 158 individuals are categorized as A, free of hip dysplasia with a Norberg angles measuring ≥102.5°. Sixty nine dogs were categorized at borderline B, in which the average Norberg angle was 99.4°.

Table 2. Evaluation of Norberg angles according to HD level (certification categories)

Evaluation of HD level	n	Average Norberg angle, °	
		Mean	SEM
A	158	103.5^{e}	0.37
B	69	99.4^{d}	0.53
C	53	95.7^{c}	0.97
D	22	91.7^{b}	0.24
E	8	85.0^{a}	1.52
All groups	310	99.9	0.32
P-value*		<0.001	

* - Tukey post hoc test (least significant difference test)
abcde – different subscribed letters show significant differences (P<0.05)

Conclusion and recommendation

None of the three Hungarian shepherd breeds are significantly more or less predisposed to HD than any of the other small and large breeds. However, some small differences are seen between the three different breeds. Similarly to previous research on CHD, the basis of development of HD is highly related to genes, in which some breeds are more predisposed than other. Furthermore, we can confirm that environmental factors like kennel, thus feeding, raising and keeping conditions adds to the already predisposed dog and makes the manifestation of the disease even more unpredictable.
Findings from this evaluation will particularly be useful for Hungarian veterinary practitioners that treat these dogs on a regular basis. Our findings will however also be of great importance to breeders and future dog owners that do not have access to the latest data and information on HD in these breeds.

References

ALEXANDER, J. (1992): Canine hip dysplasia. Philadelphia: Saunders, 503-504.

BRAGULLA, H. – KÖNIG, H. – LIEBICH, H. (2009): Veterinary anatomy of domestic mammals. Stuttgart [u.a.]: Schattauer, 215-219, 225, 237.

HEDHAMMER, Å. – WU, F. – KROOK, L. – SCHRYVER, H. – DELAHAUNTA, A. – WHALEN, J. – KALLEFELZ, F. – NUNEZ, E. – HINTZ, H. – SHEFFY, B. – RYAN, G. (1974): Overnutrition and skeletal disease. An experimental study in growing Great Dane Dogs. Cornell Vet, 64(5).

HENRIGSON, B. – NORBERG, I. – OLSSONS, S. (1966): On the Etiology and Pathogenesis of Hip Dysplasia: a Comparative Review. Journal of Small Animal Practice, 7(11), 673-688.

KEALY, R. – LAWLER, D. – BALLAM, J. – LUST, G. – SMITH, G. – BIERY, D. – OLSSON, S. (1997): Five-year longitudinal study on limited food consumption and development of osteoarthritis in coxofemoral joints in dogs. Journal of American Veterinary Medicine Association, 210, 222-225.

KRONTVEIT, R. (2011): Canine hip dysplasia in a prospective cohort study - Incidence, risk factors and long-term effects in four large breeds. http://www.knickerbockers.se/upload/Krontveit_PhD_thesis_2012.pdf [Accessed 17 Mar. 2015].

LAVRIJSEN, I. – LEEGWATER, P. – MARTIN, A. – HARRIS, S. – TRYFONIDOU, M. – HEUVEN, H. – HAZEWINKEL, H. (2014): Genome Wide Analysis Indicates Genes for Basement Membrane and Cartilage Matrix Proteins as Candidates for Hip Dysplasia in Labrador Retrievers. PLoS ONE, 9(1), p.e87735.

LUST, G. – GEARY, J. – SHEFFY, B. (1973): Development of hip dysplasia in dogs. Am J Vet Res, 34, 87-91.

MCGAVIN, M. – ZACHARY, J. (2007): Pathologic basis of veterinary disease. St.Louis: Elsevier Mosby, p.1095.

MILLER, M. – EVANS, H. – CHRISTENSEN, G. (1979): Miller's anatomy of the dog. Philadelphia: Saunders, 176, 177.

OLSON, R. (1971): Physical evaluation and selection of military dogs. Journal of the American Veterinary Medical Association, 159, 1444-1446.

RISER, W. (1975): The dog as a model for the study of hip dysplasia. Growth, form, and development of the normal and dysplastic hip joint. Veterinary Pathology, 12, 234-334.

RISER, W. – LARSEN, J. (1974): Influence of breed somatotypes on prevalence of hip dysplasia in the dog. Journal of American Veterinary Medicine Association, 165, 79-81.

RISER, W. – SHIRER, J. (1967): Correlation between canine hip dysplasia and pelvic muscle mass; a study of 95 dogs. Am J Vet Res, 28, 769-777.

STOCK, K. – KLEIN, S. – TELLHELM, B. – DISTL, O. (2011): Genetic analyses of elbow and hip dysplasia in the German shepherd dog. Journal of Animal Breeding and Genetics, 128(3), 219-229.

STUNKARD, J. – SCHWICHTENBERG, A. – GRIFFIN, T. (1969): Evaluation of hip dysplasia in German Shepherd dogs. Mod. Vet. Pract., 50, 40-44.

TOBIAS, K. – JOHNSTON, S. (2012): Veterinary surgery. St. Louis, Mo.: Elsevier, 20-21, 847.

TODHUNTER, R. – MATEESCU, R. – LUST, G. – BURTON-WURSTER, N. – DYKES, N. – BLISS, S. – WILLIAMS, A. – VERNIER-SINGER, M. – COREY, E. – HARJES, C. – QUAAS, R. – ZHANG, Z. – GILBERT, R. – VOLKMAN, D. – CASELLA, G. – WU, R. – ACLAND, G. (2005): Quantitative trait loci for hip dysplasia in a crossbreed canine pedigree. Mamm. Genome, 16(9), 720-730.

TOWNSEND, L. (1972): Hip dysplasia in military working dogs. In: Proc. Canine Hip Dysplasia Symposium and Workshop. St. Louis.

WILSON, B. – NICHOLAS, F. – JAMES, J. – WADE, C. – TAMMEN, I. – RAADSMA, H. – CASTLE, K. – THOMSON, P. (2012): Heritability and Phenotypic Variation of Canine Hip Dysplasia Radiographic Traits in a Cohort of Australian German Shepherd Dogs. PLoS ONE, 7(6), p.e39620.

ZHU, L. – ZHANG, Z. – FRIEDENBERG, S. – JUNG, S. – PHAVAPHUTANON, J. – VERNIER-SINGER, M. – COREY, E. – MATEESCU, R. – DYKES, N. – SANDLER, J. – ACLAND, G. – LUST, G. – TODHUNTER, R. (2009): The long (and winding) road to gene discovery for canine hip dysplasia. The Veterinary Journal, 181(2), 97-110.

Cryoconservation of boar semen – a genetic backup of Austrian pig breeding

BERGER, Beate[1] – KNAPP, Peter[2] – GALLNBÖCK, Markus[1]

[1] AREC Raumberg-Gumpenstein, Institute of Organic Farming and Biodiversity of Farm Animals, 4601 Thalheim, Austrasse 10, Austria
[2] Schweinezuchtverband Oberösterreich, 4641 Steinhaus, Waldstrasse 4, Austria

Abstract

Following an outbreak of Porcine Reproductive and Respiratory Syndrome at the Artificial Insemination centre of the Upper Austrian Pig breeding association in 2012 the need arose for protecting top genetics breeding material against losses caused by epidemics. The use of cryo-conserved boar semen for backup purposes was examined in this trial. A screening method which could be integrated easily into the routine work of the AI centre was developed. 28 Top Genetics boars of all 5 breeds kept at the AI centre were screened, 25 boars could be conserved successfully. Normally one complete ejaculate is sufficient to obtain at least 5 double insemination doses. In the future a genetic reserve of all freezable TOP Genetics boars will be stored as a backup collection at the Austrian Genebank for Farm Animals in a separate container provided by the pig breeding organisation for at least 5 years.

Introduction

In the Austrian Cattle Archive the Institute of Organic Farming and Biodiversity of Farm Animals has been providing genetic backup for the cattle industry for more than 15 years. Although reliable freezing methods for boar semen are in use since more than 40 years (WESTENDORF et al., 1975), still cryo-conserved semen is rarely used in routine artificial insemination (AI) in pig production. At the Austrian Genebank of Farm Animals semen of the rare pig breeds Mangalica and Turopolje is stored and used for planned mating in conservation breeding programs.

In the year 2012 an outbreak of Porcine Reproductive and Respiratory Syndrome at the AI-centre of the Upper Austrian Pig breeding association was diagnosed and the whole boar population in the centre had to be slaughtered. Besides the huge financial loss for the AI centre, pedigree breeders faced two years with no significant breeding progress. The need arose for protecting top genetics breeding material against future losses caused by epidemics.

This trial examined the possibilities of securing genetic backup using cryo-conserved boar semen. One of the goals of the trial was to develop an efficient screening method which could be integrated easily into the routine work of the AI centre.

Material and methods

Using a deep freezing method developed in a previous project (WESTENDORF et al., 1975 mod. EGERSZEGI et al., 2009) 28 Top-Genetics boars of the pig AI centre Steinhaus b. Wels were tested on suitability for deep freezing of semen. The boars were pre-selected for quality of fresh semen. The breeds included into the trial were Piétrain (15 boars), Landrace (7 boars), Large White (4 boars) Duroc (1 boar) and Schwäbisch-Hällisch (1 boar). Semen was collected at the AI centre by gloved hand technique. For the screening trial 20ml of the sperm rich fraction of the ejaculate were used.

The fresh semen was diluted 1:1 with BTS^+ extender (DiluPorc^{TM}, sinus Biochemistry & Electrophoresis GmbH, Germany) at 35°C. After motility analysis (SpermVision^{TM}, minitube, Germany) the samples were put in a styrofoam container and brought to the sperm laboratory of the Institute of Organic Farming and Biodiversity of Farm Animals for further conservation. Minimal quality parameters were set at 30% progressive motility and 30% intact acrosomes after thawing. If one ejaculate did not meet the standards at least one more ejaculate was tested. One to five ejaculates per boar were frozen.

In total 62 ejaculates were frozen in 0,5ml French straws. After thawing in a water bath of 37°C and dilution in 37°C BTS^+ extender (1:10) motility was measured by SpermVision^{TM} and acrosome integrity was evaluated before freezing and after thawing by smears stained according to the method by KOVACS and FOOTE (1992).

Results and discussion

Composition of the phospholipid membranes of sperm cells is determined genetically resulting in varied resistance against temperature shock (THURSTON et al., 2002). Therefore according to ROCA et al. (2006) freezability of semen is a highly individual trait in boars.

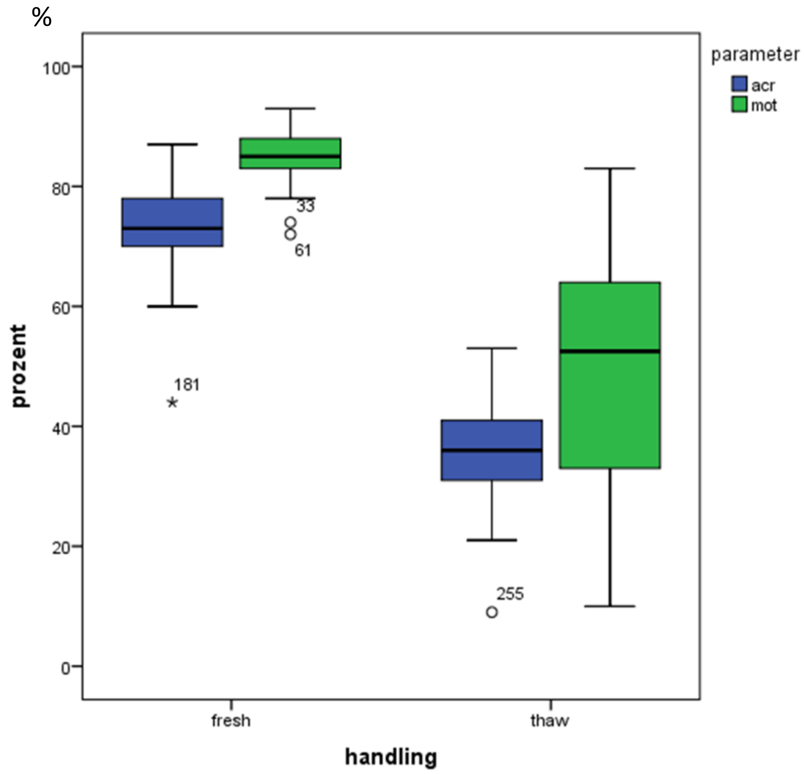
Due to the pre-selection of boars fresh semen quality was high, averaging 85.1 ± 3.8% progressive motility and 73.7 ± 6.9% intact acrosomes. After thawing 49.4 ± 18.5% progressive motile sperm cells und 35.4 ± 6.8% intact acrosomes remained (Figure 1). 19 (30.6%) of the 62 ejaculates were not suitable for deep freezing. 13 boars had at least one discarded ejaculate. These results were in the expected range (ROCA et al., 2005).

After exclusion of factors lowering semen quality like frequent collection, 25 boars could be conserved successfully. Only 3 boars (2 Piétrain, 1 Large White; 10.7%) had to be excluded as the semen was not suitable for cryo-conservation.

In contrast to ROCA et al. (2006) we found a sexual resting time of less than 5 days between collections having a negative influence on sperm survival. There was no statistical significance of the effect as the number of boars (4) and ejaculates (7) was too low.

In the second part of the trial only boars with proven freezability of semen were used. At least one complete ejaculate was frozen following the same routine as previously. All ejaculates met the quality standards before freezing and after thawing (Figure 2). 5 to 9 double insemination doses per ejaculate could be obtained depending on individual productivity of the boar and sexual resting time. The quality parameters of the fresh semen (progressive motility, acrosome integrity) allowed no prediction of the thawing quality. This result is not consistent with literature (ROCA et al., 2006).

If a boar met the standards, at least 5 double insemination doses to 5 x 10^9 sperm cells per dose were frozen. As GROSSFELD et al. (2008) mentioned, significantly lower numbers of sperm cells per insemination dose are needed, if deep intra-uterine insemination technique is used. However most of the pedigree pig breeders in Austria still use intra-cervical insemination. Therefore we opted for 5 x 10^9 sperm cells per dose in this trial.



acr	acrosome integrity
mot	progressive motility
fresh	fresh semen
thaw	frozen-thawed semen

Figure 1. Results of screening trial

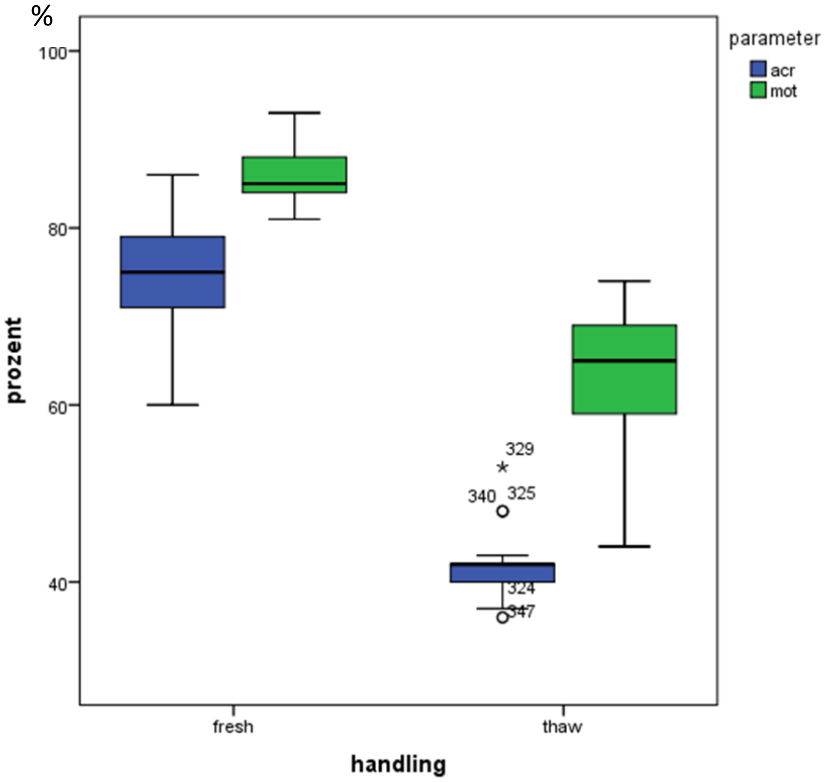
Conclusions and recommendations

The screening method developed in the trial needs only 20ml of the sperm rich phase. The other part of the ejaculate can be sold as fresh semen. This enhances the acceptance of the procedure among the pedigree breeders as the Top Genetics boars remain available in the routine collection scheme of the AI centre.

Normally one complete ejaculate is sufficient to conserve a genetic reserve of at least 5 double insemination doses ensuring the continuous breeding progress in pedigree breeding in case of an epidemic.

The genetic reserve will be stored as a backup collection at the Austrian Genebank for Farm Animals in a separate container provided by the pig breeding organisation for at least 5 years after conservation. If the reserve is not used during that time 2 double doses are transferred into the core collection for documentary reasons, the rest is destroyed.

Although freezing of boar semen will not replace fresh semen in the near future the method provides a useful tool for specific conditions (ALMLID et al., 1987) like gene banking. Deep freezing conservation of Top Genetics boar semen for export orders is planned.



acr	acrosome integrity
mot	progressive motility
fresh	fresh semen
thaw	frozen-thawed semen

Figure 2. Results of ejaculates in the genebank

References

ALMLID, T. – STAVNE, S.E. – JOHNSON, L.A. (1987): Fertility evaluation of the straw freezing technique for boar semen under practical artificial insemination conditions. Reproduction in Domestic Animals, 1987, 4, S. 193-202.

EGERSZEGI, I. – SARLÒS, P. – BERGER, B. – RÀTKY, J. (2009): Cryopreservation of semen from native Hungarian Mangalica boars – a pilot study. VIII. International Conference on Pig Reproduction Canada, Alberta, Banff 31.05. – 04.06.2009, The Banff Centre.

GROSSFELD, R. – SIEG, B. – STRUCKMANN, C. – FRENZEL, A. – MAXWELL, W.M.C. – RATH, D. (2008): New aspects of boar semen freezing strategies. Theriogenology, 70. 8, 1225-1233.

KOVÁCS, A. – FOOTE, R.H. (1992): Viability and acrosome staining of bull, boar and rabbit spermatozoa. Biotechnic & Histochemistry 67, 119 – 124

ROCA, J. – RODRÍGUEZ- MARTÍNEZ, H.V. – VÁSQUEZ, J.M. – BOLARÍN, A. – HERNÁNDEZ, M. – SARAVIA, F. – WALLGREN, M. – MARTÍNEZ, E.A. (2005): Strategies to improve the fertility of frozen-thawed boar semen for artificial insemination. Society of Reproduction and Fertility supplement, 62, 261-275.

ROCA, J. – HERNÁNDEZ, M. – CARVJAL, G. – VÁSQUEZ, J.M. – MARTÍNEZ, E.A. (2006): Factors influencing boar sperm cryosurvival. Journal of Animal Science, 84(10), 2692-2699.

THURSTON, L.M. – SIGGINS, K. – MILEHAM, A.J. – WATSON, P.F. – HOLT, W.V. (2002): Identification of amplified restriction fragment length polymorphism markers linked to genes controlling boar sperm viability following cryopreservation. Biology of Reproduction, 66 (3), 545-554.

WESTENDORF P., – RICHTER L., –TREU H. (1975): Zur Tiefgefrierung von Ebersperma. Labor- und Besamungsergebnisse mit dem Hülsenberg Pailetten-Verfahren. Dtsch. tierärztl. Wochenschrift 82, 261 – 267

Characterization of Original Braunvieh in Bavarian Allgäu based on body measurements

HELLER, Georg-Ulrich[1] – BÉKEFI, Janka[2] – ANNUS, Kata[1] – IMMLER, Stefan[3] –
BÉRI, Béla[2] – GÁSPÁRDY, András[1]

[1]Szent István University, Faculty of Veterinary Science, Institute for Animal Breeding, Nutrtition and Laboratory Animal Science, 1078 Budapest, István street 2., Hungary
[2]University of Debrecen, Faculty of Agricultural and Food Sciences and Environmental Management, Institute of Animal Science, Biotechnology and Nature Conservation Böszörményi 138, 4032 Debrecen, Hungary
[3]Arbeitsgemeinschaft Deutsches Braunvieh Allgäuer Herdebuchgesellschaft Abteilung Kempten, 87435 Kempten, Kotterner Str. 36, Bundesrepublik Deutschland

Abstract

The Original Braunvieh is a middle sized cattle breed, originated from the Alps. It is a traditionally dual-purpose breed, however today it is mostly used for milk production. In this study the current state of the breed was characterized according to body measurements and body indices as well. The measurements of 60 cows were taken in farms around Kempten (Bavaria), by use of measuring stick and tape measure. With regard to the body measurements and to the body indices, a large variance was observed. All body measurements showed significant ($p<0.10$) increase with age. It is concluded that a slow isometric growth is typical for the Original Braunvieh cows. The breed is showing characteristics of a traditional dual-purpose breed, good tendencies in both, for milk (overgrowth index) and meat (compactness index) production. This study aims to reveal the advantageous properties of the Original Braunvieh.

Introduction

The Braunvieh breed group of cattle is considered to be a descendant of the Torfrind which has been living in fore Alp region in the Early Bronze Age, however other cattle strains (like Illyrian, Ligurian-Iberian, Raetian, Alemanni, and Podolian Cattle) contributed to its development. Well defined multipurpose variants of the Braunvieh breed group (e.g. Allgäuer, Oberinntaler, Lechtaler, Montafoner, Schwyzer, and Eringer) appeared on the course of its history, and became threatened by extinction.

The term "Original Braunvieh" was created in 1979 in Switzerland, as some breeder refused to cross their originally pure bred animals with Brown Swiss (GUGGENBERGER-WAIBEL and BLANK, 2010). They wanted to clearly distinguish this breed from the crossed animals. In 1987 the breeders from Allgäu took over this name as well, to save the remnants and to continue the work with their pure breed, for better milk and meat quality. The 1950s were dominated by the fight against tuberculosis. At this time, the use of milking machines became popular. The cows were small, and this caused problems in using the new milking technology. To prevent the farmers from changing to pure dairy breeds (e.g. Holstein-Friesian), the authorities of cattle breeding decided to do a test hybridisation with Brown Swiss bulls from the USA, started in Baden Württemberg in 1965. 100 semen portions from 13 American Brown Swiss bulls were introduced. Most of them exceeded the average breeding values, based on milk and fat performance. The inseminated cows were preselected based on performance as well. 52 of the male offspring (F1 generation: 50% Brown-Swiss) were backcrossed with non-preselected herd book cows (BC1 generation: 25% Brown-Swiss). It was also bred by mating F1 cows with F1 bulls which resulted in a F2 generation (50% Brown-Swiss; BOLLMEIER, 1990). The crossbred animals were larger and gave significantly more milk. With the crossing of Brown Swiss, the original breed was dramatically repressed. Thus, the average Brown Swiss gene portion was 35.4 % in Braunvieh of Württemberg calves, randomly selected from 25 listed herd book farms in the years 1968 to 1980 (SPATSCHEK, 1981).

The Braunvieh was kept for about 80 years, both as a crossing partner, but also in pure breed. Due to its excellent properties they were widespread in large countries with beef production as well, for example Brazil, Canada, Mexico or South Africa.

Nowadays, the Original Braunvieh can be described as the autochthonous cattle breed of the Allgäu and is closely connected with the historical development of this dairy region. It is suitable for both milk and meat production under extensive and intensive conditions. The milk contains a high proportion of Kappa-Casein genotype AB and BB, these are the most favourable for cheese production.

The Original Braunvieh’s meat quality is in accordance with the highest standards on the tenderness, flavour, and juiciness and shows an ideal intramuscular fat content.

Because of the strong specialization in dairy farming in the Allgäu region, the meat production is only of minor importance. The favourable meat characteristics of the Original Braunvieh have been underestimated during the past few decades - at least in the region of its origin. However, due to the excellent mothering ability, it is particularly suitable for suckler cow husbandry. This type of farming has been increasing again during recent years. The Allgäu meat production could become more important in the future again.

The Original Braunvieh is a middle sized cattle with deep torso, solid bones, and good muscles; colour varies from dark brown to grey-brown, inner hairs of the ear are bright; horn tips, muzzle and claws are dark pigmented and the muzzle is bordered by a bright seam (“Rehmaul“).

Particular emphasis will be placed on the longevity of the animals. The durable dual purpose cow should not be too precocious, but should give birth to a calf every year. It should have a middle size frame and show healthy foundation with hard claws. The udder should be glandular and able to be milked easily with a well-developed central ligament and correct teats. In addition to good milk yield, the fattening ability gets bigger attention as well, to guarantee the economic use of these animals for fattening and slaughter. Animals should produce quality meat with a high carcass value.

Great flank-depth and wide chest for high forage intake capacity and a high feed conversion rate is to improve. As a robust, resistant and adaptable cattle, the Original Braunvieh is particularly suitable for pasture grazing both in lowlands and in the mountains. In suckler cow husbandry it is expected from the durable original Braunvieh cow a regular fertility and good breeding performance, moreover they should be frugal and undemanding. Vitale, fast-growing and well-muscled calves should be the hallmark of the Original Braunvieh with good sucking reflex. The animals shall show a calm grazing behaviour and be easy in handling for their holders.

In this study the aim were to take down the major body measurements and calculate the body indices for an up-to-date constitutional type evaluation within the frame of a thesis (HELLER, 2014).

Material and methods

The body measurements were collected from - according to the pedigree - genetically unrelated cows of different ages in order to receive good representative samples. The farms were all located around Kempten in Allgäu (Bavaria) in a radius of about 35 km. Altogether 60 cows of Original Braunvieh Cattle provided with an individual animal identification - official ear tags - were recorded form 23-26 October during 2013. All animals were under herd book control. The livestock owners helped in the careful selection of picking the defined individuals. Also birth date, the last calving date, and the actual body weight were recorded. Leader farm's owner was Mr. Ferlings from Eggenthal with 9 tested cows on 23/10/2013. Other farms were found in the Bavarian rural districts Oberallgäu (7 farms), Ostallgäu (5 farms), Unterallgäu (2 farms), Kempten (2 farms) and Lindau with one farm, as well as in the enclave of the district Reutte (Austria/Tyrol) with one farm.

To measure accurately the cows the following tools were used: a proper measuring stick and a tape measure. This tall stick, marked with measurements, with two fixable horizontal bars which slides up and down and can be fixed in wanted position on the stick. For example to measure wither height, the stick is held alongside the cow, and the upper horizontal bar is slid down until it touches the cow´s withers. The tape measure has two functions, one for measuring length in cm and second to estimate the body weight. The measurement of the heart girt is approximately proportional to the body weight. The tape measure is laid over the back of the animal and is put back around chest. It is located right behind the shoulder in perpendicular position to the floor. After declining the heart girth in cm (indicates the circumference of chest), on the back side of the tape measure from this side of view it shows the approximately body weight in kg.

All together 12 body measurements were taken, 8 with the measuring stick (height at withers, height at sacrum, rump width btw hips, rump width btw trochanters, rump width bw pins, chest depth, chest width, trunk length) and 4 with the tape measures (head length, head width, cannon girth, heart girth). The body measurements were checked in scatterplots by age. Two outliers (the youngest and the oldest cows, of age 1.2 and 14.7, respectively) were deleted from the statistical evaluation, because these greatly affected the slope of the regression line. With the body measurements there were calculated body indices (Table 1). The larger the index value, the more pronounced is the index property at the animal.

Table 1: Applied Calculation of body indices

Index of breast =	100 * (chest width / rump width)
Index of stubbiness =	100* heart girth / $\sqrt{}$ (chest depth^2 + body length^2)
Index of compactness =	100* heart girth / height at withers
Index of narrowness =	100 * body length / chest width
Index of leg length =	100* chest depth / height at withers
Index of strength, rear view =	100 * (rump width / height at withers),
Index of body capacity =	[(chest width + rump width)/2 * chest depth * body length] / 1000
Index of head =	100 * head length / body length
Index of pelvic overgrowth =	100 * height at sacrum/ height at withers
Cannon bone load index =	1000 * cannon bone circumference / body weight

Before further evaluation, the impact of the age on both the body measurements and body indices was proven by linear regressions (to determine the regression coefficient, b; and its p-value). Both were adjusted for two different ages (for 4 and 8 years of age. The adjustments were achieved for each individual with the following formula:

$$\text{age corrected value} = \text{recorded value} - \big((\text{real age} - 4 \text{ or } 8) * \text{b}\big)$$

The average age of the cows were 6.9 years (with a range of 2.8 – 12.4 years of age). On the age corrected values of both body measurements and body indices the Shapiro-Wilk W test for normality was carried out. If the p-value of this statistic is significant ($p<0.10$), the hypothesis that the respective distribution is normal should be rejected. This statistical evaluation was done with the Statistica Computer Software (STATSOFT, INC.; 2013). As results of Shapiro-Wilk W test all traits followed normal distribution.

Results and discussion

The body measurement results are shown in the Table 2. The impact of the age on the body measurements were basically without exception significant ($p<0.10$). In case of the chest width the impact of the age was proven non-significant ($p=0.132$). It means that the cows change their size by ageing. From the b-values in positive range (here not presented) it became obvious that the cows increased all their body measurements during the age section investigated. According to our results the Original Braunvieh is a really medium sized cattle breed.

Table 2: Results of adjusted body measurements (in cm, n=58)

measurement	for 4 years of age adjusted		for 8 years of age adjusted	
	mean	SD	mean	SD
height at withers	131.2	4.61	133.5	4.61
height at sacrum	137.0	3.71	138.4	3.71
rump width btw hips	55.0	2.85	56.2	2.85
rump width btw trochanters	49.6	2.78	51.1	2.78
rump width btw pins	35.2	2.89	36.6	2.89
chest depth	71.6	2.86	72.8	2.86
chest width	48.8	3.24	49.9	3.24
heart girth	199.8	7.38	203.9	7.38
body length	153.8	5.21	155.7	5.21
head length	42.0	2.76	43.1	2.76
head width	22.0	1.54	22.9	1.54
cannon girth	21.3	0.87	21.7	0.87
live weight, kg	657.7	71.0	689.8	71.0

The micro-evolutionary change of the German black pied (cattle) to the Holstein-Friesian Cattle is characterised by the breeding aims especially of the height at sacrum. These aims were in a range of 140 cm and 650 kg live weight (1977), 145 cm and 750 kg (1989) and 145-156 cm and 750 kg (in 2003). While at the same time the height at withers stays same at 132 cm (AGROBIODIVERSITÄT, 2004).

In comparison to the values of the Original Braunvieh it is obvious that the Holstein-Friesian is a very tall and large framed breed with the aim to increase milk performance. This is achieved by increasing leg length of the hind limbs to guarantee better health, milk-ability and space for larger udder at the same time.

In Table 3 are presented the adjusted body indices results, that with except of index of body capacity there were no changes found by ageing. From this observation we can conclude that a slow isometric growth is typical for the Original Braunvieh cows. Also the negative b-values (here not presented) which indicate a decline in the index property are highly accepted by us in spite of the fact that we did not found significant effect of the age.
From the basic knowledge it is obvious that a cow will become stronger in her front of the body by ageing (index of narrowness), relatively shorter legged (index of leg length), less overgrown in sacral region (index of pelvic overgrowth), and she carries relatively smaller load on a unit cross section of the extremities (cannon bone load index).

In the figures of the standard deviation (SD) of the adjusted traits (both body measurements and body indices) appeared to be low. Our results expressed in coefficient of variation (as the ratio of the standard deviation to the mean, cv %) we can state that all the values remained below 10 % (and in many cases below 5%). These inform us about the fact that a phenotypically quite heterogeneous population shows a narrowness in its adjusted characteristics.

Table 3: Results of adjusted body indices (n=58)

indices	for 4 years of age adjusted		for 8 years of age adjusted	
	mean	SD	mean	SD
index of breast	88.8	6.30	88.8	6.30
index of stubbiness	130.1	5.40	130.9	5.40
index of compactness	152.5	6.49	152.8	6.49
index of narrowness	315.4	23.41	315.2	23.41
index of leg length	183.5	7.74	183.4	7.74
index of strength, rear view	40.3	1.92	40.6	1.92
index of body capacity	571.2	55.23	604.9	55.23
index of head	27.3	2.02	27.7	2.02
index of pelvic overgrowth	104.5	2.58	103.7	2.58
cannon bone load index	32.7	3.01	31.7	3.01

Discussion and Recommendation

In a previous Carpathian Braunvieh study (GÁSPÁRDY et al., 2012), published for 5 years of age adjusted body measurements and indices it was stated that the Carpathian variant is by 5-10 cm smaller and by 20 cm shorter, and much narrower than the Original Braunvieh. The head length index 34.9, the overgrowth index 100.7, compactness 146.5, and leg length index 196.2 showed great differences from the Original Braunvieh of this work (27.3, 104.5, 152.5 and 183.5, respectively).

The advantages of the Original Braunvieh are obvious in professional point of view. Both breeds showing characteristics of a dual purpose breed, while the Original Braunvieh shows much better tendencies in both, for milk (overgrowth index) and meat (compactness index) production. At the same time, the Carpathian Braunvieh shows a more primitive type of cattle (less overgrown behind and deeper chest).

In a study about the Holstein dairy cattle measurements (TASDEMIR et al., 2011) cows were examined in the first lactation period between 26 and 36 months. We could compare their results with our adjusted measurements to 4 years. In the live weight the Braunvieh cows were heavier (657.7 kg) than the Holstein cows (570.2 kg). Although in wither height they appeared to be quite the same, 131.2 cm (Braunvieh) and 136.2 cm (Holstein). The rump width btw hips was 49.6 cm for the Braunvieh cows, the Holstein cows seemed to be wider with 54.2 cm. The Holstein cows can be considered as longer animals with the body length of 164.2 cm than the Braunvieh cows with 153.8 cm.

References

AGROBIODIVERSITÄT (2004): IÖW, Öko-Institut, Schweinfurt-Stiftung, Endbericht: FU-Berlin Kapitel 10, 28.

BOLLMEIER, S. (1990): Inzucht, Verwandtschaft und Genanteile im württembergischen Braunvieh: Dissertation, Hannover

GÁSPÁRDY, A. – UNGVÁRY, Cs. – BÉKEFI, J. – BÉRI, B. (2012): History and characterization of Carpathian Brown Cattle – through its Hungarian up-to-date news. Journal d'Ethnozootechnie de Roumanie, No. 2., 22-30.

GUGGENBERGER-WAIBEL. P. – BLANK, A. (2010): Slow Food Deutschland e.V., Arche des Geschmacks; Dokumentation/Gutachten

HELLER, G-U. (2014): A population genetic study on the Original Braunvieh in Bavaria-Allgäu. Thesis. Szent István University, Faculty of Veterinary Science, Budapest

SPATSCHECK, U. (1981): Stand und Entwicklung der Einkreuzung von amerikanischen Brown-Swiss-Tieren in das württembergische Braunvieh – dargestellt am Beispiel von 25 Herdbuchbetrieben. Dissertation. Fachhochschule Nürtingen

STATSOFT, INC. (2013): STATISTICA (data analysis software system), version 12. www.statsoft.com.

TASDEMIR, S. – URKMEZ, A, – INAL, S (2011): Determination of body measurements on the Holstein cows using digital image analysis and estimation of live weight with regression analysis. Computers and Electronics in Agriculture 76. 189–197.

Few important ancestors contribute much of the genetic material: Pedigree analysis of three highly endangered cattle breeds in Austria

BINDER, Susanne[1] – BERGER, Beate[2] – SÖLKNER, Johann[1]

[1] BOKU – Univ. Nat. Res. Life Sci. Vienna, A-1180 Vienna, Gregor Mendel Str. 33, Austria
[2] Institute of Organic Farming and Biodiversity of Farm Animals, A-4600 Wels, Austr. 10, Austria

Abstract

This study investigated the pedigrees of three highly endangered local cattle breeds of Austria: Pustertaler Spotted Cattle, Ennstaler Pied Cattle and Original Austrian Brown Cattle. The population sizes range from 236 (Ennstaler Pied) to 1601 (Original Austrian Brown) herd book cows (2010). Breeders follow the conservation program of ÖNGENE, the Austrian Association for Rare Endangered Breeds, by systematically avoiding mating of closely related animals, applying the projected inbreeding coefficient of the potential progeny as indicator. While Original Austrian Brown is derived from a large ancestral population, the two other breeds are based on very small numbers of founder animals.

The study contributes to the target of developing tools for finding bulls to collect semen in order to minimize further narrowing of these closed populations of endangered breeds.

PEDIG software was used to calculate the contributions of the most important ancestors for the three breeds. Three types of reference populations were defined, as of 2015: 1) living population; 2) male living animals of which no semen was available; 3) bulls for which semen was available.

The results indicated that Ennstaler Pied Cattle is the genetically smallest population of the three. Five most important ancestors contributed >50% of the genetic material for reference populations 1 and 2, the corresponding number for population 3 is nine. For Pustertaler Spotted Cattle, the most important ancestor (a bull called Ortner) contributed 8.35-9.63% to the genetic material of the three reference populations. Nine to 12 ancestors contributed at least 50% of the genetic material.

The Original Austrian Brown Cattle population is more diverse, due to the use of bulls from Austria, Germany and Switzerland for insemination. The most important ancestor of the two living populations contributes 6.86-7.08%. Most (17) of the 20 most important ancestors of the living Ennstaler Pied Cattle population are female while for other two breeds the majority of the most important animals are male (18 for Original Austrian Brown Cattle and 13 for Pustertaler Spotted Cattle).

Pedigree analysis indicates that the choice of young bulls to be used in artificial insemination will be crucial to minimize loss of genetic diversity in those three breeds.

Autochthonous cattle breeds in Croatia, trends and challenges

[1]IVANKOVIĆ Ante, [1]RAMLJAK Jelena

[1]Department of Animal Science and technology, Faculty of Agriculture, Svetošimunska 25,
10000 Zagreb, Croatia

Abstract

Autochthonous cattle breeds in Croatia in recent years get more attention, which is reflected in increased number of individuals and balanced population structure. These positive trends are encouraged with subsidies aimed for autochthonous breeds, also with their affirmation in public. Cattle breeds are phenotypically and genetically characterised what encouraged breeding consolidation. The knowledge of the genetic structure based on proteins polymorphism, microsatellites, *mt*DNA and *SNP* can help to maintain genetic variability and control level of inbreeding. The most important challenge to the sustainability of cattle breeds is their affirmation in programs of economic utilisation because program confirms the high sustainability risk level of economically inferior breeds. The aim of the paper was to analyse population trends, to utilize of all available indicators of genetic structure and phenotypic characteristics, and to estimate the importance of establishing a program for economic use of indigenous breeds. According to the size of the population during the last decade the average growth ranged from 9.4 to 20.3%, as well as the number of breeders actively involved in breeding. During that time number of herds per years increased from 5.7 to 13.2% as well as the average size of the herd per breeder. The average ratios of bulls vs. cows ranged from 9.4 to 16.9 indicating more uniform distribution in Busha population. Average number of calves per breeding cow in 10 years period (2005-2014) was 0.29 (Istrian cattle) to 0.44 (Slavonian Syrmian Podolian cattle) indicating insufficient reproductive efficiency. According to the parameters of the population genetic structure based on proteins polymorphisms, microsatellites, *mt*DNA and *SNP* chip, departure from observed (H_O) and expected heterozygosity (H_E) are indicated. The most vulnerable population of Slavonian Syrmian Podolian cattle experienced genetic bottleneck reflected with high inbreeding level. Due to the utilization of genetic markers, *SNP* chips are the most informative, but in terms of ratio between price and usefulness in the implementation of breeding consolidation, microsatellites as genetic markers of choice are still very usable. Effectiveness of existing programs on breeds' economic affirmation is very important for their sustainability. Economic vital programs can support more expensive methods of population control and their sustainability. Also, local community is very important in conducting the program of breed affirmation and promotion, and good example is revitalization of the Istrian cattle.

Analysis of inbreeding and average relationship of the present Hungarian Hucul Horse population

SOMOGYVÁRI, Enikő[1] – POSTA, János[1] – MIHÓK, Sándor[1]

[1]University of Debrecen, Faculty of Agricultural and Food Sciences and Environmental Management, Institute of Animal Science, Biotechnology and Nature Conservation, Department of Animal Breeding, 4032 Debrecen, Böszörményi str. 138, Hungary

Abstract

The Hungarian Hucul Horse population under gene protection was analysed using population genetic parameters. The used dataset was based on the breeding stock of 2015 and pedigree information was collected up to the founder ancestors. The population was described using inbreeding coefficient and average relationship. The parameters were computed using Endog software. The average inbreeding of the reference population was 6.8% whereas it was 5.65% for the whole population. The average relationship was 12.7% and 10.55% for the reference population and the total population, respectively.

Introduction

The aim of the study was to evaluate the genetic structure of the Hungarian Hucul population based on pedigree data, using population genetic methods. The performance of such examinations has been increasingly justified and frequent in the case of endangered breeds whose population has shrunk to a small size. These calculations may be of great help when designing or making necessary modifications to the breeding programmes. They may set the directions or even the extent of the modifications. They may imply ways for and prove the necessity of sustaining diversity within the populations, may help avoid close breeding or suggest mating systems.

The theoretical bases of pedigree analysis were first discussed by WRIGHT (1931), followed by JAMES (1962, 1971, 1972), MAC CLUER et al. (1986) and LACY (1989). Since the method of BOICHARD et al. (1997), several pedigree analyses have been published with reference to various species. Thanks to the development of computer science, today there is opportunity for performing pedigree analyses using various programmes. The programme package PEDIG written in the Fortran programming language by BOICHARD in 2002 made the analysis of bigger pedigrees possible. Three years later the ENDOG programme enabling the pedigree analysis of smaller populations was released, written in Visual Basic (GUTIÉRREZ AND GOYACHE, 2005). In 2006, SARGOLZAEI et al. designed a programme written in Visual C++ and the following year (2007) COLE wrote PyPedal in Python. In 2009, GROENEVELD et al. published the programme Poprep, creating the opportunity of comparing populations as well.

There are numerous references of inbreeding coefficients with regard to various horse breeds, which usually varies between 0.66 and 15.7. Table 1 shows results of several authors publishing inbreeding information of different horse breeds.

Table 1. Inbreeding coefficients of different horse breeds

Source	Breed	Inbreeding coefficient
Moureaux et al. (1996)	Anglo-Arab	1.17
	Arab	3.08
Pjontek et al. (2012)	Shagya Arabian horses	3.95
Cervantes et al. (2008)	Spanish Arab Horse	7
Moureaux et al. (1996)	Thoroughbred	1.02
Bokor et al. (2013)	Hungarian Thoroughbred	9.58
Cunningham et al. (2001)	English–Irish Thoroughbred	14
Pjontek et al. (2012)	Lipizzaner horse	4.02
Zechner et al. (2002)	Lipizzaner horse	10.81
Bartolomé et al. (2011)	Spanish Sport Horse	0.66
Pjontek et al. (2012)	Slovak Sport Ponies	2.67
Moureaux et al. (1996)	Selle Français	0.7
Pjontek et al. (2012)	Hucul horses	6.26
Sevinga et al. (2004)	Friesian horses	15.7

With regard to average relatedness, in the reviewed literature values (Table 2.) between 0.16 and 12.25 were reported.

Table 2. Average relatedness of different horse breeds

Source	Breed	Average relatedness
Bartolomé et al. (2011)	Spanish Sport Horse	0.16
Pjontek et al. (2012)	Shagya Arabian horses	3.08
	Lipizzaner horse	3.73
Dunner et al. (1998)	Asturcon pony	6.8
Pjontek et al. (2012)	Slovak Sport Ponies	7.19
Cervantes et al. (2008)	Spanish Arab Horse	9.1
Royo et al. (2007)	Asturcón pony	9.2
Pjontek et al. (2012)	Hucul horses	9.34
Bokor et al. (2013)	Hungarian Thoroughbred	10
Valera et al. (2005)	Andalusian horse	12.25

Material and methods

The dataset of our study based on the pedigree information of the Hungarian Hucul Horse breed which is an indigenous breed of Hungary. Pedigree information of the breed up to 2015 was used in the analysis. Animals registered in the breeding stock in 2015 were handled as reference population. The total dataset contained the pedigree information of 3,002 horses. The inbreeding coefficient and average relatedness was computed using the Endog software (GUTIÉRREZ AND GOYACHE, 2005).

The precision of the widely known and used *inbreeding coefficient* depends on the length and completeness of the pedigree (BOICHARD et al. 1997).
The Endog software calculates using WRIGHT’s formula (1922) where the inbreeding coefficient of a given individual (X) is:

$$F_X = \Sigma(1/2)^{n+n'+1} \times (1+F_A)$$

The Endog software calculates *average relatedness* with an algorithm made by COLLEAU (2002). It shows the likelihood of an allele randomly chosen from the pedigree characterising the whole population belonging to an individual.

Results and discussion

The inbreeding coefficient and average relatedness was computed for the reference and the total population, respectively. Because of the proper comparison, mare families and stallion lines were presented in figures for the total population when they have appeared also in the reference population.

Inbreeding coefficient (F_x)

Average inbreeding of the reference population was 6.8% (318 horses) whereas it was 5.65% (3,002 horses) for the total population. Our results are significantly higher than those specified by BARTOLOMÉ et al. (2011) for Spanish Sport horses (0.66%), MOUREAUX et al. (1996) for Selle Français (0.7) and Anglo-Arab (1.17%). At the same time it is lower than the 10.81 % specified by ZECHNER et al. (2002) for Lipizzan horses and SEVINGA et al. (2004) for Friesian horses (15.7%). Our results show that inbreeding is increasing within the population under study.

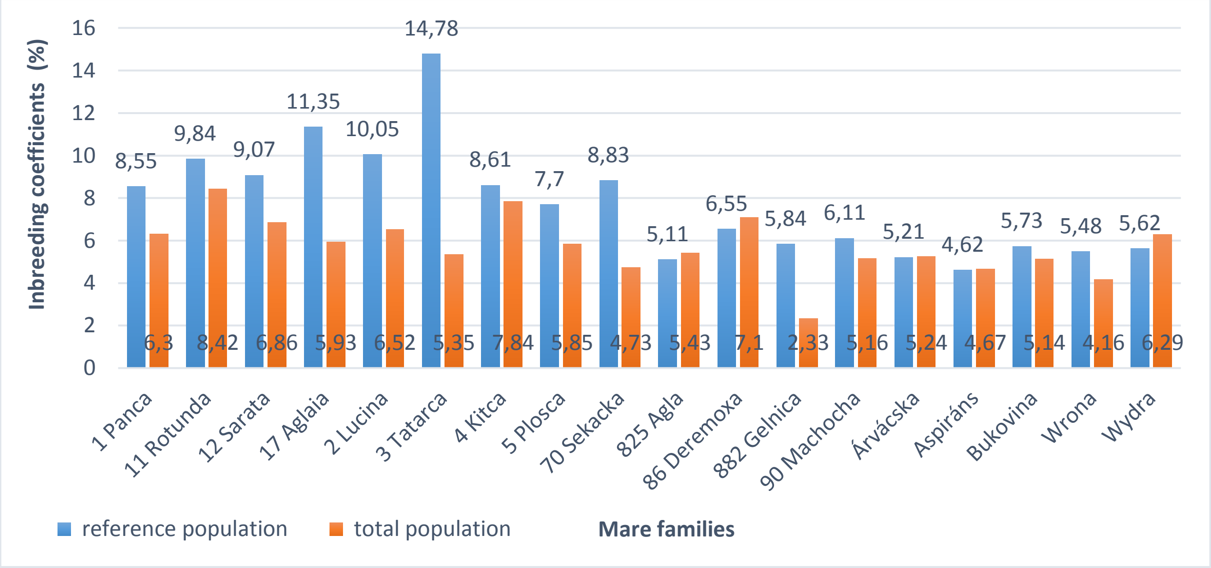


Figure 1. Average inbreeding coefficients of mare families

The average inbreeding of mare families is shown in Figure 1 for the reference and the total population, respectively. The smallest inbreeding (4.62%) belongs to the ‘Aspiráns’ mare family, whereas ‘3 Tatarca’ has the highest inbreeding (14.78%). The high inbreeding of three mares within the ‘3 Tatarca’ family (Pietrosu Parázna, Pietrosu Parázs, Pietrosu Picur) is resulted by the appearance of ‘Pietrosu IX (Lu)’, ‘Ousor IV (Lu)’ and ‘62 Prislop I-8 (Lu)’ in their 3-4-5 ancestor generation. They are followed by ‘17 Aglaia’ (11.35%) and ‘2 Lucina’ (10.05%). During the evaluation of the total population, the average inbreeding of mare families is lower than those of the reference population (values are below 9).

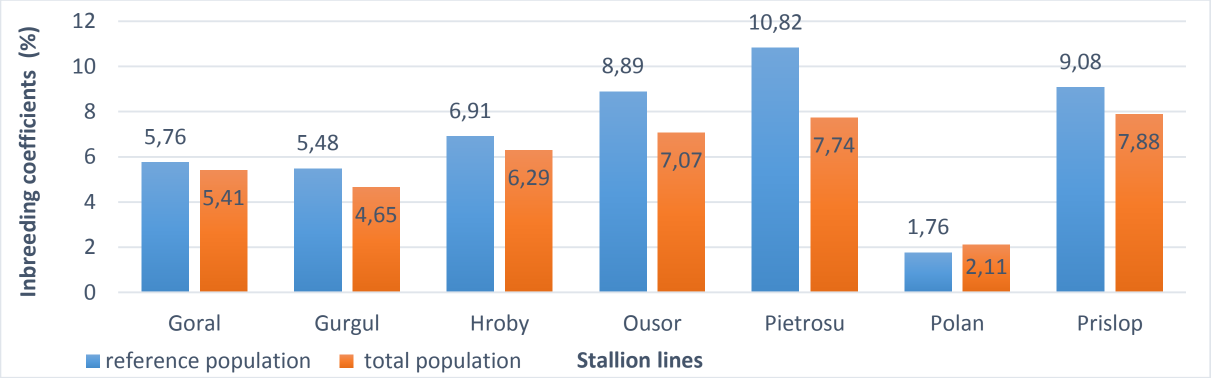


Figure 2. Average inbreeding coefficients of stallion lines

Distribution of inbreeding coefficient over stallion lines is presented in Figure 2. ‘Pietrosu’ line has the highest inbreeding (10.82%) within the reference population as the result of appearance several Pietrosu descendant horses both in the paternal and maternal background. The smallest coefficient (1.76%) was computed for the ‘Polan’ stallion line. The stallion ‘3139 Polan (Pol)’ was bred using mares originated from ‘Ousor’, ‘Hroby’, ‘Goral’, ‘Prislop’ and ‘Pietrosu’ strains and the received value might be because of the breeding method. There are only a few animals from the ‘Polan’ strain within the Hungarian breeding which also could be the reason of the low average inbreeding of this strain.

Average relatedness (AR)

Unfortunately, the average relationship of the reference population (12.7 %) is higher than that of the total population (10.55%). These values are significantly higher than the published by other authors. BARTOLOMÉ et al. (2011) published 0.16% for Spanish Sport Horses, PJONTEK et al. (2012) 3.08% for Shagya Arabian horses and 3.73% for Lipizzan horses. The highest value within previous studies was found in VALERA et al. (2005) referring to Andalusian horses, the value being 12.25%.

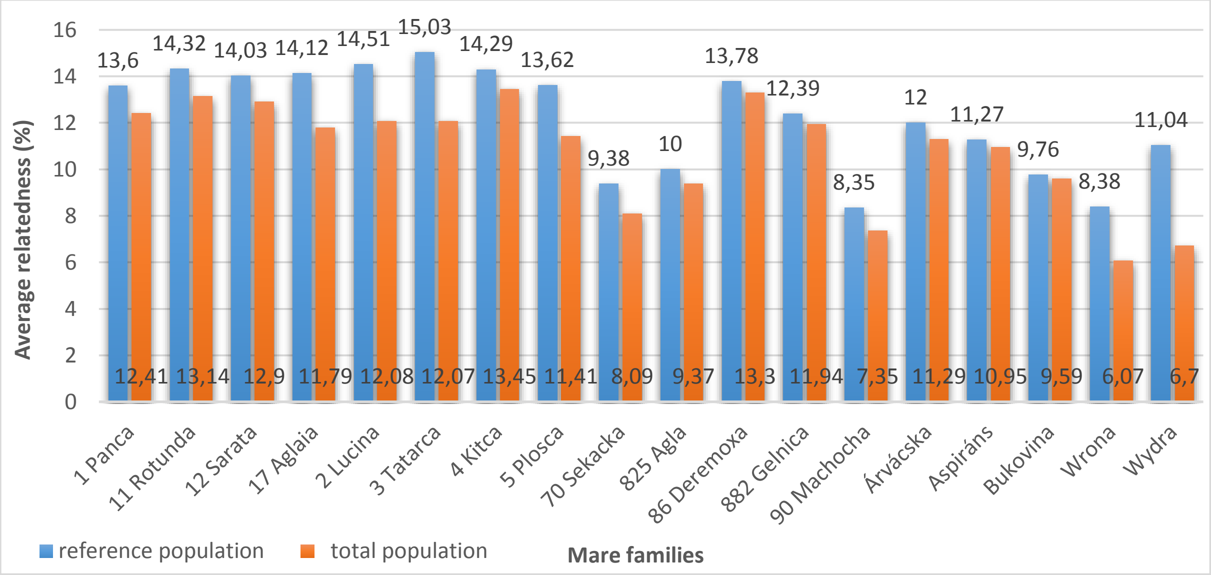


Figure 3. Average relatedness of mare families

Figure 3 shows the average relationship of mare families for the total and the reference population, respectively. The average relationship is above 13% for most of the families in the reference population. The smallest average relationship was computed (8.35%) for the ‘90 Machocha’ mare family. The moderate diversity of ‘3 Tatarca’ mare family is shown by its average relationship (15.03%).

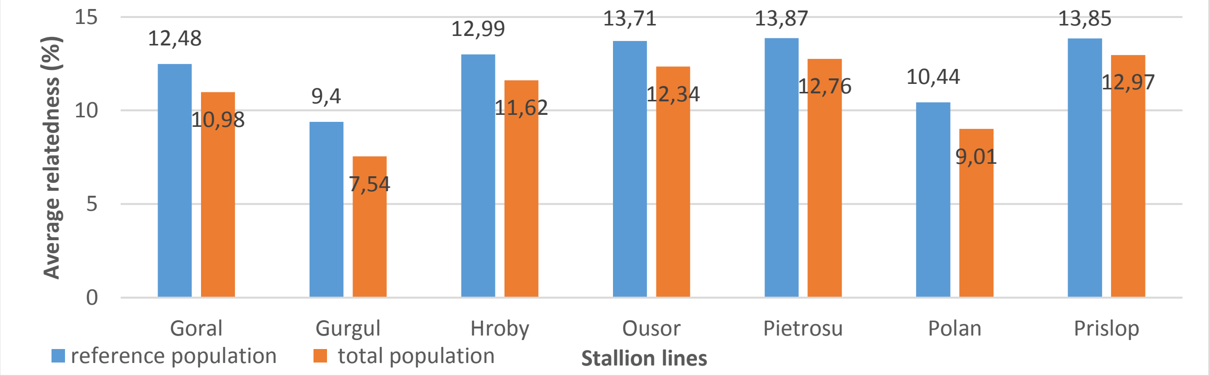


Figure 4. Average relatedness of stallion lines

Figure 4 illustrates the average relationship of the Hucul strains. The smallest value was computed for the ‘Gurgul’ strain (9.4%), whereas it was 13.87% for the ‘Pietrosu’ strain.

Conclusion and recommendation

The increasing of the inbreeding level of the population cannot be avoided both in the total and the reference population as the average relationship is much higher than the inbreeding coefficient. The inbreeding coefficient of the total population was 5.65%, the average relationship was 10.55%. The inbreeding coefficient of the reference population was 6.8%, the average relationship was 12.7%. The genetic diversity of the Hungarian Hucul Horse breeding stock is favourable based on the inbreeding level compared to other breeds (English Thoroughbred, Friesian Horse).

References

BARTOLOMÉ, E. – CERVANTES, I. – VALERA, M. – GUTIÉRREZ, J.P. (2011): Influence of foreign breeds on the genetic structure of the Spanish Sport Horse population. Livest Sci. 142. 70–79.

BOICHARD, D. (2002): PEDIG: A FORTAN package for pedigree analysis suited for large populations. In: Proc 7th World Congr. Appl. Livest. Prod. Montpellier, France, Comm. 28-13.

BOICHARD, D. – MAIGNEL, L. – VERRIER, É. (1997): The value of using probabilities of gene origin to measure genetic variability in a population. Genet Sel Evol. 29. 5–23.

BOKOR, Á. – JÓNÁS, D. – NAGY, I. – BOKOR, J. – SZABARI, M. (2013): Pedigree analysis of Hungarian Thoroughbred population. Livest Sci. 151. 1-10.

CERVANTES, I. – MOLINA, A. – GOYACHE, F. – GUTIÉRREZ, J.P. – VALERA, M. (2008): Population history and genetic variability in the Spanish Arab Horse assessed via pedigree analysis. Livest Sci. 113. 24 -33.

COLE, J.B. (2007): PyPedal: A computer program for pedigree analysis. Comput Electron Agr. 57. 107–113.

COLLEAU, J.J. (2002): An indirect approach to the extensive calculation of relationship coefficients. Genet. Sel. Evol. 34. 409–421.

CUNNINGHAM, P. – DOOLEY, J.J. – SPLAN, R.K. – BRADLEY, D.G. (2001): Microsatellite diversity, pedigree relatedness and the contributions of founder lineages to Thoroughbred horses. Anim. Genet. 32. 6: 360–364.

DUNNER, S. – CHECA, M.L. – GUTIERREZ, J.P. – MBARTIN, J.P. – CANON, J. (1998): Genetic analysis and management in small populations: the Asturcon pony as an example. Genet. Sel. Evol. 30. 397-405.

GROENEVELD, E. – WESTHUIZEN, B.V.D. – MAIWASHE, A. – VOORDEWIND, F. – FERRAZ, J.B.S. (2009): POPREP: a generic report for population management. Genet and Mol Res. 8. 3: 1158-1178.

GUTIÉRREZ, J.P. – ALTARRIBA, J. – DÍAZ, C. – QUINTANILLA, R. – CANON, J. – PIEDRAFITA J. (2003): Genetic analysis of eight Spanish beef cattle breeds. Genet Sel Evol. 35. 43-63.

GUTIÉRREZ, J.P. – GOYACHE, F. (2005): A note on ENDOG: a computer program for analysing pedigree information. J Anim Breed Genet. 122. 172-176.

JAMES, J.W. (1962): The spread of genes in random mating control population. Genet. Res. 3. 1–10.

JAMES, J.W. (1971): The founder effect and response to artificial selection. Genet. Res. 16. 241–250.

JAMES, J.W. (1972): Computation of genetic contributions from pedigrees. Theor. Appl. Genet. 42. 272–273.

LACY, R.C. (1989): Analysis of founder representation in pedigrees: founder equivalents and founder genome equivalents. Zoo Biol. 8. 2: 111– 123.

MAC CLUER, J.W. – VAN DE BERG, J.L. – READ, B. – RYDER, O.A. (1986): Pedigree analysis by computer simulation. Zoo Biol. 5. 2: 147–160.

MAIGNEL, L. – BOICHARD, D. – VERRIER, E. (1996): Genetic variability of French dairy breeds estimated from pedigree information. Interbull Bull. 14: 49-54.

MIHÓK, S. (2014): Hucul Méneskönyv I-II-III. kötet. Debrecen, Póni és Kislótenyésztők Országos Egyesülete.

MOUREAUX, S. – VERRIER, É. – RICARD, A. – MÉRIAUX, J.C. (1996): Genetic variability within French race and riding horse breeds from genealogical data and blood marker polymorphisms. Genet Sel Evol. 28. 83-102.

PJONTEK, J. – KADLEČÍK, O. – KASARDA, R. – HORNÝ, M. (2012): Pedigree analysis in four Slovak endangered horse breeds. Czech J. Anim. Sci. 57. 2: 54–64.

ROYO, L.J. – ÁLVAREZ, I. – GUTIÉRREZ, J.P. – FRENANDEZ, I. – GOYACHE, F. (2007): Genetic variability in the endangered Asturcón pony assessed using genealogical and molecular information. Livest Sci. 107. 162-169.

SARGOLZAEI, M. – IWAISKAI, H. – COLLEAU, J.J. (2006): CFC: a tool for monitoring genetic deversity. In: Commun. No. 27–28 in Proc. 8th World Congr. Genet. Appl. Livest. Prod. Belo Horizonte, Brazil.

SEVINGA, M. – VRIJENHOEK, T. – HESSELINK, J.W. – BARKEMA, H.W. – GROEN, A.F. (2004): Effect of inbreeding on the incidence of retained placenta in Friesian horses. J. Anim. Sci. 82. 982–986.

VALERA, M. – MOLINA, A. – GUTIÉRREZ, J.P. – GÓMEZ, J. – GOYACHE, F. (2005): Pedigree analysis in the Andalusian horse: population structure, genetic variability and influence of the Carthusian strain. Livest Sci. 95. 57-66.

WRIGHT, S. (1922): Coefficients of inbreeding and relationship. Am. Nat. 56. 330-33.

WRIGHT, S. (1931): Evolution in Mendelian populations. Genetics. 16. 97–159.

The technique and findings of ultrasonographic assessment of fetal well-being in Lipizzaner mares in a Hungarian stud farm (2013-2015)

VINCZE, Boglárka[1,2] – SZENCI, Ottó [2,3]

[1]Institute for Animal Breeding, Nutrition and Laboratory Animal Science, Szent István University, Budapest, 1078-Budapest, István utca 2. Hungary
[2]MTA-SZIE Large Animal Clinical Research Group, Department and Clinic for Production Animals, 2225-Üllő Dóra major, Hungary
[3]Department and Clinic for Production Animals, Szent István University, Budapest, 2225-Üllő Dóra major, Hungary

Abstract

Despite of advanced techniques in equine reproduction pregnancy loss in late term mares is still high. The evaluation of the fetus is the first step towards decreasing perinatal mortality and morbidity. REEF et al. in 1995 and 1996 made a modified biophysical profile specific to the equine fetus. This examination method became the gold standard for decades with its acute and chronic hypoxic components. The minimum 30 minutes (30-90 average time) examination is sometimes too long and not all parameters can be measured under farm conditions. Our goal was to develop a rapid assessment protocol for mares in mid- and late gestation which gives useful information about fetal well-being and viability. Late term (270-315 gestational days) pregnant broodmares (n=35) have been examined with transabdominal ultrasound in a Hungarian Stud farm. Fetal heart rate (FHR), aortic diameter (Ad), combined thickness of the uteroplacental unit (CTUP) and birth weight (BW) have been measured (mean±SD) and analyzed (R software, Vienna, Austria) related to pregnancy outcome. All examinations were performed between 5-15 minutes with a 3.5 MHz macroconvex ultrasound probe (Mindray M5 Vet®, Mindray Medical International Ltd., China). 34/35 mares had single fetuses and one had twins. In one case placentitis could be detected. FHR, Ad, CTUP, and BW were (89±11) bpm, (1.8±0.2) cm, (13.2±2.9) mm and (48.6±6.8) kg. Aortic diameter increased significantly with ongoing pregnancy and BW (P=0.0004). It has been concluded that this rapid examination protocol was a reliable and informative method for assessing fetal well-being and examinations could detect abnormal pregnancies (twins, placentitis) under farm conditions as well.

Introduction

Despite of advanced techniques in equine reproduction pregnancy loss in late term mares is still high; the rate can reach as high as 15-20% and therefore can cause significant economic loss especially in rare and endangered horse breeds. Reproduction management is therefore inevitable in horse farms breeding rare horse breeds. Veterinarians normally check pregnancy at 14-15 days after service; day 40 pregnancy check is also well known in most farms, but later, during the advanced gestation, it is not common to check the development of the equine fetus. In Hungary, ultrasonographic assessment of the foal fetus is not known and therefore not used. From year 2013, we started to work with this technique in a large breeding farm in

North-eastern Hungary to develop a reliable and low-cost sonographic method for a fast examination of the fetus. In other countries, it has been shown, that the evaluation of the fetus is the first step towards decreasing perinatal mortality and morbidity. REEF et al. in 1995 and 1996 made a modified biophysical profile (an ultrasonographic scanning method) specific to the equine fetus. In the USA, this examination method became the gold standard for decades with its acute and chronic hypoxic components. The minimum 30 minutes examination is sometimes too long and not all parameters can be measured under farm conditions. We decided to perform a pilot study in 2013 to measure as many parameters as we can in a rare and traditional horse breed: the Lipizzaner. Our goal was to develop a rapid assessment protocol for mares in mid- and late gestation which gives useful information about fetal well-being and viability.

Materials and methods

In the initial, pilot study, 20, late term pregnant broodmares were scanned in the last month of their pregnancies and the parameters that could be measured were noted in an examination sheet made by one of the authors. During these examinations we could collect the experiences regarding fetal transabdominal ultrasound in horses. The previous examinations (REEF et al., 1995) have been performed in equine clinics, with clinical equipment, hence we should have to modify it for farm circumstances. During the whole study period, a total of 35 mares have been evaluated in 2013-2015 breeding seasons.

Patient preparation

For safety reasons horses should be placed in a stock wherever they are examined (REEF et al., 1995, 1996; BASKA-VINCZE et al., 2013). For the examination it is recommended to clip the hair surgically over the ventral abdomen. The size of the clipped area depends on the gestational age (ADAMS-BRENDEMÜHL and PIPERS, 1987; BUCCA et al., 2005). In late-term mares, this area usually extends from the mammary gland to the xiphoid process and includes both sides of the abdomen. Although the use of surgical clipping has been recommended, in our experience this is not necessary.

Technique and ultrasonographic findings

The method of transabdominal ultrasonographic evaluation in the mare was described in detail previously (REEF et al., 1995). In mares, transabdominal ultrasonography of the fetus can be performed with a 2.5–3.5 MHz macro- or microconvex transducer capable of reaching 20–30 cm penetration depth. However, the uteroplacental unit can be scanned better by the use of higher frequencies, usually between 6–10 MHz with a penetration of 4–10 cm. At present, different ultrasound transducers are available for clinicians and veterinarians working under field conditions. Diluted ethanol or propanol and ultrasound gel can be used on the skin surface to increase penetration depth and image quality (BASKA-VINCZE et al., 2013).

During the examination of a pregnant mare, the scanning starts in front of the mammary gland and moves cranially. The first task is to locate the fetal thorax with the typical sight of the fetal ribs. If the fetal thorax is found, the fetal aorta should be located and the aortic diameter measured. The callipers of the ultrasound should be placed to the leading edge of the aortic walls as close to the heart as possible. It has been reported that fetal aortic diameter correlates with neonatal birth weight and maternal weight in the mare (n=30) and equations have been developed to estimate body weight (REEF et al., 1995, 1996). The uterus of the mare should be thoroughly scanned to ascertain that only one fetus is present.

Most of the ultrasound scanners make it possible to measure fetal heart rate using M-mode or B-mode.

It has been reported that fetal breathing movements are present in late-term fetuses and their absence can be a sign of acute fetal hypoxia (PALMER, 2000; BUCCA et al., 2005). Fetal breathing movements are best visualised by watching the movement of the fetal diaphragm in relation to the fetal ribs. This can be difficult because of fetal and maternal activity (PALMER, 2000; BASKA-VINCZE et al., 2013).

Fetal activity and tone are also critical components of the examinations. Fetal activity can be graded from 0 to 3 as described by REEF et al. (1995), and grade 2 or 3 is considered normal. Fetal fluid quality and quantity are important parts of fetal monitoring during transabdominal ultrasonographic assessment. Allantoic fluid (in the majority of cases) and amniotic fluid are anechoic until late gestation and, in the horse near term, increased echogenicity can occur with small particles floating in the allantoic fluid (REEF et al., 1995, 1996; BUCCA et al., 2005).

An additional scanning measurement also critical for fetal well-being is the combined thickness of the uteroplacental unit (CTUP). Thickness and continuity of this unit can be measured in the four quadrants of the mare’s abdomen, and the unit is thickened in the case of placentitis, haemorrhage or oedema. Continuity must be checked on the whole uterus, because premature separation of the placenta is a life-threatening condition for the fetus.

Ultrasonographic assessment in high-risk pregnancy

In the horse, high-risk pregnancies have been studied in more detail and the need for advanced knowledge has been recognised. Although improved diagnostic techniques are available in equine reproduction, the incidence of pregnancy loss is still high, varying between 10 and 15% during gestation (TROEDSSON, 2007).

Results and Discussion

Although the examiner is experienced in fetal sonography in mares and cows, not all of the previously mentioned parameters could be detected with this method. Fetal sex, breathing movements and other very diagnostic and important parameters in these cases could not be detected with this procedure. In order to develop a really fast and concurrently reliable examination method, 3 fetal and one neonatal parameters were built into a rapid biophysical profile adapted for farm conditions. Fetal heart rate (FHR), aortic diameter (Ad), combined thickness of the uteroplacental unit (CTUP) and birth weight (BW) have been measured (mean±SD) and analyzed (R software, Vienna, Austria) related to pregnancy outcome. As a result, 34/35 mares had single fetuses and one had twins. In one case placentitis could be detected. FHR, Ad, CTUP, and BW were (89±11) bpm, (1.8±0.2) cm, and (13.2±2.9) mm and (48.6±6.8) kg. Aortic diameter increased significantly with ongoing pregnancy and BW ($P=0.0004$).

Conclusions

According to numerous publications, transabdominal fetal ultrasonography is an effective, useful and often essential method for examining the fetus and the dam in both mares and cows. There have been attempts to create a biophysical profile for both species, but these methods should be refined in order to obtain a higher specificity and sensitivity in animals, comparable to that achieved in human medicine. In the future, simple and low-cost methods should be developed for the evaluation of the pregnant dam and its fetus, in order to develop highly effective methods for the assessment of viability. More and more advanced techniques are available for clinicians and researchers, and attempts should be made to adapt these to everyday veterinary work also in the field.

It has been concluded that this rapid examination protocol reviewed above was a reliable and informative method for assessing fetal well-being and examinations could detect abnormal pregnancies (twins, placentitis) under farm conditions as well.

References

ADAMS-BRENDEMÜHL, C. – PIPERS, F.S. (1987): Antepartum evaluations of the equine fetus. J. Reprod. Fertil. Suppl. 35, 565–573.

BASKA-VINCZE, B. – RÓZSÁS, J. – SZENCI, O. (2013): Assessment of fetal well-being by transabdominal ultrasonography in Hungarian broodmares under clinical and farm conditions. Proceedings of 13th WEVA Congress, Budapest, URL: http://www.ivis.org/proceedings/weva/2013/oral/24.pdf?LA=1.

BUCCA, S. – FOGARTY, U. – COLLINS, A. – SMALL, V. (2005): Assessment of feto-placental well-being in the mare from mid-gestation to term: Transrectal and transabdominal ultrasonographic features. Theriogenology 64, 542–557.

PALMER, J. (2000): Fetal monitoring. Proceedings of the Equine Symposium and Annual Conference , San Antonio. pp. 39–43.

REEF, V.B. – VAALA, W.E. – WORTH, L.T. – SERTICH, P.L. – SPENCER, P.A. (1996): Ultrasonographic assessment of fetal well-being during late gestation: development of an equine biophysical profile. Equine Vet. J. 28, 200–208.

REEF, V.B. – VAALA, W.E. – WORTH, L.T. – SPENCER, P.A. – HAMMETT, B. (1995): Ultrasonographic evaluation of the fetus and intrauterine environment in healthy mares during late gestation. Vet. Radiol. Ultrasound 36, 533–541.

TROEDSSON, M.H.T. (2007): High risk pregnant mare. Acta Vet. Scand. 49, Suppl. 1, S9.

Monogenetic disorders and their implications for conservation breeding programs – a practical example from the Noriker horse breed

DRUML, Thomas[1] – BREM, Gottfried[1]

[1]Institute of Animal Breeding and Genetics, University of Veterinary Sciences Vienna, Veterinärplatz 1, A-1210 Vienna, Austria

Abstract

In this study we determined the allele frequency of the glycogen synthase 1 mutation (*GYS1*) associated with PSSM type1 in the Austrian Noriker horse. We studied the influence of population structures on the distribution of the GYS1 gene mutation. The study was based upon a comprehensive population sample including a complete cohort of unselected offspring from the year 2014 (1,649 foals) and randomly selected samples of 517 adult breeding horses (208 stallions and 309 mares) born between 1989 and 2012. The mean proportion of *GYS1* carrier animals in the foal cohort was 0.32, ranging from 0.16 to 0.40 according to population substructures based on coat colours. In 517 mature breeding horses the mean carrier frequency of the *GYS1* gene mutation reached 0.44, varying on a wider scale from 0.04 to 0.62 within the population based substructures. We could show that the occurrence of the mutated *GYS1* allele is influenced by genetic bottlenecks, assortative, rotating and random mating strategies. Highest *GYS1* carrier frequencies were observed in the chestnut cohort comprising 0.40 in chestnut foals, 0.54 in chestnut mares and 0.62 in chestnut breeding stallions. This genetic subgroup of the Noriker population, characterized by the application of an assortative mating strategy, shows a reduced gene pool (effective number of founder animals = 88, population mean = 112) and a higher level of inbreeding (f ranging from 6.05 to 6.81%). Lowest *GYS1* carrier frequencies were observed in the leopard spotted Noriker subpopulation. Here the mean carrier frequency of the *GYS1* mutation reached 0.16 in foals, 0.17 in mares and 0.04 in stallions. In contrast to chestnuts, leopard spotted Noriker horses are bred according to a rotating mating system based on the recurrent use of solid black coloured and leopard spotted horses. Although leopard spotted Noriker horses are showing a genetic bottleneck represented by 25 effective ancestors (population mean = 45 effective ancestors), the founder gene pool comprised of 120 effective founders and the mean inbreeding in this genetic unit decreased from 4.88 in homozygous non-carrier horses (H/H) to 4.29% in heterozygous R/H horses and to 2.84% in homozygous carriers (R/R), respectively. In chestnut horses the opposite effect was observed: inbreeding was highest in homozygous carriers f = 6.81, and lowest in homozygous non-carriers f = 6.05. This study illustrates that lineage breeding, breeding for coat colour and specified mating strategies result in specific genetic structures, which also affect the frequency of the *GYS1* gene mutation.

Introduction

The first description of polysaccharid storage myopathy (PSSM) in 1992 was based on a study of nine horses with chronic exertional rhabdomyolysis from Quarter Horse related breeds (VALBERG et al., 1992). Since the detection of a point mutation in the skeletal muscle glycogen synthase gene (*GYS1*) associated with PSSM in a sample of 96 Quarter horses (MCCUE et al., 2008a), numerous studies determining the prevalence of PSSM in American and European draft horse breeds based on muscle biopsies (VALENTINE et al., 2001; FIRSHMAN et al., 2005; MCGOWAN et al., 2009) or genotyping for the *GYS1* mutation (MCCUE et al., 2010; BAIRD et al., 2010; SCHWARZ et al., 2011) or both (HERSZBERG et al., 2009), were published.

MCCUE et al. (2010) and BAIRD et al. (2010) attempted to determine the occurrence of the *GYS1* mutation and its frequency in samples of healthy American and European draft horse breeds. In 18 samples from European (Belgium, France, Germany, Netherland, Spain, Sweden, UK) and four samples of American draft horse breeds, the estimated mean frequency of *GYS1* mutation carrier animals comprised 0.43 (minimum=0.00, maximum=1.00, SE = 0.31. The sample sizes in these publications varied from 1 to 265 animals, with a mean of 61.6 animals and a standard deviation of 67.5, whilst animals and sample methodologies were random, non-random, stratified - and systematic random.

To date, the Austrian Noriker horse breed, which belongs to the oldest autochthonous European draft horse breeds, was not screened for PSSM and the *GYS1* mutation. Genetic diversity including the impact of colour breeding was analysed by DRUML et al. (2009) based on up to 32 generations long pedigrees. In this closed population six coat colour variants like bay, black, chestnut, Leopard, Tobiano and roan are recorded based on assortative and rotating mating strategies. Leopard spotted and roan breeding stallions in the Noriker horse breed were firstly mentioned in the year 1652 (Salzburger Landersarchiv, Hofkammer, Hofgestütsmeisterei 1652, Lit. A). A detailed breeding and selection strategy for all coat colour types is documented in the stud book of the Salzburg archbishop stud farm of Rif from the year 1789 (Salzburger Landesarchiv, Musakt. 264). Besides the breeding for colour, linage breeding is being practised in this population. Here, the male genealogies are based on five founder stallions born between 1877 and 1897, whereas the Elmar-lineage traditionally represents the male Leopard spotted subpopulation.

The Noriker horse, comprising about 10,000 registered horses in Austria, is an endangered breed with an important cultural and ecological value. The maintenance of the traditional coat colours and five sire lines are a central part of the conservation breeding program. The international interest into the PSSM complex in draft horse breeds, which arouse in the last five years, was the reason to screen this population for the *GYS1* mutation.

Therefore, the aim of this study is to determine the *GYS1* genotype frequencies in a comprehensive population sample of the Noriker horse breed (1,649 foals of the year 2013/14) and in a systematic random sample (309 active breeding mares and 208 breeding stallions, where 168 were active in 2014).

Material and Methods

Hair root samples were collected from the foal cohort in the year 2013/14 including 1,649 Noriker foals at the registration procedure. From all 208 Noriker breeding stallions hair root samples or isolated DNA, available from paternity test were used. Additional to these two population samples, 309 breeding mares were systematically randomly chosen, in order to provide a representative adult maternal basis for this study. The total number of Noriker horses used was 2,166. All horses were regarded as clinically normal at the time of sampling. This study was discussed and specifically approved by the institutional animal welfare and ethics committee (Commission for ethics and animal welfare, University of Veterinary Medicine, Vienna; protocol number ETK-06/10/2015) in accordance with GSP guidelines and national legislation.

Genotyping

Genomic DNA was extracted from hair root samples using the nexttec™ Tissue&Cells-Kit (nexttec^{TM}, Hilgertshausen, Germany) following the manufacturer's protocol. The *GYS1* genotype of each horse was obtained by applying a pyrosequencing approach on a PyroMark Q96 MD pyrosequencer (Qiagen, Hilden, Germany) where the following forward and reverse PCR primers for *GYS1* R309H: 5'-TGAAACCATGGGACCTTCTCC-3' and 5'-AGCTGTCCCCTCCCTTAGAC-3' were used, and the sequencing primer was 5'-CGAATCCAGGAGTTTGTG-3'. The PCR product was 230 bp long including the *GYS1* R309H mutation in the centre. The analysed sequence was G/ATGGCCAT (MCCUE et al., 2008a).

Pedigree analysis

Pedigree information of the 2,166 genotyped horses was extracted from a file containing the records of 51,613 Noriker horses. The resulting pedigree file contained 9,446 individual records. This restriction of pedigree length to five generations was performed in order to study the recent events of population history. An analysis based on the full pedigree record is provided by DRUML et al. (2009). Besides UELN number, father ID and mother ID, coat colour and sire linage were retained for further analysis. The 73 different shades of coat colours of the dataset were reduced to their base colour (black, bay, chestnut) or base pattern (Leopard spotted, roan, Tobiano).

The genealogic data was used to calculate following measures of genetic variability: effective number of founders (f_e) and ancestors (n_a) described by BOICHARD et al. (1997), inbreeding coefficients complete generation and equivalent generation interval. Inbreeding coefficients were calculated for pedigrees considering all available generations (f_{all}). The parameters were calculated using the software package ENDOG v.4.6 (GUTIÉRREZ and GOYACHE 2005).

Results

Carrier frequencies of GYS1 genotypes in the Noriker population

From 1,649 foals born in 2013/14, 1,126 animals were homozygote (R/R) for the wild allele R at the *GYS1* locus, 456 animals were heterozygous (H/R) and 67 animals were homozygous for the *GYS1* mutation (H/H). The frequency of GYS1 carrier animals in this sample, which is representing the allele pool of the actual and unselected Noriker population, was 0.32 and it was not equally distributed across the population. Between the sexes no deviations could be detected, but between the six coat colour branches significant differences were noticed. The carrier-animal proportion was highest among chestnut foals with 0.40, followed by roan foals with a proportion of 0.33, bay foals with 0.32; black foals with 0.29, Tobianos with 0.21 and it was lowest in Leopard spotted foals with 0.16 (Table 1). Selection intensity in the Noriker horse is high, as on the male side only 2 % of colts will be used as breeding stallions and on the female side 37.5% of fillies will enter the main stud book on average. Therefore we can assume that the distribution of *GYS1* genotype frequencies will change, when studying adult and reproductive horses.

Table 1. Number of genotyped Noriker foals from the year 2013/14, genotyped Noriker stallions and mares structured by *GYS1* genotype (R = wildtype allele; H = mutated allele)

	Foals		Breeding horses			
	N	H Carrier%	N	H Carrier% total	H Carrier% stallions	H Carrier% mares
Brown	424	32	135	35	38	33
Chestnut	434	40	99	58	62	54
Roan	86	33	38	26	32	21
Black	535	29	201	28	31	26
Tobiano	29	21	5	20	20	-
Leopard spotted	141	16	39	8	4	17
All	1649	32	517	34		

In this sample of mature breeding horses comprising 517 animals, the mean *GYS1* carrier frequency increased to 0.44 and the differences in genotype frequencies between the coat colour branches remained roughly the same, but with more emphasis on the extremes like chestnut (carrier frequency of 0.58) and Leopard spotted horses (carrier frequency of 0.08). In breeding stallions the frequencies of carrier animals was higher than in mares and ranged from 0.31 (black stallions) to 0.62 (chestnut stallions), except for Leopard spotted horses, where only 4% of stallions were carriers (Table 1). Among these two samples a co-linearity between the grade of accumulation of GYS1 carrier animals and the intensity of selection could be observed in chestnut and bay horses. In the Leopard spotted branch the opposite effect was detected.

Table 2. *GYS1* genotype frequencies in 168 actual Noriker breeding stallions by sire linage (R = wildtype allele; H = mutated allele)

	n	%	R/R	H/R	H/H	% R/H	% H/H	H carrier animals
Diamant	22	0.13	7	14	1	0.64	0.05	0.68
Elmar	24	0.14	21	3	-	0.13	0.00	0.13
Schaunitz	25	0.15	19	6	-	0.24	0.00	0.24
Nero	32	0.20	16	14	2	0.42	0.06	0.50
Vulkan	65	0.38	42	20	3	0.31	0.05	0.35
	168	1	105	57	6	0.34	0.04	0.38

Frequencies of *GYS1* genotypes within five male genealogies (Diamant, Elmar, Nero, Schaunitz and Vulkan sire linage) were derived from 168 actual breeding stallions. From the 169 breeding stallions 65 (38%) belong to the Vulkan linage, 32 (20%) to the Nero linage, 25 (15%) to the Schaunitz linage, 24 (14%) to the Elmar linage and 22 (13%) to the Diamant linage. Carrier frequency of *GYS1* mutation carriers in this sample collection of breeding stallions varied between 0.13 (Elmar linage) and 0.68 (Diamant linage) (see Tab. 2). In the Leopard spotted Elmar linage and in the spotted branches of the Vulkan linage the *GYS1* mutation did not segregate. The three heterozygous Elmar stallions (two of them were solid coloured) were out cross animals with dams from branches with higher *GYS1* frequencies.

Gene pool, inbreeding and GYS1 carrier frequencies

From the 9,446 animals in the pedigree file, 1,054 horses were founder animals. In this study, the complete generation equivalent (GE) was 9.05 +- 0.49. The generation interval (GI) based on the last two generations was 8.40 +- 4.31 in foals and 8.32 +-3.66 years in adult horses.
Diversity parameters as effective number of founders (f_e), effective number of ancestors (f_a) and number of ancestors explaining 50% of the gene pool (n_{a50}) did not differ significantly between the three samples and were around 111 effective founders, 43 effective ancestors and 16 ancestors explaining 50% of the gene pool. In Table 3 these parameters are given for the five coat colour branches of the foal sample.

Table 3. Genetic diversity parameters effective number of founders (f_e) and effective number of ancestors (n_a), number of ancestors contributing to 50% of the gene pool (n_{a50}) for Noriker foals, the single coat colour branches within the foal cohort, adult horses, stallions and mares

	n	n founder	f_e	n_a	n_{a50}
Foals 2014	1553	1046	112	45	18
Leopard spotted	136	636	120	25	9
Chestnut	343	734	88	32	12
Roan	86	581	125	32	12
Brown	424	816	104	37	14
Black	535	839	115	42	16
Adult horses	517	770	111	43	16
Adult stallions	208	660	111	44	17
Adult mares	309	710	111	41	15

Here in these genetic subgroups differences in effective population sizes (f_e and f_a) indicate an unbalanced use of breeding animals in the sample of chestnut foals (f_e=88) and a genetic bottleneck in the sample of Leopard spotted foals (f_a=25). At the same time the number of effective founders in Leopard spotted foals (f_e=120) is higher than the average and the chestnut subpopulation. Although there have been limitations in population size of the Leopard spotted branch in the history up to present, the use of breeding animals, especially stallions, was more moderate, whereas in chestnut horses a tendency towards mass selection could be observed. These differences in population parameters also were similar in the two samples of adult Noriker breeding mares and stallions (Table 3). In Table 4 the five ancestors with the highest gene proportion are given for the gene pool in the samples of chestnut and Leopard spotted foals.

Table 4. Most important ancestors contributing to 50% of the gene-pool and their gene proportions and genotyped ancestors within the sample of adult Leopard spotted breeding horses (n = 39) and within the sample of adult chestnut breeding horses (n = 99). (R = rank; *GYS1* = *GYS1* genotype)

Leopard spotted horses:

R	Gene proportion	Cum. gene proportion	Name	Sex	Coat colour *	Birth year	*GYS1*
1	14.58	0.15	Lohninger Vulk. XV	H	L.	1989	-
2	10.84	0.25	Jank Elmar X	H	L.	1963	-
3	7.70	0.33	Toni Vulkan XI	H	L.	1968	-
4	5.77	0.39	Stef Elmar XIII	H	L.	1998	R/R
5	4.75	0.44	Prinz Elmar XII	H	L.	1977	-
6	4.41	0.48	Glück Elmar XIII	H	L.	1997	R/R
7	3.53	0.52	Hoffeldhof Vulkan XVII	H	L.	1998	R/R
8	3.42		Pongau Elmar XIV	H	L.	2002	R/R
9	2.80		Franz Elmar XIII	H	B.	1999	R/R
11	2.40		Jubel Elmar XII	H	L.	2000	R/R
14	2.16		Linox Vulkan XVII	H	L.	2000	R/R
13	2.16		Grenzland Vulkan XIV	H	L.	1994	R/R

Chestnut horses:

R	Gene proportion	Cum. gene proportion	Name	Sex	Coat colour**	Birth year	*GYS1*
1	10.05	0.10	Mailing Vulkan XI	H	C.	1962	-
2	7.55	0.18	Vogl Vulkan XI	H	Br.	1958	-
3	6.43	0.24	Gulden Diamant XIII	H	C.	1992	R/H
4	5.34	0.29	Bichl-Vulkan IX	H	C.	1953	-
5	4.90	0.34	Schieder Vulkan XIV	H	C.	1978	-
6	4.04	0.38	Engelbert Vulkan XV	H	C.	1990	R/H
7	3.45	0.42	Bandit Nero XI	H	C.	1982	
8	3.32	0.45	Steindorf Vulkan X	H	C.	1953	-
9	3.15	0.48	Stock Nero VII	H	C.	1959	-
10	2.93	0.51	Recke Vulkan XIII	H	C.	1977	-
11	2.44		Schimmer Vulkan XVII	H	C.	2000	H/H
14	2.03		Pölsen Vulkan XVI	H	C.	2001	R/H
25	0.99		Zirrus Schaunitz XVI	H	C.	2001	R/R

* L =Leopard spotted; B. = Black
** C. = Chestnut; Br. = Brown

In Table 5 the mean inbreeding coefficients for the coat colour branches of the foal sample structured by *GYS1* genotype are given. Chestnut foals show the highest inbreeding of all subpopulations and the inbreeding coefficients (f_{all}) are increasing from 6.05 % in R/R horses to 6.81 % in H/H horses (Tab. 5). In this subpopulation the highest carrier genotype frequencies and the highest proportion of H/H genotypes exist. This result follows the genetic drift and the inbreeding theory, where higher inbreeding and reduced variability result in an increase of homozygosity, in this case homozygous H/H horses. At the same time within the Leopard spotted subpopulation the opposite effect can be observed: inbreeding is lowest in the homozygous H/H horses f = 2.84%, followed by the heterozygous H/R horses f = 4.29% and it is highest in non-carriers f = 4.88% (R/R). The relative higher inbreeding coefficients related to the absence of the GYS1 allele can be described as purging effect in this subpopulation of the Noriker breed.

Table 5. Mean inbreeding coefficients f_{all} structured by colour and *GYS1* genotype (H/H, H/R, R/R) in the complete Noriker foal cohort of the year 2014

	R/R f_{all}	H/R f_{all}	H/H f_{all}
Brown	4.92	5.12	4.54
Chestnut	6.05	6.34	6.81
Roan	4.70	4.43	4.58
Black	4.89	4.75	5.00
Tobiano	4.68	4.56	-
Leopard spotted	4.88	4.29	2.84
all	5.10	5.31	5.83

Conclusion

In this study we present the *GYS1* genotype frequencies in a whole draft horse population based on 2,166 healthy Noriker horses. The resulting *GYS1* carrier animal frequency was on average 0.32 and within the lower range of reported values for American and European draft horse breeds, where the mean carrier frequencies of the *GYS1* mutation was 0.43, ranging from 0 to 1 (BAIRD et al., 2010; MCCUE et al., 2010). In the existing literature sample sizes are variable and on a lower level for studies which are designed to screen for allele variants in a population. Although MCCUE et al. (2010) refer to this issue, and propose a sample size of 300 animals in order to have a 95% probability to detect an allele, when the true frequency is below 0.01, none of *GYS1* related studies matched this number in their population samples (MCCUE et al., 2010; BAIRD et al., 2010; SCHWARZ et al., 2011; HERSZBERG et al., 2009). Furthermore MCGOWAN et al. (2009) mentioned the sampling problem in PSSM publications. A series of PSSM prevalence necropsy studies concentrated on horses for euthanasia or referral stations with focus on neuromuscular disorders and on retrograde samples from neuromuscular disease databases (VALENTINE and COOPER, 2005; VALENTINE et al., 2001; MCCUE et al., 2008b). Resulting prevalences may be distorted and not be representative for single breeds or populations. In *GYS1* mutation screening studies in healthy populations sampling strategies were described as non-random, simple random, systematic random, stratified random (MCCUE et al., 2010; BAIRD et al., 2010), but insufficient information about relationship of sampled individuals and genetic structure are given. In our study we could show, that even in one population the mean carrier frequency of the *GYS1* mutation can vary from 0.04 to 0.62. Furthermore, we demonstrated that both – linage breeding and assortative mating strategies – have considerable effects on the segregation of the *GYS1* allele. ALVAREZ et al. (2010) reported a loss of genetic variability within a breeding program where a major objective is coat colour. In the case of chestnut Noriker horses, characterized by a limited effective population size, the assortative mating strategy and linage breeding led to an increase of the frequency of *GYS1* gene mutation, increase of inbreeding and number of homozygous H/H horses. Furthermore, a misbalance in use of breeding animals was detected, which is due to a “popular sire effect”, where five chestnut “impact stallions” out of three sire linages determine 18.4% of the chestnut gene pool. Four of these five stallions were carriers of the *GYS1* mutation and one stallion was H/H homozygous. The results from the chestnut horse sample correspond to current inbreeding and drift theory. In Leopard spotted Noriker horses, especially in mature breeding stallions, the *GYS1* carrier frequency tends to zero and within the Leopard spotted male genealogies of the Elmar and Vulkan sire linages, the *GYS1* gene mutation did not segregate. The Leopard spotted gene pool is substantially different from all other coat colour strains, which is also documented by a higher genetic distance especially to chestnut horses (DRUML et al. 2009). This genetic differentiation can be explained by the interaction of a high phenotypic selection intensity with predominantly applied rotating mating strategies, where solid coloured black horses out of Leopard spotted linages are used for optimizing the spotting pattern. This mating system has been recently confirmed by HOLL et al. (2012) and BELLONE et al. (2013), who published evidence that the interaction between the *LP* gene and the *PATN1* gene lead to different spotting phenotypes. In Leopard spotted horses the non-carrier animals are characterized by higher inbreeding coefficients than carriers indicating a purging effect. Comparable results are reported by LANGE et al. (2005), where the prevalence of insect bite hypersensitivity decreased, when the inbreeding of individuals was increased.

In this study we could demonstrate, that frequencies of the *GYS1* gene mutation are varying in different genetic substructures of the Noriker horse breed. It is important to notice, when selecting against the *GYS1* mutation, to consider the genealogical and genetical structures. Generalized conservation genetic strategies like minimizing the increase of inbreeding or maximizing the relationship coefficients can have negative effects, as the *GYS1* mutation may spread across the whole population. As the *GYS1* gene mutation occurs at higher frequencies in 13 European draft horse breeds (BAIRD et al. 2010), all of them representing endangered animal genetic resources, in the context of conservation breeding programs well differentiated selection approaches and long-term breeding strategies should be developed and applied.

References

ALVAREZ, I. – ROYO, L.J. – PEREZ-PARDAL, L. – FERNANDEZ, I. – PAYERAS, L. – GOYACHE, F. (2010): Assessing losses of genetic variability in the endangered Mallorqui horse. Czech Journal of Animal Science 55(10), 456-462.

BAIRD, J.D. – VALBERG, S.J. – ANDERSON, S.M. – MCCUE, M.E. – MICKELSON, J.R. (2010): Presence of the glycogen synthase 1 (GYS1) mutation causing type 1 polysaccharide storage myopathy in continental European draught horse breeds. Veterinary Record 167, 781-784.

BELLONE, R.R. – HOLL, H. – SETALURI, V. – DEVI, S. – MADDODI, N. – ARCHER, S. – SANDMEYER, L. – LUDWIG, A. – FOERSTER, D. – PRUVOST, M. – REISSMANN, M. – BORTFELDT, R. – ADELSON, D.L. – LIM, S.L. – NELSON, J. – HAASE, B. – ENGENSTEINER, M. – LEEB, T. – FORSYTH, G. – MIENALTOWSKI, M.J. – MAHADEVAN, P. – HOFREITER, M. – PAIJMANS, J.L.A. – GONZALEZ-FORTES, G. – GRAHN, B. – BROOKS, S.A. (2013): Evidence for a retroviral insertion in TRPM1 as the cause of congenital stationary Night Blindness and Leopard Complex Spotting in the horse. PLoS ONE 8(10):e78280 (doi:10.1371/journal.pone.0078280).

BOICHARD, D. – MAIGNEL, L. – VERRIER, E. (1997): The value of using probabilities of gene origin to measure genetic variability in a population. Genetics Selection Evolution 29, 5-23.

DRUML, T. – BAUMUNG, R. – SÖLKNER, J. (2009): Pedigree analysis in the Austrian Noriker draught horse: genetic diversity and the impact of breeding for coat colour on population structure. Journal of Animal Breeding and Genetics 126, 348-356.

FIRSHMAN, A.M. – BAIRD, J.D. – VALBERG, S.J. (2005): Prevalences and clinical signs of polysaccharide storage myopathy and shivers in Belgian draft horses. Journal of the American Veterinary Medical Association 227, 1958-1964.

GUTIÉRREZ, J.P. – GOYACHE, F. (2005): A note on ENDOG: a computer program for analysing pedigree information. Journal of Animal Breeding and Genetics 122, 357-360.

HERSZBERG, B. – MCCUE, M.E. – LARCHER, T. – MATA, X. – VAIMAN, A. – CHAFFAUX, S. – CHÉREL, Y. – VALBERG, S.J. – MICKELSON, J.R. – GUÉRIN, G. (2009): A GYS1 gene mutation is highly associated with polysaccharide storage myopathy in Cob Normand draught horses. Animal Genetics 40, 94-96.

HOLL, H. – BROOKS, S.A. – ARCHER, S. – BELLONE, R. (2012): Whole transcriptome analysis of a pattern modifier (PATN1) of Leopard Complex spotting (LP). Poster presented by H. Holl at the Plant and Animal Genome Conference XX, San Diego, CA, January 2012.

LANGE, S. – HAMANN, H. – DEEGEN, E. – OHNESORGE, B. – DISTL, 0. (2005): Investigation of the prevalence of summer eczema in Icelandic horses in northern Germany, Berliner und Münchner Tierärztliche Wochenschrift 118 (11-12), 481-489.

MCCUE, M.E. – VALBERG, S.J. – MILLER, M.B. – WADE, C. – DIMAURO, S. – AKMAN, H.O. – MICKELSON, J.R. (2008a): Glycogen synthase (GYS1) mutation causes a novel skeletal muscle glycogenesis. Genomics 91, 458-466.

MCCUE, M.E. – VALBERG, S.J. – LUCIO, M. – MICKELSON. J.R. (2008b): Glycogen synthase 1 (GYS1) mutation in diverse breeds with polysaccharide storage myopathy. Journal of Veterinary Internal Medicine 22, 1228-1233.

MCCUE, M.E. – ANDERSON, S.M. – VALBERG, S.J. – PIERCY, R.J. – BARAKZAI, S.Z. – BINNS, M.M. – DISTL, O. – PENEDO, M.C.T. – WAGNER, M.L. – MICKELSON, J.R. (2010): Estimated prevalence of the Type 1 Polysacharide Storage Myopathy mutation in selected North American and European Breeds. Animal Genetics 41, 145-149.

MCGOWAN, C.M. – MCGOWAN, T.W. – PATTERSON-KANE, J.C. (2009): Prevalence of equine polysaccharide storage myopathy and other myopathies in two equine populations in the United Kingdom. The Veterinary Journal 180, 330-336.

Salzburger Landesarchiv, Hofkammer, Hofgestütsmeisterei 1652, Lit. A.

Salzburger Landesarchiv, Musakt. 264

SCHWARZ, B. – ERTL, R. – ZIMMER, S. – NETZMANN, Y. – KLEIN, D. – SCHWENDENWEIN, I. – HOVEN, R.V.D. (2011): Estimated prevalence of the GYS-1 mutation in healthy Austrian Haflingers. Veterinary Record 169, doi: 10.1136-vr.d5438.

VALBERG, S.J. – CARDINET, G.H. – CARLSON, G.P. – DIMAURO, S. (1992): Polysaccharide storage myopathy associated with recurrent exertional rhabdomyolysis in horses. Neuromuscular Disorders 2, 351-359

VALENTINE, B.A. – HABECKER, P.L. – PATTERSON, J.S. – NJAA, B.L. – SHAPIRO, J. – HOLSHUH, H.J. – BILDFELL, R.J. – BIRD, K.E. (2001): Incidence of polysaccharide storage myopathy in draft related breeds: a necropsy study of 37 horses and a mule. Journal of Veterinary Diagnostic Investigation 13, 63-68.

VALENTINE, B.A. – COOPER, B.J. (2005): Incidence of polysaccharide storage myopathy: necropsy study of 225 horses. Veterinary Pathology 42, 823-827.