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Genetic analysis of growth parameters and survival potential of Jamunapari goats in semiarid tropics

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ABSTRACT

Goats are adaptable to varied farming environments and contribute significantly towards sustainable livestock production and food security. Selective breeding of goats for improved performance is an important component of sustainable production. The objectives of the present study were to determine the most appropriate models of analysis for growth traits, to estimate genetic parameters, survival potential of kids from birth to 12 months of age and to estimate genetic trends for growth traits of Jamunapari kids at different ages. Genetic parameter estimates were obtained from 6590 records generated between 1982 and 2012 from 5922 animals with a pedigree covering over 13 generations. The most parsimonious model for early growth traits included permanent environmental effects due to the dam (PE) and litter effects. Similarly, the most appropriate model for early average daily gain (ADG) between birth and 3 or 6 months also included PE and litter effects. The estimates of heritability for survival from birth to 12 months of age ranged from 0.10 to 0.43. The estimates of heritability for ADG varied from 0.04 to 0.41. In general, higher estimates of heritability were observed when a sire model was fitted in the random effect. There was no genetic variation observed for survival between birth and 3 months of age. However, heritability estimates of between 0.18 and 0.39 were observed for survivability during post-weaning period to 12 months of age. The genetic trend at 9 months of age and 12 months of age was 0.144 kg 0.189 kg per year respectively. The genetic trend at all the ages was positive during the study period.

1. Introduction

The rapidly growing livestock market and the opportunity for global trade offer the potential to increase the income of livestock farmers. Moreover, the global preference for animal protein consumption has increased over last decade. Since goats (*Capra hircus*) can utilize fibrous plant materials to produce meat, which offers a reliable source of animal protein in developing countries, their abundance may have led to an increasing preference for goat meat in developed countries (Devendra, 2010; Webb et al., 2005). Goat meat (chevon) is the most preferred meat in India and the domestic demand outstrips its supply (Sen et al., 2004). More importantly, goats produce meat and milk in different types of agro climatic zone and supplement the nutritional requirement of human-beings in several disadvantaged geographical locations. Goats are adaptable and resilient animals for sustainable livestock production and have the potential to fulfill the protein requirement of growing population, with most of the approximately 1 billion world goat population, 56 and 30% located in Asia and Africa respectively (FAO, 2015). Moreover the carcass fat content of goat meat

is low and virtually all the parts of carcass are consumed (Webb, 2014). Therefore, it is necessary to optimize productivity of goat breeds with naturally available feed resources and goat producers have to adopt new technologies and better feeding practices to improve the performance and yield of goats (Webb, 2014). Body weights and average daily gains are important selection traits for improving production performance by selective breeding. Selection is primarily based on body weight between 6 and 12 months of age, with increasing body weight considered as important breeding goal. However, in practice, the most appropriate genetic model should be considered when breeding for any trait that is evaluated. Goats are not generally well studied, resulting in limited genetic parameter estimates available on growth, milk and reproduction traits (Bosso et al., 2007; Boujenane and El-Hazzab, 2008; Zhang et al., 2008; Gowane et al., 2011; Rashidi et al., 2011). Genetic parameters on growth traits have been reported in different breeds and locations (Snyman and Olivier, 1996; Roy et al., 2008; Hermiz et al., 2009; Thiruvenkadan et al., 2009; Alade et al., 2010; Ekambaram et al., 2010; Roy et al., 2011). The heritability of growth traits at different ages varied from 0.06 to 0.88 in different breeds (Mukundan and Bhat,

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1978; Madeli and Patro, 1984; Jin and Zhang, 1995; Bishop and Russel, 1996; Snyman and Olivier, 1996; Schoeman et al., 1997; Rashidi et al., 2000; Rashidi et al., 2008; Roy et al., 2008; Hermiz et al., 2009; Thiruvankadan et al., 2009; Ekambaram et al., 2010; Faruque et al., 2010; Roy et al., 2011). There are few reports on genetic parameter estimation of average daily gain between different growth stages and survival potential. Moreover genetic trend of growth traits has not been reported in goat breeds in different regions. Therefore, the objectives of the present study were (a) to determine the most appropriate models of analysis for body weight and average daily gain (ADG) of Jamunapari kids at different ages; (b) to estimate genetic parameters of these traits; (c) to estimate the genetic parameter of survival potential of kids up to 12 months of age; and (d) to evaluate the genetic trends in body weight during the last 31 years of selective breeding.

2. Material and methods

2.1. Animals

The Jamunapari goats were introduced to the study area (CIRG) from their natural habitat, the Chakarnagar area of Etawah district of Uttar Pradesh, which is situated 150 km from the Central Institute for Research on Goats (CIRG) in Mathura, India. The study area has semi-arid climate and an average annual rainfall of about 375 mm which is scattered during the months of June to September. The soils are sandy with natural pasture and bush as the main vegetation type. The pastures are mainly *Cenchrus ciliaris* and *C. setigerus*, along with native annual and perennial flora. The temperature varies from 4.0 °C to 24.3 °C during winter and 27.5 °C to 42.4 °C during summer.

The Jamunapari goat is a milk-producing breed with average body weight of 28.0 kg at 12 months of age with 1.5 kidding rate. It has a majestic white colour coat with long pendulous ear, Roman nose and has *trans*-boundary distribution (Rout et al., 2000). The breed has been used extensively for upgrading local breeds in neighboring Southeast Asian countries and is an ancestor to the Anglo-Nubian goat (Rout et al., 2004).

The goats were maintained under a semi-intensive system of management with 6–7 h of grazing and stall feeding with seasonally available green fodder, supplemented with concentrate mixtures (70% maize and 10–15% oil cake, 10–15% bran and mineral mixture) depending upon the status and age category of the animals. Generally, animals were housed separately according to their ages, sex, physiological status and health status. Controlled breeding was practiced with the does being bred during May to June and October to November followed by kidding in the months of October to November and March to April, respectively. Does were exposed to the bucks twice at each oestrus. At kidding, each kid was assigned an identification number by ear tattooing and date of birth, sex, birth type and live body weights were recorded. Kids were stall-fed up to weaning at 3 months of age, and then allowed to graze nearby areas for very short periods for up to 6 months of age. The preventive health care measures were regular vaccination of pestis-de-petitis (PPR), Foot and Mouth disease (FMD), and Enterotoxaemia (ET) of the flock. Targeted deworming for the control of gastrointestinal nematodes was carried out during the pre-monsoon season (May to June) and in the post-monsoon season (September to October). Animals were regularly dipped to control ectoparasites in the flock.

2.2. Traits analysed

Growth data and pedigree were available from 1982 to 2012 on Jamunapari flocks maintained at the ICAR-Central Institute for Research on Goats (CIRG). The traits analysed were those for body weights at: (a) birth (BWT), 3 months (M3WT), 6 month (M6WT), 9 month (M9WT) and 12 months (M12WT) of age; (b) average daily body weight gain (ADG) between birth to 12 months of age within the

Table 1

Summary of pedigree data structures and number of records.

Source	Numbers
Phenotype records	6590
Pedigree records	5922
Sires	292
Sire of sires	125
Dam of sires	196
Dams	1819
Sire of dams	207
Dam of dams	784
Generations	13

following periods: birth to 3 months (0–3 M), 3–6 months (3–6 M), 6–12 months (6–12 M), birth to 6 months (0–6 M), birth to 9 months (0–9 M), birth to 12 months (0–12 M), 3–9 months (3–9 M), 3–12 months (3–12 M); and (c) survivability of kids from birth to 12 months of age (whether a kid born alive was still alive at weaning, 3 month, 6 month, 9 month and 12 month of age). Pedigree records on 5922 animals over 13 generations were used for genetic parameter analysis (Table 1).

2.3. Data analysis

Initially data were explored for summary statistics and normality using SAS (SAS, 2013). The models fitted accounted for environmental effects for parity (with all parities above 6 fitted as one class), year (1982–2012), season (autumn and spring) and birth type (TOB, singles and multiple with 2 plus treated as one class). Random effects for animal, sire, maternal (m) and permanent environmental (PE) effects due to the dam were fitted. Estimates of variance and co-variance components were obtained using the ASReml program (Gilmour et al., 2009), initially fitting the univariate models. The following models were fitted:

$$\text{Model 1: } y = Xb + Z_a + e \quad (1)$$

$$\text{Model 2: } y = Xb + Z_a + Z_m + e \quad (2)$$

$$\text{Model 3: } y = Xb + Z_s + e \quad (3)$$

$$\text{Model 4: } y = Xb + Z_a + Z_{pe} + e \quad (4)$$

$$\text{Model 5: } y = Xb + Z_a + Z_{pe} + Z_{lit} + e \quad (5)$$

$$\text{Model 6: } y = Xb + Z_s + Z_{pe} + Z_{lit} + e \quad (6)$$

Where y is a vector of observations on specific traits of the animal; b is a vector of fixed effects; a , m , s , pe , lit are vectors of random effects describing additive genetic, maternal additive, sire, litter and permanent environment effects due to dam; X , Z are corresponding incidence matrices relating to each effect to y ; and e is the vector of residuals. Normal distributions were assumed for the random effects: direct additive $\sim N(0, A\sigma_a^2)$, sire $\sim N(0, A\sigma_{sire}^2)$, $pe \sim N(0, I\sigma_{pe}^2)$, litter $\sim N(0, I\sigma_{lit}^2)$, $e \sim N(0, I\sigma_e^2)$, where A is the numerator relationship matrix, and I denotes the identity matrices of the order equal to the number of litters and records. Likelihood ratio tests (LRT) were carried out to determine the most suitable model for each trait in univariate analyses (Morrell, 1998). The test statistic was $-2[\ln L_{(2)} - \ln L_{(1)}]$ where $L_{(n)}$ is the likelihood of Model n . Critical values for the LRT were taken from a mixture distribution $\frac{1}{2}\chi^2_{(1)}$ and $\frac{1}{2}\chi^2_{(0)}$ (Self and Liang, 1987).

Breeding values of individual animals were estimated with ASReml. In order to estimate the genetic trends, means of estimated breeding values of the kids within year of birth were calculated. Genetic trends were obtained by regression means of estimated breeding values on year of birth for each trait.

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