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A REVIEW OF SOME IMPORTANT VIRAL DISEASES OF WILD BOARS

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Review Paper

Abstract: Wild boars are one of the widest-ranging mammals worldwide and represent reservoirs for many important viruses. Disease outbreaks in domestic swine are often described as a consequence of contact with wild boars, and traditional rearing conditions are a particular risk factor. Examples of such diseases include classical swine fever (CSF), African swine fever (ASF), Aujeszky’s disease (AD), and diseases caused by porcine circoviruses and parvoviruses. Some viral infections causing high mortality rates are easily noticeable and thus reported, though many viruses infecting wildlife are insidious impacting survival rates and reproduction in wild animals. Samples from wild boars for laboratory testing are usually collected postmortem and include various tissues or blood sera. The recovery of viable viruses during virus isolation depends on the virus species and the condition of the sample. Since this method does not yield timely results, most diagnostic procedures are based on PCR or antigen detection methods. Serological surveys are inexpensive and appropriate for prevalence studies. When interpreting the results of diagnostic tests, both virus and host characteristics, and the epizootiological situation must be accounted for. Disease control techniques such as fencing or feeding wild boars cause animal aggregation and give rise to population density which favors pathogen maintenance in the environment. Hunting reduces the number of susceptible animals and is helpful as an additional control measure and for sampling. Available data on infectious disease dynamics in wild boars is scarce, and constant knowledge improvement on pathogenesis, clinical symptoms, risk factors, and adequate control measures are required.

Key words: CSFV, ASFV, PCV, PPV, SuHV1, wild boar

Introduction

Wild boars (*Sus scrofa*) are one of the widest-ranging mammalian species worldwide, and this species gradually spreads, occupying new areas (*Ruiz-Fons et al., 2008*). The behavioral and ecological characteristics of the species favor its abundance, while the high reproduction rate is further aided by climate change that prolongs the mating season (*Acevedo et al., 2007; Massei et al., 2015*). Human-driven factors also play a major role in wild boar expansion, namely abandoning rural areas, as well as the intensification of wild boar farming and supplementary feeding in line with the expansion in commercial hunting (*Acevedo et al., 2007*). Moreover, recreational hunting has little effect on reducing wild boar population sizes (*Massei et al., 2015*). Wild boars represent practically perfect reservoirs for many important infectious diseases of veterinary importance owing to their natural susceptibility to various pathogens, worldwide distribution, biological and ecological traits (*Ruiz-Fons et al., 2008; Meng et al., 2009*). Wild boars tend to roam large distances, and host movement is known as an essential component of the dynamics of infectious diseases depending on the mobility of the animals, as well as the biological characteristics of infectious agents (*Podgorski and Smietanka, 2018; Nišavić et al., 2021a,b*). For example, in extreme conditions such as hunting pressure, wild boars can cross distances of up to 250 km (*Milićević, 2016*). Many disease outbreaks in domestic swine, especially animals reared in traditional conditions, have been described as a consequence of contact with wild boars, and human activities in rural areas have only further increased the possibilities of such events (*Gibbs, 1997*; *Turcitu et al., 2011; Franzo et al., 2020; Petrović et al., 2021*). The estimated density of the wild boar population in Serbia is 0.2 - 1.38 animals per km^2, while the country has the highest pig density in the Western Balkans with around 2.7 million domestic pigs, and traditional farming with low or without any biosecurity measures is still very common (*Milićević et al., 2016; Petrović et al., 2021*). Wild boars abandon densely populated areas, and households with traditional pig rearing systems become ideal food sources for these wild animals (*Milićević, 2016*). The constantly growing wild boar population in Europe, along with rising animal density enables pathogen persistence in nature, thus leading to health risks for domestic pigs along with the potential economic losses to the livestock industry. This review concerns several viral diseases of swine that also implicate wild boars as significant factors for pathogen tenacity and transmission.

Classical swine fever (CSF)

Classical swine fever is the cause of major economic losses around the world, particularly in countries with widespread pig farming (*Zhou, 2019*). The

CSF virus (CSFV) is an enveloped positive-stranded RNA virus categorized in the genus Pestivirus within the *Flaviviridae* family (*ICTV, 2021*). A single CSFV serotype has been described to date, however, serological cross-reactions with other viruses from the same genus such as bovine viral diarrhea virus (BVDV) or border disease virus (BDV) can impair the results of serological diagnostics (*Beer et al., 2015; Moennig, 2015; OIE, 2019a*). The virus is sensitive to commonly used disinfectants and detergents, but it can survive for months in various pork meat products and moist conditions (*Moennig, 2015*). Domestic pigs have been the subject of extensive studies concerning the clinical course of CSF, however, wild boars are just as susceptible to CSFV infection (*Artois et al., 2002; Milićević et al., 2013; Moennig, 2015; Zhou, 2019*). Classical swine fever occurs throughout the world and is endemic in areas such as Asia, South, and Central America, parts of Europe, and Africa (*Brown and Bevins, 2018*). The presence of the virus in wild boar populations poses a constant threat of CSFV introduction into domestic pig populations and even reintroduction of the virus in certain countries (*Beer et al., 2015; Zhou, 2019*). The virus was found to be readily transmitted between domestic and wild pig populations in regions with extensive pig farming. Wild boars are viewed as important reservoirs of CSFV in nature (*Artois et al., 2002; Kaden et al., 2005; Moennig, 2015; Zhou, 2019*). The clinical course of the disease can be acute, chronic, or late-onset, which occurs as a consequence of prenatal infection of piglets (*Moennig, 2015*). After crossing the placental barrier in pregnant sows, CSFV infection of fetuses most commonly results in stillbirth or abortion. However, if the infection occurs in late gestation, persistently infected piglets are born and represent a major source of the virus since these animals shed the virus for weeks until they die. These late-onset infections may pass unnoticed, with wasting as the most common symptom. This clinical form of the disease has not been observed in wild boars since it is difficult to track such occurrences in the wild, however, it has been demonstrated experimentally (*Kaden et al., 2005; Moennig, 2015*). It is thought that adult animals are less important as virus shedders in wild boar populations and that the persistent infection of piglets is the main route for the spread of CSF in these animals (*Artois et al., 2002*). The acute course of CSF lasts a few weeks (usually 1 to 3, or up to 4 weeks) and passes with complete recovery or death of affected animals. The outcome of the acute disease form depends on various factors, such as the virulence of the infecting viral strain or the immune status of the animal (*Moennig, 2015; Zhou, 2019*). Clinical manifestation of CSF is milder in older animals with less specific symptoms and frequent recovery. The main clinical symptoms include fever, inappetence, conjunctivitis, nasal discharge, diarrhea, convulsions, and loss of coordination (*Zhou, 2019*). Characteristic signs also include the appearance of petechial and ecchymotic bleeding on the skin and internal organs on postmortem examination (*Artois et al., 2002; Zhou, 2019*). Chronically infected animals are mostly adult pigs and this disease course lasts more than 4 weeks during which the specific disease signs seen in the acute form are replaced by less specific and include intermittent fever, chronic enteritis with consequential wasting (*Artois et al., 2002*). This disease form has not been fully described in wild boars, and it can be questioned whether these chronically infected animals could survive for a long period in a natural setting (*Kaden et al., 2005; Moennig, 2015*). The oro-nasal route is the most common infection pathway, and the virus primarily replicates in the tonsils wherefrom it is transmitted to corresponding lymph nodes, while the onset of viremia enables the infection of internal organs (*Artois et al., 2002*). CSFV is transmitted in susceptible animal populations through direct contact or indirectly through fomites (*Zhou, 2019*). Contaminated meat products are also an important source of the virus and can lead to the introduction of CSFV in areas free of infection (*Moennig, 2015*). Wild boars get infected through direct contact with domestic pigs or by feeding in contaminated areas (*Artois et al., 2002; Ito et al., 2019; Zhou, 2019*). The virus persists and becomes endemic, especially in large and dense populations of wild boars where it is transmitted within a group of animals as well as between different groups, both by direct or indirect contact. This occurs through contaminated excretions, carcasses, during rutting, or after hunting seasons which drives the formation of new groups of animals (*Moennig, 2015*). Adult wild boars that survive the infection become immune, however, piglets lacking passive immunity to CSFV act as reservoirs (*Artois et al., 2002; Moennig, 2015*). Maternal antibodies against CSFV protect newborn animals during the first several weeks however, they do not prevent the shedding of the virus (*Artois et al., 2002*). The outbreak of CSF in wild boar populations is suspected in cases of high mortality detected within a certain population, along with noticing atypical behavior in live animals. Pathological findings include the appearance of widespread hemorrhages, particularly in lymph nodes that are marbled red, tonsils, larynx, and other internal organs (*Artois et al., 2002; OIE, 2019a*). Splenic infarctions and necrotic ulcerations in the gastrointestinal tract are also frequently observed (*OIE, 2019a*). Suspicion of CSFV infection must be confirmed using laboratory tests, and tonsils, lymph nodes, spleen, ileum, and kidneys are usually sent for analysis (*OIE, 2019a*). The virus can be isolated in cell cultures of porcine origin (e.g. PK-15 cell line), however, CSFV is not cytopathic, and its presence must be indirectly identified using immunofluorescence or immunoperoxidase staining (*Moenning, 2015; Petrović et al., 2019; OIE, 2019a*). Since virus isolation is often time-consuming, reverse transcription polymerase chain reaction (RT-PCR) is the method of choice due to its sensitivity, speed, and the potential for analysis of multiple samples (*Milićević et al., 2013; Nišavić et al., 2016*). Serology is performed in sera collected from shot wild boars and recommended tests include the virus neutralization test (VN) and the ELISA using monoclonal antibodies that discriminate between CSF and BVD/BD antibodies (*Artois et al., 2002; OIE, 2019a*). Until now, three CSFV genotypes containing various subgenotypes have been discovered, and the occurence of novel genotypes is being constantly monitored (*Beer et al., 2015*). Studies conducted in Serbia show that all examined isolates belonged to the 2.3 CSFV subgroup (*Milićević et al., 2013; Petrović et al., 2019*). In December 2019, Serbia has stopped vaccination against CSF which brings the country one step closer to being declared as free of CSF (*Službeni Glasnik RS, Br . 87, 2019*).

African swine fever (ASF)

African swine fever is one of the most important viral diseases of pigs, and the lack of vaccine combined with the presence of infected wild boars further complicates the implementation of effective control measures (*Podgorski and Smietanka, 2018; OIE, 2019b*). The causative agent is the African swine fever virus (ASFV), a double-stranded DNA virus from the *Asfarviridae* family (*ICTV, 2021*). Unlike most DNA viruses, ASFV replicates in the cytoplasm of infected cells, and its main target cells are macrophages which aid virus dissemination throughout the body of the infected animal (*Blome et al., 2020*). This virus is very stable, especially in moist conditions (blood, manure, etc.) as well as in raw pork products where it survives for months, however, proper cooking results in virus inactivation (*Dixon et al., 2019*). Outbreaks of this disease must be reported to the World Organisation for Animal Health (OIE), and trade restrictions are imposed on countries with reported cases of ASF (*OIE, 2019b; Blome et al., 2020*). African swine fever is endemic to sub-Saharan Africa, Sardinia, and parts of the Caucasus and Eastern Europe (*Beltran-Alcrudo et al., 2017*). ASFV infects domestic pigs and wild suids (warthogs and bushpigs in Africa; wild boars in Europe and Asia) (*Beltran-Alcrudo et al., 2017; Milićević et al., 2019; Petrović et al., 2021*). The virus circulates between *Ornithodoros moubata* soft tick species and warthogs in Africa in which it causes no clinical symptoms (*Blome et al., 2020*). This sylvatic cycle is maintained since warthogs are naturally resistant to ASFV, and the virus remains in tick populations due to transovarial, transstadial, and transsexual transmission (*Dixon et al., 2019*). Conversely, the Eurasian wild boars manifest clinical symptoms similar to domestic pigs and excrete high levels of virus (*Blome et al., 2020; Dixon et al., 2019*). Wild boar populations in Sardinia, Eastern Europe, and the Caucasus are important for maintaining the cycle of ASFV infection (*Beltran-Alcrudo et al., 2017*; *Dixon et al., 2019*). The virus is transmitted through scavenging, as well as by human factors such as supplementary feeding, fencing, or hunting (*Beltran-Alcrudo et al., 2017*). In Europe and Asia, domestic pigs can be infected by wild boars both through direct and indirect routes (*Podgorski and Smietanka, 2018; Blome et al., 2020*). Wild boars can move across borders and therefore represent important means of virus transmission and a reservoir for domestic pigs, especially in areas with low biosecurity measures on extensive pig farms (*Podgorski and Smietanka, 2018; Chenais et al., 2019*). In areas with low wild boar population densities, the infection of these animals originated from domestic pigs, however, in regions with dense wildlife populations, wild boars are reservoirs of ASFV for domestic pigs (*Beltran-Alcrudo et al., 2017*; *Petrović et al., 2021*). The clinical presentation of ASF is variable and dependent on virulence of the virus, infectious dose, exposure route, as well as the affected breed of swine (*Dixon et al., 2019*; *OIE, 2019b*). Peracute and acute disease forms are caused by highly virulent strains and often result in the death of affected animals. Acute ASF is characterized by inappetence, high fever, lethargy, ocular and nasal discharge, vomiting, melaena, purple areas and hemorrhages on the ears, abdomen, and legs (*Dixon et al., 2019; Milićević et al., 2019; Blome et al., 2020*). These characteristic hemorrhages are difficult to observe in wild boars due to dark skin and thick hair (*Beltran-Alcrudo et al., 2017*). Infection with viruses of moderate virulence leads to acute and subacute forms of the disease characterized by somewhat lower mortality rates of 30-70% (*Blome et al., 2020*). Clinical signs are usually less severe than in acute cases, however, hemorrhages and edemas are more evident, as well as impaired movement due to joint swelling as a result of fluid and fibrin accumulation (*Beltran-Alcrudo et al., 2017; Blome et al., 2020*). Virus isolates of low virulence are present in endemic areas, and the infection is more dependent on the exposure route and infectious dose. These strains cause chronic disease manifested by mild fever, wasting, arthritis, skin ulcers, and respiratory symptoms (*Dixon et al., 2019*). Characteristic pathological findings include enlarged hemorrhagic lymph nodes, splenomegaly (the spleen is dark red to black with round edges), petechiae in the kidneys and other organs (*Beltran-Alcrudo et al., 2017; OIE, 2019b*). Clinical manifestations of ASF may not be easily distinguished from other viral and bacterial diseases of pigs, and a definitive diagnosis is established based on laboratory tests (*Beltran-Alcrudo et al., 2017*). Laboratory diagnostic methods are based on the identification of viral DNA, antigens, or specific antibodies, and the choice of proper methods is based on the disease course and epizootiological situation (*Nišavić et al., 2016*). Samples for testing include blood in anticoagulant, serum, spleen, lymph nodes, bone marrow, lung, tonsil, and kidney (*Milićević et al., 2019*; *OIE, 2019b*). Virus isolation is performed by inoculation of pig leukocyte or bone marrow cultures with sampled material and the replication of ASFV produces a cytopathic effect (CPE) in the infected cells (*Beltran-Alcrudo et al., 2017; OIE, 2019b*). The haemadsorption (HAD) test is often performed since a positive result in the HAD test is definitive for ASF diagnosis. Pig erythrocytes adhere to the surface of pig monocyte or macrophage cells cultured *in vitro* and infected with ASFV which is a unique trait for this virus (*Beltran-Alcrudo et al., 2017*). The presence of the virus can also be confirmed in cell cultures by immunofluorescence or PCR (*OIE, 2019b*). The viral antigen can also be directly detected in sampled tissues by antigen ELISA test or immunofluorescence, however, these methods are most sensitive for diagnosing acute ASF (*Beltran-Alcrudo et al., 2017*). Conventional and real-time PCR is most often used for the detection of the ASFV genome in samples from both pigs and ticks (*Milićević et al., 2019*; *Blome et al., 2020*). This method is equally applicable unrelated to the disease course in suspected infections (*Beltran-Alcrudo et al., 2017*). The presence of anti-ASFV antibodies is mostly detected using ELISA and immunofluorescence and is indicative of current infection or past exposure since there is no vaccine available (*OIE, 2019b*). However, serological diagnostic methods are not applicable in acute and peracute cases of infection (*Beltran-Alcrudo et al., 2017*). ASFV is a genetically stable virus with low rates of mutation. Today, the molecular epizootiology of ASF is mostly based on whole-genome sequencing that enables a more detailed analysis of potential genetic changes and an understanding of virulence factors (*Blome et al., 2020*). The first reported case of ASF in Serbia was detected on July 30, 2019, in a domestic pig population in Mladenovac municipality (*Milićević et al., 2019*). The epizootiological situation in Romania, Bulgaria, and Hungary during 2017 and 2018 lead to the establishment of programs of surveillance of wild boar populations in bordering areas with Serbia (*Petrović et al., 2021*). However, the virus was introduced due to human activities, most probably including the illegal trade of pork products (*Milićević et al., 2019*). Since then, numerous outbreaks in both domestic pigs and wild boars have been reported, and the epidemiological pattern shows that ASFV circulates among small farms, wild boars, but also affects large farms with intensive rearing systems (*Petrović et al., 2021*).

Aujeszky's disease (AD)

Aujeszky's disease (AD) is an economically important viral disease primarily associated with pigs or wild boars as natural hosts (*OIE, 2018; Tan et al., 2021*). The disease is caused by Suid Herpesvirus 1 (SuHV1), a double-stranded DNA virus from the genus *Varicellovirus*, subfamily *Alphaherpesvirinae* of the *Herpesviridae* family (*ICTV, 2021*). The virus exists in a single serotype and four genotypes circulating worldwide (*Milićević et al., 2016; Sehl and Teifke*, *2020*). SuHV1 causes the infection of multiple organs, dominantly the central nervous system of diverse mammalian species (carnivores, rabbits, cattle, etc.), however, it is not zoonotic (*Sehl and Teifke*, *2020*). The pigs are the only species that survive the infection and remain latently infected after recovery, making them ideal reservoir hosts (*OIE, 2018*). Clinical manifestations of AD in pigs depend primarily on the age of the animal and its immunological status as well as the virulence of the infecting SuHV1 strain (*Helke et al., 2015*). Piglets in the first two weeks of life are highly susceptible to infection and show severe neurological symptoms followed by death (*Sehl and Teifke*, *2020*). Older categories of pigs mostly have respiratory disease symptoms that are frequently complicated by secondary bacterial infections, and pregnant sows abort due to the ability of the virus to cross the placental barrier (*Helke et al., 2015*). The disease in other animal species is fatal and also known as pseudorabies (similar to rabies) or "mad-itch" since it leads to behavioral and nervous disorders often manifested by scratching due to intense pruritus that in turn causes severe tissue damage (*Sehl and Teifke*, *2020*). SuHV1 is shed in large quantities by infected pigs and is spread in the population by direct and indirect contact (*Nišavić and Milić, 2017a*). Cattle, sheep, and goats mostly acquire the infection through direct contact with infected pigs, whilst carnivores get infected through unprocessed pig meat (*Helke et al., 2015; Sehl and Teifke*, *2020*). After replication in the respiratory tract of the pig, the virus is transported to tonsils and regional lymph nodes, and it spreads throughout the body during the viraemic phase of infection (*Nišavić and Milić, 2017a*). SuHV1 demonstrates tropism towards various tissues including the endothelium, lymphocytes, macrophages, and epithelial cells (*Sehl and Teifke*, *2020*). Similar to other herpesviruses, latency is established in the trigeminal and sacral ganglia as well as in the tonsils (*Helke et al., 2015*; *Nišavić et al., 2018; Radalj et al., 2021*). Herpesviruses are successfully maintained in animal populations through constant cycles of latency and reactivation of the virus which results in shedding and infection of other susceptible animals (*Radalj et al., 2021*). Clinical symptoms of AD are rarely observed in wild boars, and disease outbreaks may pass unnoticed, while some studies demonstrate that younger animals are mostly affected (*OIE, 2018*; *Sehl and Teifke*, *2020*). The occurrence of AD in wild boar populations can be triggered by stress-induced by various factors including environmental conditions or human activities (*Meier et al., 2015*). In extensive pig farming systems, domestic pigs are often exposed to contact with wild boars, and on the other hand, human factors can influence the distribution of wild boars that potentially induce interactions with domestic pigs (*Charrier et al., 2018*). On pathological examination, notable changes can be seen in younger animals and include congestion of the brain and lymph nodes, and necrotic alterations in tonsilar tissue and parenchymatous organs (*Sehl and Teifke*, *2020*). The appearance of white spots on the liver indicates AD infection in very young piglets (*OIE, 2018*). Laboratory diagnosis of AD is based on virus isolation, PCR, and serology (*Nišavić and Milić, 2017a*). Suitable samples for analysis include oral fluid and nasopharyngeal swabs from living animals (*OIE, 2018*). In the case of wild boars, tissues taken on post-mortem examination are usually sampled and often include samples of brain, spleen, tonsils, lungs, kidneys, or blood (*Milićević et al., 2016; OIE, 2018*). Neural tissue is the sample of choice for attempting virus isolation in latently infected animals (*Radalj et al., 2021*). SuHV1 can be successfully isolated in various cell lines, with PK-15 being the most preferred, and virus replication induces the development of CPE within 24 to 72h of specimen inoculation. Following isolation, SuHV1 is further identified by virus neutralization, immunofluorescence, or PCR (*OIE, 2018*). Conventional or real-time PCR is the method of choice since it is reliable in detecting both active infection and latently present virus and enables the examination of multiple samples in a relatively short time (*Nišavić et al., 2016*). ELISA is most frequently used for serological diagnosis and is especially suitable for large-scale studies on wild boar populations (*Boadella et al., 2012; Charrier et al., 2018*). Seroprevalences in wild boars are highly variable from country to country, with the highest being in Spain, Italy, and neighboring Croatia and Romania (*Meier et al., 2015*). Even though AD occurs worldwide, some countries have managed to eradicate the disease in domestic pigs (Canada, USA, New Zealand, and some EU states) (*OIE, 2018*). However, wild boar populations still pose a threat since these animals are risk factors for introducing the virus into previously free areas (*Boadella et al., 2012*). For example, in Spain, where AD has been eradicated in domestic pigs, occasional spillovers from wild boars to extensively reared pigs still occur and this is controlled by mandatory vaccination (*Muller et al., 2021*). Conversely, in Serbia, there are no eradication or vaccination programs, and domestic pigs are mostly vaccinated on large commercial farms due to economic reasons. In Serbia, SuHV1 was successfully isolated from wild boars demonstrating respiratory symptoms during the winter of 2014/2015. The isolates were genetically analyzed, and the results showed little difference from domestic pig SuHV1 isolates, again emphasizing the importance of establishing adequate biosecurity measures in some areas of the country where pigs are extensively farmed (*Milićević et al., 2016*).

Porcine circovirus infections

Porcine circoviruses (PCVs) are known etiological agents of disease in both domestic pigs and wild boars, however, due to the widespread use of advanced molecular techniques, novel PCVs are still being detected (*Nišavić and Milić, 2017b; Zhang et al., 2020*; *Nišavić et al., 2021a*). These viruses are one of the smallest DNA viruses with a circular single-stranded genome and are members of the *Circoviridae* family (*ICTV, 2021*). To date, PCVs have been divided into four species, i.e., PCV1-4 (*Opriessnig et al., 2020*). PCV1 does not cause diseases in pigs and was discovered as a contaminant of porcine cell lines. However, PCV2 is listed as one of the most important viruses of swine and causes various disease syndromes in these susceptible animals also known as a porcine-circovirus-associated disease (PCVAD) (*Segales et al., 2012; Zhai et al., 2019*). PCVAD includes the postweaning multisystemic wasting syndrome (PMWS), pneumonia, reproductive problems, and porcine dermatitis and nephropathy syndrome (PDNS). Available literature information dominantly concerns PCV2 since it was the most studied of all circoviruses. It is well-known that aside from infection with PCV2, other factors are required to induce severe disease (*Segales et al., 2019*). PCV3 has been identified recently in domestic pigs and wild boars and is also connected with similar disorders as PCV2, however, this virus was also detected in healthy animals, and it is suggested that PCV3-associated disease is most often subclinical and also dependent on the influence of other factors (*Prinz et al. 2019; Saporiti et* *al. 2021*). PCV4 was identified very recently in China, however, its global distribution and potential disease association are still largely unknown (*Zhang et al., 2020*). PCV2 easily spreads in the susceptible population, mostly through direct contact, and is shed for a long time, thus exposing susceptible pigs to contaminated respiratory, digestive, and urinary secretions (*Rose et al., 2012*). Definitive diagnosis of infectious diseases includes laboratory confirmation of the etiological agent after clinical sign assessment. This may be difficult in the wild, and thus most studies concern the analysis of wild boar samples collected postmortem (*Prinz et al. 2019; Nišavić et al. 2021a*). The most suitable samples for conventional or real-time PCR analysis include the spleen, liver, tonsils, lymph nodes, and sera (*Amoroso et al., 2021; Nišavić et al., 2021a*). PCV2 affects the immune system in wild boars leadings to the aggravation of other diseases present in these animals (*Rose et al., 2012*). Some wild boar hunting grounds are fenced and correspond to domestic pig extensive breeding farms that can also deteriorate PCVAD (*Ellis et al., 2003*). Overall, it is considered that wild boars are PCV2 reservoirs and represent a substantial risk for domestic pigs (*Amoroso et al., 2021*). A study conducted in Italy emphasizes the limited efficacy of biosecurity control measures considering high PCV2 infection prevalence in both domestic pig and wild boar populations (*Franzo et al., 2020*). PCV2 prevalence in wild boars is variable from one country to another, and often, PCV2-positive domestic pigs are detected in areas with high densities of wild boar populations and where pigs are traditionally farmed (*Turcitu et al., 2011; Franzo et al., 2020*). Traditional pig production with irregular vaccination strategies is common in Serbia, indicating the possible role of domestic pigs as an infection source for the wild boar population (*Nišavić et al., 2021a*). PCV2 isolates are genetically heterogeneous and are currently divided into eight genotypes, i.e. (PCV2a-PCV2h) (*Franzo and Segales, 2018*). In a recent study by *Nišavić et al. (2021a),* the presence of PCV2 was confirmed in 40.32% of organ samples from 124 wild boars hunted in areas with widespread traditional pig farms. The sampled animals were clinically healthy, showing the importance of cofactors that support disease development. The most prevalent genotype in wild boars in Serbia was PCV2d which corresponds to the current global PCV2 genotype shift (*Song et al., 2020; Nišavić et al., 2021a*). Nevertheless, the emergence of new PCV2 strains and genotypes is probably driven by vaccine immunity and shows the necessity for more effective preventive measures that also include limiting possible contact of wild boars and domestic pigs, creating the flux of PCV2 strains in both directions (*Franzo and Segales, 2018*; *Franzo et al., 2020*). Accumulating results from different studies demonstrate that PCV3 is also highly prevalent in wild boar populations around worldwide, however, the presence of this virus was not determined in wild boars in Serbia (*Prinz et al., 2019; Amoroso et al., 2021; Nišavić et al., 2021a*).

Porcine parvovirus infections

Porcine parvoviruses (PPVs) are small single-stranded DNA viruses classified within the *Parvoviridae* family (*ICTV, 2021*). New PPVs are being successively discovered in recent years, and currently, PPV1-7 have been detected in samples from both domestic pigs and wild boars around the world (*Xiao et al., 2013; Nišavić et al., 2021b*; *Park et al., 2021*). One of the main characteristics of parvoviruses is replication in cells with a high mitotic index, and therefore fetal tissues provide an ideal environment (*Nišavić and Milić, 2017c; Truyen and Streck, 2019*). It is known that PPV1 causes infection in pigs and wild boars manifested by stillbirths, mummification, embryonic death, and infertility (SMEDI), while the exact role of other parvoviruses in causing disease remains to be determined (*Streck et al., 2015; Truyen and Streck, 2019*). The outcome of infection in pregnant sows depends on the gestation stage, namely, early infections lead to reproductive failure and fetal mummification, while fetuses infected in the second half of gestation may survive the infection. Moreover, the virulence of the infecting strain plays a major role, and more virulent PPV1 strains cross the placental barrier more efficiently (*Truyen and Streck, 2019*). PPV is highly resistant in the environment facilitating its indirect transmission, and it is shed through feces and other secretions (*Helke et al., 2015*). The transmission of PPV between wild boars and domestic pigs is very probable due to the prolonged survival of this virus in the environment (*Nišavić and Milić, 2017c; Malmsten et al., 2018*). The virus primarily replicates in the tonsils, after which it reaches regional lymph nodes, causes viremia, and reaches the placenta causing clinical manifestations of the disease (*Helke et al., 2015*). PPV1 is highly prevalent in wild boars across Europe and recent studies also concern the presence of other newly discovered parvoviruses (*Malmsten et al., 2018; Nišavić et al., 2021b*; *Park et al., 2021*). PPV3 is related to human parvovirus 4, and a recent study from Italy speculates that it has an immunosuppressive effect on wild boars, however, this virus is mostly detected in healthy animals (*Amoroso et al., 2019; ICTV, 2021; Nišavić et al., 2021b*). PPV3 was the most common parvovirus in wild boars in Serbia with a detection rate of 69.6% amongst all positive samples, and different PPV3 strains were found to be circulating amongst Serbian domestic pigs and wild boars (*Nišavić et al., 2021b*). All novel PPVs except for PPV2 have been described in the organs of Korean wild boars, with frequent findings of co-infection (*Park et al., 2021*). The study conducted by *Nišavić et al. (2021b)* in Serbia also aimed to investigate the presence of different PPVs in wild boars for the first time. Similar to the results of other studies, co-infections were a frequent finding, and PPV1, PPV2, and PPV3 were determined in the samples of lymph nodes, spleen, and tonsils of wild boars. Laboratory submissions for the confirmation of PPV1 usually include mummified fetuses and fetal tissues, however, when analyzing the presence of PPV1 or other related PPVs in wild boar populations, samples of lymphatic tissue and parenchymatous organs are usually taken from animals shot on hunting grounds (*Helke et al., 2015; Nišavić et al., 2021b*). Isolation of PPV1 can be attempted, however, it is seldom successful if samples are not processed on time, i.e. the recovery of viable viruses depends on the condition of the sample. The virus is further confirmed by immunofluorescence, hemagglutination, or PCR (*Truyen and Streck, 2019*). Routinely, all PPVs are detected using molecular methods that are generally more sensitive, specific, and suitable for the analysis of autolyzed tissue samples (*Nišavić et al., 2016; Nišavić et al., 2021b; Park et al., 2021*). Serological methods such as ELISA or hemagglutination-inhibition test are performed to determine the previous exposition of certain wild boar populations to PPV (*Malmsten et al., 2018; Truyen and Streck, 2019*). High seroprevalence is detected in wild boar populations from regions with more developed extensive domestic pig production (*Roić et al., 2005*).

Control of viral diseases in wild boars

Wild boars represent an exceptional species for investigating the epidemiology of wildlife diseases since the species is indigenous around the world, adapts easily to new habitats, has a high reproductive rate, and shares common infectious agents with domestic pigs (*Ruiz-Fons et al., 2008; Massei et al., 2015*). These animals are reservoirs for some viral pathogens of domestic pigs thus, disease control programs must address the issue of contact prevention between wild and domestic swine (*Moennig, 2015*). However, it must be noted that the spillover events can occur both ways, and that wild boar can be infected by domestic pigs thus, becoming pathogen reservoirs in nature (*Nišavić et al., 2021a; Petrović et al., 2021*). Pathogen eradication is arduous in wild animals, and control measures should not be limited to wildlife only and should begin with the domestic pig population (*Meier and Ryser-Degiorgis, 2018*). Disease prevention in domestic swine includes surveillance programs, implementation of adequate biosecurity measures, and vaccination if applicable (*Ruiz-Fons et al., 2008; Meier and Ryser-Degiorgis, 2018*). Some control techniques such as the use of fencing or feeding of wild boars cause the aggregation of these animals in certain areas and give rise to population density which favors efficient disease transmission and pathogen maintenance in the environment (*Ruiz-Fons et al., 2008; Moennig, 2015; Beltran-Alcrudo et al., 2017*). High population densities are found to be connected to high prevalences of ADV, CSF, PCV2, and are important for maintaining and spreading ASF, thus ideal measures would include population control without animal aggregation (*Meier and Ryser-Degiorgis, 2018*). Hunting is another method that reduces the number of susceptible animals in the wild, however, available data show that regular hunting did not lead to the decrease of the wild boar population over time (*Massei et al., 2015*). Therefore, this is useful as an additional control measure, also valuable in terms of sample collection for laboratory diagnosis

(*Moennig, 2015; Milićević et al., 2016; Nišavić et al., 2021a; Nišavić et al., 2021b*). Serological surveys are appropriate for epizootiological studies and are inexpensive, practical, and demonstrate the previous contact with certain viruses, while virological assays require more samples to correctly determine prevalence rates (*Boadella et al., 2012; Charrier et al.,* 2018; *OIE, 2019b; Tryen and Streck, 2019; Nišavić et al., 2021b*). Attention must be paid to the interpretation of results of diagnostic tests since the detection of a virus does not automatically determine its excretion (*Beltran-Alcrudo et al., 2017; Radalj et al., 2021*). Therefore, virus and host characteristics, as well as the epizootiological situation on-site must be taken into account when choosing the appropriate diagnostic approach.

Conclusion

Wild boars are similarly affected by viral diseases as domestic pigs and have great reservoir potential for certain pathogens. Some viral diseases characterized by high mortality rates can significantly influence wild boar populations in the wild, and are more easily noticeable and thus reported. On the other hand, many viruses infecting wildlife are more insidious and impact survival rates and reproduction in wild animals. In some cases, wild boars might be less susceptible to disease than domestic pigs, particularly due to the absence of factors that aid disease development present in farmed animals. There is still no sufficient data available on all aspects of infectious disease dynamics in these animals in the wild, and many available studies give opposing conclusions on the same subjects of investigation. This seeks the constant improvement of knowledge on pathogenesis, clinical aspects of the disease, risk factors for disease development, epizootiology, and adequate control measures of viral diseases of these animals.

Pregled značajnih virusnih oboljenja divljih svinja

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Rezime

Divlje svinje su jedna on najrasprostranjenijih vrsta sisara na planeti, a ujedno predstavljaju i rezervoare mnogih značajnih virusa. Pojava oboljenja u populacijama domaćih svinja se javlja kao posledica kontakta sa divljim svinjama pri čemu tradicionalan način uzgoja životinja predstavlja faktor rizika. Primeri takvih obljenja su: klasična kuga svinja, afrička kuga svinja, Aujeckijeva bolest i oboljenja izazvana svinjskim cirkovirusima i parvovirusima. Određene virusne infekcije sa visokom stopom mortaliteta se mogu lako detektovati, a samim tim i prijaviti, međutim neki virusi divljih svinja ne dovode do vidljivih promena što otežava njihovo otkrivanje. Uzorci za laboratorijska ispitivanja poreklom od divljih svinja se najčešće prikupljaju postmortalno i uključuju različita tkiva ili krvni serum. Uspešnost izolacije virusa u kulturi ćelija zavisi od vrste virusa kao i od stanja dostavljenog uzorka. S obzirom da primena navedene metode oduzima vreme, većina procedura se zasniva na PCR ili metodama detekcije antigena. Pored toga, serološke metode su ekonomski isplative i pogodne za izvođenje studija prevalencije. Prilikom interpretacije rezultata laboratorijskih analiza je izuzetno značajno uzeti u obzir više parametara uključujući osobine virusa i domaćina kao i epizootiološku situaciju na terenu. Metode kontrole zaraznih bolesti divljih svinja poput ograđivanja ili dohranjivanja životinja dovode do povećanja gustine populacije što pogoduje transmisiji patogena. Lov dovodi do smanjenja broja osetljivih životinja u određenoj sredini, međutim koristan je kao dodatna mera kontrole i omogućuje prikupljanje uzoraka. Dostupni podaci o dinamici infektivnih oboljenja divljih svinja su ograničeni i neophodno je konstantno izučavanje njihove patogeneze, kliničkih osobenosti, faktora rizika kao i procena primene određenih mera kontrole.

Ključne reči: CSFV, ASFV, PCV, PPV, SuHV1, divlje svinje

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Author Contributions

JN and AR conceptualized the paper, which was developed further in discussion with NM, AS, AŽ, and DB, JN, AR, and IP collated articles for review, wrote and critically reviewed various drafts. NM, AŽ, AS, DB, and IP contributed to the preparation of the final version and provided consent for submission.

Conflicts of Interest

The authors declare no conflicts of interest.

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EFFECT OF YEAR, LAMBING SEASON, SEX AND BIRTH TYPE ON EARLY PERFORMANCE IN MIS LAMBS

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Original scientific paper

Abstract: Considering the fact that sheep production has an important role in agriculture of Serbia, lamb performance is essential. Objective of the study was to investigate effect of year, lambing season, sex and birth type on growth performances in lambs of MIS breed. Animal data (birth date, birth type, sex, birth weight -BW0, body weight after 30 days - BW30 and body weight after 60 days – BW60) are gained from control of productive parameters maintained from 2011 to 2020. Research was conducted on the sample of 1592 lambs. Average daily gain from birth to 30 days (ADG1), from 30 to 60 days (ADG2), and from birth until 60 days (ADG3), were calculated and included in analysis. Calendar year was divided in four seasons, each season consists from 3 months: winter, spring, summer and autumn. Average body weights (± standard deviation) at birth, after 30 and 60 days were 4.41 kg (± 0.99), 14.11 kg (± 2.80), 24.05 kg (± 3.86), respectively. Average daily gains were 319.87 g (± 74.97), 329.84 g (± 70.90) and 324.99 g (± 55.48) for ADG1, ADG2 and ADG3, respectively. Lambing type and sex of the lambs affected all of the observed traits very significantly ($p < 0.01$). Lambing year had very significant effect ($p < 0.01$) on BW30, on ADG1 and ADG2, while lambing season significantly ($p < 0.05$) affected BW60, ADG2 and ADG3.Based on the results it can be concluded that birth type and sex had strongest effects in early productive parameters of lambs.

Key words: growth traits, sheep, small ruminants, gains

Introduction

Sheep production has an important role in agriculture of Serbia. With production of 34 thousand tones in 2019. it holds third place in the production of red meat *(Statistical Office of the Republic of Serbia, 2020)*.

The MIS sheep was bred at the Institute of Animal Husbandry in Zemun during the period 1991-2006., by a complex combination of representatives of three sheep breeds: Pirotska pramenka, Merinolandschaf (Wurtemberg) and Ile de France (*Petrović, 2006*). This is a meaty type of sheep, with a strong constitution, with a pronounced carcass conformation and exceptional meat properties. Females enter brood at 10-12 months of age, and rams at 12 months of age. Fertile estrus occurs during most of the year. An average of 130-160 lambs are obtained from 100 sheep (lambing index 1.3 – 1.6).

Production of lamb meat obtained from young lambs up to 60 days old, and of the carcass weight of 10 to 12 kg, i.e. about 25 kg live weight, is a predominant one (*Zeljić et al., 2019*). Body weight and growth are important in the total productivity, especially when the meat production is the main objective; a high birth weight allows the animal to well start his career, and grow rapidly before and after weaning predisposes, to a better diseases resistance and to reach quickly puberty and maturity (*Zidane et al., 2015*). Body weight at birth and weaning depends on many environmental factors, and among them are year and season, which is primarily reflected through nutrition, housing and care of animals during the production cycle, especially during pregnancy (*Petrović et al., 2015*). Among other important factors on the growth of lambs maternal age, maternal body weight, type of birth and sex of lambs should be mentioned (*Caro Petrović et al., 2015*). An understanding of the factors which influence the development and growth of lambs will permit changes in the breeding and management schemes to minimize influences, which reduce production efficiency (*Bermejo et al., 2010*).

Considering the above mentioned, the aim of this study is to evaluate the influence of year, lambing season, sex and birth type on growth traits of lambs.

Material and Methods

Animal data (birth date, birth type, sex, birth weight (BW0), body weight after 30 days (BW30) and body weight after 60 days (BW60)) are gained from control of productive parameters maintained from 2011 to 2020 on Experimental sheep farm in Institute for Animal husbandry in Zemun, Serbia. Research was conducted on the sample of 1592 lambs, offspring of 303 ewes. Average daily gain from birth to 30 days (ADG1), from 30 to 60 days (ADG2), and from birth until 60 days (ADG3) were calculated and included in analysis. Calendar year was divided in four seasons, each season consists from 3 months: winter (december, january, february), spring (march, april, may), summer (june, july, august) and autumn (september, october, november).

Basic statistical parameters of phenotypic manifestation and variability of examined properties (body weight on birth, after 30 and 60 days and average daily gains – ADG1, ADG2, ADG3) were calculated using standard statistical procedures in PROC MEAN procedure in SAS statistical package (SAS Inst., Inc., Cary, NC). Using the PROC CORR procedure in the same statistical package, correlation coefficients for examined traits were calculated, and using GLM procedure, effects of fixed factors were examined. Fixed factors were year, lambing season, birth type (single, twin, triplets, quadruplets) and sex of the lambs.

An applied fixed model was such as follows:

$$Yijkl= \mu + Gi + Sj + Tk + Pl + eijkl$$

In which:
Yijkl- is a phenotypic expression of a studied trait
μ- population general average
Gi- fixed effect of i year of birth (i=2011,...2020)
Sj- fixed effect of j lambing season (j=1, 2, 3, 4)
Tk- fixed effect of k type of birth (k=1, 2, 3, 4)
Pl- fixed effect of l lamb`s sex (l=1, 2)
eijkl- random error.

Results and Discussion

Average body weights (at birth, after 30 days and on weaning), as well as ADGs are shown in table 1. Body weight of lambs at birth has an important role in achieving a good production, because of the initial body weight depends not only growth, but also vitality and mortality of sheep (*Petrović et al., 2009*). In this study, BW0 showed the highest coefficient of variation - CV (22.55%), and can be explained by lot of factors influencing on this trait. Birth weight of lambs is influenced by breed, sex of lambs, birth type, age of dam, feeding conditions and production system (*Sušić et al., 2005*).

Body weight at 60 days is higher, but ADG2 is lower than reported in *Petrović (2006)*, where values were 22.14 kg and 370.83 g, respectively. The average daily gain of lambs, can be influenced by a lot of factors. In addition to the ewe's milk production, ADG of lambs can be affected by litter size, management in lamb rearing, by available feeds on the farm, in terms of quality and quantity, but also by individual performance of lambs. For these reasons, large variations are noticeable in the ten-year observation of these parameters, especially in minimum values, showed in table 1.

Concerning the ADG, highest CV was reported in ADG1 and ADG2, which is in line with results reported in study of *Latifi and Mohammadi (2018)*.

Table 1. Average values and variability of studied traits

Traits	n	x̄	SD	Variance	Min	Max	CV (%)
BW0, kg	1573	4.41	0.99	0.99	1.80	7.80	22.55
BW30, kg	1414	14.11	2.80	7.86	4.10	23.50	19.87
BW90, kg	1383	24.05	3.86	14.93	12.00	36.50	16.07
ADG1, g	1412	319.87	74.97	5619.89	6.67	653.33	23.44
ADG2, g	1382	164.98	35.39	1252.73	16.67	353.33	21.45
ADG3, g	1382	216.88	36.86	1358.40	91.11	346.67	16.99

*BW0= birth weight; BW30= body weight at 30 days; BW60= body weight at 60 days; ADG1= average daily gain from birth to 30 days; ADG2= average daily gain from 30 days to 60 days; ADG3= average daily gain from birth to 60 days.

In table 2 values of F-test for body weights and ADGs are presented. Body weights (from birth to 60 days). Lambing type and sex of the lambs had significantly influences on birth weight of the lambs, which is in line with results reported in *Dixit et al. (2001)* and *Latifi and Mohammadi (2018)*. Lambing year, lambing type and sex significantly influences on lamb weight after 30 days.

Lambing type and lambing season, as well as sex of the lambs, significantly influenced on the BW60.

Table 2. Values of F- test for studied factors

Traits	Factors				
	Lambing year	Lambing season	Lambing type	Sex	R^2
BW0	1.17^{ns}	1.59^{ns}	1066.58**	25.53**	0.41
BW30	27.13**	1.00^{ns}	659.60**	35.45**	0.34
BW90	0.02^{ns}	5.31*	577.17**	63.01**	0.32
ADG1	34.09**	0.59^{ns}	359.09**	22.52**	0.23
ADG2	41.16**	4.61*	86.08**	36.88**	0.10
ADG3	0.15^{ns}	4.30*	369.94**	55.51**	0.24

^{ns}=P>0.05; *=P<0.05; **=P<0.01; R^2= coefficient of determination.

Lambing year significantly affected BW30, ADG1 and ADG2. *Staikova and Stancheva (2009)* found out in their study that the year of birth significantly influenced the live weight at all ages. On the contrary to results of this study, *Petrović et al. (2011)* reported that lambing year significantly influenced birth weight of the lambs.

Lambing season significantly influenced only on ADG2 and ADG3. Although differences depending on the lambing season can be interpreted as the factor of food, in other words, the effect of pasture grass and natural environment

(Petrović et al., 2011), these effects wasn't established in this study. This can be explained by the practice that lambs stay with their mother indoor until weaning. Dams receive sufficient amounts of hay and concentrate mixture, and creep feeding of lambs starts 7-10 days after lambing, so lambs have similar conditions throughout the year, with fulfilled nutritive demands After weaning, lambs are, depending on season, or in pastures or fed indoors, and that explains differences in ADG2 and ADG3.

Table 3. Values of Pearson correlation coefficients for studied traits

Traits					Traits
BW30	BW60	ADG1	ADG2	ADG3	
0.68^{**}	0.66^{**}	0.43^{**}	0.30^{**}	0.48^{**}	BW0
	0.84^{**}	0.95^{**}	0.22^{**}	0.79^{**}	BW30
		0.77^{**}	0.71^{**}	0.98^{**}	BW60
			0.15^{**}	0.77^{**}	ADG1
				0.74^{**}	ADG2

^{ns}=P>0.05; *=P<0.05; **=P<0.01.

Lambing type had very significant effect on all of the observed traits, which is in line with *Baneh and Hafezian (2009)* and *Rahimi et al. (2014),* who reported that type of birth was significant on weight traits from lambing to weaning. Single lamb's body weight in all ages and their average daily gain were more than twins because of competition between twins to fed on their mother's milk resulting in suckling less milk compared to the singles *(Petrović et al., 2015)*.

Sex of the lambs significantly influenced on all of the observed traits. These results are in line with *Rashidi et al. (2008), Rahimi et al. (2014)* and *Caro Petrović et al. (2015).* Type and measure of hormone secretion especially sexual hormones, lead to difference in animal growth, estrogen hormone has a limited effect on the growth of long bones in females, which leads to smaller body weight in females than in males (*Petrović et al., 2015*). *Ilić et al. (2013)* reported that male lambs were heavier than females, and that effects of lamb sex were significant on the body weight of lambs on birth, after 30, 60 and 90 days. On the contrary, *Caro Petrović et al. (2013)* didn't found effect of the sex on body weight.

In table 3. correlation coefficients of observed trait are shown, which can give more detailed information about physical development of lambs. Statistical significance was found among all of the traits. Birth body weight is strongly correlated with BW30 and BW60. These results are in line with study of *Petrović et al. (2014)* who reported that highest correlation indexes were found between birth body weight and body weight after 30 days. Higher body weight of lambs at birth affects the higher birth weight of lambs at 60 days of age (*London and Weniger, 1995*).

Conclusion

The obtained results showed that birth body weight had biggest coefficient of correlation, with interval of values from 1.80 kg to 7.80 kg.

Lambing year had very significant effect ($p < 0.01$) on BW30,on ADG1 and ADG2, while lambing season significantly ($p < 0.05$) affected BW60, ADG2 and ADG3. Lambing type and sex of the lambs had strongest effects ($p < 0.01$) on BW0, BW30, BW60, ADG1, ADG2, ADG3.

Body weight on birth had strongest correlation coefficients with BW30 and BW60.

Based on the obtained data and results, it can be concluded that lambing type and sex of the lambs very significantly affected observed parameters.

Uticaj godine, sezone, pola i tipa jagnjenja na rane performanse MIS jagnjadi

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Rezime

S obzirom na to da ovčarstvo ima važnu ulogu u poljoprivredi Srbije, produktivnost jagnjadi je od izuzetnog značaja. Cilj istraživanja je bio da se ispita uticaj godine, sezone jagnjenja, pola i tipa rođenja na produktivne parametre jagnjadi MIS rase. Podaci o životinjama (datum rođenja, tip rođenja, pol, telesna masa na rođenju -BW0, telesna masa posle 30 dana - BW30 i telesna masa nakon 60 dana - BW60) su dobijeni kontrolom proizvodnih parametara održanih od 2011. do 2020. godine, na uzorku od 1592 jagnjadi. Prosečan dnevni prirast od rođenja do 30 dana (ADG1), od 30 do 60 dana (ADG2), i od rođenja do 60 dana (ADG3), izračunat je i uključen u analizu. Kalendarska godina je podeljena na četiri godišnja doba (zima, proleće, leto i jesen), a svako godišnje doba sastoji se od 3 meseca. Prosečna telesna masa (± standardna devijacija) pri rođenju, posle 30 i 60 dana bila je 4.41 kg (± 0.99), 14.11 kg (± 2.80), 24.05 kg (± 3.86), redom. Prosečni dnevni prirasti iznosili su 319.87 g (± 74.97), 329.84 g (± 70.90) and 324.99 g (± 55.48) za ADG1, ADG2 i ADG3, redom. Tip rođenja i pol jagnjadi značajno su uticali na sve ispitivane osobine ($p < 0.01$). Godina rođenja imala je veoma značajan uticaj ($p < 0.01$) na BW30, na ADG1 i ADG2, dok je sezona jagnjenja značajno ($p < 0.05$)

uticala na BW60, ADG2 i ADG3. Na osnovu rezultata može se zaključiti da su tip i pol rođenja imali najjače efekti u ranim produktivnim parametrima jagnjadi.

Ključne reči: osobine porasta, ovce, sitni preživari, prirasti

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GENETIC PARAMETERS OF SOME PRODUCTIVE AND REPRODUCTIVE TRAITS IN SHEEP FROM THE BULGARIAN DAIRY SYNTHETIC POPULATION (BDSP) AND ITS CROSSES WITH LACAUNE AND ASSAF

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Original scientific paper

Abstract: Dominating in recent years in Bulgaria are the sheep from the Bulgarian Dairy Synthetic Population (BDSP) and its crosses with other dairy breeds. This in turn leads to significant, scientifically based genetic and phenotypic diversity and different levels of productivity. The aim of the study is to research and characterize the genotypic parameters of the main productive and reproductive traits in sheep from the Bulgarian dairy synthetic population and its crosses with the breeds Lacaune and Assaf. The study includes a total of 3212 ewes reared in 15 farms, as from Bulgarian dairy synthetic population - 1114 ewes, BDSP crosses with Assaf - 1052 ewes and BDSP crosses with Lacaune - 1046 ewes, born in the period from 2014 to 2019 including. Studied trait were: milk yield for a standard 120-day period of I, II and III lactation, biological fertility of the 1st, 2nd and 3rd lambing and the trait - live weight of different age categories. The statistical model used was based on the model of animal /Animalmodel /, using the software product VCE and PEST (Groeneveld). Heritability in the main selection trait milk yield of the 1st, 2nd and 3rd lactation reaches from low to moderate and medium values. The lowest level of genetic diversity is in BDSP - h^2 varies from 0.125 to 0.157, in BDSP x Assaf from 0.131 to 0.202, and with the highest genetic diversity in the studied trait are ewes BDSP x Lacaune, respectively from 0.342 to 0.397. The rates of fertility in all three studied groups were from low to moderate h^2 - in BDSP from 0.133 to 0.156, in BDSP x Lacaune - from 0.040 to 0.112 and in BDSP x Assaf - from 0.100 to 0.122.

Key words: sheep, BDSP, Lacaune, Assaf, heritability, genetic corelation

Introduction

Dairy sheep are the most numerous part of the population in the country, which determines their main place in the structure of the national gene pool. The main directions of selection in this productive direction are increase of milk yield and fertility, improvement of the suitability of the udders for machine milking, increase of the resistance to the climatic factors and optimal utilization of the feed. This was the main goal in the creation of the recognized in 2005. The Bulgarian dairy synthetic population, in which the valuable qualities of the breeds included in the breeding scheme are combined.

The competitiveness and economic sustainability of productive systems in sheep breeding are a key factor for the successful business of farmers today. This also explains their desire to genetically renew their herds faster than is possible through purebred breeding. A typical example of this is the Bulgarian dairy synthetic population sheep, which is in the process of continuous genetic renewal. The method of creating the population allows in its intrabreed structure to use an "open nucleus" - it is characterized by an open system of selection. This allows, in addition to the main purebred breeding, in some cases to periodically apply ennobling crossbreeding with breeding material from the breeds involved in the creation of BDSP and from other world famous dairy breeds *(Stancheva et al., 2014).*

Recently, in the course of continuous genetic renewal, the breeds Assaf and Lakaune have been included. In the process of crossbreeding in the first generation, animals are undoubtedly obtained, which are generally superior in their productivity and fertility to their maternal forms. These are expected results due to the heterosis effect, the fundamental theoretical foundations of which have been well studied and described for years. *Boikovski (2006) and Baer et al. (2012)* presenting an analysis of the genetic effects caused by cross-breeding native breeds with Lacaune and East Frisian sheep breeds. The real problems with such an approach appear in the next management of the genetic changes of the obtained crosses *(Stancheva et al., 2013).* In our country the researches of the results from the breeding proces of the Bulgarian dairy synthetic population are limited. One of the main reasons for genetic losses in the population is the lack of a preliminary strategy that clearly presents the priorities in the breeding goals and the way in which they will be achieved.

The current work in dairy sheep breeding in the country leaves some unresolved problems related to the achievement of greater genetic progress in the synthetic population (*Nedelchev, 2010; Lazarov, 2011*).

The genetic parameters for different selection traits in sheep breeds with different productive direction are the subject of wide scientific interest. *El Fadili and Leroy (2001)* report that the use of crossbred schemes between local and sheep breeds with high milk yield can accelerate productivity gains through the exploitation of additive and non-additive genetic variations. *Tibbo (2006)* presents aspects related to the importance of maintaining adaptability to local conditions in the process of striving to improve productive qualities with different cross-breeding schemes.

In the beginning there is a high variability in all signs, including the main ones - milk yield and fertility, due to the influence of the final breeds or of the original Bulgarian breeds. After the creation of the different types of multi-breed crosses, selection begins in order to typify the created population (*Stancheva et al., 2014*). The breeding process is carried out in order to reduce, above all, the differences in milk yield and fertility. This system has been used for more than 30 years and by 1992 the Synthetic Population had a volume of 548,320 ewes.

The research conducted so far related to establishing the effect of some factors - sequence of lactation, parity, year of birth, linear differentiation, age of insemination, udder type and method of calculation on the variation of phenotypic parameters of productive traits in sheep from BDSP, report highly reliably influence of the year of birth factor (*Djorbineva et al., 1995; Stancheva, 2003; Boikovski et al., 2006; Hinkovski et al., 2008; Ivanova and Raicheva, 2009; Ivanova, 2013; Stancheva and Staykova, 2013*).

The improvement of the population in the current structure is carried out on the principle of rotation of the males of the individual genotypes and of the existing genealogical lines. This allows to typify the population and at the same time to avoid the increase of the inbreeding coefficient *(Slavova et al., 2015)*. The maintenance of genealogical lines and their use is a dynamic process, as the changes in it are determined by the effect of the realized genetic progress and depend on a number of economic factors.

The development and improvement of this genetic resource from the national gene pool of the country should continue by preserving and improving the high values of the main selection traits and improving the quality of the products, according to modern market trends and requirements *(Stancheva et al., 2014).*

In search of ways to increase genetic progress and in response to the increased interest of farmers in the world-famous high milk yield dairy sheep breeds, research teams are working on projects aimed at optimizing breeding schemes for individual flocks and specialized lines with the participation of foreign breeds. The results are related to the evaluation of the productive traits of the obtained crosses and use in the scheme for creating lines with high milk yield and fertility of the breeds Lacaune, Chios and Assaf to improve the Bulgarian dairy synthetic population *(Boikovski et al., 2013).*

The aim of the study is to research and characterize the genotypic parameters of the main productive and reproductive traits in sheep from the Bulgarian dairy synthetic population and its crosses with the breeds Lacaune and Assaf.

Materials and Methods

Due to the great interest about the Bulgarian dairy synthetic population, as well as its crossbreeding with the highly productive Assaf and Lakaune, also the increase in the number of animals under breeding control, the idea arose to study the genotypic parameters of some productive and reproductive traits of these population.

The genotypic parameters of the productive and reproductive indicators of the Bulgarian dairy synthetic population and its crosses were studied taking into account the influence of genetic and non-genetic factors on the studied traits.

The study included flocks bred in private farms in Bulgaria from region of Burgas, owned by members of the NGO “Association for breeding and rearing of dairy Sheep”, with headquarters in Aytos city, from region of Burgas.

A total of 3212 ewes reared in 15 farms, constitute of Bulgarian dairy synthetic population - 1114 ewes, BDSP crosses with Assaf - 1052 ewes, and BDSP crosses with Lacaune - 1046 ewes, born in the period from 2014 to 2019. The sheep are being raised semi-intensive not only on pasture but additionally fed a traditional technology typical of the flat lands of the Burgas region.

All fifteen farms included in the study are members of the NGO “Association for breeding and rearing of dairy Sheep”. Studied traits were: milk yield for a standard 120-day period of I, II and III lactation, biological fertility of the 1st, 2nd and 3rd lambing and the trait - live weight of the different age categories.

The necessary primary information for the study was obtained from the herd books and primary documentation kept in the “Association for breeding and rearing of dairy Sheep”.

The analysis of genetic and environmental varianses is based on the hypothesis that genetic variation is influenced by the effects: breed, herd-year-season, year of birth, line, parity, permanent environmental effect and other effects reported in the error.

The general statistical working model is based on the model of animal /Animal model/:

$$Yijklm = BREED\ i + Lam\ j + SL\ k + Lact\ l + LW\ m + eij\text{к}lmno$$

where:

$Yijklm$ – observation of the respective trait;

$BREED\ i$– effect of **i** th breed - genetic group;

$Lam\ j$ - fixed effect of the size of **j** th lambing;

SL k - fixed effect of **k** th consecutive lambing;

Lact l –effect of the **l** th consecutive lactation;

LW m – effect of the **m** th live weight level of the animal – on weening, 18 months and 2,5 years of age;

Eijklmno - random effect of unobserved factors;

Used software products to perform statistical analysis was PEST to calculate heritability and VCE (Groeneveld) for calculation the genetic correlations between the main productive and reproductive traits of BDSP, and its crosses with Lacaune and Assaf.

Results and Disscusion

Heritability estimates obtained by us for the main selection traits: live weight at weaning, at 18 months and at 2.5 years of age; fertility in the first, second and third lambing and milk yield of the first, second and third lactation for a standardised milking period of 120 days of the Bulgarian dairy synthetic population and crosses with Lacaune and Assaf are presented in Table 1.

The main reproductive traits included in our study were fertility in the first, second and third lambing. The highest value of h^2 is characterized by the group of BDSP - 0.133; 0.156 and 0.147 from 1st to 3rd lambing. The crosses BDSP with Assaf are close to these values in terms of heritability; 0,120, 0.122 and 0.100 in the 1st, 2nd and 3rd lambing. In the genetic group crosses with Lacaune, we established the lowest heritability of the reproductive traits. The values of heritability found by us corresponds to those established by *Vatankhah et al. (2008)* and *Collins and Conington (2014)* with values of 0.13 and 0.10 for the first lambing and 0.19 for the second lambing. *Walkom and Brown (2017)* present significantly higher h^2 for the trait fertility of the third lambing - 0.51.

The values obtained by us for the coefficient of heredity of the traits characterizing the intensity of growth - live weights of the animals during the different periods of their development are determined by low values for all three groups included in our study.

The lowest values of the indicators have the representatives of BDSP 0.064; 0.010 and 0.024 respectively - live weight at weaning, at 18 months and at 2.5 years of age. The values of h^2 are also low in the other two groups included in the study, they are presented in Table 1.

Established values for heritability for growth intensity traits does not correspond to those reported by *Collins and Conington (2014)* **-** 0.21 live weight at weaning and 0.44 at 18 months of age, as well as slightly higher presented by *Vatankhah et al. (2008)* - 0.28 at weaning.

Slightly higher heritability was found in our study at a live weight of 2.5 years of age in the BDSP x Assaf group - 0.175, which fully corresponds to that published by *Walkom et al. (2017)* - 0.17.

Milk production is the main productive trait of the included in our study specialized in this area Bulgarian dairy synthetic population. The results obtained by us for the crosses BDSP x Lacaune show the highest levels of heritability in the milk yield of the first, second and third lactation - 0.342; 0.397 and 0.386 respectively. Published by *Barillet et al. (2001)* and *Ligda et al. (2002)* values of h^2 - 0.32 and 0.35 for the 1st, and 0.34 and 0.40 for the second lactation correspond to those found by us. With a slightly lower coefficient of heredity are the group of crosses BDSP x Assaf 0.131; 0.202 and 0.184, for the 1st, 2nd and 3rd lactation. The obtained values of heritability of the studied trait in the Bulgarian dairy synthetic population are lowest - 0.156; 0.125 and 0.157, respectively from 1st to 3rd lactation. From genetically point of view the best result and promising potential had genetic group BDSP crosses with Lacaune.

The results of our study describing the genetic correlations between traits: fertility in first, second and third lambing; live weight at weaning, at 18 months and at 2.5 years of age; milk yield of the first second and third lactation for a standardized milking period of 120 days in the Bulgarian dairy synthetic population are presented in Table 2.

Table 1. Heritability (h^2) of the main selection traits of BDSP and its crosses with Lacaune and Assaf

Trait	BDSP	BDSPxLacaune	BDSPxAssaf
Fertility at 1st lambing	0.133 ± 0.031	0.040 ± 0.013	0.120 ± 0.021
Fertility at 2nd lambing	0.156 ± 0.035	0.112 ± 0.035	0.122 ± 0.020
Fertility at 3rd lambing	0.147 ± 0.054	0.090 ± 0.014	0.100 ± 0.012
Live weight at weaning	0.064 ± 0.026	0.065 ± 0.016	0.044 ± 0.024
Live weight at 18 months	0.010 ± 0.002	0.095 ± 0.010	0.067 ± 0.025
Live weight at 2.5 years	0.024 ± 0.004	0.057 ± 0.005	0.175 ± 0.038
Milk yield at 1st lactation	0.156 ± 0.047	0.342 ± 0.037	0.131 ± 0.032
Milk yield at 2nd lactation	0.125 ± 0.054	0.397 ± 0.049	0.202 ± 0.045
Milk yield at 3rd lactation	0.157 ± 0.060	0.386 ± 0.051	0.184 ± 0.095

The correlations regarding the fertility traits of the 1st, 2nd and 3rd lambing are high and positive. The variation between them is insignificant from 0.788 - 0.803. This gives reason to believe that the selection in fertility of the first lambing will give a high positive result in the next, ie. can rely on early indirect selection on this trait.

The values of the correlations with regards to the same trait in the age aspect, ie. the repeatability of the trait is indicative of the degree of its age variability. This is of great importance for selection, allowing for the optimization of the number of controls on productive traits and earlier indirect selection and assessment of animals.

The correlation between fertility and live weight at different stages of development of individuals is characterized by positive values. There is only a negative correlation between the fertility of the third lambing with a live weight of 2.5 years (-0.288). The obtained results give grounds to believe that in the future selection activity in terms of fertility and live weight traits should be conducted independent selection, according to the selection limits for the breed.

The correlations between the traits determining the intensity of growth at different stages of development of individuals are highly negative, with the exception of the relation between live weight at weaning and live weight at 2.5 years 0.024. This is indicative that it is appropriate to carry out the selection by live weight up to 2.5 years of age.

Table 2. Genetic correlations between the main productive and reproductive traits in BDSP

Trait	Fertility at 1^{st} lambing	Fertility at 2nd lambing	Fertility at 3rd lambing	Live weight at weaning	Live weight at 18 months	Live weight at 2.5 years	Milk yield at 1^{st} lactation	Milk yield at 2nd lactation	Milk yield at 3rd lactation
Fertility at 1^{st} lambing		0.803*	0.788	0.129	0.094***	0.125	0.334**	0.308	0.097
Fertility at 2nd ambing			0.794*	0.074	0.048*	0.130**	-0.024	-0.187**	-0.233
Fertility at 3rd lambing				0.194	0.792*	-0.288	-0.575	-0.605	-0.755*
Live weight at weaning					-0.633*	0.024	-0.103	-0.418	-0.048
Live weight at 18 months						-0.789	-0.571**	-0.362	-0.434
Live weight at 2.5 years							-0.393	-0.189**	0.558
Milk yield at 1^{st} lactation								0.979***	0.574**
Milk yield at 2nd lactation									0.731**
Milk yield at 3rd lactation									

statistical significance *: $p<0.05$ **: $p<0.01$ ***: $p<0.001$

The main productive trait milk yield is in a high positive correlation at different stages of lactation. Between the first and second lactation we report the highest value 0.979, between the second and third 0.731 and between the first and third 0.574, and also the correlations are statisticaly significant. The obtained results give reason to believe that the selection on the basis of milk yield of the first lactation would be with a high positive effect in terms of the levels of the trait in later stages of development of the individuals. This would also be an argument to recommend optimization of milk control in age (up to 2nd lactation), according to their complexity and high intensity.

It is noteworthy that the trait milk yield is negatively correlated, to varying degrees, with all the traits included in the study. An exception is the fertility of first lambing, as the correlation between it and the milk yield of the first, second and third lactation is 0.334; 0.308 and 0.097, respectively. We also report a positive correlation of 0.558 between the milk yield of the third lactation and the live weight at 2.5 years. This trait is directly related to both milk production and fertility of ewes. According to our results, animals with a higher live weight at 2.5 years have a higher level of milk yield of 3rd - lactation.

The obtained results and the analyzes we made are the reason to consider that in the future breeding activity in the studied herds of the breed BDSP it would be expedient to conduct independent selection on the main productive traits - live weight, milk yield and fertility, according to the accepted selection limits for the breed. It is recommended to control the live weight of female animals until the age of 2.5 years, the fertility of the first and second lambing, and the milk yield of the first and second lactations.

The results describing the genetic correlations between the traits: fertility in the first, second and third lambing; live weight at weaning, at 18 months and at 2.5 years of age; milk yield of the first, second and third lactation for a standardized milking period of 120 days at crosses of BDSP x Lacaune are presented in Table 3.

The correlations established by us between the reproductive traits - fertility of the 1st, 2nd and 3rd lambing are from moderate to high positive and are in the range from 0.328 to 0.570. The obtained values are reason to believe again that the selection of fertility of the first lambing will give positive results in later stages of development of the sheep and can successfully serve as a basis for preliminary evaluation of animals on this important reproductive trait.

The correlation between fertility and live weight at different stages of development of individuals varies from high positive to moderate negative. The highest positive is between live weight at 18 months and fertility of the first lambing 0.729. This is indicative that when entering in breeding age, well-prepared in terms of live weight, well-grown and physiologically well-developed young female animals achieve higher fertility on the first lambing. It should be noted the moderate negative correlation between live weight at 2.5 years and fertility of 2nd lambing (-0.424).This shows that the high live weight of ewes at this age is not a reason to achieve high fertility of 2nd lambing, i.e. independent selection must be headed on both grounds. From a zootechnical point of view, well-prepared ewes with optimal live weight will have higher fertility rate.

The correlations between the traits determining the intensity of growth at different stages of development of individuals are from moderate to high positive. The correlation between live weight at weaning and live weight at 2.5 years is impressive, which is marked by an extremely high positive value 0.907. From the point of view of selection, the obtained results give reason to believe that the selection of lambs and young animals with higher intensity of weight, according to the requirements for the breed and the direction, will give a positive result at a later stages of development.

Table 3. Genetic correlations between the main productive and reproductive traits in BDSP crosses with Lacaune

Trait	Fertility at 1st lambing	Fertility at 2nd lambing	Fertility at 3rd lambing	Live weight at weaning	Live weight at 18 months	Live weight at 2.5 years	Milk yield at 1st lactation	Milk yield at 2nd lactation	Milk yield at 3rd lactation
Fertility at 1st lambing		0.570**	0.328*	-0.027	0.792**	0.032	0.333***	-0.715	0.565
Fertility at 2nd lambing			0.493***	0.055	0.243	-0.424**	-0.475	-0.831*	0.817
Fertility at 3rd lambing				0.009	-0.310	0.158*	0.298	-0.202	-0.970*
Live weight at weaning					0.202*	0.907	-0.307	-0.146	0.084
Live weight at 18 months						0.279**	-0.255*	-0.486	0.330
Live weight at 2.5 years							-0.014	0.189**	0.175
Milk yield at 1st lactation								0.877***	0.555**
Milk yield at 2nd lactation									0.884**
Milk yield at 3rd lactation									

statistical significance *: $p<0.05$ **: $p<0.01$ ***: $p<0.001$

The trait milk yield is in a high positive correlation in the different sequences of lactations. Between the second and third lactation we report the highest value of

0.884. The correlation between the first and second lactation is almost identical - 0.877, and between the first and third is 0.555. This gives grounds to conclude again that the selection by milk yield of the first lactation, indirectly will lead to high values of the trait in subsequent lactations, can serve as a basis for preliminary assessment and optimization of the number of controls in terms of age.

It is noteworthy that the trait of milk yield is negatively correlated to varying degrees with most of the traits included in the study. The milk yield of the first lactation is in a moderate positive correlation with the fertility of the first lambing 0.333. Surprisingly, the milk yield of the second and third lactations is in an extremely high negative correlation with the fertility of the second and third lambing with values of (-0.831) and (-0.970), respectively. On the other hand, the milk yield of the third lactation is in a high positive correlation with the fertility of the 1st and 2nd lambsing - 0.565 and 0.817, respectively.

The obtained results are grounds to believe that in the future selection activity in the studied flocks it will be expedient to conduct an independent selection with regard to the milk yield of the sheep, on the one hand, and the other selection traits, on the other.

The results describing the genetic correlations between the traits: fertility in the first, second and third lambing; live weight at weaning, at 18 months and at 2.5 years of age; milk yield of the first, second and third lactation for a standardized milking period of 120 days at crosses of BDSP x Assaf are presented in Table 4.

The correlations between the reproductive traits in the first two groups - BDSP and BDSP x Lacaune (Table 2. and Table 3.) were characterized entirely by positive values. In the third group BDSP x Assaf the correlations vary from low positive to moderate negative. The correlation between the fertility of 1st and 3rd lambing has a moderate negative value of (-0.409). This means that the selection in fertility of the first lambing alone could not give a guaranteed indirect positive result for the levels of the trait at later ages, ie. it is imperative that the selection of fertility in the studied population be continued on 2nd and 3rd lambing.

The correlation between fertility and live weight at different stages of development of individuals do not differ much from the previous two groups, as here again we find a very high negative correlation between live weight at 2.5 years and fertility of 2nd lambing (-0.962), while that between live weight at 2.5 years and fertility of 3rd lambing is a high positive 0.875. This is a reason to recommend again for the future breeding work in the studied herds, with regard to these two traits, to conduct an independent selection in terms of age, according to the accepted standards. Indirect selection would not give good results. We report from moderate negative to highly positive correlation between the traits determining the intensity of growth at different stages of animal development. The correlation between live weight at weaning and live weight at 18 months is a high positive value 0.686, between live weight at weaning and live weight at 2.5 years is moderately negative (-0.381), and the correlation between live weight at 18 months and live weight at 2.5 years has a negative sign, but with a value close to zero (-0.002). This requires, on one hand, the lambs to be weaned at a sufficiently high live weight of 23-25 kg, which would ensure their normal growth and development until they enter breeding age at 16-18 months, but also selection of live weight at 1.5 and 2.5 years of age.

Milk yield has moderate to high positive correlations in different lactations. Between the first and second lactation we report the highest value 0.878, between the first and third 0.482 and moderate between the second and third lactation 0.368.

Table 4. Genetic correlations between the main productive and reproductive traits in BDSP crosses with Assaf

Trait	Fertility at 1st lambing	Fertility at 2nd lambing	Fertility at 3rd lambing	Live weight at weaning	Live weight at 18 months	Live weight at 2.5 years	Milk yield at 1st lactation	Milk yield at 2nd lactation	Milk yield at 3rd lactation
Fertility at 1st lambing		0.130**	-0.409	0.019*	0.099***	-0.720*	0.872***	0.781*	0.118
Fertility at 2nd lambing			0.125*	-0.215	0.817	-0.962*	0.783	0.335**	0.431
Fertility at 3rd lambing				0.116	0.574	0.875*	0.808	0.631*	0.890**
Live weight at weaning					0.686*	-0.381	0.369	-0.111	0.119
Live weight at 18 months						-0.002*	0.621**	0.467	0.800
Live weight at 2.5 years							-0.383	-0.393	-0.089*
Milk yield at 1st lactation								0.878***	0.482**
Milk yield at 2nd lactation									0.368**
Milk yield at 3rd lactation									

statistical significance *: $p<0.05$ **: $p<0.01$ ***: $p<0.001$

In the group of crosses of BDSP with Assaf the results show that the trait milk yield of 1st, 2nd and 3rd lactation are in high and positive correlation with the trait of live weight at 18 months, respectively - 0.621, 0.467 and 0.800 and with low up to moderate negative correlation with the sign of live weight at 2.5 years, respectively (-0.383); (-0.393) and (-0.089) for the 1st, 2nd and 3rd lactations. This is indicative that in future breeding work it is necessary to focus on the selection of young female animals with sufficiently high live weight and good physical condition when they enter breeding age at 1.5 years, given the expectations of them to achieve high milk yield. In this group of crosses we also report high positive correlations between milk yield of lactations and fertility in the diferent lambings. The milk yield of the 2nd lactation is in a moderate positive correlation with the fertility of the 2nd lamb 0.335, and the milk yield of the 1st and 3rd lactation is in high and positive correlation with the fertility of the 1st and 3rd lambs with values of 0.872 and 0.890. The obtained results give us reason to believe that the selection of milk yield in the studied group BDSP x Assaf would give positive results in terms of fertility and oposite. In fact, these are two of the most important, with the greatest economic significance traits that are the basis of breeding and production activities in the dairy sector.

Conclusions

1. Low values of heritability for the traits characterizing the growth intensity show consolidation of the studied part of the population. h^2 in BDSP ranges from 0.010 to 0.064; in BDSP x Lacaune from 0.057 to 0.095; in BDSP x Assaf from 0.044 to 0.175. Low levels of genetic diversity of the trait minimize the chances to conduct effective breeding based on phenotype.
2. A reliable basis for the management of a mass selection (by phenotype) and indirect selection by fertility and milk yield are the high and positive correlations between the two traits in the crosses BDSP x Assaf, with values of sequence lactations and lambing from 1st to 3rd 0.872, 0.783 and 0.631 respectively.
3. From low to moderate positive values of h^2 are established for the trait fertility in all three studied groups. The values are as follows - for BDSP from 0.133 to 0.156, for BDSP x Lacaune - from 0.040 to 0.112 and for BDSP x Assaf - from 0.100 to 0.122.
4. Heritability in the main selection trait milk yield of 1st, 2nd and 3rd lactation reaches from low to moderate values. The lowest level of genetic diversity is in BDSP - h^2 varies from 0.125 to 0.157. In BDSP x Assaf the values of h^2 mark slightly higher levels - from 0.131 to 0.202. The highest is the genetic diversity according to the studied trait in the sheep BDSP x Lakaune, respectively from 0.342 to 0.397.

Genetski parametri proizvodnih i reproduktivnih osobina ovaca bugarske mlečne sintetičke populacije (BDSP) i njenih meleza sa rasama Lacaune i Assaf

Georgi Kalaydzhiev

Rezime

Poslednjih godina u Bugarskoj dominiraju ovce bugarske mlečne sintetičke populacije (BDSP) i njeni melezi sa drugim mlečnim rasama. Ovo dovodi do značajnog, naučno zasnovanog genetičkog i fenotipskog diverziteta i različitih nivoa produktivnosti. Cilj rada je istraživanje i karakterizacija genotipskih parametara glavnih proizvodnih i reproduktivnih osobina ovaca bugarske mlečne sintetičke populacije i njenih meleza sa rasama Lacaune i Assaf. Istraživanje je obuhvatalo ukupno 3212 ovaca gajenih na 15 farmi, i to grla bugarske mlečne sintetičke populacije - 1114 ovaca, BDSP melezi sa rasom Assaf - 1052 ovce, i BDSP melezi sa rasom Lacaune - 1046 ovaca, rođenih u periodu od 2014. do 2019. godine. Ispitivane osobine su: mlečnost za standardni period od 120 dana I, II i III laktacije, biološka plodnost 1., 2. i 3. jagnjenja i osobina - živa masa različitih starosnih kategorija. Korišćen je statistički model zasnovan na Animal modelu, uz korišćenje softverskog proizvoda VCE i PEST (Groeneveld). Heritabilitet u glavnoj selekcijskoj osobini mlečnost u 1., 2. i 3. laktaciji pokazuje niske do umerene i srednje vrednosti. Najniži nivo genetičke raznovrsnosti je kod BDSP - h^2 varira od 0,125 do 0,157, kod BDSP x Assaf od 0,131 do 0,202, a najveći genetski diverzitet u proučavanom svojstvu imaju ovce BDSP x Lacaune, odnosno od 0,342 do 0,347. Stope fertiliteta u sve tri ispitivane grupe bile su od niske do umerene h^2 - u BDSP od 0,133 do 0,156, u BDSP x Lacaune - od 0,040 do 0,112, i u slučaju BDSP x Assaf - od 0,100 do 0,122.

Ključne reči: ovce, BDSP, Lacaune, Assaf, heritabilitet, genetska korelacija

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SOME PRODUCTIVE AND REPRODUCTIVE TRAITS IN SHEEP FROM THE BULGARIAN DAIRY SYNTHETIC POPULATION (BDSP) AND ITS CROSSES WITH LACAUNE AND ASSAF: 2. PHENOTYPIC PARAMETERS

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Abstract: Bulgarian Dairy Synthetic Population (BDSP) and its crosses with other dairy breeds are the most numerous sheep population in Bulgaria. There are significant phenotypic diversities and different levels of productivity. The aim of the study is to research and characterize the phenotypic parameters of the main productive and reproductive traits in sheep from the Bulgarian dairy synthetic population and its crosses with the breeds Lacaune and Assaf. The study includes a total of 3212 ewes BDSP and their crosses with Assaf and Lacaune. Studied trait were: milk yield for a standard 120-day period of I, II and III lactation, biological fertility of the 1st, 2nd and 3rd lambing and the trait - live weight of different age categories. The software product SYSTST 13 and SPSS - Descripive statistics were used to conduct the study. With the highest milk yield of the 1st, 2nd and 3rd lactation were the sheep BDSP x Lacaune - 186.28 l, 194.03 l, 200.56 l, followed by BDSP x Assaf - 184.27 l, 191.87 l and 198.64 l and those of BDSP - 134.18 l, 139.48 l and 144.33 l. The average phenotypic values of the traits live weight at weaning, at 18 months and 2.5 years are close - respectively in BDSP - 25.21 kg, 60.59 kg and 65.50 kg, for BDSP x Lacaune - 25.17 kg, 60.52 kg, 65.44 kg and for BDSP x Assaf - 25.19 kg, 60.58 kg, 65.67 kg. Fertility indicates the highest average values of the crosses BDSP with Lacaune from 1.53 to 1.59, followed by BDSP x Assaf from 1.40 to 1.46. The lowest fertility rate had the ewes from BDSP from 1.22 to 1.25.

Key words: BDSP, Lacaune, Assaf, phenotipic, milk yield, fertility

Introduction

Globally, the consumption and demand for sheep's milk is constantly increasing, but on the other hand the trend of its production is negative. This is caused by decreasing intersts in the rearing of dairy breeds of sheep and the shift of farmers to raise sheep for meet. This trend is observed in most developed countries, including Bulgaria, and the fact is due to several reasons. The lack of skilled labor, excessive urbanization, as well as the existence of milking costs and additional wages. Sheep's milk products are gaining more and more market size due to their quality and nutritional value - the higher content of protein, fat, vitamins and minerals compared to milk obtained from other species (*Park et al., 2007; Pandya and Ghodke, 2007*). From here come the favorable prospects for increasing the production and processing of sheep's milk.

Purposeful work on the establishment of specialized dairy sheep in Bulgaria began in the late 70's on a pre-defined program. Currently, the most numerous, most widespread and newest Bulgarian specialized breed of sheep for milk is the Bulgarian Dairy Synthetic Population (BDSP). It is created through complex reproductive crossbreeding and purposeful selection. Bulgarian dairy synthetic population was registered with certificate №10645 (property of AI-Shumen) from 30.06.2005 (*Stancheva et al., 2014*). Sheep and rams of the breeds: Blackhead Pleven, local Stara Zagora, Avasi, East Friesian and others take part in the breed formation. The average genetic potential of ewes for the milking period is about 150 to 200 liters, and the realization of this trait depends mainly on the provided conditions of feeding and rearing. The first insemination usually takes place at 18 months, but is also possible at 9-10 months of age. Biological fertility is about 150 lambs per 100 ewes.

In the methodological guidelines for creating the synthetic population of sheep for milk, *Hinkovski et al. (1984)* indicate that the breeding target is 250 to 300 liters of milk per lactation. The results of studies by a number of authors on the milk productivity of different types of crossbred sheep, which later formed the synthetic population of sheep for milk (*Boikovski, 1982; Djorbineva, 1984; Todorova, 1987; Tsvetanov, 1989; Ahmed, 1991; Dimov, 1995; Stancheva, 2003; Iliev, 2011; Ivanova, 2013; Slavova et al., 2015; Stancheva et al., 2018.*) show that the breeding goal in the creation of the synthetic population has not been achieved. The achieved level of milk productivity - below 200 liters during lactation is much lower than the set breeding goal.

According *to Stancheva (2003*), the milk yield of sheep from the synthetic population of the herd at the Agricultural Institute in Shumen for animals born in 1987-1999 is an average of 99.18 liters for first lactation and 101.96 liters for second lactation and an average biological fertility of 1.37. In a study by the same author for 2008, the milk yield of the herd in ZI - Shumen averaged at 104.24 l

(*Stancheva et al., 2011*). In the herd of the Institute of Animal Sciences - Kostinbrod for the period 2006 - 2009 an average milk yield was established for a 120-day milking period for ewes of I lactation - 95.86 l, II - 95.89 l and 111.68 l of III lactation *(Ivanova, 2013*). The fertility rate of sheep from the synthetic population established by *Stancheva (2003)* were - 1.335 - 1.412, respectively of I and II lactation for the Shumen region and by *Dimov and Kuzmanova (2007)* 1.34 for the Plovdiv region. Against the background of the high achievements in the field of dairy sheep breeding in the developed western European countries *(Fuente et al., 2006; Gutierrez et al., 2007)* for the breeds Awasi and Asaf - 297 l, and in Israel *(Pollot and Gootwine, 2004)* for the breed - Asaf 334 l. *Slavova et al. (2021)* reports low levels of grow intensity traits in BDSP reared in AI. Stara Zagora. The above-cited results obtained by our specialized breed for milk are significantly lower.

Dominant in recent years are sheep from BDSP and its crosses with other dairy breeds, bred in most private herds. This in turn leads to the existence of significant, scientifically based phenotypic and genetic diversity and different levels of productivity (*Stancheva et al., 2014*).

In addition to the traditional Bulgarian sheep breeds, more and more sheep breeders are turning to various foreign breeds in search of more profitable animals for breeding.

The Lacaune and Assaf breeds are exactly the ones that many sheep breeders already prefer because of their good productivity and the suitable conditions in our country for their breeding.

Assaf is a synthetic population and was created by crossing the local Awasi breed with rams from the German East Frisian dairy breed. The average milk yield for lactation from Assaf in different years varies from 330 to 350 liters. In some farms it reaches 400 liters. The average fertility is 150-160 lambs per 100 sheep every 8 months. This high fertility rate is one of the reasons why these breed particularly is profitable to raise.

Another extremely valuable breed is the Lacaune breed. It is one of the sheep breeds with highest milk yield in the world. It was created in France in the 19th century on the basis of several local sheep populations. The breed is characterized by high milk yield - 270-320 liters. The fertility of the sheep is between 190-200 lambs per 100 sheep.

Among the dairy breeds, the total share of sheep belonging to the Bulgarian dairy synthetic population is the largest (about 70%). This in itself means that a lot of effort and serious selection work is needed to build its breeding structure and its development. The fact is that there is a significant phenotypic and genetic diversity and different levels of productivity in sheep from BDSP, it is necessary to consolidate the population *(Stancheva et al., 2014).*

The aim of the study is to research and characterize the phenotypic parameters of the main productive and reproductive traits in sheep from the

Bulgarian dairy synthetic population and its crosses with the breeds Lacaune and Assaf.

Material and Methods

The increasing number of animals under breeding control from Bulgarian dairy synthetic population in the country is one of the reasons to study the phenotypic parameters of some productive and reproductive traits of these sheep.

The study includes a total of 3212 ewes from Bulgarian dairy synthetic population and crosses with Assaf and Lacaune, this is a continuation of research of the genotypic parameters of some productive and reproductive traits BDSP and its crosses and it was conducted on the same sheep population.

All fifteen farms included in the study are members of the NGO “Association for breeding and rearing of dairy Sheep”. Studied traits were: milk yield for a standard 120-day period of I, II and III lactation, biological fertility of the 1st, 2nd and 3rd lambing and the trait - live weight of the different age categories.

The control of milk yield was performed during the milking period, and over the years four controls were performed. The milk yield data refer only to the milk obtained from the ewes after complete weaning of the lambs. The quantity of milk is presented in volume units (ml). The individual milk yield of each ewe for the control day was calculated by multiplying the amount of milk obtained by the morning individual control by a herd ratio representing the ratio: morning + evening milk / morning milk. The milk yield for a 120-day milking period was calculated as the sum of the milk yields from the individual control periods of each sheep. Live weight was measured individually at weaning, at 18 months and 2.5 years.

The examined traits are controlled and registered according to a standard method and instructions, provided in the Instruction for control of the productive qualities and grading of the sheep in Bulgarian legistration (2003-2013). The necessary primary information for the study was obtained from the herd books and primary documentation kept in the “Association for breeding and rearing of dairy Sheep”.

The phenotypic parameters of the productive and reproductive indicators of the Bulgarian dairy synthetic population and its crosses were studied taking into account the influence of genetic and non-genetic factors on the studied traits.

Used software products to perform the statistical analysis of phenotypical values of the productive and reproductive traits in BDSP and its crosses, mean phenotypic values of ferttility traits in 1st, 2nd and 3rd lambing and mean phenotypic values of traits live weight at weaning, at 18 months and 2.5 years, mean phenotypic values of the trait milk yield for 120 days at the 1st, 2nd and 3rd lactation were SYSTST 13 and SPSS.

Results and Discussion

Table 1 presents the phenotypic values of the main statistical parameters of the traits: fertility in the first, second and third lambing; live weight at weaning, at 18 months and at 2.5 years of age and milk yield in the first, second and third lactation for a standardized milking period of 120 days. The average values of the listed traits are presented graphically, such as the fertility in Figure 1, live weights in Figure 2, and milk yield in Figure 3.

One of the traits that has received serious attention in recent years, and which is currently one of the main selection traits, is fertility. The phenotypic indicators of the trait are determined mainly for three of the periods of development of the ewes - the first, the second and the third lambing, as mentioned in the literature the limits of the biological fertility for the breed BDSP is from 1.2 to 1.5, and for Lacaune and Assaf, respectively, from 1.5 to 1.9 and 1.3 to 1.6.

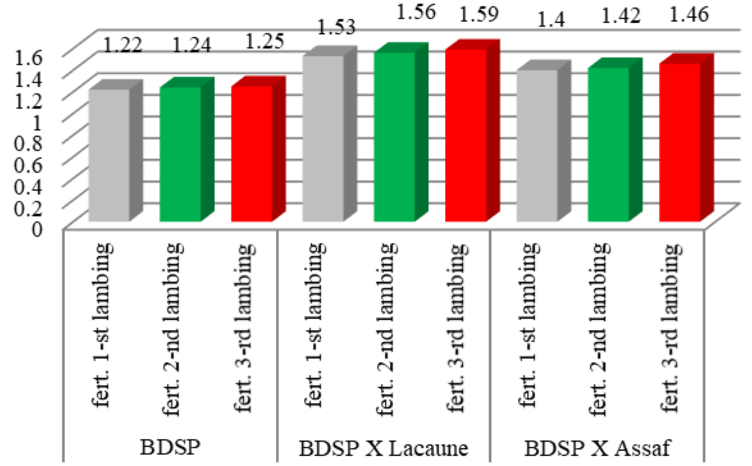
The results reported by us are in unison with those published in the literature *(Stancheva, 2003; Ivanova, 2013; Dimov and Kuzmanova, 2007; Stancheva et al., 2018)*. It is worth noting that in all three lambings in a row the minimum and maximum values of fertility remain the same in all three studied groups BDSP 1-2 BDSP x Assaf 1-2 and BDSP x Lakaune 1-3, taking into account that only in animals crossed with Lacaune had triplets. In the fertility trait, the differences between the standard deviation and the coefficient of variation (CV) are very small in all three groups, but on the other hand we report the highest CV from 31% to 35% in this indicator, compared to the others included in the study. This is due to the fact that the minimum and maximum values are from 1 to 3, and the standard deviation from the average is from 0.416 to 0.506. At such low minimum and maximum values and such Std., naturally CV is so high.

Figure 1 shows the average phenotypic values of fertility in 1st, 2nd and 3rd lambing. The results show that with the highest average values are characterized the crosses of BDSP with Lacune from 1.53 to 1.59, followed by BDSP x Assaf from 1.40 to 1.46 and with the lowest fertility rate are the ewes from BDSP from 1.22 to 1.25. The presented graph clearly shows the positive trend in fertility from the 1st to the 3rd lambing and in the three groups included in the study, as the highest average values were reported in the 3rd lambing.

Table 1. Phenotypic values of the main statistical parameters of the productive and reproductive traits in SPBM and its crosses

Trait	Main statistical parameters	BDSP n=1114	BDSP x Lacaune n=1046	BDSP x Assaf n=1052
Ferility at 1st lambing	Min. value	1	1	1
	Max. value	2	3	2
	Standard Deviation	0.416	0.506	0.491
	Coefficient of variation	34	33	35
Ferility at 2nd lambing	Min. value	1	1	1
	Max. value	2	3	2
	Standard Deviation	0.424	0.501	0.495
	Coefficient of variation	34	32	35
Ferility at 3rd lambing	Min. value	1	1	1
	Max. value	2	3	2
	Standard Deviation	0.431	0.496	0.499
	Coefficient of variation	35	31	34
Live weight at weaning	Min. value	23	24	23
	Max. value	27	27	27
	Standard Deviation	0.766	0.784	0.797
	Coefficient of variation	3	3	3
Live weight at 18 months	Min. value	57	58	56
	Max. value	63	63	63
	Standard Deviation	1.138	1.090	1.146
	Coefficient of variation	2	2	2
Live weight at 2.5 yars	Min. value	62	60	62
	Max. value	68	68	70
	Standard Deviation	1.061	1.222	1.249
	Coefficient of variation	2	2	2
Milk yield at 1st lactation	Min. value	123	168	166
	Max. value	148	216	204
	Standard Deviation	5.347	7.628	8.214
	Coefficient of variation	4	4	4
Milk yield at 2nd lactation	Min. value	130	174	176
	Max. value	150	216	216
	Standard Deviation	5.384	6.814	7.117
	Coefficient of variation	4	4	4
Milk yield at 3rd lactation	Min. value	132	180	178
	Max. value	152	234	236
	Standard Deviation	4.425	6.979	7.039
	Coefficient of variation	3	3	3

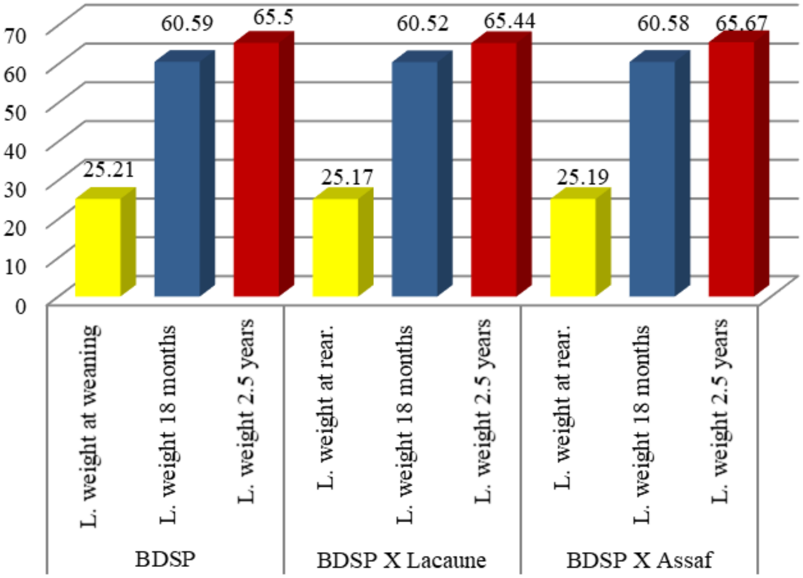
Figure 1. Mean phenotypic values of fertility traits in 1st, 2nd and 3rd lambings



The obtained values for the traits characterizing the growth intensity - live weights of the animals during the different periods of their development are not characterized by great variability. We report very similar phenotypic values in live weight at weaning. The maximum of the trait is the same for all farms - 27 kg, and the minimum differs by one kilogram in plus for crosses with Lacaune - 24 kg, so the average, as well as the standard deviation and coefficient of variation are almost identical. With the highest standard deviation for the above-mentioned trait are, the crosses with Assaf - 0.797. We established also the highest average value of 25.21 kg in BDSP.

The other trait that is not only decisive in terms of growth intensity, but is also related to the fertility and milk productivity of sheep, is the live weight at 18 months of age. Here we also report a slight variation, as the lowest minimum value is for crosses with Assaf - 56 kg and the highest is for crosses with Lacaune - 58 kg. At the maximum of the indicator there are no differences in the three groups - 63 kg. The average values vary within extremely narrow limits. The standard deviation and the coefficient of variation are almost identical and are presented in Table1.

Figure 2. Mean phenotypic values of traits live weight at weaning, at 18 months and at 2.5 years



The live weight at 2.5 years in ewes is essential for fertility, prolificacy and subsequently for milk productivity. Both too low and too high weight lead to unsatisfactory results in the above-mentioned trait. From the reported phenotypic values of the indicator live weight of 2.5 years in Table 1 it can be seen that the difference in the minimum values for the trait is within narrow limits, with a lower minimum value are the crosses with Lacaune - 60 kg, and in BDSP and its crosses with Assaf we established 62 kg. At the maximum, BDSP x Assaf have the highest value - 70 kg, they also have the highest average phenotypic value for the trait - 65.67 kg. The differences in the mean values are presented in Fig. 2. As can be seen, the values of the traits that determine the intensity of growth are in extremely narrow limits, which determines the low values of the standard deviation and the coefficient of variation.

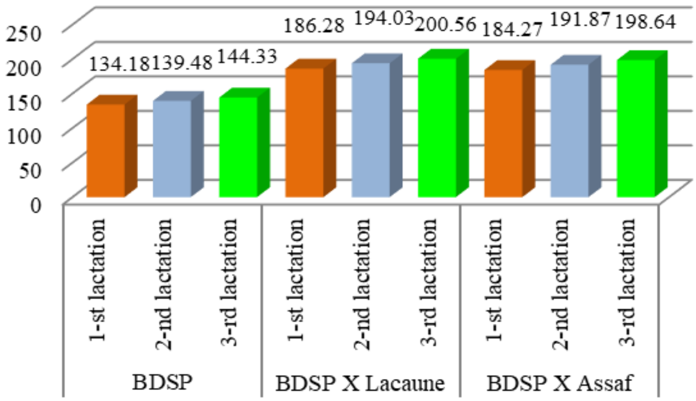
The slight variation of the phenotypic values of the traits characterizing the growth intensity - live weights of the animals during the different periods of their development are indicative of the presence of consolidation of the studied sample of the population.

The main selection trait, which is also the main productive one in the Bulgarian dairy synthetic population, as well as in its crosses is the milk yield for a

120-day standardized milking period. In the Beeding program of the NGO the control of the milk productivity is set as main, therefore in our research we have included the phenotypic values of the main statistical parameters for the three stages of production 1st, 2nd and 3rd lactation. The results obtained by us are presented in Table 1 and Fig. 3.

The highest phenotypic mean value of the milk yield of the 1st lactation is characterized by crosses with Lacon - 186.28 l, and the lowest is BDSP - 134.18 l. In BDSP x Assaf the average milk yield is 184.28 l. The lowest minimum was reported for BDSP - 123 l, and for crosses with Lacaune we have established the highest minimum and maximum milk yield for the period with values of 168 l and 216 l. With this indicator the variability is clear, so the standard deviation is in ranges from 5.35 for BDSP to 8.21 for BDSP x Assaf. The coefficient of variation has similar values for the three studied groups.

Figure 3. Mean phenotypic values of the trait milk yield for 120 days at the 1st, 2nd and 3rd lactation



In our analysis of the results we found that the average phenotypic values of milk yield for the 1st, 2nd and 3rd lactation for 120 days have a positive trend with the progression of lactations to the 3rd and for the three included in the study genetic groups. With the highest average value for the 2nd lactation are again the crosses with Lacune - 194.03 l, and with the lowest BDSP - 139.48 l, as with the crosses with Assaf the average milk yield is 191.87 l. It gives the impression the close values, and apparently the equalized genetic potential wich have the crosses of BDSP with Assaf and Lacune. In the third lactation in a row, the values established by us are in unison with the previous two lactations. The crosses with Lacaune are characterized by the highest phenotypic mean value - 200.56 l, the reported value for crosses with Assaf is slightly lower - 198.64 l. The lowest average for the trait again belongs to the animals from the Bulgarian dairy synthetic population - 144.33 l. The coefficient of variation for the third lactation is 3 for all three groups, and Std. is in the range of 4,425 to 7,039. For the trait milk yield, the highest value was reported on the 3rd lactation at the crosses with Assaf - 236 l for 120 - day standardized milking period.

Conclusions

1. The average phenotypic values of the traits characterizing the growth intensity of the three studied groups of sheep - live weight at weaning, at 18 months and 2.5 years are close - respectively in BDSP - 25.21 kg, 60.59 kg and 65.50 kg, in BDSP x Lacaune - 25.17 kg, 60.52 kg, 65.44 kg and in BDSP x Assaf - 25.19 kg, 60.58 kg, 65.67 kg, as the standard deviation vary within very narrow limits, and the coefficient of variation is from 2 to 3%.
2. The fertility trait, which is the main reproductive trait, indicates the highest average values at the crosses of BDSP with Lacaune from 1.53 to 1.59, followed by BDSP x Assaf from 1.40 to 1.46. The lowest fertility rate had the ewes from BDSP from 1.22 to 1.25, as the coefficient of variation of the trait is from 31 to 35%.
3. With the highest milk yield of the 1st, 2nd and 3rd lactation are the ewes BDSP x Lacaune - 186.28 l, 194.03 l, 200.56 l, followed by BDSP x Assaf - 184.27 l, 191 , 87 l, 198.64 l and with the lowest value of the trait were BDSP - 134.18 l, 139.48 l and 144.33 l. The mean standard deviation levels for this indicator are relatively low at 3 to 4%.
4. From the obtained results we can conclude that the crosses F1 of BDSP with the breeds Assaf and Lakaune significantly increase the values of the main selection traits milk yield and fertility.
5. The controlled inclusion of the Lacaune and Assaf breeds in the BDSP breeding schemes could lead to a phenotypic consolidation of the traits, as well as an increase in the milk yield and fertility of the population.

Proizvodne i reproduktivne osobine ovaca bugarske mlečne sintetičke populacije (BDSP) i njenih meleza sa rasama Lacaune i Assaf: 2. Fenotipski parametri

Georgi Kalaydzhiev

Rezime

Bugarska mlečna sintetička populacija (BDSP) i njeni melezi sa drugim mlečnim rasama su najbrojnija populacija ovaca u Bugarskoj. Postoje značajne fenotipske raznolikosti i različiti nivoi produktivnosti. Cilj rada je istraživanje i karakterizacija fenotipskih parametara glavnih proizvodnih i reproduktivnih osobina ovaca bugarske mlečne sintetičke populacije i njenih meleza sa rasama Lacaune i Assaf.
Istraživanje je obuhvatalo ukupno 3212 ovaca i njenih meleza sa rasama Lacaune i Assaf. Ispitivane osobine su: mlečnost za standardni period od 120 dana I, II i III laktacije, biološka plodnost 1., 2. i 3. jagnjenja i osobina - živa masa različitih starosnih kategorija. Za sprovođenje studije korišćen je softverski proizvod SYSTST 13 i SPSS – deskriptivna statistika. Sa najvećim prinosom mleka u 1., 2. i 3. laktaciji bile su ovce BDSP x Lacaune - 186,28 litara, 194,03 litara, 200,56 litara, zatim BDSP x Assaf - 184,27 litara, 191,87 litara i 198,64 litara – BDSP 134,18 litara , 139,48 litara i 144,33 litara. Prosečne fenotipske vrednosti osobina mase pri odbijanju, sa 18 meseci i uzrastu od 2,5 godine su bliske - respektivno - kod BDSP - 25,21 kg, 60,59 kg i 65,50 kg, kod BDSP x Lacaune - 25,17 kg, 60,52 kg, 65,4 kg, i kod BDSP x Asaf - 25,19 kg, 60,58 kg, 65,67 kg. Plodnost ukazuje na najveće prosečne vrednosti kod meleza BDSP x Lacaune od 1,53 do 1,59, zatim BDSP x Assaf od 1,40 do 1,46. Najnižu stopu fertiliteta imale su ovce BDSP od 1,22 do 1,25.

Ključne reči: BDSP, Lacaune, Assaf, fenotip, mlečnost, plodnost

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REGRESSION TREE ANALYSIS TO PREDICT BODY WEIGHT OF SOUTH AFRICAN NON-DESCRIPT GOATS RAISED AT SYFERKUIL FARM, CAPRICORN DISTRICT OF SOUTH AFRICA

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Abstract: Regression tree is the data mining algorithm method which contains a series of calculations that creates a model from collected data. Present study aimed to develop model to estimate body weight (BW) from biometric traits viz. withers height (WH), sternum height (SH), body length (BL), heart girth (HG) and rump height (RH). A total of eighty-three (n = 83) South African non-descript indigenous goats (54 females and 29 males) aged three months and above were used in the study. Pearson's correlations and classification and regression tree (CART) as statistical techniques were used for data analysis. Correlation results indicated that there was a positive highly statistical significant ($P < 0.01$) correlation between BW and all biometric traits in both males and females, the positive highly statistical significant correlation was observed between BW and WH ($r = 0.82$) in female goats while in males the highest positive statistical significant correlation was detected between BW and BL ($r = 0.83$). CART model indicated that the BW mean was 29.868 kilograms (kg) as dependent variable and BL had the highest remarkable role in BW followed by SH, RH while the age had the least remarkable role in BW. This study suggests that BL, SH and RH might be used by South African non-descript goats' farmers as a selection criterion during breeding to improve BW of animal. More completive studies and experiments need to be done using CART to predict BW in more sample size of South African non-descript goats or other goat breeds.

Keywords: Biometric traits, body length, heart girth, rump height, sternum height.

Introduction

Classification and regression tree is one of the data mining algorithm that can predict categorical dependent variables referred as classification and continuous dependent variables referred as regression by constructing trees *(Breiman et al., 1984)*. This data mining algorithm has been practiced world widely in animal breeding to predict body weight (BW) and it is also used in livestock; Potchefstroom Koekoek chickens *(Tyasi et al., 2020a)*, in Beetal goats of Pakistan *(Eyduran et al., 2017)*, in Turkish Tazi dogs *(Celik and Yilmaz, 2018)* and also in Balochi sheep *(Huma and Iqbal, 2019)*. South African non-descript goat is commonly kept in rural areas of South Africa, mainly with traditional methods *(Webb et al., 2003*; *Norris et al., 2015)*. According to *Tyasi et al. (2020b)* non-descript indigenous goats are more resistance to diseases and parasites in comparison with other breeds. This breed is one of the non-selective browsers and survive well in harsh environment *(Mara et al., 2013)*. Goat production contribute to economy by producing meat and milk which serve as part of human diet, moreover they play a role when performing religious and cultural ceremonies *(Hassen and Tesfay, 2014)*. Challenges experienced in rural areas are that farmers are disadvantaged when it comes to selling, feeding, and providing medication to their goats due to lack of weighing scales, as they are expensive *(Eyduran et al., 2017)*. There is limited information of prediction of BW from morphological traits and characterizes using classification and regression tree in non-descript goats of South Africa. Hence, the objective of the study was to establish a model to predict the BW using withers height, sternum height, body length hearth girth and rump height of South African non-descript indigenous goats. The study will provide information which will help the farmer to select the best biometric traits that might be used to predict BW.

Materials and Methods

Study area

The study was conducted in Limpopo province, Syferkruil Experimental farm (Figure 1) which is situated 9 kilometres northwest from University of Limpopo. Temperatures in winter range between 5 ^{O}C and 28 ^{O}C and in summer ranges from 10 ^{O}C to 36 ^{O}C and the mean annual rainfall is less than 400mm.

Research animals, design, and management

South African non-descript indigenous goats of 3 months and above one year of age were used in the current study. Cross-sectional design was used with one replicate per goat. The farm was visited, and data was collected once from 83 goats (54 female and 29 male). Goats were kept under extensive production whereby the animals lived in a constricted area called a kraal. They grazed during the day and the animals were placed in the kraal during the evenings. Fresh, clean water was provided to the animals daily.

Data collection

BW and five biometric traits were measured on each goat in the morning before they are released for grazing or feeding. Biometric traits measured were: withers height (WH), sternum height (SH), heart girth (HG), rump height (RH) and body length (BL). BW was measured in kilograms (kg) using a balance scale while biometric traits were measured using a measuring tape in centimetres (cm). All measurements were taken according to the suggestion of *Norris et al. (2015)*. Briefly, WH: distance from the highest point of the shoulder (wither) to the ground surface in relation to level of the fore legs, BL: distance between anterior shoulder point to the posterior extremity of the pin bone, SH: vertical distance from lower tip of the sternum to the ground as the animal standing, RH: distance from the top of the pelvic girdle to the ground surface in relation to the level of hind legs and HG: vertical distance from the ground to the top of the pelvic. All the measurements were taken by one person to avoid errors.

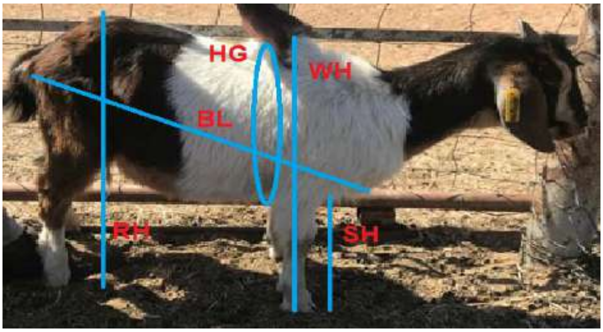

Figure 1. Biometric traits measured in the study

Classification and regression tree (CART) algorithm

CART algorithm is a tree decision technique which as was developed by *Breiman et al. (1984)* and its mostly used in the animal industry because it is very simple, easy, and applied to visualize. CART was performed as described by *Eyduran et al. (2019)* and *Tyasi et al. (2021)*. Briefly, CART was applied to estimate BW as the dependent variable from five biometric traits viz. WH, SH, HG, RH and BL. Age and sex of the animal was also included in the model as the independent variables. Ten (10) fold cross-validation was used as an error estimation method documented to be the most acceptable method of prediction to offer estimate of the future error of prediction for each node and explained the variation observed in the dependent-variable was predicted as follows:

$S^2_x = (1 - S^2_e) \times 100$

$S^2_e = \text{risk value}/S^2_y$

Where in details:

S^2_x = explained variation, S^2_e = unexplained variation and S^2_y = variance of the root node (standard deviation of the root node)^2.

Data analysis

The current experimental data were analysed using Statistical Package for Social Sciences (IBM SPSS, 2019) version 26 software. Probability of 5% for significant was used and probability of 1% for highly significant between traits was also used. Descriptive statistics such as average, standard deviation, standard error, and coefficient of variation were calculated. Pearson's correlation coefficient was used to estimate the relationships between all the measured traits while classification and regression tree (CART) was computed to develop a model.

Results

Descriptive statistics

The summary of all examined traits on South African non-descript indigenous goats (male and female) which are less than one-year-old and above is presented in Table 1. In goats younger than a year, BW mean numerical value of female kids were higher than those of male kids. Descriptive statistics of biometric traits recognised that female kids had higher mean numerical values in all traits, HG, RH, BL, WH and SH respectively. While in goats older than a year, BW mean numerical value of male goats were higher than those of female goats. The summary of biometric traits showed that male goats had higher mean numerical values in all traits, HG, RH, BL, WH and SH. Coefficient of variation of goats that are lower than one year of age ranged from 9.03% to 60.51% while animals above or equals to one year of age had coefficient of variation ranging from 7.22% to 20.35%.

Table 1. Descriptive statistics for body weight and biometric traits of male and female South African non-descript goats

Age group	Traits	Sex	Mean±SE	SD	CV (%)	Min	Max
< 1 year	BW (kg)	M	24.82±3.20	15.02	60.51	7.00	60.00
		F	40.36±2.49	10.28	25.47	25.30	58.00
	HG (cm)	M	64.02±3.02	14.17	22.13	37.50	82.60
		F	87.49±2.68	11.06	12.64	75.00	104.90
	RH (cm)	M	49.59±1.99	9.31	18.77	32.50	64.00
		F	58.87±1.68	6.94	11.79	43.00	66.00
	BL (cm)	M	59.00±2.56	12.01	20.35	38.00	76.40
		F	77.95±1.93	7.95	10.20	66.40	90.00
	WH (cm)	M	50.70±2.02	9.49	18.72	35.00	69.00
		F	67.31±2.20	9.06	13.46	50.00	79.00
	SH (cm)	M	35.33±1.13	5.32	15.06	27.00	42.50
		F	40.31±0.88	3.64	9.03	32.00	45.00
≥ 1 year	BW (kg)	M	42.51±3.27	8.65	20.35	30.60	55.00
		F	25.66±1.49	9.04	35.23	9.00	43.00
	HG (cm)	M	83.93±3.10	8.20	9.77	78.00	96.50
		F	70.37±1.85	11.25	15.99	45.00	83.00
	RH (cm)	M	61.14±2.79	7.38	12.07	51.00	68.00
		F	52.42±1.42	8.62	16.44	39.00	68.00
	BL (cm)	M	77.41±3.84	10.17	13.14	66.40	89.50
		F	62.16±1.43	8.68	13.96	41.00	76.40
	WH (cm)	M	72.14±1.97	5.21	7.22	65.00	78.00
		F	55.42±1.62	9.84	17.76	40.00	75.00
	SH (cm)	M	41.07±1.51	4.00	9.74	36.00	45.00
		F	35.62±0.78	4.74	13.31	26.00	43.00

SE: Standard Error, CV: Coefficient of Variation, SD: Standard Deviation, BW: Body Weight, HG: Heart Girth, RH: Rump Height, BL: Body Length, WH: Withers Height, SH: Sternum Height, < 1 year: Younger than one year, ≥ 1 year: Older than a year.

Phenotypic correlations among measured traits

Pearson's correlation was used to examine the relationship between BW and biometric traits of South African non-descript goats for both sexes (Table 2). The results above diagonal line show correlation results of female goats. The results indicated that BW had a positive highly statistical significant ($P < 0.01$) correlation with HG, RH, BL, WH and SH. However, phenotypic correlation findings of male below the diagonal line showed that BW had a positive highly significant correlation ($P < 0.01$) with HG, RH, BL, WH and SH .

Table 2. Phenotypic correlation between body weight and biometric traits of female above diagonal and male below diagonal

Traits	BW	HG	RH	BL	WH	SH
BW (kg)		0.79^{**}	0.80^{**}	0.83^{**}	0.76^{**}	0.66^{**}
HG (cm)	0.68^{**}		0.82^{**}	0.88^{**}	0.78^{**}	0.60^{**}
RH (cm)	0.62^{**}	0.58^{**}		0.88^{**}	0.84^{**}	0.72^{**}
BL (cm)	0.77^{**}	0.87^{**}	0.62^{**}		0.88^{**}	0.73^{**}
WH (cm)	0.82^{**}	0.66^{**}	0.86^{**}	0.73^{**}		0.73^{**}
SH (cm)	0.63^{**}	0.50^{**}	0.81^{**}	0.63^{**}	0.83^{**}	

**P<0.01; BW: Body weight; HG: Heart girth; RH: Rump height; BL: Body length; WH: Withers height; SH: Sternum height

CART algorithm

CART model in South African non-descript goats (Figure 2) with BW as a dependent variable and biometric traits, sex and age as the independent variables. This model contained a total of fourteen (14) nodes on which eight of them were terminal nodes (node 3, 6, 8, 10, 11, 12, 13, 14), respectively. Node 0 is the root node containing the descriptive statistics of BW (mean = 29.868kg, standard deviation = 13.080 and n = 83). Node 0 based on BL was divided into node 1 (<= 63.050cm) and node 2 (> 63.050cm), respectively. Node 1 was divided based on HG into node 3 (<=56.500cm) and node 4 (> 56.500 cm). Node 4 was divided based on HG into node 7 (<=70.500cm) and node 8 (>70.500 cm). Node 7 was divided on the basis of RH into node 11 (<= 50.500 cm) and node 12 (> 50.500cm), respectively. Node 2 on the other hand was divided based on SH into node 5 (<= 43.250cm) and node 6 (>43.250cm). Node 5 was divided based on BL into node 9 (<=72.050cm) and node10 (>72.050cm). The last node to be divided in this model was node 9 which was divided on the basis of age into node 13 (goats that are two years and four years old) and node 14 (goats that are one year and eleven years old), respectively. In all the terminal nodes, node 6 appeared to be the best node as it was recorded the highest predicted mean (54.00kg) than node 3 (10.939kg), node 8 (25.500kg), node 10 (39.467kg), node 11 (18.444kg), node 12 (20.600kg), node 13 (38.333kg) and node 14 (30.750kg), respectively. The model showed that node 12 had the lowest variance $(0.894)^2 = 0.799$ and the variance of the root node or dependent variable (BW) was $S^2_y = (13.080)^2 = 171.086$. The unexplained variation in the BW was S^2_e = risk value $\div S^2_y = 25.316 \div 171.086 = 0.148$ and the variation in the model was explained as $S^2y = (1 - S^2_e) \times 100 = (1- 0.148) \times 100 = 0.85 \times 100 = 85\%$, respectively.

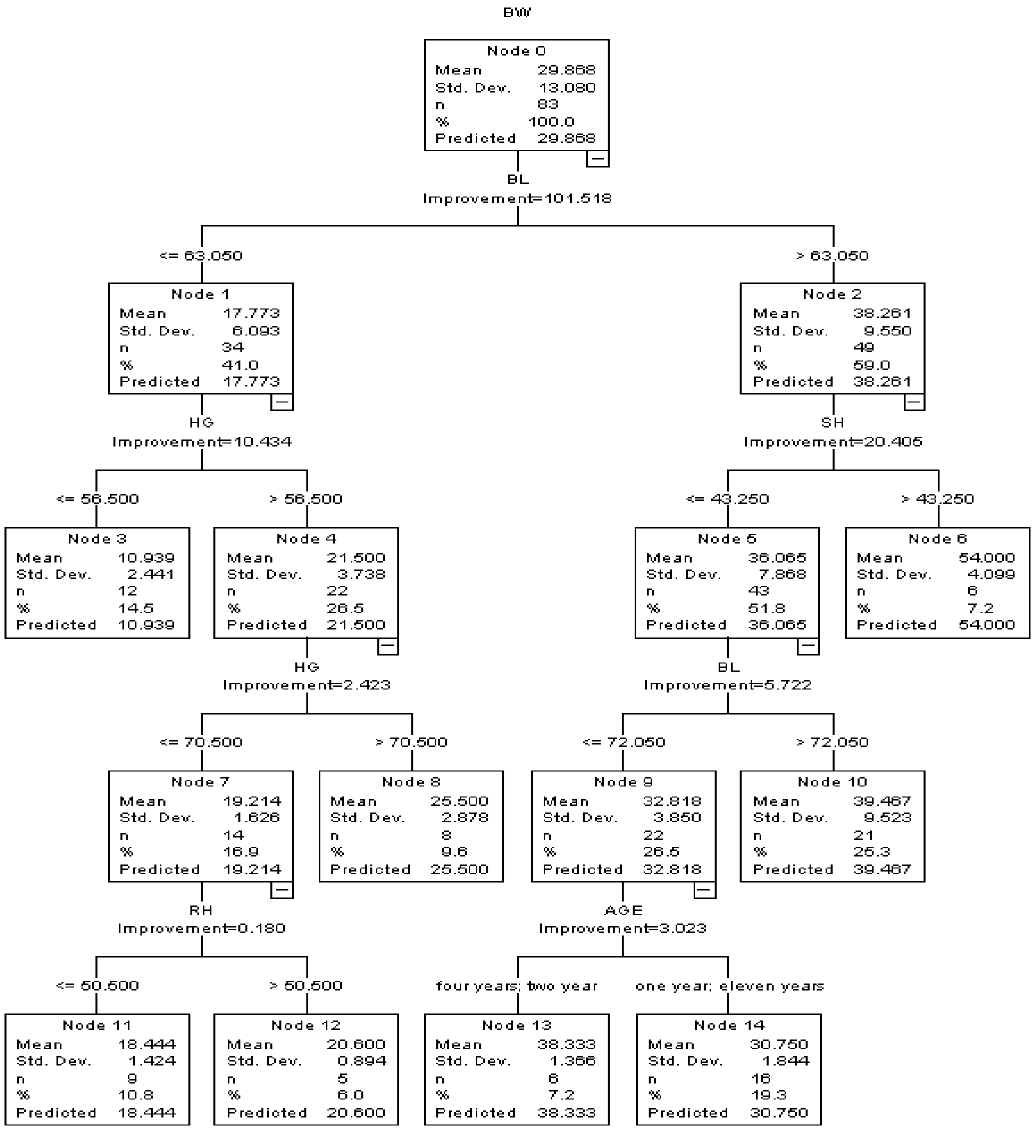

Figure 2. Classification and regression tree model (CART)

Discussion

Biometric traits are alternatives which can be used to predict BW mostly at rural areas where the weighing scale is not available *(Norris et al., 2015*; *Eyduran et al., 2017*, *Tyasi et al., 2020b)*. Classification and regression tree is the best decision tree technique for recognizing biometric traits playing a critical role on live BW of animal *(Eyduran et al., 2017*; *Tyasi et al., 2021)*. The current study firstly determined the relationship between body weight, rump height, body length, withers height and sternum height of South African non-descript goats. Correlation findings in both sexes indicated that BW had positive highly significant correlation with body length, rump height, heart girth, withers height and sternum height. Increasing body length, rump height, heart girth, withers height and sternum height in both sexes might cause an increase in BW. Therefore, body length, rump height, heart girth, withers height and sternum height might be used for genetic improvement of BW during breeding. Contrary to the current study was reported by *Tyasi et al. (2020b)* where BW showed the lowest correlation with heart girth, no correlation with rump length and high correlation with withers height, rump height and body length in South African non-descript indigenous female goats. Study differences might be due to age group of goats used in the study. Similar studies concluded that body weight had positive high significant correlation with the biometric traits. *Yakubu and Mohammed (2012)*, agrees with the current study where there is positive highly significant correlation between body weight and body length, body weight and heart girth in red Sokoto goats. *Yakubu (2009)*, observations are in harmony with the current study where there is positive highly significant correlation between BW and withers height, rump height, body length, heart girth in West African dwarf goats. *Norris et al. (2015)*, had a positive highly significant correlation between BW and heart girth in female meanwhile, *Berhe (2017)* observed positive high significant correlation between body weight and heart girth, body weight and withers height.

CART algorithm was used in the current study to develop a model to predict the BW from withers height, sternum height, body weight, body length hearth girth and rump height of South African non-descript. Our findings indicated that body length, heart girth, sternum height, rump height and age explained 85% of variation in body weight of South African non-descript goats. Model developed from the current study suggests that body length had the highest remarkable role in body weight followed by heart girth, sternum height, rump height, respectively. It was also shown that age also played a significant role in body weight of South African non-descript indigenous goats *Celik and Yilmaz (2018)* conducted CART in Turkish Tazi dogs and had disagreement with the current study, where 68.90% of the variability of the BW was explained with withers height, rump height and abdominal width and chest depth, while withers height played the highest role and chest depth played the lowest role on BW. The reason for variation may be due to type of species differences. Contrary to the current study was also reported by *Celik et al. (2017)* in Beetal goats of Pakistan where age played a significant role on body weight followed by scrotal length, the traits found on CART explained 91.97% of variation in the body weight. The difference may be due to different breed and sample size. *Tyasi et al. (2020a)* performed a study on Potchefstroom Koekkoek laying hens and discovered that wing length played a higher role on body weight than other traits using. Classification and regression tree followed by beak length, and the traits found on CART explained 57% of the variation in body weight. The variation may be due to the type of species used, based on current study results.

Conclusion

It can be concluded that there is a positive highly significant relationship between body weight and biometric traits (rump height, body length, withers height, sternum height) of South African non-descript indigenous goats. The study suggests that all the biometric traits can be used as a selection criterion to improve body weight of South African non-descript indigenous goats, moreover they may assist in decision making when feeding, medicating, marketing and breeding their animals. Furthermore, the study emphasized that body length and withers height can be used as single traits to improve body weight in males and female goats, respectively. CART model can be used to predict body weight of South African non-descript indigenous goats precisely due to its high coefficient of determination. The model suggests that body length alone can be used to predict body weight of South African non-descript indigenous goats. The current study will help communal farmers in determining the feed amount, drug dose, and market price of an animal and in improving profitability of animal farms. It is recommended that prediction of body weight using biometric traits especially at rural areas might save farmers expenses for scales, help in decision making for breeding purposes for economic importance traits such as body weight. However, further studies need to be performed on the prediction of body weight using CART algorithm in different goat breeds or more sample size of the same breed.

Analiza regresijskog stabla za predviđanje telesne mase južnoafričkih autohtonih koza uzgajanih na farmi Syferkuil, u okrugu Kaprikorn u južnoj Africi

Thobela Louis Tyasi, Amanda Tshegofatso Mkhonto, Madumetja Cyril Mathapo, Kagisho Madikadike Molabe

Rezime

Regresijsko stablo je metoda algoritma za dobijanje podataka koja sadrži niz proračuna koji kreiraju model od prikupljenih podataka. Ova studija je imala za cilj da razvije model za procenu telesne mase (BW) na osnovu biometrijskih osobina, tj. visine grebena (WH), visine grudne kosti (SH), dužine tela (BL), obima srca (HG) i visine zadnjeg dela tela, kukova (RH). U istraživanju je korišćeno ukupno osamdeset tri (n = 83) južnoafričke autohtone koze (54 ženke i 29 mužjaka) starosti od tri meseca i više. Za analizu podataka korišćene su Pirsonove korelacije i stablo klasifikacije i regresije (CART - classification and regression tree) kao statističke tehnike. Rezultati korelacije su pokazali da postoji pozitivna visoko statistički značajna ($P < 0{,}01$) korelacija između BW i svih biometrijskih osobina, i kod muških i ženskih grla, pozitivna visoko statistički značajna korelacija je primećena između BW i WH ($r = 0{,}82$) kod ženskih grla koza dok kod muških grla, najveća pozitivna statistički značajna korelacija otkrivena je između BW i BL ($r = 0{,}83$). CART model je pokazao da je srednja vrednost BW bila 29,868 kilograma (kg) kao zavisna varijabla i BL je imao najveću značajnu ulogu u BW, praćen SH, RH, dok je starost imala najmanje značajnu ulogu kod BW. Ovo istraživanje sugeriše da bi BL, SH i RH mogli da koriste farmeri koji uzgajaju južnoafričke autohtone koze, kao kriterijum selekcije tokom uzgoja za poboljšanje telesne mase životinja. Sveobuhvatnija istraživanja i eksperimenti treba da se urade korišćenjem CART-a da se predvidi BW u većoj veličini uzorka južnoafričkih autohtonih koza ili drugih rasa koza.

Ključne reči: biometrijske osobine, dužina tela, obim srca, visina kukova, visina grudne kosti.

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Author's contributions

Thobela Louis Tyasi designed the experiment, analyzed the data, and wrote the manuscript. Amanda Tshegofatso Mkhonto, Madumetja Cyril Mathapo and Kagisho Madikadike Molabe performed the fieldwork and wrote the manuscript. Thobela Louis Tyasi read, edited, and approved the final manuscript.

Competing interests

The authors declare that they have no conflict of interest.

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Affiliations of authors – Times New Roman, font size 9, normal, under affiliations of authors should be mentioned e-mail of corresponding author and after that category of paper.

Example 1

POTENTIALS OF SERBIAN LIVESTOCK PRODUCTION – OUTLOOK AND FUTURE

Milan M. Petrović[1], Stevica Aleksić[1], Milan P. Petrović[1], Milica Petrović[2], Vlada Pantelić[1], Željko Novaković[1], Dragana Ružić-Muslić[1]

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[2]University of Belgrade, Faculty of Agriculture, Nemanjina 6, 11080 Zemun, Serbia
Corresponding author: Milan M.Petrović, **e-mail address**
Review paper

Example 2

EFFECTS OF REARING SYSTEM AND BODY WEIGHT OF REDBRO BROILERS ON THE FREQUENCY AND SEVERITY OF FOOTPAD DERMATITIS

Zdenka Škrbić, Zlatica Pavlovski, Miloš Lukić, Veselin Petričević

Institute for Animal Husbandry, Autoput 16, 11080 Belgrade, Serbia
Corresponding author: Zdenka Škrbić, **e-mail address**
Original scientific paper

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Abstract: up to 250 words, Times New Roman, font size 11, justify. Abstract should contain a brief overview of the methods and the most important results of the work without giving reference. Abstract submitted in English language.

Key words: not more than 6. The selection carried out by relying on widely accepted international source such as a list of keywords Web of Science.

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Materials and Methods – state methods applied in the paper; experimental research design. Use SI system of measurement units.

Results and Discussion – present investigation results separately from discussion or together in one paragraph. Presentation of the results should be precise and without repetitions, and include the evaluation of significant differences and other parameters.

Text and titles of tables, figures and graphs, Times New Roman, font size 9, **bold**, in the following form:

Table 1. Least square means for the reproductive traits of cows

Tables and figures should be numbered and with adequate title and legend, width and height not exceeding 12 cm and 17 cm, respectively. Tables should be prepared according to instruction for forming of tables in Office Word. Each column in table must have heading and, when necessary, abbreviations should be explained in the legend/footnote.

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After Conclusion the title of the paper in Serbian in Times New Roman 14 **bold**, is stated, followed by authors in Times New Roman 11 *italic*, example:

Potencijali srpske stočarske proizvodnje – izgledi i budućnost

Milan M. Petrović, Stevica Aleksić, Milan P.Petrović, Milica Petrović, Vlada Pantelić, Željko Novaković, Dragana Ružić-Muslić

Summary – in Serbian language, 250 max. words (non-Serbian authors should provide Summary in English language that will be translated to Serbian by Editor's office)

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Research was financed by the Ministry of Science and Technological Development, Republic of Serbia, project TR 6885.

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In scientific journals:

PETROVIĆ M. M., SRETENOVIĆ LJ., BOGDANOVIĆ V., PERIŠIĆ P., ALEKSIĆ S., PANTELIĆ V., PETROVIĆ D. M., NOVAKOVIĆ Ž. (2009): Quantitative analysis of genetic improvement of milk production phenotypes in Simmental cows. Biotechnology in Animal Husbandry, 25,1-2, 45-51.

ŠKRBIĆ Z., PAVLOVSKI Z., LUKIĆ M. (2007): Uticaj dužine tova u različitim sistemima gajenja na klanične osobine brojlerskih pilića genotipa Redbro. Biotechnology in Animal Husbandry 23, 3-4, 67-74.

WEBB E., O'NEILL H. (2008): The animal fat paradox and meat quality. Meat Science, 80, 28-36.

PhD Thesis:

RUŽIĆ-MUSLIĆ D. (2006): Uticaj različitih izvora proteina u obroku na proizvodne rezultate jagnjadi u tovu. Doktorska disertacija. Univerzitet u Beogradu, Poljoprivredni fakultet.

CAETANO A.R. (1999): Comparative mapping of the horse (*Equss caballus*) genome by synteny assignment of type-I genes with a horse-mouse somatic cell hybrid panel. Ph.D. Dissertation, University of California, Davis.

In Scientific Books:

PETROVIĆ P.M (2000): Genetika i oplemenjivanje ovaca. Naučna knjiga, Beograd, pp365.

FITZGERALD M. (1994): Neurobiology of Fetal and Neonatal Pain. In: Textbook of Pain. 3rd edition. Eds Wall P. and Melzack R. Churchchill Livingstone, London, UK, 153-163.

At Scientific Meetings:

ŠKRBIĆ Z., LUKIĆ M., BOGOSAVLJEVIĆ-BOŠKOVIĆ S., RAKONJAC S., PETRIČEVIĆ V., DOSKOVIĆ V., STANOJKOVIĆ A. (2015): Importance of farm management in reducing broilers skin lesions. Proceedings of the 4th International Congress “New Perspectives and Challenges of Sustainable Livestock Production”, October 7 – 9, Belgrade, 145-158.

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