Genetic and phenotypic parameters for feed and water efficiency in Senepol cattle

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Summary

The sustainability of beef production in the world demands the identification and selection of efficient animals that can produce more products with fewer inputs. Feed accounts for around 50-70% of variable costs of beef cattle systems, depending on the level of intensification adopted. Water has been traditionally considered an inexpensive, readily available, and renewable natural resource. However, growing concerns about the availability of drinkable water have increasingly pushed pressure on livestock production, especially cattle. Thus, genetic and phenotypic parameters were estimated for feed and water efficiency in Senepol cattle in order to evaluate their use as selection criteria. Records on 587 Senepol heifers, involved in performance tests, were used. Traits studied included residual feed intake (RFI), residual water intake (RWI), average daily feed intake (ADFI), average daily water intake (ADWI) and average daily gain (ADG). Individual daily feed and water intake records were collected over a 70-day period, using electronic feed and water bunks developed by Intergado Ltd. The ADG was calculated dividing the total weight gained during the test by its duration. A linear regression model of ADFI on metabolic weight (mean weight$^{0.75}$) and ADG was fitted, within each test edition. RFI was calculated as ADFI minus that predicted using the regression equation. The same was performed for calculating RWI by using ADWI instead of ADFI in the linear regression model. Genetic (co)variances were estimated using two-trait animal models and software AIREMLF90. Direct heritability estimates for RFI, RWI, ADFI, ADWI and ADG were 0.12 ± 0.10, 0.39 ± 0.12, 0.23 ± 0.11, 0.47 ± 0.12 and 0.15 ± 0.09 (averaged across all analyses), respectively. RFI was genetically (r_g = 0.50 ± 0.65) and phenotypically (r_p = 0.37 ± 0.04) correlated with RWI. Both RFI and RWI presented phenotypic correlations near to zero with ADG (r_p = -0.11 ± 0.05 and -0.09 ± 0.05, respectively). Genetically, RFI was not correlated (r_g = 0.06 ± 1.12) with ADG, whereas RWI was (r_g = 0.45 ± 0.79). The correlations between the pairs RFI-ADFI and RWI-ADWI were all positive (r_g = 0.68 ± 0.91, r_p = 0.78 ± 0.02; and r_g = 0.90 ± 0.11, r_p = 0.84 ± 0.01, respectively). ADFI was positive correlated with ADWI (r_g = 0.75 ± 0.41, r_p = 0.57 ± 0.03), and both traits presented similar correlations with ADG (r_g = 0.61 ± 0.77, r_p = 0.28 ± 0.04; and r_g = 0.70 ± 0.69, r_p = 0.29 ± 0.04, respectively).

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Introduction

Increasing food production for the growing human population of a constraining land base will require greater efficiency of production (Berry and Crowley, 2013). With limited resources available for production, there is a need to identify and select for efficient animals that can produce more product with fewer inputs (Ahlberg *et al.*, 2017).

Feed accounts for around 50-70% of variable costs of beef cattle systems, depending on the level of intensification adopted. Hence, feed efficiency, undoubtedly, has a major role to play in increasing production efficiency (Berry and Crowley, 2013).

Water has been traditionally considered an inexpensive, readily available, and renewable natural resource (Brew *et al.*, 2011). However, with the increasing demand for animal products in the coming decades, balancing animal productivity with water use will require a concerted effort among producers, scientists, agroindustries, and consumers to reduce the risks associated with animal water demand and scarcity (Palhares *et al.*, 2017). According to Nardone *et al.* (2010), the efficiency of water utilization will be the primary mission necessary to achieve sustainability of animal agriculture.

The Senepol breed was developed from the beginning of the twentieth century on the Virgin Island of Saint Croix as a tropically adapted taurine breed. Since the arrival of the first animals in Brazil in 2000, the population has increased its census considerably. Considering only taurine breeds with semen produced in Brazil in 2014, the Senepol breed was surpassed only by the Angus breed (ASBIA, 2015).

Thus, genetic and phenotypic parameters were estimated for feed and water efficiency in Senepol cattle in order to evaluate their use as selection criteria.

Material and methods

Records from 587 Senepol heifers (*Bos taurus taurus*), progenies of 61 sires and 264 dams, were used. The pedigree contained 1,965 animals. The data were obtained from a compilation of eight commercial performance tests performed on Grama Farm, Pirajuí, São Paulo, Brazil (21º 59' S; 49º 27' W), between 2014 and 2016. The animals started the tests with an average weight of 397 ± 52 kg and age of 520 ± 59 days.

Animals were housed in collective pens, where individual daily feed and water intake records were collected over, approximately, a 70-day period, using Intergado® System (Intergado® Ltd, Contagem, Minas Gerais, Brazil). For more information about Intergado® System, see Chizzotti *et al.* (2015) and Oliveira Jr *et al.* (2017). Prior to the tests, the animals were allowed to adapt to the diet and facilities for a minimum period of 14 days. The animals had ad libitum access to diet and water. The feed composition of the diet offered was modified over the tests, but was equivalent in energy and protein content, with 2.64 Mcal of metabolizable energy and 14% of crude protein in dry matter basis (DM).

The studied traits included average daily gain (ADG – kg d^{-1}), average daily feed intake (ADFI – kg DM d^{-1}), average daily water intake (ADWI – L d^{-1}), residual feed intake (RFI – kg DM d^{-1}) and residual water intake (RWI – L d^{-1}). The ADG was calculated dividing the total weight gained during the test by its duration. A linear regression model of ADFI on mid-test metabolic body weight (mid-test body weight$^{0.75}$) and ADG was fitted (Koch *et al.*, 1963), within each test edition. RFI was calculated as ADFI minus that predicted using the regression equation. The same was performed for calculating RWI by using ADWI instead of ADFI in the linear regression model.

The contemporary groups were defined as test edition and farm of origin of the heifer. Records outside the interval of ± 3.0 standard deviations from the mean of the contemporary group were eliminated. Only animals with valid records for all five traits studied were kept. Animals from contemporary groups with less than five individuals were also discarded. Table 1 shows the data structure and descriptive statistics of the traits.

The (co)variance components were estimated by the restricted maximum likelihood method under a two-trait animal model using the AIREMLF90 program (Misztal *et al.*, 2002). The model included random direct additive genetic effects, the fixed effects of contemporary group and age of animal nested in the respective contemporary group as a covariate (linear effect). Direct heritability estimates for each trait were obtained by averaging across all two-trait analyses.

Results and discussion

The direct heritability estimates for the studied traits ranged from 0.12 to 0.47 (Table 2). These results, which are pioneers for Senepol cattle, indicate that selection can be used for increasing feed and water efficiency. However, genetics gains for ADWI and RWI are expected to be quite superior to those for ADFI and RFI due to the significant differences in heritabilities. Berry and Crowley (2013) performed a meta-analysis of genetic parameters for feed efficiency in beef cattle and reported higher values than the ones found in the present study (pooled heritabilities of 0.40 ± 0.01 for ADFI and 0.33 ± 0.01 for RFI). No study was found in the literature with genetic parameters for water intake and efficiency in cattle.

RFI was genetically and phenotypically correlated with RWI (Table 2). These results indicate that selection for animals with better feed efficiency could also lead to genetic progress for water efficiency. Despite water is often thought of as an irrelevant factor in beef cattle production, increasing water efficiency could be strategic, especially, in a long-term context. According to Nardone *et al.* (2010), all effects of global warming on water availability could force the livestock sector to establish a new priority in producing animal products that need less water. Both RFI and RWI presented phenotypic correlations (r_p) near to zero with ADG (Table 2). Genetically (r_g), RFI was

Table 1. Description of the final data set of studied traits.

Trait[1]	Mean ± SD	Number of animals with records	Number of contemporary groups
ADG (kg d^{-1})	0.87 ± 0.21	587	51
ADFI (kg d^{-1})	7.49 ± 1.16	587	51
ADWI (L d^{-1})	24.68 ± 3.99	587	51
RFI (kg d^{-1})	0.00 ± 0.79	587	51
RWI (L d^{-1})	0.00 ± 2.96	587	51

[1]ADG, average daily gain; ADFI, average daily feed intake in dry matter basis; ADWI, average daily water intake; RFI, residual feed intake in dry matter basis; RWI, residual water intake.

Table 2. Heritability (diagonal), phenotypic correlation (below the diagonal) and genetic correlation (above the diagonal) estimates for the studied traits.

Traits[1]	ADG	ADFI	ADWI	RFI	RWI
ADG	**0.15 ± 0.09[2]**	0.61 ± 0.77	0.70 ± 0.69	0.06 ± 1.12	0.45 ± 0.79
ADFI	0.28 ± 0.04	**0.23 ± 0.11**	0.75 ± 0.41	0.68 ± 0.91	0.57 ± 0.40
ADWI	0.29 ± 0.04	0.57 ± 0.03	**0.47 ± 0.12**	0.39 ± 0.90	0.90 ± 0.11
RFI	-0.11 ± 0.05	0.78 ± 0.02	0.30 ± 0.04	**0.12 ± 0.10**	0.50 ± 0.65
RWI	-0.09 ± 0.05	0.29 ± 0.02	0.84 ± 0.01	0.37 ± 0.04	**0.39 ± 0.12**

[1] ADG, average daily gain; ADFI, average daily feed intake; ADWI, average daily water intake; RFI, residual feed intake; RWI, residual water intake.
[2] standard error.

not correlated with ADG, whereas RWI was (Table 2). Berry and Crowley (2013) reported similar estimates (pooled) for r_p and r_g between RFI and ADG. For r_p, these authors found a range of -0.06 to +0.04; while for r_g, a range of -0.15 to +0.53. Guimarães *et al.* (2017) also estimated r_p close to zero between RFI and ADG for Senepol cattle. Kennedy *et al.* (1993) pointed out that although RFI is phenotypically independent of the component traits, except ADFI, it is not genetically independent. As RWI is calculated similarly to RFI, the same could be said for this trait.

The r_p and r_g between the pairs RFI-ADFI and RWI-ADWI were all positive (Table 2). Berry and Crowley (2013) and Guimarães *et al.* (2017) found results of similar magnitude and sign of the ones estimated in the present study. ADFI was highly positive correlated with ADWI (Table 2), both genetically and phenotypically. It suggests that ADWI could be used to estimate ADFI in cattle what would be useful since measuring the former is easier and cheaper than the latter. This would be especially advantageable in grazing systems where evaluating ADFI in large scale is not yet a feasible alternative. ADG presented similar correlations with both intake traits (Table 2), corroborating the findings of Berry and Crowley (2013).

Conclusions

Genetic improvement for feed and water efficiency in Senepol cattle can be achieved through selection. Genetic progress for water efficiency is expected to be superior to the one for feed efficiency. Feed intake and efficiency can be genetically improved by selecting animals for water intake and efficiency**.**

Acknowledgements

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First national recording of health traits in dairy cows in the Czech Republic

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Summary

This study presents a basic description and analysis of 20 common health disorders/diseases monitored in 289 802 dairy cows in the Czech Republic. The data were provided by farmers on a one-time basis from 1 183 herds and were collected between July 2015 and June 2016. In 55 % of cows, no disorders/diseases were treated, while in 45 % of cows, at least 1 of 20 monitored disorders/diseases was recorded. The most frequent disease was mastitis (19.8 % treated lactations, i.e., lactational incidence risk, *LIR*), followed by metritis (*LIR* 11.3 %) and foot and claw diseases (*LIR* 11.0 %). Treatment of metabolic disorders was rather seldom (*LIR* 1-3.2 %). Not all farms recorded all diagnoses; while almost 90 % of farmers reported the incidence of mastitis, less than 50 % of them recorded the incidence of metabolic diseases. Additionally, the comparison of the incidence of foot and claw diseases with studies based on hoof trimmer records showed possible under-reporting. Despite those limitations, our basic analysis is important for intended genetic evaluation of health traits and gave us an idea about the health conditions and disease recording in Czech dairy cattle.

Keywords: cattle, lactational incidence risk, mastitis, reproduction disorders, metabolic disorders, foot and claw diseases.

Introduction

Health traits in dairy cattle attract attention not only for their influence on farm profitability and production efficiency but also for the impact of the diseases and their veterinary treatment on animal welfare, food safety and quality (Egger-Danner *et al.*, 2013). Growing attention is also paid to the impact of drugs used in veterinary medicine, such as the spread of antibiotic-resistant strains of bacteria that can negatively impact human health (Egger-Danner *et al.,* 2014).

Health traits have generally low heritability; however, there is a possibility that health traits can be selected, as they show sufficient genetic variability and that genetic improvement can occur; however, for this purpose, we need a large amount of reliable data (Heringstad and Osteras, 2013).

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The incidence of diseases in Czech dairy cattle is high, where more than 80% of culling is due to health reasons. The most frequent reasons for culling in 2016 were reproduction disorders (21.5%), dystocia (10.1%) and udder diseases (8.5%); the remaining 43.9 % were other unspecified health reasons (Kvapilík *et al.,* 2017). According to Bauer *et al.* (2016), Czech farmers use approximately 20 different farm management software packages for recording different farm data, including data on health situations (61% of farmers), veterinary treatments and drug applications (59% of farmers). Based on the Law of Veterinary Care, the farmers are obliged to keep records about the use of medication bound by a prescription and to keep records of the reason for those diagnoses. These records have not been standardized, nor have they been gathered or stored in a joint database yet, which would enable their processing and utilization for the purposes of genetic evaluation and selection. Our aim was to describe the health conditions and to gather and evaluate data on the incidence of 20 common diseases/disorders in Czech dairy cows over one year.

Materials and methods

The data on disease incidences were provided retrospectively by farmers via electronic survey. The observation period covered the period from the 1st of July 2015 until the 30th of June 2016. The survey contained information on the identification numbers of farms and cows, health status of each cow (treated/not treated), diagnosis (chosen from 20 common diseases listed in Table 1), use of antibiotics and their dose and way of application. Other data (breed of cow, date of calving, parity, milk yield) were filled in from the database of lifelong performance.

The first occurrence/incidence of each disease (or group of diseases in case of foot and claw) during lactation, was coded as 0- not treated, 1- treated (lactational incidence risk – *LIR*). Repetitions of the same diagnosis during the same lactation period were not considered.

Data were edited, so that only lactations which started with calvings from July 2015 until 7 days (for dystocia, parturient paresis, retained placenta), 20 days (for metritis) or 60 days (for other diseases) before the end of observation period were included in the evaluation. To differentiate the farms with incomplete data, each herd with a minimum of 20 lactations was required to have at least 1 record of disease/group of diseases. For smaller farms (<20 lactations) no minimum *LIR* was required. For editing of the database and basic calculations we used *SAS 9.4.*

Results and discussion

The data set contained information from 1 183 herds and 289 802 cows, which account 78 % of the total number of dairy cows in the Czech Republic. The distribution of breeds was as follows: 138 643 Holstein (H100; 48%), 64 304 of Czech Pied cattle (C100; 22%), and the rest were crossbreds (28%) or other dairy breeds (Ayrshire, Braunvieh, Montbéliarde, Normande, Red Holstein; 2%). A total of 130 244 cows (45%) had at least 1 diagnosis, while 159 558 (55 %) cows were stated as "not treated". Description of edited data structure and *LIR* of diseases are presented in Table 1. The most frequently treated disease was mastitis (*LIR* = 19.8 %), followed by metritis (*LIR* = 11.3%) and groups of foot and claw diseases (*LIR* = 11.0%).

Lactation incidents of mastitis and reproductive disorders were comparable to frequencies stated in other national studies (Govignon-Gion, *et al.,* 2012, Egger-Danner *et al.,* 2012, Vukasinovic *et al.,* 2017, Zwald *et al.,* 2004). On the other hand, *LIR* of foot and claw diseases was rather low. As the study of Krpálková *et al.* (2016) showed,

Table 1. The structure of edited data and lactational incidence risk LIR of monitored diseases.

Disease / disorder	No. of herds	No. of lactations	No. of treated lactations	% of treated lactations
Mastitis	1 026	209 147	41 505	19.8
Dystocia and/or retained placenta	815	192 741	9993	5.2
Metritis	802	191 438	21 549	11.3
Endometritis and/or cystic ovaries	810	165 198	17 627	10.7
Milk fever	581	136 877	2 290	1.7
Other recumbency	357	54 405	521	1.0
Primary ketosis	348	63 373	1704	2.7
Subclinical primary ketosis	337	58 180	1830	3.2
Secondary ketosis	263	37 468	564	1.5
Foot and claw[1]	907	187 450	20 673	11.0

[1]group of 9 diseases/disorders including lameness, interdigital hyperplasia, claw ulcer, toe ulcer, typical sole ulcer (Rusterholz), sole ulcer in atypical location, white line disease, interdigital phlegmon, digital dermatitis.

the frequency of claw diseases often exceeds 50%, and better care combined with more control of legs leads to higher recording of diseases. Additionally, van der Spek *et al.* (2013) examined hoof trimmer records and found that more than half of the scored cows had at least one claw disorder. The same authors pointed to the importance of trimming status, which is a heritable trait correlated with claw disorders and therefore an interesting trait to include in the genetic evaluation. Additionally, *LIR* of metabolic diseases was rather low, compared to the meta-analysis of Pryce *et al.* (2016), where the median incidence of ketosis was 3.3 %, the incidence of subclinical ketosis was up to 34 %, and the median incidence of milk fever was 2.8 %.

The quality of data is determined by their objectivity, reliability and validity. In retrospective studies, the quality of on-farm documentation plays a key role. According to Pryce *et al.* (2016), many farm computer systems still do not ensure that data captured for health traits are consistent and accurate, and thus there is a potential for underestimated/over-reported incidences. Reporting of disease is more likely when it is treated by medication, where evidence is mandatory. As mentioned by Egger-Danner *et al.* (2012), the main reasons for incomplete data were missing documentation, a fact that farmers emphasize different health aspects at different times, or situations, when not all farms record all diagnoses. The last reason was also present in our study, where almost 90 % of farmers reported the incidence of mastitis, but less than 25 % of them recorded the incidence of metabolic diseases except for milk fever, which was reported by almost 50 % of farmers.

A clear and unambiguous definition of diagnosis is very important. It is not unusual that the farmer describes the symptoms, applies the medication, but hesitates to name the disease. Additionally, Pryce *et al.* (2016) mentioned under-reporting of metabolic diseases due to differences in producer interpretation of symptoms. Likewise, Krpálková *et al.* (2016) noted the possibility of bad recognition and consequent under-reporting of the incidence of foot and claw diseases by farmers, especially in large herds.

Generally, differentiating between farms with incomplete recording and farms with very low incidence rates is a challenge (Egger-Danner *et al.,* 2012), especially in small farms. Basic measure for data validation is therefore their careful editing, which consisted mainly in determination of their minimum incidence per herd, year and/or

season (Egger-Danner *et al.*, 2012, Vukasinovic *et al.*, 2017). Only data from farms with regular and complete registration of diagnoses should be included in the genetic analysis.

Conclusions

This study presents the first step on the way to the national recording of health traits in dairy cattle and for subsequent use of such data for genetic parameter estimation and genetic evaluation. Despite the limitations, our analysis provides valuable information for future processing and validation of data and identifies the weak points that could negatively affect the recording and reporting of incidence of diseases/disorders in cattle populations.

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