GENETIC ANALYSIS OF WOOL TRAITS AND ITS ASSOCIATION WITH KERATIN GENES IN MAGRA SHEEP

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M.V.Sc.

THESIS

DOCTOR OF PHILOSOPHY

(Animal Genetics and Breeding)



2017

Department of Animal Genetics and Breeding

College of Veterinary and Animal Science, Rajasthan University of Veterinary and Animal Sciences, Bikaner-334001 GENETIC ANALYSIS OF WOOL TRAITS AND ITS ASSOCIATION WITH KERATIN GENES IN MAGRA SHEEP

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THESIS

Submitted to the Rajasthan University of Veterinary and Animal Sciences, Bikaner

In partial fulfillment of the requirements for the degree of

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(Animal Genetics and Breeding)

FACULTY OF VETERINARY AND ANIMAL SCIENCE

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(HARVINDER SINGH)

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1. INTRODUCTION

The sheep. an important economic livestock species. contributes greatly to the agrarian Indian economy, especially in arid, semiarid and mountainous areas. They play an important role in the livelihood of a large percentage of small and marginal farmers and landless labourers engaged in sheep breeding. Sheep husbandry strengthens the backbone of rural economy of north-western arid habitat because of uncertainty of agricultural crops due to scanty rainfall, lack of irrigation facilities and low productivity of soil. Domestication of animals was an essential step in human demographic and cultural development. Sheep (Ovis aries) were domesticated in South-western Asia about 12,000 years ago being one of the earliest species (Zeder et al., 2006). Sheep are gregarious in nature. They have a unique niche in small holder agriculture from the fact that they require small investments; have shorter production cycles, faster growth rates and greater environmental adaptability as compared to large ruminants. Major sources of income from meat, wool, skin, and manure make sheep industry a very profitable enterprise. The profitability of sheep production largely depends on the growth and wool production performance. A rich source of nitrogen, phosphorus and potash present in droppings of sheep improves the soil fertility.

The total livestock population consisting of Cattle, Buffalo, Sheep, Goat, pig, Horses & Ponies, Mules, Donkeys, Camels, Mithun and Yak in the country is 512.05 million numbers (Livestock census, 2012). The total livestock population has decreased by about 3.33% over the previous census. India is endowed with 44 descript breeds of sheep distributed in different agro-climatic conditions. The country stands second in sheep population in the world. The total sheep in the country is 65.06 million numbers, contributing around 12.71 % of the total livestock population of India (Livestock census, 2012). The population has declined by about 9.07% over the previous census. Total livestock population of Rajasthan is 57.73 millions. The state stands third in sheep population in India, sharing around 13.95 % of the

total sheep population. Around 9 million sheep is concentrated in Rajasthan.

India is sixth largest producer of raw wool in the world, accounting for 1.8 % of world wool production with about 4.2 % of the total sheep population. The total wool production of the country is 46.1 million kg. Rajasthan is the largest producer of wool in the country which produces about 30.4 % of the total wool production. Annual production of wool in Rajasthan is about 14 million kg, with an annual growth rate of 6.2 % (BAHS, 2014).

Magra breed of sheep is an important carpet wool breed of Rajasthan. The lustrous wool produced by Magra is the most suitable for carpet production. The breed is characterized by well built body with light pink skin covering. The head is without any wool but covered with white hairs, with light brown patches round about the eyes, flat forehead, medium in size and hornless. The breed is widely distributed in and around Bikaner, Churu and Nagaur districts of Rajasthan. Magra breed produces the best quality carpet wool, besides this it is also known for survivability in harsh climatic condition, scarce feed and fodder resources.

The woolen sector in India plays an important role by linking the rural economy with the manufacturing industry, represented by small, medium, and large-scale units. This industry caters to civil and defence requirements for warmer clothing. Most of the wool produced (85%) is of coarse quality, used mainly in the manufacturing of hand-knotted carpets, 5% is apparel grade and 10% is coarse grade, used mainly for the production of low quality carpets, blankets, etc. Hence, to increase the value of its handmade carpets, the country imports raw wool. India is the fourth largest importer from Australia. It is important to exploit the inherent potential of indigenous sheep in order to improve the quality of their wool and bring it at par with its exotic counterparts.

The economics of sheep production is greatly affected by the wool performance. Wool quality traits like fibre diameter, staple length,

number of crimps per cm of wool fibre etc contribute to price variation due to their effect on fibre processing properties and the ultimate quality of the products. Wool traits are largely affected by both genetic and non genetic factors, which must be evaluated before planning and implementing a sheep breeding plan.

During the growth of fibre from its follicle, control is exercised by several multigene families to produce a coordinated synthesis of the Keratin proteins. The relative proportions of Keratin proteins of these families in the fibre vary between species and within species and these ratios are known to fluctuate in response to dietary, chemical and hormonal changes (Gillespie and Marshall, 1980). Consequently, variations in family of Keratin genes play an important role in quality and production of the animal fibre. Identification of these genes controlling the wool quality in terms of fibre diameter and length will offer an opportunity to improve production efficiency, product quality and product diversity, through utilizing them in the breeding programs for developing specific lines. The capacity to modify the structural components of wool fibre using knowledge of the genes controlling the KIF/KAP protein content and balance was demonstrated in Merino sheep (Bawden *et al.,* 1998).

The wool fibre consists of three main structures, the cuticle, the cortex, and in some coarse wools, the medulla (Onions, 1962). The cortex comprises 90% of the wool fibre and consists of filamentous microfibrils embedded in a matrix of Keratin associated proteins (KAPs) (Marshall *et al.*, 1991; Powell and Rogers, 1986). The microfibrils consist of keratin intermediate-filaments (KIFs), which are also known as the "hard" α -keratins. They are low-sulphur proteins, which are classified into two protein families, Type I keratins (acidic) and Type II keratins (non-acidic) (Powell, 1996, Schweizer *et al.*, 2006). The keratin associated proteins in an organized fashion, are the major proteins of the wool fibre. The genes coding for these wool proteins might have an impact on wool quality, and so are candidate genes for

further selective breeding. Sheep Type I and Type II genes are at 11q25-q29 and 3q14-q22 (Dolling and Brooker, 1966; Hediger *et al.*, 1991), with the Type I gene about 4-5 kb in length and containing 6 introns and Type II genes about 7-9 kb in length and containing 8 introns (Powell and Roggers, 1997). Linkage mapping using the AgResearch IMF flock has confirmed these physical map positions (McLaren *et al.*, 1997). The Type 1 IF wool keratin gene on ovine chromosome 11 was identified as a QTL for wool staple strength (Rogers et al., 1994a; Purvis and Franklin, 2005). Polymorphism associated with the candidate gene for this wool keratin has been described in several exotic sheep breeds. Recurrent studies have further documented the relationship between the allelic variant of Type 1 IF wool keratin gene and staple strength (Purvis and Franklin, 2005). However, very little studies of this potential gene marker have been done in Indian sheep breeds.

The matrix KAPs are divided into three groups based on their amino acid compositions: the high-sulphur proteins (KAP1.n, KAP2.n, KAP3.n), ultra-high-sulphur proteins (KAP4.n, KAP5.n, KAP10.n) and high-glycine-tyrosine proteins (KAP6.n, KAP7.n, KAP8.n) (Marshall et al., 1991, Plowman, 2003). The KAPs characteristically contain an unusually high percentage of cysteine, or glycine and tyrosine residues, and based on their amino acid composition can be grouped into the high sulphur (16-30 mol % cysteine), the ultrahigh sulphur (30 mol % cysteine) and the high glycine/ tyrosine KAPs (Powell and Rogers, 1997). The KAPs have been divided into families using the nomenclature proposed by Powell and Rogers (1997), and to date, a total of 27 families have been identified from sheep, rabbit, mouse and humans (Rogers, 2006; Rogers et. al., 2007). Of these, KAP families 1-3, 10-16 and 23-27 are high sulphur (HS) KAPs, KAP families 4, 5, 9 and 17 are ultra-high sulphur (UHS) KAPs, and KAP families 6-8 and 18-22 belong to the high glycine and tyrosine (HGT) KAPs (Rogers, 2006; Rogers et. al., 2007). The genes encoding KAPs appear to be organized into domains. In humans, KAP genes from all of the 27 families identified are clustered and located in five chromosomal

regions. Of these, chromosomal region 21q22.1 harbours 17 functional HGT and 11 functional HS KAP genes, constituting all of the seven HGT and eight of the 12 HS KAP gene families (Rogers *et al.*, 2002; Rogers *et al.*, 2007). Of these HS KAP genes, the KAP11-1 gene (KRTAP11-1) is the only gene that exhibits strong expression and that is uniquely expressed in the late matrix and the entire cortex (Rogers *et al.*, 2002). This early expression pattern seems to conflict with the view that KAPs are expressed after keratins, and that co-expression of KAPs and keratins is restricted to the mid and upper cortex region of the fibre where KAP/KAP or KAP/keratin cross-linking occurs (Rogers, 2004). The KAP11-1 gene is the only known gene member of the KAP11 family. The gene has been identified in human (Rogers *et al.*, 2002), mouse (Huh *et al.*, 1994), cattle (Zimin *et al.*, 2009) and sheep (Gong *et al.*, 2011b). Moreover, there has been no identification and investigation of variation in KAP11-1 in any breed of sheep in India.

There is a large amount of variation in the wool fibre proteins, particularly in the matrix proteins, and it is notable that such hetrogeneity is still present despite thousands of years of selective breeding to improve the quality of the wool fibre and to reduce variation. Many studies (Beh *et al.*, 2001; McLaren *et al.*, 1997; Parsons *et al.*, 1994a; Rogers *et al.*, 1993; Rogers *et al.*, 1994a; Rogers *et al.*, 1993; Rogers *et al.*, 1994a; Rogers *et al.*, 1994b) have reported polymorphism in members of the keratin and KAP gene families. Furthermore, there have been some reports associating variation in the KIF and KAP loci with variation in fibre diameter (Beh *et al.*, 2001; Parsons *et al.*, 1994b), staple strength (Rogers *et al.*, 1994a) etc.

Thus, this study was conducted to identify genetic polymorphism of KIF type-I gene by RFLP and KAP11-1 gene by SSCP that may be useful in marking variation in economically important wool traits such as greasy fleece yield, staple length, fibre diameter, crimp frequency etc with the following objectives:

1. To study the effect of genetic and non-genetic factors on wool traits.

- 2. To estimate genetic and phenotypic parameters for wool traits.
- 3. To identify the polymorphism of keratin genes in Magra sheep.
- 4. To study the association of polymorphism of keratin genes with wool traits.

2. REVIEW OF LITERATURE

The requirements of livestock industry are never static hence rates of improvement are to be constantly reviewed. Research work on Magra sheep is very scanty and limited, especially on the aspects considered in the present investigation. Therefore, review has been extended to other breeds of sheep.

The available literature regarding relevant aspect of the study has been reviewed and presented under the following heads:

2.1 Wool performance viz. wool yield and wool quality

2.2 Genetic and non-genetic factors affecting the wool yield and wool quality

2.3 Genetic and phenotypic parameters

2.4 Polymorphism of Keratin genes (KIF- I and KAP 11-1 genes)

2.5 Association of polymorphism of Keratin genes with wool traits

2.1 Wool performance

Wool production is important from economic point of view since the quantity and quality of wool produced determines the net economic returns from the sheep flock.

Wool production is affected by (i) supply to the follicles of the substances needed in fibre growth (ii) effectiveness with which the follicle utilize the supply of precursors (iii) productivity of the different follicle types within the group relative to each other and (iv) competition between follicles during follicle development or between mature follicles for precursor. The first two factors affect amount of wool whereas last two components affect the quality of fleece. Fibre forming substances may be (a) amino acids or other materials needed for the formation of new cells in the follicle bulb, (b) energy sources needed for this cellular proliferation, or (c) specific substances needed for the synthesis of keratin at later stages of fibre formation. Limitation to the supply of these materials could result from genetic effects that control the metabolic level of sheep, the blood supply of the follicles and poor nutrition of the animal.

The reports given by various workers regarding the genetic analysis of wool traits in sheep are summarized below:

2.1.1 Wool yield

The estimates of greasy fleece yield reported by various workers at different clips have been presented in Table 2.1. Greasy fleece yield at first clip ranged from 437 g in Deccani to 1880 g in Buchi sheep. Greasy fleece yield at second clip ranged from 493 g in Muzaffarnagri to 1840 g in Buchi sheep. Greasy fleece yield at third clip ranged from 549 g in Pugal to 875 g in Nali breed of sheep.

2.1.2 Wool quality

The quality of wool fibres is determined by several traits like staple length, crimp frequency, fibre diameter; and percentage of pure, hairy, hetro and medullated fibres. Various workers estimated these wool quality traits and their estimates are summarized below:

Table 2.1 Average greasy fleece yield of lambs up to three clips estimated by different workers

Author (s)	Least-	Breed/genetic		
	GFY I	GFY II	GFY III	group
Singh and Kushwaha (1995)	860±0.03	1090±0.03	-	Bharat Merino
Sinha and Singh (1997)	511.00±11.90	-	-	Muzaffarnagri
Sharma <i>et al.</i> (1999)	965±0.02	667±0.02	875±0.03	Nali
Tomar <i>et al.</i> (2000)	820±0.02	-	-	Bharat Merino
Dass and Singh (2001)	577.73±5.81	586.55±8.53	-	Marwari
Ganai <i>et al.</i> (2002)	996±0.01	-	-	Rambouillet X Gaddi
Mandal <i>et al.</i> (2002)	533.39±12.83	493.13±15.75	-	Muzaffarnagri
Dass <i>et al.</i> (2003)	638.7±8.67	578.0±9.73	-	Magra
Murdia <i>et al.</i> (2003)	933±0.003	-	-	Magra
Sharma <i>et al.</i> (2003)	578	-	-	Malpura
Mehta <i>et al.</i> (2004)	584.11±12.77	536.93±20.33	-	Magra
Nimbalkar <i>et al.</i> (2005)	437±0.01	-	-	Deccani
Kumar <i>et al.</i> (2005)	950±0.33	-	-	Chokla
Ahmad <i>et al.</i> (2005)	1060±0.23	-	-	Avikalin
Nehra <i>et al.</i> (2005)	543.20±14.28	-	-	Marwari
Dass (2006)	558	513	549	Pugal
Kumar <i>et al.</i> (2006)	821± 0.01	-	-	Avikalin
Poonia (2006)	930±0.03	900±0.03	-	Munjal
Arora <i>et al.</i> (2007)	788±8	-	-	Jaisalmeri
Dass (2007)	557.55±5.97	513.79±5.15	549.23±6.46	Pugal
Dass <i>et al.</i> (2008)	505.28±3.39	552.77±4.75	-	Marwari
Dixit <i>et al.</i> (2009)	874±0.02	1010±0.02	-	Bharat Merino

Chopra <i>et al.</i> (2010)	896.20±13.06	-	-	Bharat Merino
Gowane <i>et al.</i> (2010c)	751.19	-	-	Bharat Merino
Dixit <i>et al.</i> (2011)	874±0.02	1010±0.02	-	Bharat Merino
Kumar and Singh (2011)	950±0.01	-	-	Chokla
Narula <i>et al.</i> (2011)	755.77 ± 5.63	949.62 ± 6.59	-	Magra
Narula <i>et al.</i> (2012)	568.58 ± 4.19	692.40 ± 5.53	-	Marwari
Kumar <i>et al.</i> (2013)	950 ± 0.01	-	-	Chokla
Akhtar <i>et al.</i> (2014)	1880±0.11	1840±0.01	-	Buchi
Gupta <i>et al.</i> (2015)	579.61±4.65	-	-	Patanwadi

2.1.2.1 Staple length

The average staple length as estimated by various workers has been summarized in Table 2.2. The lowest and highest staple length was reported by Chopra *et al.* (2010) and Tabbaa *et al.* (2001) as 3.30 and 14 cm in Bharat Merino and Awassi sheep, respectively.

2.1.2.2 Crimp frequency

Crimp frequency refers to waviness of wool per cm of wool fibre. Various workers estimated the crimp frequency of wool fibre in different breeds of sheep.

Mehta *et al.* (1998) and Gopal and Singh (2001) estimated the crimp frequencies as 1.05 ± 0.06 and 0.56 ± 0.01 in Magra and Marwari sheep, respectively. Dass *et al.* (2003) reported the estimate of crimp frequency as 0.86 ± 0.02 in Magra breed of sheep.

In Pugal breed of sheep, Dass (2007) estimated the crimp frequency as 0.77 ± 0.03 . Dass *et al.* (2008) and Devendran *et al.* (2008) reported the estimates of crimp frequency as 0.49 ± 0.01 and 0.20 ± 0.02 in Marwari and Coimbatore breed of sheep, respectively. Narula *et al.* (2011) and Narula *et*

al. (2012) estimated the crimp frequency as 0.80 ± 0.01 and 0.67 ± 0.01 in Magra and Marwari sheep, respectively.

2.1.2.3 Fibre diameter

Fibre diameter is probably the most important factor for determining the quality of wool and its value. As the fibre diameter increases, it changes the way wool is used. Larger diameter fibre do not work well in the felting process, but because they are stronger and less likely to break during the carding and combing process, they are very well suited for carpets and rugs. Small diameter fibre or fine wool

Table 2.2 Average staple length of wool fibre estimated by different workers

Author (c)	Stanla longth (om)	Breed/ genetic
Author (S)	Staple length (cm)	group
Mehta and Nivsarkar (1997)	4.61±0.17	Sonadi
Mehta and Nivsarkar (1997)	5.09±0.30	Malpura
Mehta <i>et al.</i> (1998)	4.26±0.16	Magra
Gopal and Singh (2001)	4.69±0.05	Marwari
Tabbaa <i>et al.</i> (2001)	14±0.18	Awassi
Ganai <i>et al.</i> (2002)	5.73±0.15	Rambouillet X Gaddi
Dass et al. (2003)	6.16±0.07	Magra
Naidoo <i>et al.</i> (2004)	8.32±0.27	Merino
Nimbalkar <i>et al.</i> (2005)	6.64±0.16	Deccani
Dass (2006)	6.07±0.13	Pugal
Poonia (2006)	6.95±0.12	Munjal
Arora <i>et al.</i> (2007)	4.62	Jaisalmeri
Dass (2007)	6.07±0.13	Pugal

Dass <i>et al.</i> (2008)	5.16±0.04	Marwari
Devendran <i>et al.</i> (2008)	5.50±0.18	Coimbatore
Dixit <i>et al.</i> (2009)	3.32±0.07	Bharat Merino
Chopra <i>et al.</i> (2010)	3.30±0.04	Bharat Merino
Gowane <i>et al.</i> (2010b)	3.38±0.03	Bharat Merino
Dixit <i>et al.</i> (2011)	3.32±0.07	Bharat Merino
Narula <i>et al.</i> (2011)	6.81±0.04	Magra
Narula <i>et al.</i> (2012)	4.85±0.03	Marwari
Behdad <i>et al.</i> (2013)	12.88±24.19	Bakhtiari
Ciappesoni <i>et al.</i> (2013)	7.89	Merino
Das <i>et al.</i> (2014)	5.22 ± 0.11	Kashmir Merino
Khan <i>et al.</i> (2015)	5.52±0.02	Rambouillet

Author (s)	Fibre diameter (µ)	Breed/ genetic group
Snyman (1995)	21.47±0.09	Afrino
Parthasarthy et al. (1997)	28.76	Nali
Mehta and Nivsarkar (1997)	42.76±1.07	Sonadi
Mehta and Nivsarkar (1997)	45.01±1.55	Malpura
Mehta <i>et al.</i> (1998)	30.84±0.67	Magra
Sharma <i>et al.</i> (2000)	32.92±0.53	Marwari
Sharma <i>et al.</i> (2000)	28.34±0.46	Nali
Gopal and Singh (2001)	36.15±0.27	Marwari
Tabbaa <i>et al.</i> (2001)	36±0.33	Awassi
Ganai <i>et al.</i> (2002)	21.69±0.19	Rambouillet X Gaddi
Dass <i>et al.</i> (2003)	32.31±0.17	Magra
Mehta <i>et al.</i> (2004)	32.41±0.28	Magra
Naidoo <i>et al.</i> (2004)	19.8±0.03	Merino
Nehra <i>et al.</i> (2005)	32.53±0.38	Marwari
Dass (2006)	34.42±0.45	Pugal
Poonia (2006)	38.70±0.51	Munjal
Dass (2007)	34.42±0.45	Pugals
Arora <i>et al.</i> (2007)	34.59	Jaisalmeri
Dass et. al (2008)	33.66±0.28	Marwari
Devendran <i>et al.</i> (2008)	45.8±2.20	Coimbatore
Dixit <i>et al.</i> (2009)	18.89±0.15	Bharat Merino
Chopra <i>et al.</i> (2010)	18.34±0.09	Bharat Merino

Table 2.3 Average fibre diameter (µ) of wool fibre estimated by different workers

Gowane <i>et al.</i> (2010b)	18.08±0.04	Bharat Merino
Dixit <i>et al.</i> (2011)	18.89±0.15	Bharat Merino
Narula <i>et al.</i> (2011)	31.80±0.18	Magra
Narula <i>et al.</i> (2012)	33.38±0.18	Marwari
Behdad <i>et al.</i> (2013)	36.70±8.06	Bakhtiari
Ciappesoni <i>et al.</i> (2013)	16.99	Merino
Das <i>et al.</i> (2014)	20.95± 0.07	Kashmir Merino
Khan <i>et al.</i> (2015)	21.25±0.01	Rambouillet

are best suited for clothing and textiles. Fibre diameter is used to determine the wool grade.

The average fibre diameter as estimated by various workers in different breeds of sheep has been summarized in Table 2.3. The minimum and maximum fibre diameter was reported by Ciappesoni *et al.* (2013) and Mehta and Nivsarkar (1997) as 16.99 and 45.01 μ in Merino and Malpura sheep, respectively.

2.1.2.4 Pure fibres (%)

Various workers estimated the percentage of pure fibres of wool as shown below.

Mehta *et al.* (1998) and Mehta *et al.* (2004) estimated the percentage of pure fibres of wool as 57.75 \pm 2.67 and 63.31 \pm 1.58 %, respectively in Magra sheep. Nehra *et al.* (2005) and Poonia (2006) observed the percentage of pure fibres of wool as 40.39 \pm 0.72 and 36.84 \pm 1.24 %, in Marwari and Munjal sheep, respectively.

Behdad *et al.* (2013) estimated the percentage of pure fibres of wool as 89.99 ± 8.74 % in Bakhtiari sheep.

2.1.2.5 Hetro fibres (%)

The average percentage of hetro fibres in wool as estimated by certain workers has been summarized below.

Mehta *et al.* (1998) and Dass *et al.* (2003) estimated the percentage of hetro fibres in wool as 8.68 ± 0.91 and 31.32 ± 0.72 %, respectively in Magra sheep.

Gopal and Singh (2001) and Nehra *et al.* (2005) estimated the percentage of hetro fibres of wool as 32.77 ± 0.61 and 23.06 ± 0.42 %, respectively in Marwari sheep. Dass (2006) and Poonia (2006) observed 28.19 ± 0.67 and 14.47 ± 0.60 % of hetro fibres in Pugal and Munjal breeds of sheep, respectively.

Dass (2007) and Dass *et al.* (2008) estimated the percentage of hetro fibres in wool as 28.19 ± 0.67 and 30.46 ± 0.68 % in Pugal and Marwari breed of sheep, respectively.

Narula *et al.* (2011) and Narula *et al.* (2012) estimated the hetro fibres as 33.29 ± 0.50 and 37.81 ± 0.49 % in Magra and Marwari sheep, respectively. Behdad *et al.* (2013) reported the estimate of hetro fibres as 4.91 ± 5.37 % in Bakhtiari sheep.

2.1.2.6 Hairy fibres

Certain workers estimated the percentage of hairy fibres in wool as shown below.

Mehta *et al.* (1998) and Dass *et al.* (2003) estimated the percentage of hairy fibres in wool as 33.63 ± 2.44 and $12.46 \pm 0.47\%$, respectively in Magra sheep. Gopal and Singh (2001) observed estimates the percentage of hairy fibres of wool as $18.34 \pm 0.42\%$ in Marwari sheep.

Dass (2007), Dass *et al.* (2008) and Narula *et al.* (2011) estimated the percentage of hairy fibres in wool as 30.94 ± 1.22 , 20.27 ± 0.52 and 16.03 ± 0.42 % in Pugal, Marwari and Magra breed of sheep, respectively. Behdad *et al.* (2013) reported the estimate of hairy fibres as 5.11 ± 5.23 % in Bakhtiari sheep.

2.1.2.7 Medullation percentage (%)

Medullation per centage is one of the most important economic traits for determining the suitability of wool for carpet manufacturing. The medullated fibres are blended with pure fibres to impart the Table 2.4 Average medullation percentage (%) of wool fibre estimated by different workers

	Medullation	Breed/
Author (s)		
	percentage (%)	genetic group
Parthasarthy et al. (1997)	62.78	Nali
Sharma <i>et al.</i> (2000)	51.42±2.05	Marwari
Sharma <i>et al.</i> (2000)	50.80±1.77	Nali
Gopal and Singh (2001)	51.22±0.73	Marwari
Tabbaa <i>et al.</i> (2001)	11.60±0.33	Awassi
Dass <i>et al.</i> (2003)	42.67±0.91	Magra
Mehta <i>et al.</i> (2004)	36.68±1.59	Magra
Nehra <i>et al.</i> (2005)	39.33±0.67	Marwari
Dass (2006)	59.14±1.37	Pugal
Poonia (2006)	62.10±1.24	Munjal
Arora <i>et al.</i> (2007)	39.75	Jaisalmeri
Dass (2007)	59.14±1.37	Pugal
Dass <i>et al.</i> (2008)	50.72±0.90	Marwari
Devendran <i>et al.</i> (2008)	48.76±2.85	Coimbatore
Dixit <i>et al.</i> (2009)	4.39±0.49	Bharat Merino
Chopra <i>et al.</i> (2010)	1.95±0.03	Bharat Merino
Gowane <i>et al.</i> (2010b)	1.25±0.07	Bharat Merino
Dixit <i>et al.</i> (2011)	4.39±0.49	Bharat Merino
Narula <i>et al.</i> (2011)	49.32±0.79	Magra
Narula <i>et al.</i> (2012)	52.54±0.60	Marwari

desirable properties of resilience, durability and appearance retention. Generally, the medullated fibres should not be more than 45 %.

The average medullation percentage of wool fibre as estimated by various workers has been summarized in Table 2.4. The lowest and highest medullation percentage were estimated by Gowane *et al.* (2010b) and Parthasarthy *et al.* (1997) as 1.25 and 62.78 % in Bharat Merino and Nali breed of sheep, respectively.

2.2 Genetic and non-genetic factors affecting the wool yield and wool quality

Different workers observed effects of various factors like sire, year of shearing, sex of lamb, season of birth and age at shearing on wool traits and their literature has been revived and presented below:

2.2.1 Factors affecting the wool yield

Various workers have studied the significant effect of the following factors on first, second and third greasy fleece yield in different breeds of sheep.

2.2.1.1 Effect of sire

The information on effect of sire on greasy fleece yield is very scanty in literature. Singh and Kushwaha (1995) observed significant effect of sire on greasy fleece yield at first and second clip in Bharat Merino sheep.

Significant effect of sire on first greasy fleece yield was also observed by Kushwaha *et al.* (1995), Singh and Kushwaha (1995), and Sinha and Singh (1997) in Avivastra, Bharat Merino, Muzaffarnagri sheep, respectively.

Table 2.5 Reports showing significant effect of the year of shearingon greasy fleece yield of lambs

Author (s)	Wool yield	Breed/genetic group
Singh and Kushwaha (1995)	GFY I and GFY II	Bharat Merino
Sinha and Singh (1997)	GFY I	Muzaffarnagri
Sharma <i>et al.</i> (1999)	GFY I, GFY II and GFY III	Nali
Tomar <i>et al.</i> (2000)	GFY I	Bharat Merino
Gopal and Singh (2001)	GFY I and GFY II	Marwari
Mandal <i>et al.</i> (2002)	GFY II	Muzaffarnagri
Ganai <i>et al.</i> (2002)	GFY I	Rambouillet X Gaddi
Sharma (2003)	GFY I	Malpura
Mehta <i>et al.</i> (2004)	GFY I	Magra
Nehra <i>et al.</i> (2005)	GFY I	Marwari
Kumar <i>et al.</i> (2006)	GFY I	Avikalin
Poonia (2006)	GFY I and GFY II	Munjal
Singh <i>et al.</i> (2007)	GFY I	Corriedale
Dass <i>et al.</i> (2008)	GFY I and GFY II	Marwari
Dixit <i>et al.</i> (2009)	GFY I and GFY II	Bharat Merino
Chopra <i>et al.</i> (2010)	GFY I	Bharat Merino
Kumar and Singh (2011)	GFY I	Chokla
Dixit <i>et al.</i> (2011)	GFY I and GFY II	Bharat Merino
Narula <i>et al.</i> (2011)	GFY I and GFY II	Magra
Narula <i>et al.</i> (2012)	GFY I and GFY II	Marwari

Kumar <i>et al.</i> (2013)	GFY I	Chokla
Akhtar <i>et al.</i> (2014)	GFY I and GFY II	Buchi
Gupta <i>et al.</i> (2015)	GFY I	Patanwadi
Khan <i>et al.</i> (2015)	GFY I	Rambouillet

Kumar (2000), Tomar *et al.* (2000) and Ahmad (2002) observed significant effect of sire on greasy fleece yield at first clip in Chokla, Bharat Merino and Avikalin breed of sheep, respectively. Kumar *et al.* (2013) also reported significant effect of sire on first greasy fleece yield in Chokla sheep.

2.2.1.2 Effect of year/ period of shearing

The year differences could be due to varying degree of availability of feed and fodders, physical environment and other managemental factors prevailing in different years. The reports regarding fixed significant effect of year on greasy fleece yield is shown in Table 2.5.

However, few workers also reported non-significant effect of the year/period on greasy fleece yield. Mandal *et al.* (2002) found non significant effect of year on first greasy fleece yield in Muzaffarnagari sheep. Similarly, in Magra sheep, non-significant effect of year was reported by Dass *et al.* (2003) and Mehta *et al.* (2004) on first and second greasy fleece yield, respectively. Non-significant effect of the year on greasy fleece yield was reported by Dass *et al.* (2014) in Kashmir Merino sheep.

2.2.1.3 Effect of sex of lamb

Sex hormones that are released from gonads influence the animal's physiological system and are responsible for differences in body weights and wool yield in different sexes. The females have slower growth rate than males because of early maturing body and reach a smaller mature size due to effect of estrogen, which restrict the growth of long bones. Castration of rams results in increased growth rate resulting in higher body weight and higher wool yield as compared to females. Various workers have reported the significant effect of sex

Table 2.6: Reports showing significant effect of the sex of lamb on greasy fleece yield of lambs

Author (s)	Wool yield	Breed/genetic group
Singh and Kushwaha (1995)	GFY I	Bharat Merino
Sinha and Singh (1997)	GFY I	Muzaffarnagri
Tomar <i>et al.</i> (2000)	GFY I	Bharat Merino
Mandal <i>et al.</i> (2002)	GFY II	Muzaffarnagri
Sharma (2003)	GFY I	Malpura
Mehta <i>et al.</i> (2004)	GFY II	Magra
Nehra <i>et al.</i> (2005)	GFY I	Marwari
Dass, (2006)	GFY I, GFY II and GFY III	Pugal
Kumar <i>et al.</i> (2006)	GFY I	Avikalin
Arora <i>et al.</i> (2007)	GFY I	Jaisalmeri
Dass (2007)	GFY I, GFY II and GFY III	Pugal
Dass <i>et al.</i> (2008)	GFY I and GFY II	Marwari
Dixit <i>et al.</i> (2009)	GFY I	Bharat Merino
Chopra <i>et al.</i> (2010)	GFY I	Bharat Merino
Dixit <i>et al.</i> (2011)	GFY I	Bharat Merino
Narula <i>et al.</i> (2011)	GFY I and GFY II	Magra
Narula <i>et al.</i> (2012)	GFY I and GFY II	Marwari
Behdad <i>et al.</i> (2013)	GFY I	Bakhtiari
Akhtar <i>et al.</i> (2014)	GFY I and GFY II	Buchi
Gupta <i>et al.</i> (2015)	GFY I	Patanwadi
Khan <i>et al.</i> (2015)	GFY I	Rambouillet

of lambs and their observations and results are summarized in Table 2.6.
However, non-significant effect of the sex of lamb on second greasy fleece yield was observed by Singh and Kushwaha (1995) in Bharat Merino sheep. Sharma *et al.* (1999) observed non-significant effect of the sex of lamb on first, second and third greasy fleece yield in Nali sheep. Non-significant effect of the sex of lamb on first and second greasy fleece yield was reported by Gopal and Singh (2001) in Marwari sheep.

Tabbaa *et al.* (2001) and Mandal *et al.* (2002) also found nonsignificant effect of the sex of lamb on first greasy fleece yield in Nali sheep. Similarly, in Magra sheep, non-significant effect of sex of lamb was reported by Dass *et al.* (2003) and Mehta *et al.* (2004) on first greasy fleece yield. Kumar and Singh (2011) found non-significant effect of the sex of lamb on first greasy fleece yield in Chokla sheep. Non-significant effect of the sex of lamb on second greasy fleece yield was also reported by Dixit *et al.* (2011) in Bharat Merino sheep. Kumar *et al.* (2013) also reported non-significant effect of the sex of lamb on first greasy fleece yield in Chokla sheep.

2.2.1.4 Effect of season of birth

The reports regarding fixed significant effect of season of birth on greasy fleece yield at different clips is shown in Table 2.7.

However, few workers also reported non-significant effect of the season on greasy fleece yield. Mandal *et al.* (2002) reported non-significant effect of season on second greasy fleece yield in Muzaffarnagri sheep. Non-significant effect of season on first and second greasy fleece yield was reported by Poonia (2006) and Akhtar *et al.* (2014) in Munjal and Buchi breed of sheep, respectively.

Table 2.7: Reports showing significant effect of season on greasy fleece yield of lambs

Author (s)	Wool yield	Breed/genetic group
Sinha and Singh (1997)	GFY I	Muzaffarnagri
Tomar <i>et al.</i> (2000)	GFY I	Bharat Merino
Mandal <i>et al.</i> (2002)	GFY I	Muzaffarnagri

Sharma (2003)	GFY I	Malpura
Mehta <i>et al.</i> (2004)	GFY I and GFY II	Magra
Nehra <i>et al.</i> (2005)	GFY I	Marwari
Kumar <i>et al.</i> (2006)	GFY I	Avikalin
Singh <i>et al.</i> (2007)	GFY I	Corriedale
Arora <i>et al.</i> (2007)	GFY I	Jaisalmeri
Dixit <i>et al.</i> (2009)	GFY I	Bharat Merino
Dixit <i>et al.</i> (2011)	GFY I	Bharat Merino
Gupta <i>et al.</i> (2015)	GFY I	Patanwadi

Dixit *et al.* (2009) and Dixit *et al.* (2011) found non-significant effect of season on second greasy fleece yield in Bharat Merino sheep. Das *et al.* (2014) and Khan *et al.* (2015) also reported non-significant effect of season on first greasy fleece yield in Kashmir Merino and Rambouillet breed of sheep.

2.2.1.5 Effect of age at shearing

Lamb's age at shearing was found to have significant effect on greasy fleece yield as reported by various workers and is summarized below:

Tabbaa *et al.* (2001), Kumar *et al.* (2006) and Singh *et al.* (2007) reported significant effect of age at shearing on first greasy fleece yield in Awassi, Avikalin and Corriedale breed of sheep, respectively. Dixit *et al.* (2009) observed significant effect of age at shearing on first greasy fleece yield in Bharat Merino sheep. Significant effect of age at shearing on first greasy fleece yield in Bharat Merino sheep was also found by Chopra *et al.* (2010).

Dixit *et al.* (2011) observed significant effect of age at shearing on first greasy fleece yield in Bharat Merino sheep. Significant effect of age at shearing on first greasy fleece yield in Bakhtiari sheep was also found by Behdad *et al.* (2013).

However, Dixit *et al.* (2009) and Dixit *et al.* (2011) reported nonsignificant effect of age at shearing on second greasy fleece yield in Bharat Merino sheep.

2.2.2 Factors affecting the wool quality

The reports given by various workers regarding the factors affecting wool quality traits in sheep are given below:

2.2.2.1 Effect of sire

The information on effect of sire on wool quality traits is very scanty in literature. Dixit *et al.* (2009) observed significant effect of sire on staple length, fibre diameter amd medullation percentage in Bharat Merino sheep.

2.2.2.2 Effect of year/ period of shearing

Various workers have reported the significant effect of year on wool quality traits. Snyman (2000) observed significant effect of year on fibre diameter in Afrino sheep. Gopal and Singh (2001) and Dass and Singh (2002) found significant effect of year on fibre diameter, staple length, crimps, hetro fibres, hairy fibres and medullation percentage in Marwari sheep. Dass *et al.* (2003) also found significant effect of year on fibres and medullation percentage in Marwari sheep.

Significant effect of year on fibre diameter and percentage of pure, hetro and medullated fibres was reported by Nehra *et al.* (2005) in Marwari sheep. Poonia (2006) found significant effect of year on staple length and hetro fibres percentage in Munjal breed of sheep. Dass *et al.* (2008) found significant effect of year on fibre diameter, staple length, crimps, pure fibres, hetro fibres, hairy fibres and medullation percentage in Marwari sheep.

In Bharat Merino, significant effect of year on fibre diameter, staple length and medullation percentage was observed by Dixit *et al.* (2009), Chopra *et al.* (2010) and Dixit *et al.* (2011).

Narula *et al.* (2011) reported significant effect of year on staple length, crimp frequency, fibre diameter, hetro and hairy fibres in Magra sheep. Narula *et al.* (2012) also found significant effect of year on staple length, crimp frequency, fibre diameter and hetro fibres in Marwari sheep. Staple length

and fibre diameter were significantly affected by year as per the report of Khan *et al.* (2015) in Rambouillet breed of sheep.

However, few workers also reported non-significant effect of year on wool quality traits. Mehta *et al.* (2004) and Poonia (2006) observed non-significant effect of year on fibre diameter and percentage of pure and medullated fibres in Magra and Munjal breed of sheep, respectively. Narula *et al.* (2011) and Narula *et al.* (2012) found non-significant effect of year on medullation per centage. Non- significant effect of year on fibre diameter and staple length was reported by Dass *et al.* (2014) in Kashmir Merino sheep.

2.2.2.3 Effect of sex of lamb

The reports given by various workers regarding the significant effect of sex on different wool quality traits in sheep are shown in Table 2.8.

However, few workers also reported non-significant effect of sex on wool quality traits that are summarized in Table 2.9.

2.2.2.4 Effect of season of birth

Various workers have reported the significant effect of season on wool quality traits. Nehra *et al.* (2005) observed significant effect of season of birth on fibre diameter and percentage of pure and medullated fibres in Marwari sheep. In Bharat Merino sheep, Dixit *et al.* (2009) found significant effect of season on staple length and fibre diameter while Chopra *et al.* (2010) reported significant effect of season only on staple length.

Significant effect of season on fibre diameter and staple length was also found by Dixit *et al.* (2011), in Bharat Merino sheep. Das *et al.* (2014) reported significant effect of season only on staple length in Kashmir Merino sheep.

Non-significant effect of season on wool quality traits was also reported by few workers that are shown below:

Mehta *et al.* (2004) found non-significant effect of season on fibre diameter, pure and hetro fibres in Magra sheep. Nehra *et al.* (2005) also reported non-significant effect of season on hetro fibres in Marwari sheep. Dixit *et al.* (2009), Chopra *et al.* (2010) and Dixit *et al.* (2011) found non-significant effect of season on medullation percentage in Bharat Merino

sheep. In addition to medullation percentage, Chopra *et al.* (2010) reported non-significant effect of season on fibre diameter also in Bharat Merino sheep. Non-significant effect of season on staple length and fibre diameter was also reported by Khan *et al.* (2015) in Rambouillet breed of sheep.

		Breed/	
Author (s)	Wool quality	genetic group	
Snyman (2000)	Fibre diameter	Afrino	
Sharma <i>et al.</i> (2000)	Medullation percentage	Marwari & Nali	
Gopal and Singh	Staple length, Crimp,	Marwari	
(2001)	Hairy fibre		
Dass <i>et al.</i> (2003)	Staple length	Magra	
Mehta <i>et al.</i> (2004)	Pure fibre, Medullation percentage	Magra	
Dass <i>et al.</i> (2008)	Staple length, Crimp, Hairy fibre	Marwari	
Devendran <i>et al.</i>	Fibre diameter	Coimbatore	
(2008)			
Dixit <i>et al.</i> (2009)	Fibre diameter, Staple length	Bharat Merino	
Chopra <i>et al.</i> (2010)	al. (2010) Medullation percentage		
Dixit <i>et al.</i> (2011)	Dixit <i>et al.</i> (2011) Staple length, Fibre diameter		
Narula <i>et al.</i> (2011)	Crimp frequency	Magra	
Narula <i>et al.</i> (2012)	Fibre diameter	Marwari	
Behdad <i>et al.</i> (2013)	Staple length, True fibre,	Bakhtiari	
	Hetro fibre		

Table 2.8: Reports showing significant effect of sex of lamb on wool quality traits in different breeds of sheep

Table 2.9: Reports showing non-significant effect of sex on wool qualitytraits

Author (s)	Wool quality	Breed/ genetic group
Sharma <i>et al.</i> (2000)	Fibre diameter	Marwari & Nali
Dass and Singh (2001)	Fibre diameter, Hetro fibre, Medullation percentage	Marwari
Dass <i>et al.</i> (2003)	Fibre diameter, Crimp, Hetro fibre, Hairy fibre, Medullation percentage	Magra
Mehta <i>et al.</i> (2004)	Fibre diameter	Magra
Nehra <i>et al.</i> (2005)	Fibre diameter, Pure fibre, Hetro fibre Medullation percentage	Marwari
Dass (2006)Staple length, Crimp, Fibre diameter, Hetro fibre, Hairy fibre, Medullation percentage		Pugal
Dass (2007)Staple length, Crimp, Fibre diameter, Hetro fibre, Hairy fibre, Medullation percentage		Pugal
Dass <i>et al.</i> (2008)	ass <i>et al.</i> (2008) Fibre diameter, Hetro fibre, Medullation percentage	
Devendran <i>et al.</i> (2008)	Staple length, Crimp, Medullation percentage	Coimbatore
Dixit <i>et al.</i> (2009)	Medullation percentage	Bharat Merino
Chopra <i>et al.</i> (2010)	Fibre diameter, Staple length	Bharat Merino
Dixit <i>et al.</i> (2011)	Medullation percentage	Bharat Merino
Narula <i>et al.</i> (2011)	Staple length, Hetro fibre, Medullation percentage	Magra
Narula <i>et al.</i> (2012)	Staple length, Crimp, Hetro fibre, Hairy fibre, Medullation percentage	Marwari
Behdad <i>et al.</i> (2013)	Hairy fibre	Bakhtiari
Khan <i>et al.</i> (2015)	Staple length, Fibre diameter	Rambouillet

2.2.2.5 Effect of age at shearing

Lamb's age at shearing affects staple length and fibre diameter significantly as per the reports of Devendran *et al.* (2008) in Coimbatore sheep. Behdad *et al.* (2013) found significant effect of age at shearing on staple length and percentage of true and hetro fibres in Bakhtiari breed of sheep.

However, non- significant effect of age at shearing on the staple length and fibre diameter was found by Tabbaa *et al.* (2001) in Awassi sheep. Devendran *et al.* (2008) reported non-significant effect of age at shearing on crimp and medullation percentage in Bharat Merino sheep. Behdad *et al.* (2013) found non-significant effect of age at shearing on percentage of hairy fibres in Bakhtiari sheep.

2.3 Genetic and phenotypic parameters

To bring the desired change in genotypes, the precise estimates of phenotypic and genetic parameters, *viz.* heritability, phenotypic and genetic correlations among economic traits and breeding values of the traits are essential for making a decision regarding efficient breeding system and selection programme.

2.3.1 Heritability estimates

The potential for genetic improvement of a trait is largely dependent upon its heritability and its genetic correlations with other traits. The heritability of the traits varies from one population to another population and changes from time to time. In India, paternal half sib method (sire model like LSMLMW package of Harvey, 1990) is generally used for the estimation of heritability. However, animal model like WOMBAT gives more precise and accurate value of heritability by taking into account partitioning of the total heritability into its direct, maternal genetic and maternal permanent environmental components.

The reports given by various workers regarding the heritability estimates of wool yield and wool quality traits in sheep by sire model and animal model are summarized below:

2.3.1.1 Heritability estimates by sire model

The heritability estimates of wool yield and wool quality as estimated by various workers are presented as follows:

2.3.1.1.1 Heritability estimates for wool yield

The heritability estimates of first greasy fleece yield as estimated by various workers are presented in Table 2.10.

However, certain workers also reported heritability for second greasy fleece yield. Singh and Kushwaha (1995) and Sharma *et al.* (1999) estimated heritability for second greasy fleece yield as 0.18 ± 0.13 and 0.02 ± 0.14 in Bharat Merino and Nali sheep, respectively. Mandal *et al.* (2002) and Dixit *et al.* (2011) reported the heritability estimates as 0.38 ± 0.06 and 0.54 ± 0.13 for second greasy fleece yield in Muzaffarnagri and Bharat Merino sheep, respectively.

2.3.1.1.2 Heritability estimates for wool quality

Heritability estimates of wool quality traits as estimated by various workers are presented as follows:

Nimbalkar *et al.* (2005) and Dixit *et al.* (2011) found heritability estimates as 0.18 ± 0.15 and 0.76 ± 0.15 for staple length in Deccani and Bharat Merino sheep, respectively. Behdad *et al.* (2013) and Dashab *et al.* (2012) reported heritability estimates as 0.36 ± 0.33 and 0.48 ± 0.18 for staple length in Bakhtiari and Baluchi sheep, respectively. Khan *et al.* (2015) reported 0.15 \pm 0.05 as heritability estimate for staple length in Rambouillet breed of sheep.

Table 2.10: Reports showing heritability estimates for greasy fleece yield at first clip

Author (s)	GFY I	Breed/genetic group
Pannu (1994)	0.21	Marwari
Singh and Kushwaha (1995)	0.52±0.15	Bharat Merino
Sinha and Singh (1997)	0.15±0.07	Muzaffarnagri
Sharma (1998)	0.35 ± 0.08	Marwari
Singh <i>et al.</i> (1998)	0.51 ± 0.06	Marwari
Sharma <i>et al.</i> (1999)	0.57 ± 0.29	Nali
Tomar <i>et al.</i> (2000)	0.50±0.10	Bharat Merino
Joshi (2001)	0.70±0.15	Marwari
Mandal <i>et al.</i> (2002)	0.23±0.05	Muzaffarnagri
Nimbalkar <i>et al.</i> (2005)	0.11±0.17	Deccani
Nehra <i>et al.</i> (2005)	0.16±0.12	Marwari
Kumar <i>et al.</i> (2005)	0.24±0.08	Chokla
Ahmad <i>et al.</i> (2005)	0.41	Avikalin
Dixit <i>et al.</i> (2009)	0.54±0.13	Bharat Merino
Dixit <i>et al.</i> (2011)	0.54±0.13	Bharat Merino
Behdad <i>et al.</i> (2013)	0.09±0.39	Bakhtiari
Dashab <i>et al.</i> (2012)	0.19±0.08	Baluchi
Khan <i>et al.</i> (2015)	0.49±0.08	Rambouillet

Heritability estimates for fibre diameter were estimated by Nehra *et al.* (2005) and Dixit *et al.* (2011) as 0.22 ± 0.12 and 0.46 ± 0.13 in Marwari and

Bharat Merino breed of sheep, respectively. Dashab *et al.* (2012) and Khan *et al.* (2015) reported heritability estimates as 0.32±0.07 and 0.55±0.09 in Baluchi and Rambouillet sheep, respectively.

Sharma *et al.* (2000) estimated heritability for medullation percentage as 0.75 ± 0.35 in Marwari & Nali breed of sheep. Nehra *et al.* (2005) reported heritability estimates for percentage of pure and hetro fibres as 0.02 ± 0.10 and 0.03 ± 0.10 , respectively in Marwari sheep. Dixit *et al.* (2009) observed heritability estimate as 0.15 ± 0.10 for medullation percentage in Bharat Merino breed of sheep. Behdad *et al.* (2013) reported heritability estimate for percentage of pure fibres as 0.34 ± 0.38 in Bakhtiari sheep. Dashab *et al.* (2012) estimated heritability for percentage of pure, hetro and hairy fibres as 0.65 ± 0.44 , 0.16 ± 0.09 and 0.20 ± 0.08 , respectively, in Baluchi breed of sheep.

2.3.1.2 Estimation of heritability by animal model

Estimation of heritability by restricted maximum likelihood (REML) procedures fitting an animal model and ignoring or including maternal genetic or permanent environmental effects was carried out by various workers shown below:

2.3.1.2.1 Heritability estimates for wool yield

Reports available on sheep wool genetics highlighted the role of maternal effects governing the wool traits. Fogarty (1995) reported the heritability estimates for greasy fleece yield as 0.34 ± 0.03 and 0.36 ± 0.03 in different wool and dual purpose sheep, respectively. Snyman *et al.* (1996) estimated heritability for first greasy fleece yield as 0.20 in Merino sheep.

Bromley *et al.* (2000) reported estimates of permanent environmental effect of dam ranging from 0.08 to 0.17 for wool yield. Ahmad *et al.* (2005) and Kumar *et al.* (2005) estimated heritability for first greasy fleece yield as 0.11 and 0.10 \pm 0.06 in Avikalin and Chokla sheep.

Safari *et al.* (2005) estimated the direct heritability, maternal genetic and permanent environmental effect as 0.25 ± 0.06 , 0.08 ± 0.01 and 0.15 ± 0.09 , respectively, for greasy fleece yield in different wool breeds of sheep (average from diverse studies that included maternal effects in the model). However, for dual purpose breeds of sheep, the estimates were 0.31 ± 0.04 , 0.02 ± 0.01 and 0.11 ± 0.02 , for direct heritability, maternal genetic and permanent environmental effect, respectively. Safari *et al.* (2005) also reported highly variable permanent environmental effect for fleece weight in the wool. They concluded that for genetic evaluation of fleece weight, a model with direct animal and maternal genetic effects as well as an animal permanent environmental effect needs to be evaluated.

Swan *et al.* (2008) reported estimates of direct heritability, maternal genetic and permanent environmental effect as 0.43 ± 0.04 , 0.07 ± 0.02 and 0.05 ± 0.02 , respectively, from the best model for greasy fleece yield in Merino sheep. However, Mandal *et al.* (2009) reported non-significant influence of maternal genetic and permanent environmental effect on greasy fleece yield in Muzaffarnagri sheep.

Gowane *et al.* (2010a) estimated the heritability for first greasy fleece yield as 0.30 ± 0.00 and reported that the maternal permanent environmental effect accounted for 4% of the total phenotypic variation in greasy fleece yield in Malpura sheep; suggesting that maternal effects were not important and thus, may not be included for selection. For Bharat Merino sheep, there was no evidence of direct maternal effect for greasy fleece yield; however estimates of 0.26 ± 0.01 and 0.11 ± 0.03 for permanent environmental effect were observed by Gowane *et al.* (2010b) and Gowane *et al.* (2010c), respectively. Gowane *et al.* (2010c) reported heritability as 0.05 ± 0.03 for first greasy fleece yield in Bharat Merino sheep.

Di *et al.* (2011) reported estimates of direct heritability and maternal genetic effect as 0.14 ± 0.02 and 0.12 ± 0.04 , respectively, from the best model for greasy fleece yield in Chinese superfine Merino sheep. Ciappesoni *et al.* (2013) reported estimates of direct, maternal genetic and total heritability as 0.294, 0.158 and 0.275, respectively, from the best model for greasy fleece yield in Merino sheep.

2.3.1.2.2 Heritability estimates for wool quality

The information regarding estimation of heritability and maternal effects for wool quality traits using animal model is very scanty in literature. Fogarty (1995) estimated the heritability for fibre diameter as 0.51 ± 0.03 and 0.52 ± 0.03 in different wool and dual purpose sheep, respectively.

Naidoo *et al.* (2004) reported the heritability estimates for staple length and fibre diameter as 0.25 ± 0.04 and 0.61 ± 0.04 in Merino breed of sheep.

Safari *et al.* (2005) estimated the heritability for staple length, crimp frequency and fibre diameter as 0.46 ± 0.04 , 0.41 ± 0.03 and 0.59 ± 0.02 , respectively in different wool breeds of sheep while in dual purpose breeds the estimates were 0.48 ± 0.03 and 0.57 ± 0.05 for staple length and fibre diameter, respectively.

Swan *et al.* (2008) reported direct heritability estimates as 0.66 ± 0.02 and 0.54 ± 0.03 , for fibre diameter and staple length, respectively, in Merino sheep. Gowane *et al.* (2010b) studied wool quality parameters for Bharat Merino sheep and revealed non-significant effect of maternal influence on wool quality attributes.

Di *et al.* (2011) reported the direct genetic heritability estimates for staple length and fibre diameter as 0.22 ± 0.04 and 0.26 ± 0.05 , respectively in Chinese superfine Merino sheep. Ciappesoni *et al.* (2013) reported the direct genetic, maternal genetic and total heritability estimates for staple length as 0.399, 0.057 and 0.362, respectively; and for fibre diameter as 0.74, 0.06 and 0.56, respectively, from the best fitted model in Merino sheep.

2.3.2 Genetic correlations

Genetic correlations among different traits are mainly attributed to pleiotropic action of genes and their estimates are useful to know the correlated response in one character while selection is based on other character.

Sharma *et al.* (1999) and Mandal *et al.* (2002) found genetic correlation between greasy fleece yield at first and second shearing as >1 and 0.32 ± 0.19 in Nali and Muzaffarnagri sheep, respectively.

Nehra *et al.* (2005) estimated genetic correlation of greasy fleece yield with fibre diameter, pure fibres and hetro fibres as 1.09 ± 0.46 , -2.74 ± 6.00 and 0.46 ± 1.54 , respectively; fibre diameter with pure fibres and hetro fibres as -1.00 ± 3.25 and 0.39 ± 1.25 , respectively; and pure with hetro fibres as -1.03 ± 5.30 , in Marwari sheep.

Safari *et al.* (2005) estimated the genetic correlations of greasy fleece yield with staple length and fibre diameter as 0.44 and 0.36, respectively; and staple length with fibre diameter as 0.19 in different wool breeds of sheep. Safari *et al.* (2007) estimated genetic correlation between greasy fleece yield and fibre diameter as 0.27 \pm 0.02, in Merino sheep.

Dixit *et al.* (2011) found genetic correlation of greasy fleece yield at first shearing with second shearing, fibre diameter, staple length and medullation percentage as 0.16 ± 0.03 , 0.16 ± 0.03 , 0.20 ± 0.03 and 0.12 ± 0.03 , respectively, in Bharat Merino sheep.

Di *et al.* (2011) observed the genetic correlations of greasy fleece yield with staple length and fibre diameter as 0.21 and 0.60, respectively; and staple length with fibre diameter as 0.11 in Chinese superfine Merino sheep. Ciappesoni *et al.* (2013) estimated the genetic correlations of greasy fleece yield with staple length and fibre diameter as 0.35 ± 0.04 and 0.42 ± 0.04 , respectively; and staple length with fibre diameter as 0.09 ± 0.04 in Merino sheep.

Khan *et al.* (2015) estimated genetic correlation of greasy fleece yield with fibre diameter and staple length as -0.23 ± 0.13 and 0.05 ± 0.18 , respectively; and staple length with fibre diameter as -0.29 ± 0.17 , in Rambouillet sheep.

2.3.3 Phenotypic correlations

The correlation of phenotypic values, which can be directly measured, is the association between two traits. This is estimated by measurement of the two traits on an individual in the population.

Mehta *et al.* (1998) estimated phenotypic correlation of fibre diameter with staple length, number of crimps, pure, hairy and hetro fibres as 0.028, 0.563, - 0.846, 0.832 and 0.318, respectively; staple length with number of crimps, pure, hairy and hetro fibres as -0.230, 0.642, 0.133 and 0.0045, respectively; hetro fibres with crimp, pure and hairy as -0.050, -0.422 and 0.196; crimp with hairy fibres and hetro with hairy fibres as -0.688 and - 0.968, respectively, in Magra sheep.

Sharma *et al.* (1999) and Mandal *et al.* (2002) estimated phenotypic correlation between greasy fleece yield at first and second shearing as 0.140

and 0.089, in Nali and Muzaffarnagri sheep, respectively. Sharma *et al.* (2000) found phenotypic correlation between medullation percentage and fibre diameter as 0.55, in Marwari and Nali sheep. Nimbalkar *et al.* (2005) estimated phenotypic correlation between greasy fleece yield and staple length as 0.81 ± 0.03 , in Deccani sheep.

Nehra *et al.* (2005) estimated phenotypic correlation of greasy fleece yield with fibre diameter, medullation percentage, pure fibres and hetro fibres as 0.161 ± 0.04 , 0.08 ± 0.04 , -0.03 ± 0.04 and -0.09 ± 0.04 , respectively; fibre diameter with medullated fibres, pure fibres and hetro fibres as 0.60 ± 0.03 , -0.60 ± 0.03 and 0.03 ± 0.04 , respectively; and pure with medullated and hetro fibres as -0.80 ± 0.52 and -0.31 ± 0.04 , respectively, in Marwari sheep.

Safari *et al.* (2005) estimated the phenotypic correlations of greasy fleece yield with staple length and fibre diameter as 0.32 and 0.31, respectively; and staple length with fibre diameter as 0.19 in different wool breeds of sheep. Safari *et al.* (2007) estimated phenotypic correlation between greasy fleece yield and fibre diameter as 0.24 \pm 0.01 in Merino sheep.

Di *et al.* (2011) observed the phenotypic correlations of greasy fleece yield with staple length and fibre diameter as 0.18 and 0.12, respectively; and staple length with fibre diameter as 0.13, in Chinese superfine Merino sheep.

Dixit *et al.* (2011) found phenotypic correlation of greasy fleece yield at first shearing with second shearing, fibre diameter, staple length and medullation percentage as 0.13 ± 0.18 , 0.48 ± 0.18 , 0.24 ± 0.17 and 0.30 ± 0.29 , respectively, in Bharat Merino sheep. Khan *et al.* (2015) estimated phenotypic correlation of greasy fleece yield with fibre diameter and staple length as - 0.003 ± 0.02 and 0.009 ± 0.02 , respectively; and staple length with fibre diameter as - 0.03 ± 0.02 , in Rambouillet sheep.

2.4 Polymorphism of Keratin genes

Keratin proteins are the major components of wool and are responsible for most of their structural properties. The keratins can be divided into two groups: the keratin intermediate filament (KIF) proteins and keratin associated (KAP) proteins. Genetic differences at both KIF and KAP protein controlling loci may play an important role in determining phenotypes for different wool production and quality traits. However, the study regarding polymorphism of keratin genes that affects wool production and quality traits is very scanty in literature.

2.4.1 Polymorphism of Keratin intermediate filament type I (KIF- I) gene

Rogers *et al.* (1993) described the polymorphism associated with KIF-I gene in several sheep breeds. An RFLP was identified when the amplified DNA (480 bp) was cleaved with Msp I restriction enzyme. Comparison of fragment sizes revealed the polymorphism to be the result of the presence or absence of the Msp I restriction site beginning at nucleotide 159 of the PCR product. This resulted in 100 bp + 159 bp (Allele M) or 259 bp (Allele N) DNA fragments respectively. Both alleles had invariant DNA fragments of 126 bp and 95 bp.

Similar banding patterns were obtained by Arora *et al.* (2008) in native Indian sheep breeds. In indigenous sheep, an Msp I RFLP revealed two alleles (M and N) and three genotypes (MM, MN, NN). The Type 1 IF wool keratin allele M yielded two bands of 100 and 159 bp, and allele N gave one fragment of 259 bp. Invariant fragments of 126 and 95 bp were present in both the alleles. Arora *et al.* (2008) concluded that with respect to the PCR product size of 480 bp, the indigenous Indian sheep breeds were observed to be similar to European sheep breeds.

Liu *et al.* (2009) found polymorphism of KIF- I gene in cashmere goats. The amplified product (459 bp) on Hae III RFLP revealed two alleles (A and C) and three genotypes (AA, AC, CC). Genotypic pattern AA yielded bands at 204, 110, 102, and 43 bp; pattern CC gave fragments at 163, 110, 102, 43 and 41 bp; and pattern AC yielded bands at 204, 163, 110, 102, 43 and 41 bp.

The above results were further confirmed by Ahlawat *et al.* (2014) in Patanwari, Marwari and Dumba breeds of sheep. At locus KRT 1.2 of the gene, 3 genotypes, viz. MM, MN and NN with genotype frequencies of 0.74, 0.24 and 0.02; 0.54, 0.42 and 0.04; and 0.64, 0.36 and 0.00 for Marwari, Patanwadi and Dumba breeds, respectively. The overall genotypic frequencies at KRT 1.2 locus for MM, MN and NN were estimated as 0.64, 0.34 and 0.02 respectively. The overall allele frequencies for allele M and allele N were 0.81 and 0.19 respectively. The restriction fragments generated were of 159, 126 and 100 bp for MM genotype; 259, 159 and 100 bp for MN genotype; and 259 and 126 bp for NN genotype.

2.4.2 Polymorphism of Keratin associated proteins 11-1 (KAP 11- 1) gene

Keratin-associated proteins (KAPs) are a structural component of the wool fibre and form the matrix between the keratin intermediate filaments (KIFs). Variation in the KAP genes may affect the structure of KAPs and hence wool characteristics. While the KAP genes (or *KRTAP*s) have been identified in humans, only limited efforts have been made to fully understand the presence of nucleotide variation within those genes. To date, it has only been described for the KAP1 and KAP4 families and studies only undertaken in Caucasian and Japanese populations (Shimomura *et al.* 2002; Kariya *et al.* 2005; Rogers *et al.* 2006). In contrast, variation has been extensively looked for in ovine KAP genes, including KAP1, KAP3, KAP5, KAP6-KAP8, KAP11, KAP13 and KAP24 genes. This likely reflects the importance of wool in the production of apparel and interior textile products.

Parsons *et al.* (1993) studied polymorphism in KRTAP- 6 gene and identified RFLP using Bam HI enzyme. Two allelic polymorphic bands of 24.5 and 14.1 kb; and three rare polymorphic bands of 12.5, 10.2 and 7.6 kb were detected.

In the KAP1 family, Rogers *et al.* (1994b) described three variant sequences containing 13 SNPs and length variation (having between three to five repeats of a 30 bp sequence) for KRTAP1-1. Nine variant sequences containing 20 SNPs have been described for KRTAP1-3 by them.

In the KAP3 family, variation has only been revealed in KRTAP3-2 by McLaren *et al.* (1997). Two variants of ovine KRTAP3-2 detected by PCR-SSCP have been reported, but as no sequence information describing the nucleotide variation has been reported, the nature of the variation is currently unknown. McLaren *et al.* (1997) also reported two sequence variants in KRTAP7-1 using the restriction endonuclease Bgl II and four sequence variants using the restriction fragment Length Polymorphism (RFLP) analysis. No specific information on nucleotide sequence variation was given.

Itenge Mweza *et al.* (2007) used PCR-SSCP analysis to identify sequence variation in the KAP1.3 (formerly known as B2C) and K33 (formerly known as KRT 1.2) genes; whereas PCR- agarose gel electrophoresis was used to identify length polymorphism in the KAP 1.1 (formerly known as B2A gene). They reported three alleles at the KAP1.1 locus, nine alleles at the KAP1.3 locus and five alleles at the K33 locus of Merino sheep.

Nine variant sequences containing 14 SNPs have been reported for KRTAP1-4 by Gong *et al.* (2010a). In the KAP5 family, Gong *et al.* (2010b) five sequence variants have been described for ovine KRTAP5-4. There are six SNPs and one length polymorphism in this gene. Non-synonymous SNPs predominate and there is variation in copy number of a 30-bp repeat sequence encoding a cysteine-rich deca peptide "RPCCSQSSCC" in the C-terminal region. Either one or two copies of the repeat sequence are present in each variant.

Using PCR-stem loop conformational polymorphism (PCR-SLCP), Zhou *et al.* (2011) reported four sequence variants of ovine KRTAP24-1. Seven SNPs were described in ovine KRTAP24-1 and four of them are non-synonymous.

Gong *et al.* (2011a) described KRTAP6-1 to have three sequence variants that are comprised of three SNPs and a 57-bp insertion/deletion. Gong *et al.* (2011b) and Gong *et al.* (2011c) identified six and five sequence variants in ovine KRTAP11-1 and KRTAP13-3, respectively. There are five and four SNPs in these genes respectively, and four of the five SNPs in KRTAP11-1 are synonymous, while three of the four SNPs in KRTAP13-3 are non-synonymous. Gong *et al.* (2011d) found 11 variant sequences containing 10 SNPs for KRTAP1-2.

The SNPs described above in KRTAP1-1 and KRTAP1-4 were predominantly non-synonymous, whereas those described in KRTAP1-2 and KRTAP1-3 were predominantly synonymous. It should however be noted that the sequence variants described above for KRTAP1-1 have been detected by PCR and agarose gel electrophoresis. This approach is inadequate for detecting SNPs and thus the variation described to date for KRTAP1-1 may be an under-estimation of what actually exists in sheep. Further investigation using other nucleotide variation screening techniques is required to reveal the full extent of variation in this gene, if it exists.

Variation in KRTAP7-1 has been investigated by Gong *et al.* (2011e) who used PCR- SSCP to screen the entire coding region of KRTAP7-1 and reported two sequence variants resulting from one non-synonymous SNP.

In the KAP8 family, variation has been investigated in both KRTAP8-1 and KRTAP8-2 (Gong *et al.*, 2011e; Gong *et al.* 2014). Gong *et al.* (2011e) reported that KRTAP8-1 has five sequence variants containing four SNPs, whereas Gong *et al.* (2014) described that KRTAP8-2 has only two sequence variants containing one SNP. The majority of SNPs found in KRTAP8-1 are synonymous (Gong *et al.*, 2011e), while the sole SNP found to date in *KRTAP8-2* is located 21 bp upstream of the nominal TATA box sequence (Gong *et al.*, 2014). Gong *et al.* (2015) also reported 11 variant sequences containing 10 SNPs for KRTAP1-2.

In the KAP6 family, Zhou *et al.* (2015) described KRTAP6-1 to have three sequence variants that are comprised of three SNPs and a 57-bp insertion/deletion. Zhou *et al.* (2016) reported that KRTAP6-2 has six sequence variants containing five SNPs. Zhou *et al.* (2016) also detected five sequence variants for KRTAP6-3 that are comprised of three SNPs and a 45-bp insertion/deletion. As per the report of Zhou *et al.* (2016), KRTAP6-4 has three SNPs resulting in three sequence variants. Six sequence variants were identified by Zhou *et al.* (2016) for KRTAP6-3 that contains five SNPs and an 18-bp insertion/deletion. The SNPs found in KRTAP6-3 and KRTAP6-5 was predominantly non-synonymous, whereas synonymous SNPs predominated in KRTAP6-1, KRTAP6-2 and KRTAP6-4. The nature of the polymorphism did not

appear to coincide with the physical locations of the genes on the chromosome, but it was in some respects consistent with KRTAP6-1, KRTAP6-2 and KRTAP6-4 being located in the middle of a region that is flanked by KRTAP6-5 and KRTAP6-3.

In summary, variation has been found in all of the ovine KAP genes investigated to date. The apparent higher degree of variation found in sheep when compared to humans, is possibly due to a greater number of individuals having been screened. Genetic variation in human KAP genes could therefore potentially be significantly higher than previously thought based on comparison with ovine KAP genes, although this remains to be revealed.

2.6 Association of polymorphism of keratin genes with wool traits

There have been few studies describing associations between wool traits and variation in KIF and KAP genes.

Parson *et al.* (1994) reported that variation in a KAP6 gene was associated with Mean Fibre Diameter in medium wool Peppin Merinos. The KAP6 gene maps to ovine chromosome 1 in a chromosome region where Beh *et al.* (2001) detected a QTL affecting mean fibre diameter in medium wool Merinos. Allain *et al.* (2006) also detected a QTL on chromosome 1 for the "objectionable fibre content" (being defined as a large medulated fibres with a latticed medulla deficient in sulphur) in backcross Sarda × Lacaune sheep. Itenge-Mweza (2007a) reported an association between variation in KRTAP1-1 (KAP1-1) and wool yield in one half-sib family and with mean staple length and wool brightness in another half-sib family.

On chromosome 11, Roldan *et al.* (2010) did not find any QTL for mean fibre diameter, but instead they found a QTL for other wool traits including curvature and wool yield. Roldan *et al.* (2010) detected a QTL for wool weight, staple strength and coefficient of variation of fibre diameter.

Ahlawat *et al.* (2014) reported non-significant effect of variation due to different genotypes on staple length, fibre diameter and medullation percentage in Marwari, Patanwadi and Dumba breeds of sheep. The observed least square means for staple length, fibre diameter and medullation percentage for all the three genotypes (MM, MN, NN) were reported as 5.93 ± 0.29 , 6.20 ± 0.27 and 6.25 ± 0.74 ; 42.43 ± 1.33 , 43.03 ± 1.23 , 42.77 ± 3.43 ; and 77.48 ± 2.78 , 75.75 ± 2.58 and 88.21 ± 7.19 , respectively.

Wool crimp is thought to be affected by the composition of KAPs in the wool fibre. A recent report in Chinese Merino sheep by Wang *et al.* (2014) described an OAR11 QTL for crimp that is approximately 30 MB from the known KAP genes on that chromosome. They also described two chromosomes 1 QTLs for fibre diameter, but they are at least 100 MB from the known OAR1 KAP genes.

Recently, Zhou *et al.* (2015) reported that variation in KRTAP6-1 (KAP6-1) was found to be associated with variation in wool fibre diameter associated traits. An association between variation in KRTAP1-2 (KAP1-2) and Greasy Fleece Weight (GFW) and Clean Fleece Weight (CFW) was revealed by Gong *et al.* (2015), suggesting that KRTAP1-2 (KAP1-2) mainly affects wool weights in Merino sheep.

3. MATERIALS AND METHODS

The material and methods for the present study have been divided into following subheads:

3.1 Phenotypic and Genetic Aspect of Study

3.1.1 Source of Data

The data for the proposed work were collected from the records of the sheep research project under Network Project on Sheep Improvement, located at the Arid Region Campus of the Central Sheep and Wool Research Institute (ICAR- C.S.W.R.I), Bikaner.

This station was established in July, 1974 near village Beechwal on Bikaner-Sri Ganganagar highway approximately six kilometers away from the Bikaner city in Rajasthan state. The geographical location of the station is at an altitude of 234.84 meters above mean sea level on 28° 3' N Latitude and 37° 5' E Longitude.

The farm is spread over 636 hectares. The soil is sandy. The maximum temperature goes as high as 49° C during the month of May and June and falls to the level of 0° C during winter months. Low and erratic rainfall is a common feature with an annual precipitation of 260 millimeters.

3.1.2 History of the Flock

The research project was initiated in 1996 as an institute project of CSWRI. This project was converted into Network Project in 2013. The Magra sheep is being improved through selection since the starting of the project. At present, there are 300 breedable ewes in the flock.

3.1.3 Management and Feeding

All the sheep were maintained on natural pastures and allowed free range grazing. The pasture consisted primarily of annual grasses such as Aristida funcunilata (Lampla) and Cenchrus sagitarus (Bhurat); perennial grasses such as Lasiurus sindicus (Sewan), Dactyloctenium sindicum (Ganthia) and Cenchrus ciliarus (Anjan); legumes like Indigofera spp. (Bakaria), Tephrosis purpurea and Tribulus terrestris (Gokhru) and trees and shrubs like *Prosopis cineraia* (khejri), *Zizyphus* nummularia (Pala), Calligoneum polygonoides (Phog), Aerva Crotolaria burchea and pseudotomentosa, Cymbopogan Spp. Supplementary feeding was provided to the advance pregnant and lactating ewes and young lambs. Green fodder such as Avena sativa (Oats), Pennisetum typhoides (Bajra) and Lucerne were fed to the flocks according to their availability and dry hay was supplemented particularly during lean period when the grazing resources available in the pasture were depleted. All the sheep were allowed to graze from 8.00 AM to 6.00 PM daily except during summer months from April to September when split grazing during cooler hours of the day was observed from 6.00 AM to 12 Noon and 3.00 PM to 7.00 PM.

The animals were watered twice, once in morning and again in evening. The supplementary feeding of concentrate was carried out in evening hours as per schedule in Table 3.1.

3.1.4 Housing

The sheep were housed during night in sheds covered with asbestos sheets with open sides during winter and in open corrals made by chain link fencing during summer months. Space of about 1.5 sq. meters per sheep was provided.

Table 3.1: Schedule of supplementary feeding of concentrate

Class of animal	Concentrate	Period
	(g /day)	r enou

Pame	300	180 days (breeding	
Nams	500	season and lean period)	
		120 days (advanced	
Ewes	300	Pregnancy and	
		lactation)	
(I) Lambs of 15-90 days age	ad libitum	75 days	
(II) Lambs of 91-180 days	300	aveb 00	
age	500	90 uays	
(III) Lambs of 181-365 days	250	180 davs	
age	200	100 days	

3.1.5 Shearing

Until 2008, the shearing of animals was carried out twice a year in March and August by hand scissors. From 2009, the shearing was done thrice a year. The first shearing was done at the age of approximately six months. The sheep were dipped in clean water before shearing.

3.1.6 Mating Programme

The breeding season generally commenced towards the mid of August and continued for 2-3 oestrus cycles (up to beginning of November). However, a minor season of mating was also executed in the month of March-April to augment the more lambing per year. Accordingly, two season of lambing were observed in the data. The ewes in heat were detected both in morning and evening by teaser rams. The ewes showing oestrus were mated randomly to breeding rams once during oestrus cycle and their identification number were noted. Repeat breeders were again mated to rams in subsequent cycles randomly within selection line. The mating was continued for three oestrus cycles.

3.1.7 Health Cover

Emphasis was laid on preventive measures rather than curative therapy. The prophylactic measures such as vaccination, deworming,

dipping and hygienic measures like dusting, spraying, disinfection of sheds, watering channels, feeding troughs and protection of lambs against inclement weather conditions and prophylactic antibiotic treatment of lambs were implemented. The animals were vaccinated against sheep pox once a year. All the animals were protected against enterotoxaemia and other clostridial infections. Anthelmentic drenching of all the animals was carried out mostly once a year or as per the requirement. Coccidiostats to young lambs were given in drinking water. Post shearing dipping with organophosphorous compounds was carried out.

3.1.8 Collection of Data

The data used in the present study were collected over a period of 15 years from 2000-2014 from the database of Magra sheep, maintained at Arid Region Campus of Central Sheep and Wool Research Institute, Dist. Bikaner, Rajasthan. The following information was recorded:

- i) Animal No.
- ii) Sire No.
- iii) Dam No.
- iv) Dam's age at shearing
- v) Period of shearing
- vi) Sex
- vii) Season of birth

Criteria		GFY I	GFY II	GFY III
	P1 (2000-2002)	349	247	-
	P2 (2003-2005)	574	424	-
Period of shearing	P3 (2006-2008)	534	376	-
	P4 (2009-2011)	703	685	401
	P5 (2012-2014)	713	610	378
Sex of	Male	1447	1121	360
lamb	Female	1426	1221	419
Season of birth	1 st	2273	1812	381
	2 nd	600	530	398

Table 3.2: Frequency distribution on the basis of period ofshearing, sex and season of birth for wool production traits

Table 3.3: Frequency distribution on the basis of period ofshearing, sex and season of birth for wool quality traits

Criteria		SL	NC	FD	PURE	HET	HAIRY	MED
	P1 (2000- 2002)	309	309	309	309	309	309	309
Deried	P2 (2003- 2005)	378	378	378	378	378	378	378
of	P3 (2006- 2008)	421	421	421	421	421	421	421
snearing	P4 (2009- 2011)	576	576	576	576	576	576	576
	P5 (2012- 2014)	389	389	389	389	389	389	389
Sex of	Male	1142	1142	1142	1142	1142	1142	1142
lamb	Female	931	931	931	931	931	931	931
Season	1 st	1617	1617	1617	1617	1617	1617	1617
of birth	2 nd	456	456	456	456	456	456	456

viii) Wool production traits *viz.,* greasy fleece yield at 1st, 2nd and 3rd shearing.

 ix) Wool quality traits *viz.*, staple length, crimp frequency, fibre diameter, pure fibres, hetro fibres, hairy fibres and medullation percentage.

The frequency distribution of data on the basis of period of shearing, sex and season of birth for different traits under study are given in Table 3.2 and 3.3. The data were divided into five periods of three years each.

3.1.9 Standardization of Records

The animals with known pedigree and complete records on all target traits, viz. wool production traits *viz.*, greasy fleece yield at 1st, 2nd and 3rd shearing, and wool quality traits *viz.*, staple length, crimp frequency, fibre diameter, pure fibres, hetro fibres, hairy fibres and medullation percentage were considered for the present study. The sires with less than 4 progenies were excluded in the analysis.

3.1.10. Statistical Analysis

3.1.10.1. Estimation of performance of wool traits along with genetic and non-genetic factors affecting them

The data were adjusted for the effect of non-genetic factors viz. sex, season of birth and period of shearing as fixed effects and lamb's age at shearing as a covariate. The data were analyzed by the Least squares procedure of fitting constants using LSMLMW programme (Harvey, 1990). The model that was employed to examine the effect of genetic and non-genetic factors on various wool production and quality traits is as follows:

$$Y_{ijklm} = \mu + a_i + B_j + C_k + D_l + b (DA_{ijkl} - DA) + e_{ijklm}$$

Where,

 Y_{ijklm} = Performance record of the mth progeny of ith sire, jth period, kth sex and lth season

 μ = Overall population mean

ai = Effect of ith sire

 B_j = Effect of jth period of shearing

 $C_k = Effect of k^{th} sex$

 $D_I = Effect of I^{th} season of birth$

b ($DA_{ijkl} - DA$) = The regression of the trait on age at shearing.

 e_{ijklm} = Random error NID(0, σ^2).

3.1.10.2 Estimation of Genetic and Phenotypic Parameters

The genetic and phenotypic parameters *viz.,* heritability, genetic correlation and phenotypic correlation were estimated both by sire model i.e., model 2 of LSMLMW programme (Harvey, 1990), and by animal model i.e., WOMBAT programme (Meyer, 2007).

3.1.10.2. Estimation of Genetic and Phenotypic Parameters by Sire Model

3.1.10.2.1. Estimation of Heritability

Paternal half sib correlation method given by Becker (1968) was used to estimate the heritability of different traits. The sires with less than four progeny were excluded for the estimation of heritability. The model for estimating the heritability is:

$$Y_{ij} = M + S_i + e_{ij}$$

Where,

Y_{ij} = Observation of the jth progeny of the ith sire

M = Overall mean

 S_i = Random effect of the ith sire NID (0, σ^2_s)

 e_{ij} = Random error NID (0, σ^2_e)

The analysis of variance for obtaining the between sire and within sire components of variance needed for computing the heritability estimates was carried out as per the procedure given in the Table 3.4.

Table 3.4: Analysis of variance for estimation of heritability by siremodel

Source of variation	D.F	M.S.S.	E.M.S
Between sire	s - 1	MS₅	σ^2_w + k σ^2_s
Progeny within sire	N – s	MSw	σ^2_w

Where,

K= 1 / (s-1) {N- ($\sum n_i^2$ / N)} = weighted number of progeny per sire

s = total number of sire

 $n_i = no.$ of progeny of ith sire, and

N= total no. of progeny (N = $\sum n_i$)

The sire component of variance was obtained as,

$$\sigma^{2}{}_{s} = \frac{MS_{S} - MS_{W}}{K}$$

And the heritability (h²) was computed by the following formula,

$$h^2 = 4t = 4 \sigma_s^2 / (\sigma_s^2 + \sigma_w^2) = \sigma_A^2 / \sigma_p^2$$

Where,

 σ^{2}_{s} = sire component of variance

 σ^2_w = within sire component of variance

 σ^{2}_{A} = additive genetic variance

 σ^{2}_{p} = total phenotypic variance

Standard Error of Heritability

The standard error of heritability was estimated using the formula given by Swinger *et al.* (1964), as follows:

S.E. $(h^2) = 4 S \sqrt{\{[2(N-1)(1-t)^2(1 + (K-1)t)^2] / [K^2(N-s)(s-1)]\}}$

Where,

N = number of observations,

t = intra-class correlation,

s = total number of sires and

K = weighted number of progenies per sire

$$K = \{ [1/(s - 1)] [N - (\Sigma n_i^2) / N] \}$$

3.1.10.2.2. Estimation of Genetic Correlations

The genetic correlation is the measure of the degree of association between the two traits at the genetic level. The choice of the method however depends upon the kind and nature of available data. In the present study, the genetic correlations were estimated as the ratio of the genetic covariance between the two traits to the square root of the product of the genetic variances of the two traits by using the formula given below:

$$r_{g(XY)} = \text{Cov } S_{XY} / \sqrt{[(\sigma^2 s_X) (\sigma^2 s_Y)]}$$

Where,

X and Y are traits of the same individual,

Cov S_{XY} = Sire component of covariance between traits X and Y

 σ^2_{SX} and σ^2_{SY} = Sire components of variance for traits X and

Y, respectively

Standard Error of Genetic Correlation

The standard error of genetic correlation was calculated by the following formula:

S.E.
$$(r_g) = [(1-r_g^2) / \sqrt{2}] * \{\sqrt{[SE(h_x^2) SE(h_y^2)]} / \sqrt{[(h_x^2) (h_y^2)]}\}$$

Where,

 r_g = the estimate of genetic correlation between traits X and Y

 h^{2}_{x} and h^{2}_{y} = the estimates of heritability of the two traits X

and Y, respectively

S.E h_x^2 and S.E h_y^2 = the standard errors of the heritability of

the two traits X and Y, respectively.

The statistical significance of genetic correlation was tested using the 't-test'.

3.1.10.2.3. Estimation of Phenotypic Correlations

The phenotypic correlation is the measure of the degree of association between the observed values of the two traits measured on the same animal. Phenotypic correlation was estimated by using the following formula:

$$r_{p}(xy) = \frac{Cov_{s}(xy) + Cov_{e}(xy)}{\sqrt{\{[\sigma^{2}_{s}(x) + \sigma^{2}_{e}(x)] [\sigma^{2}_{s}(y) + \sigma^{2}_{e}(y)]}}$$

Where,

Covs (xy) = Sire component of covariance between traits X and Y Cove (xy) = Error component of covariance between traits X and Y σ^{2}_{e} (x) and σ^{2}_{e} (y) = Error components of variance for traits X and Y, respectively.

Standard Error of Phenotypic Correlation

The standard error of phenotypic correlations can be calculated as:

Where,

 $r_{p(XY)}$ = Phenotypic correlation between the traits X and Y in the

same individual

N - 2 = Degree of freedom

The statistical significance of correlations was tested by using the't-test'.

3.1.10.2. Estimation of Genetic and Phenotypic Parameters by Animal Model

For different wool traits, (co) variance components along with the genetic and phenotypic parameters i.e. heritability (h^2), genetic correlation (r_G) and phenotypic correlation (r_p) was estimated using the WOMBAT programme (Meyer, 2007) by fitting an animal model throughout. Maternal genetic and permanent environmental effects will be taken into account by including appropriate random effects into the model of analysis (Meyer, 1989).

Six different single traits linear models as described by Meyer (1992) that accounts for the direct and maternal effects, allowing for and ignoring genetic covariance between direct and maternal effects were fitted initially as follows:

$$Y = X\beta + Z_a a + \epsilon \tag{1}$$

$$Y = X\beta + Z_aa + Z_mm + \varepsilon \text{ with Cov } (a_m, m_o) = 0$$
(2)

$$Y = X\beta + Z_aa + Z_mm + \varepsilon \text{ with Cov } (a_m, m_o) = A\sigma_{am}$$
(3)

$$Y = X\beta + Z_a a + Z_c c + \epsilon$$
(4)

$$Y = X\beta + Z_aa + Z_mm + Z_cc + \varepsilon \text{ with Cov } (a_m, m_o) = 0$$
 (5)

$$Y = X\beta + Z_aa + Z_mm + Z_cc + \varepsilon \text{ with Cov } (a_m, m_o) = A\sigma_{am}$$
 (6)

Where,

Y = the vector of record

 β , a, m, c, and ϵ = vectors of fixed, direct additive genetic, maternal additive genetic, permanent environmental effects of the dam, and residual effects, respectively.

X, Z_a , Z_m , and Z_c = incidence matrices that relate these effects to the records

A = the numerator relationship matrix between animals

 σ_{am} = the covariance between additive direct and maternal genetic effects.

Assumptions for variance (V) and covariance (Cov) matrices involving random effects were:

$$V(a) = A\sigma_a^2$$
$$V(m) = A\sigma_m^2$$
$$V(c) = I\sigma_c^2$$
$$V(e) = I\sigma_e^2$$
$$Cov (a,m) = A\sigma_{am}$$

I represents identity matrix; σ_a^2 , σ_m^2 , σ_c^2 , σ_e^2 are additive genetic variance, additive maternal, maternal permanent environmental and residual variances, respectively. The direct-maternal correlation (r_{am}) was obtained for all the traits under analysis.

Maternal across year repeatability for ewe performance was calculated for all the traits as follows:

$$t_m = (\frac{1}{4})h^2 + m^2 + c^2 + r_{am}\sqrt{m^2\sqrt{h^2}}$$
; (Al-Shorepy, 2001)

The total heritability (h^2_t) , was calculated using the following formula:

$$h^{2}_{t} = (\sigma_{a}^{2} + 0.5 \sigma_{m}^{2} + 1.5\sigma_{am}) / \sigma_{p}^{2}$$
; (Willham, 1972)

The most appropriate model for each trait was selected based on log likelihood ratio test (Meyer, 1992). Significance of an effect will be tested at p<0.05 by comparing the differences in log likelihoods (-2 log L) with values for a chi square distribution with degrees of freedom equal to the differences in the number of (co)variance components fitted for the two models. The model with fewest random terms was chosen where log-L values did not differ significantly. Subsequently, a series of bivariate animal model analysis will be carried out in order to estimate genetic and phenotypic correlations between the traits. Estimates from single trait analysis were used to obtain starting values for bivariate analysis.

3.2 Molecular Aspect of Study

3.2.1 Experimental Animals

Whole blood samples were collected from 162 animals of Magra sheep maintained at Central Sheep and Wool Research Institute (C.S.W.R.I), Arid Region Campus, Beechwal, Bikaner.

3.2.2 Equipments

DNA Thermal Cycler (Chino Scientific Instrument Mfg); Alphaimager Gel Documentation System (Chino Scientific Instrument Mfg); Refrigerated Micro Centrifuge (Eltek), Submarine Gel Electrophoresis (Genaxy); System Deep freeze (Remi); Electrophoresis power supply (Sebia); PAGE, Microcentrifuge (Genaxy); Microwave (Samsung); Digital balance (Adaie Dutt); Vortex mixture (Chino Scientific Instrument Mfg); Autoclave; Water bath; Incubator; and Rapid dry system (Atto); Micro pipettes- p10, p200,

p500 and p1000 (eppendorff/ Finni pipette) present at Molecular genetics laboratory of the department were used.

3.2.3 Chemicals

Agarose (Genei), Ethidium Bromide (SISCO), 6X Loading dye (Genei), Sodium chloride (Qualigenes), Magnesium chloride (Qualigenes), Tris base (SISCO), Sodium acetate (Qualigenes), Ethylene dichloride tetra acetic acid (EDTA) (SISCO), Xylene cyanol (S.D. fine chem. Ltd.). Bromo-phenolblue (SISCO).

3.2.4 Kit and Other Chemicals

Genomic DNA Isolation Kit (Himedia), PCR amplification Kit (Promega Ltd.), dNTP (Promega), Synthetic oligonucleotide primers (Merck Ltd.), Taq DNA buffer (Promega Ltd.), Taq DNA Polymerase (Promega Ltd.), *Mspl* Restriction enzyme (Merck).

3.2.5 Collection of Blood Samples

Blood sample was collected from each animal by jugular vein puncture. About 2-3 ml of venous blood was collected in a 5 ml vaccutainer tube containing EDTA as an anticoagulant under sterile conditions. After collection of blood, the vials were shaken gently to facilitate thorough mixing of blood. The vials were then kept immediately in ice box containing ice and gel cool pack and transported to the laboratory immediately. After reaching to laboratory, the samples were stored at -20° C. Processing of the samples for DNA extraction was performed on the same day of sample collection.

3.2.6 Extraction of Genomic DNA

Genomic DNA was extracted from blood by Blood Genomic DNA Purification Kit supplied by HIMEDIA Ltd. Various steps followed are as follows:

 The blood samples were taken out of ice box and were thawed at room temperature.

- (ii) 200 µl of the fresh whole blood was taken in a 2.0 ml collection tube.
- (iii) 20 µl of the Proteinase K solution was added into the above collection tube containing blood. The tube was vortexed (10-15 seconds) to ensure thorough mixing of the enzyme.
- (iv) 20 μl of RNase A solution was added. Vortexing (10-15 seconds) was done to ensure thorough mixing of the enzyme and incubated for 2 minutes at room temperature.
- (v) Lysis reaction-200 µl of the lysis solution was added to the sample and vortexed thoroughly for a few seconds to obtain a homogenous mixture. The mixture was incubated at 55°C for 10 minutes.
- (vi) Preparing for binding to the spin column 200 µl of ethanol was added to the lysate obtained from step V and mixed thoroughly by gentle pipetting for 5-10 seconds.
- (vii) Loading lysate in Hi Elute mini prep spin column- The entire lysate obtained from step VI was transferred into Hi Elute mini prep spin column. Centrifuging was done at 10,000 rpm for 1 minute. The flow-through liquid was discarded and the column was placed in a same 2.0 ml collection tube.
- (viii) Prewash- 500 µl of prewash solution was added to the Hi Elute mini prep spin column and centrifuged at 10,000 rpm for 1minute. The flow-through liquid was discarded and the same collection tube with the column was re-used.
- (ix) Wash-500 µl of wash solution was added to the column and centrifuged at 13,000 rpm for 3 minutes. The flow through liquid was discarded and the column was placed in the same collection tube and it was centrifuged for an additional one minute at 13,000 rpm to remove traces of wash solution. The
collection tube was discarded and the column was placed in a new uncapped 2.0 ml collection tube.

- (x) DNA Elution-100 µl of the elution buffer was directly added into the column without spilling to the sides and incubated for 1 minute at room temperature (15-25°C). Centrifuging was done at 10,000 rpm for 1 minute to elute the DNA.
- (xi) The eluate was transferred to a fresh capped 2 ml collection tube and stored at -20°C till further use.

3.2.7 Checking the Quality of DNA

The genomic DNA isolated from the blood samples was checked for quality, purity and concentration. Only the samples with good quality of DNA were used for further analysis.

Horizontal submarine agarose gel electrophoresis was carried out to check the quality of genomic DNA using 1.2 % agarose.

At the start, the gel casting tray was prepared by sealing it's both end with adhesive tape and then the comb was set over it in a way to keep a gap of at least 0.5 mm between the tips of comb teeth and floor of the casting tray, so that the wells got completely sealed by agarose.

Subsequently, 1.2% agarose suspension in 1 X TBE buffer was made and heated on in microwave until the agarose was completely melted and dissolved to give a clear transparent solution. After cooling it at 60° C, ethidium bromide (10 mg/ml) @ 2µl per 25 ml of agarose solution was added to a final concentration of 0.5 µg/ml and was mixed gently.

The agarose solution was poured into the sealed casting tray. The gel was prepared to about 4 mm thickness. The agarose gel was allowed to set completely at 4^o C temperature before the comb was gently removed. The adhesive tape was also detached and gel casting platform was submerged in the electrophoresis tank containing 1 X TBE buffer.

For loading the samples, 5 μ l DNA sample was mixed with 1 μ l of 6 X gel loading dye and was loaded into the well with the help of microtips. A marker DNA was also run in one of well. Electrophoresis was performed at 70 volt for 1 hrs. Once the electrophoresis was over, the gel was visualized under UV trans-illuminator and documented by photography. DNA sample showing intact bands were used for further analysis.

The concentration and purity of DNA was checked by nanospectrophotometer. The samples showing 360/380 absorbance ratio between 1.7-1.9 and concentration above 30 ng/µl were used for further analysis.

3.2.8 PCR Amplification of the Genes

From the purified genomic DNA, the KIF type-I gene and KAP11-1 gene fragments were amplified using two different sets of primers (forward and reverse) by using standard PCR protocols.

3.2.8.1 Designing of PCR Primer

Primers were designed from gene sequence for sheep (GenBank accession No. M_23912) for KIF type-I gene; and from mRNA sequence (GenBank accession No. NM_001080740) for KAP11-1 gene using Primer 3.0 software. The primer sequences used for the polymorphism study of KIF type-I gene and KAP11-1 gene are shown in Table 3.5. Primers were synthesized by Integrated DNA technologies (Coralville, IA, USA).

3.2.8.2 PCR Components for Each Reaction

The amplification for both the genes were performed in a final volume of 25 μ l, containing 4 μ l DNA template, 0.5 μ l each primer, 1.0 μ l dNTPs, 0.5 μ l *Taq* DNA polymerase, 5 μ l 5X reaction buffer, 1.5 μ l

MgCl₂ and 12 μ l nuclease free water (Details of PCR components are given in Table 3.6).

3.2.8.3 Protocol for PCR Amplification

At first, a PCR master mixture, containing all the reaction components except genomic DNA, was prepared in ice under sterile condition. Care was taken to add *Taq* DNA polymerase at the end of preparation. After addition of all the components, the master mix was mixed gently, followed by spinning by table top micro centrifuge. Then, 21μ I of master mix was added to each pre labelled PCR tubes (eppendorff tube) of 0.2 ml capacity. Finally, 4μ I of good quality genomic DNA was added to each tube. The contents of tube were mixed gently and spinned at 9000 rpm at 10 sec. Finally, the PCR tubes were arranged in a pre-programmed thermo cycler. PCR products obtained, after the completion of the programme, were kept at -20 °C in refrigerator until further processing.

3.2.8.4 PCR Programme

Various combinations of reaction chemicals were tried to optimize the concentration of each component. The PCR parameters, viz. annealing temperature and cycling conditions were optimized to obtain a specific amplified product in sufficient quantity and best quality. The standardized programme followed for amplification of KIF type I and KAP 11-1 gene are given in Table 3.7 and 3.8, respectively. Table 3.5 Primer sequences used to amplify Keratin genes inMagra sheep

Primer	Forward and Reverse Sequence (5' to 3')	Expected product size (bp)
KIF type-I	Forward: 5' CAC AAC TGT GGC TTG GTG AAC TTG 3'	480
gene	Reverse: 5' CTT AGC CAT ATC TCG GAT TCC CTC 3'	400
KAP11-1	Forward: 5' TGC ATC TCT CAA CCA GCA C 3'	532
gene	Reverse: 5' TGG AAT CTT GAT TCA CTC ATG 3'	552

Table 3.6 PCR components for each reaction for all primers.

Sr. No	PCR component	Volume added per sample
1.	5X PCR assay buffer (Mg-free)	5 µl
2.	25 mM MgCl ₂	1.5 µl
3.	dNTPs mix (10mM)	1 µl
4.	Primer Forward (F) (10 picomoles/ µI)	0.5 µl
5.	Primer Reverse (R) (10 picomoles/ µl)	0.5 µl
6.	Taq DNA polymerase (5 units/ μι)	0.5 µl
7.	Template DNA	4 µl
8.	DNAase free MiliQ water (Nuclease free water)	12 µl
Total Volume		25 µl

Step	Temperature Time		No. of cycles	
I. Initial	95°C	5 minutes	One	
Denaturation				
II. Cycle				
(i) Denaturation	94°C	45 seconds	Over all total	
(ii) Annealing	58°C	45 seconds	40 cycles	
(iii) Synthesis	72°C	1 minute		
III. Final extension	72°C	10 minutes	One	
IV. Holding	4°C			

Table 3.7 PCR conditions for amplification of KIF type I gene in Magra sheep

Table 3.8 PCR conditions for amplification of KAP 11-1 gene inMagra sheep

Step	Temperature	mperature Time	
I. Initial	95°C	5 minutes	One
Denaturation			
II. Cycle			
(i) Denaturation	94°C	45 seconds	Over all total
(ii) Annealing	53.5°C	45 seconds	40 cycles
(iii) Synthesis	72°C	1 minute	
III. Final extension	72°C	10 minutes	One
IV. Holding	4°C		

3.2.8.5 CHECKING OF THE AMPLIFIED PRODUCT

PCR amplified DNA were analyzed by analytical agarose gel electrophoresis as per the procedure described by Sambrook and Russel (2002). Appropriate quantity of agarose (analytical grade) was boiled in 30ml of 1X TBE buffer to obtain uniform molten agarose (of desired 2% for KIF type I and 1% for KAP 11-1 amplicons) which was cast in appropriate gel-casting tray fitted with acrylic comb and left for setting. Prior to casting the gel, the molten agarose was allowed to cool to about 50°C after which ethidium bromide was added to make a final concentration of 0.5 µg/ml and mixed thoroughly. The acrylic comb was carefully removed after the gel had set perfectly. The tray with gel was then transferred to and submerged in an electrophoresis tank containing 1X TBE buffer. DNA to be analyzed was mixed with appropriate volume of 6X DNA loading dye and charged into wells alongside DNA molecular weight marker. Electrophoresis was carried out at 90 volt until the tracking dye (6X loading dye) had just passed out of the gel. The DNA bands were visualized under UV illuminator and documented. The molecular sizes of the DNA bands were analyzed in relation to molecular weight marker.

3.2.9 Detection of Genetic Variation

Genetic variation of KIF type-I gene was detected by PCR-RFLP assay using Msp I restriction enzyme.

Genetic variation of KAP11-1 gene was detected by PCR-SSCP assay.

3.2.9.1 Detection of Genetic Variation in KIF Type I Gene by Restriction Fragment Length Polymorphism (RFLP)

The PCR amplified product of KIF type I gene was cleaved by Msp I restriction enzyme at 37 °C for 16 hrs. The RE digested products were electrophoresed in 8% non denaturing polyacrylmide gel. The program was run at 90 volt for 2-3 hours at room temperature in 1 X TBE buffer. The genotypic patterns were visualised by ethidium bromide staining.

3.2.9.2 Detection of Genetic Variation in KAP 11-1 Gene by Single Strand Conformational Polymorphism (SSCP)

The single strand conformation polymorphism detection was done using Polyacrylamide gel electrophoresis (PAGE). For detecting SSCP, 7% native PAGE was run in Hoefer SE 600 series electrophoresis unit. The unit was assembled as given in instruction manual. The glass plates measuring 18 x 16 cm were cleaned thoroughly with mild detergent under tap water, rinsed with distilled water and allowed to dry. If required wiped with ethanol to remove any grease spots and allowed to dry. The plates were adjusted on the gel caster with 1.5 mm spacers using screws and checked for any leakage using distilled water. 40 ml of 7% polyacrylamide gel solution was prepared (after appropriate optimization) with the components given in Table 3.9 (Sambrook and Russel, 2002).

The gel solution was gently poured in between the glass plates and comb was set. The gel was allowed to polymerize for 30-60 minutes without any disturbance. The comb was removed carefully and the wells were washed with 0.5 X TBE buffer. The gel was clammed with a cam operated system provided in the unit to upper buffer chamber and the lower chamber tank and upper buffer chamber was filled with cold 0.5 X TBE buffer.

Proper amount of sample was aliquoted into separate tubes and an equal volume of 2 X SSCP gel loading dye (98% formamide, 10 mM EDTA, 0.025% bromophenol blue, 0.025% xylene cyanol) was added to it. Prior to loading, the samples were denatured at 95°C for 5 min and then rapidly cooled on wet ice for around 10-15 minutes. Finally, the samples were loaded into the wells.

Table 3.9 Composition of 7% Polyacrylamide gel for detection ofpolymorphism of KAP11-1 gene

Sr. Component V	Volume
-----------------	--------

No.		
1.	Acrylamide and N', N', N', N' Bis-acrylamide	6 ml
	(37.5:1)	
2.	5XTBE	8 ml
3.	Sterilized distilled water	26 ml
4.	10% Ammonium per sulphate	360 µl
5.	TEMED	30 µl

The electrodes were connected appropriately to the electrophoresis power supply and the program was run at 200 volt for 10-12 hours at 10°C in 0.5 X TBE buffer. After the run was completed the glass plates were retrieved from the assembly and very carefully apart those with the help of scale provided in the unit. The gel still attached to one of the glass plate was carefully transferred to container having ethidium bromide solution and rocked gently to remove gel from glass plate. The gel was stained for about 15-20 minutes with gentle shaking. The gel was analyzed under UV light and documented by gel-documentation system.

3.2.10 Estimation of Genotypic and Gene Frequencies

The genotypes were detected by the RFLP and SSCP pattern of each sample in the gels. The gene and genotypic frequencies were estimated by standard procedure (Falconer and Mackey, 1998).

Total no. of individuals of a particular genotype Genotype frequency = ------Total no. of individuals of all genotype

Gene frequency = $D + \frac{1}{2} H$

Where,

D= No. of homozygotes for a particular allele in total

samples

H= No. of Hetrozygotes in total samples

N= No. of Animals

Testing of the population for Hardy Weinberg equilibrium was done by Chi-squares test using PopGene32 software (Yeh *et al.*, 2000).

3.2.11 ASSOCIATION OF POLYMORPHISM OF KERATIN GENES WITH WOOL TRAITS

The data on wool production traits *viz.*, greasy fleece yield at 1st, 2nd and 3rd shearing, and wool quality traits *viz.*, staple length, number of crimps per cm of wool fibre, fibre diameter, pure fibres, hetro fibres, hairy fibres and medullation percentage were collected, compiled and analysed to study the association of these traits with the keratin genes under study.

The statistical analysis involving association of polymorphism of keratin genes with wool traits in Magra sheep was done using software programme LSMLMW (Harvey 1990).

$$Y_{ij} = \mu + A_i + e_{ij}$$

Where,

 $Y_{ij} = \text{Performance record of the } j^{\text{th}} \text{ animal of } i^{\text{th}} \text{ genotype}$

µ = Overall mean

 A_i = Fixed effect of ith genotype

 e_{ij} = Random error NID ($0,\sigma^2$).

4. RESULTS AND DISCUSSION

The results of present investigation have been presented and discussed under the following headings as per the objectives of the study:

4.1 Performance of wool production and quality traits

4.2 Genetic and phenotypic parameters for wool traits

4.3 Polymorphism of keratin genes (KIF- I and KAP 11-1 genes)

4.4 Association of polymorphism of keratin genes with wool traits

4.1 Performance of wool traits

The wool performance of Magra sheep was evaluated in terms of wool production *viz* greasy fleece yield at first, second and third clip; and wool quality *viz* staple length, crimp frequency, fibre diameter and proportion of pure, hetro, hairy and medullated fibres. The leastsquares means and effects of sire, period, sex, season and age at shearing have been discussed under the following headings:

4.1.1 Performance of wool production traits

The least-squares means for greasy fleece yield at first, second and third clip have been presented in Table 4.1. The overall leastsquares means were observed to be 690.50 ± 4.713 , 754.83 ± 5.571 and 670.93 ± 5.386 g for greasy fleece yield at first, second and third clip, respectively.

4.1.1.1 Greasy fleece yield at first shearing

The least-squares means of first greasy fleece yield for different periods, sex and season along with the regression on age at shearing are presented in Table 4.1. The overall least-squares means of first greasy fleece yield was estimated to be 690.50 ± 4.713 g.

The lower estimates for first greasy fleece yield were reported as 638.7 ± 8.67 and 584.11 ± 12.77 g by Dass *et. al.* (2003) and Mehta *et al.* (2004), respectively, in Magra sheep; 511.00 ± 11.90 and 533.39 ± 12.83 g by Sinha and Singh (1997) and Mandal *et al.* (2002), respectively, in Muzaffarnagari sheep; 577.73 ± 5.81 , 543.20 ± 14.28 and 505.28 ± 3.39 g by Dass and Singh (2001), Nehra *et al.* (2005) and Dass *et al.* (2008), respectively in Marwari lambs; and 579.61 ± 4.65 g by Gupta *et al.* (2015) in Patanwadi breed of sheep.

However, Arora *et al.* (2007), Chopra *et al.* (2010), Narula et al. (2011) and Kumar *et al.* (2013) reported higher estimates of first greasy

fleece yield as 788 \pm 8.00, 896.20 \pm 13.06, 755.77 \pm 5.63 and 950 \pm 0.01 g in Jaisalmeri, Bharat Merino, Magra and Chokla sheep, respectively.

4.1.1.1.1 Effect of sire

The effect of sire on first greasy fleece yield was estimated to be highly significant ($P \le 0.01$).

This shows that if greasy fleece weight of sire is higher, the lamb born will also produce high greasy fleece yield. This may be due to the genes of greasy fleece yield present in the sire. This result resembles with that of Sinha and Singh (1997) in Muzaffarnagri sheep, Tomar *et al.* (2000) in Bharat Merino sheep, Ahmad (2002) in Avikalin sheep and Kumar *et al.* (2013) in Chokla sheep.

4.1.1.1.2 Effect of period

The effect of the period was highly significant (P≤ 0.01) on greasy fleece yield at first clip. The first greasy fleece yield was lowest in the period P4 (2009-2011) as 599.69 \pm 7.115 g and highest in the period P3 (2006-2008) as 858.17 \pm 9.294 g. There was significant reduction in GFYI in P4 (2009-11) because as per recommendations, management adopted practice of three shearing per year inspite of two shearing per year prior to P4. It resulted in early shearing of lambs which consequently reduced the fleece weight. Other factors like variability in rainfall, nutrition, management etc might also have contributed in variability in first greasy fleece yield over different periods. These results were in agreement with the findings of Mehta *et al.* (2004), Dass *et. al.* (2008), Dixit *et al.* (2011) and Kumar *et al.* (2013) in Magra, Marwari, Bharat Merino and Chokla breed of sheep, respectively.

4.1.1.1.3 Effect of sex

The least-squares means for first greasy fleece yield was estimated as 723.72 \pm 5.814 and 657.28 \pm 5.833 g in males and

females, respectively. The effect of sex on first greasy fleece yield was found to be highly significant ($P \le 0.01$). On an average, the males produced 66.44 g more wool than the female lambs. Wool production is directly proportional to the body surface area of the sheep (Owen, 1976) and the surface area has positive correlation with body weight of the animal. The males being heavier in body weight and having a larger body size had more surface area and produced more wool. Similar results were reported by Arora *et al.* (2007), Dass (2007), Dass *et. al.* (2008), Dixit *et al.* (2011) and Gupta *et al.* (2015) in Jaisalmeri, Pugal, Marwari, Bharat Merino and Patanwadi breed of sheep. However, non-significant effect of sex of lamb on first greasy fleece yield was reported by Dass *et al.* (2003) and Mehta *et al.* (2004) in Magra sheep.

4.1.1.1.4 Effect of season of birth

The least-squares means for first greasy fleece yield was estimated as 704.62 \pm 3.931 and 676.37 \pm 8.704 g in season 1st (January- June) and 2nd (July- December), respectively. The effect of season on greasy fleece yield at first clip was found to be highly significant (P≤ 0.01). Lambs born during season 1st achieved higher fleece weight. The possible reason for heavier first clip of the season 1st born lambs may be the better nutrition and also due to plentiful succulent grasses available and coincided with favourable weather conditions. The first greasy fleece yield was significantly affected by season as reported by Mehta *et al.* (2004), Nehra *et al.* (2005), Arora *et al.* (2007) and Dixit *et al.* (2011) in Magra, Marwari, Jaisalmeri and Bharat Merino sheep, respectively. However, Das *et al.* (2014) and Khan *et al.* (2015) reported non-significant effect of season of birth on first greasy fleece yield in Kashmir Merino and Rambouillet breed of sheep, respectively.

4.1.1.1.5 Regression of age at shearing

Regression of age at shearing had highly significant influence (P \leq 0.01) on the first greasy fleece yield of the lamb. The regression coefficient of first greasy fleece yield was 0.414 ± 0.1320. Positive

regression coefficient indicates that the more fleece yield was produced by lambs whose age at shearing was higher. Significant effect of age at shearing on first greasy fleece yield was reported by Kumar *et al.* (2006) in Avikalin sheep; and Chopra *et al.* (2010) and Dixit *et al.* (2011) in Bharat Merino sheep.

Table 4.1: Least-squares means (± S.E) of greasy fleece yield (g) at first, second and third shearing in Magra lambs.

TRAITS/ FACTORS	AITS/ GFY I GFY II		GFY III
Overall Mean	690.50 ± 4.713	754.83 ± 5.571	670.93 ± 5.386
(µ)	(2873)	(2342)	(779)
SIRE	**	**	*
PERIOD	**	**	NS
P1 (2000-2002)	691.44 ± 10.603 ^c (349)	540.08 ± 13.070 ^a (247)	-
P2 (2003-2005)	671.80 ± 9.049° (574)	872.16 ± 10.958 ^d (424)	-
P3 (2006-2008)	858.17 ± 9.294 ^d (534)	931.34 ± 11.489 ^e (376)	-
P4 (2009-2011)	599.69 ± 7.115 ^a (703)	751.60 ± 7.966 ^c (685)	667.34 ± 7.822 (401)
P5 (2012-2014)	631.39 ± 6.863 ^b (713)	678.95 ± 7.867 ^b (610)	674.53 ± 8.445 (378)
SEX	**	**	**
Male	723.72 ± 5.814 ^b (1447)	820.72 ± 7.037 ^b (1121)	746.95 ± 7.985 ^b (360)
Female	657.28 ± 5.833 ^a (1426)	688.93 ± 6.699 ^a (1221)	594.91 ± 7.248ª (419)
SEASON	**	**	**
1 st (Jan- June)	704.62 ± 3.931 ^b (2273)	810.80 ± 4.745 ^b (1812)	613.46 ± 8.329 ^a (381)
2 nd (July- Dec) 676.37 ± 8.704 ^a (600)		698.85 ± 10.104 ^a (530)	728.41 ± 7.894 ^b (398)
AGE AT ** SHEARING		**	**
Regression coefficient	0.414 ± 0.1320	1.473 ± 0.1546	-0.893 ± 0.2961

No. of observations are given in parenthesis. Figure with different superscripts differ significantly.

** - Highly significant (P≤ 0.01) ; * - Significant (P≤0.05); NS - Non-significant

4.1.1.2 Greasy fleece yield at second shearing

The least-squares means of greasy fleece yield at second clip for different periods, sex and season along with the regression on age at shearing are presented in Table 4.1. The overall least-squares means for second greasy fleece weight was estimated to be 754.83 \pm 5.571 g. The lower estimates for second greasy fleece yield were reported as 578.0 \pm 9.73 and 536.93 \pm 20.33 g by Dass *et. al.* (2003) and Mehta *et al.* (2004) in Magra sheep, respectively; and 586.55 \pm 8.53 and 552.77 \pm 4.75 g by Dass and Singh (2001) and Dass *et al.* (2008) in Marwari lambs, respectively.

However, Singh and Kushwaha (1995) and Dixit *et al.* (2011) reported higher estimates of second greasy fleece yield than the present findings as 1090 ± 0.03 and 1010 ± 0.02 g in Bharat Merino sheep.

4.1.1.2.1 Effect of sire

The effect of sire on greasy fleece weight at second clip was estimated to be highly significant ($P \le 0.01$). This shows that if fleece weight of sire is higher, then their lamb's fleece weight at second clip will also be higher. This result resembles with that of Singh and Kushwaha (1995) in Bharat Merino sheep.

4.1.1.2.2 Effect of period

The effect of the period was highly significant ($P \le 0.01$) on second greasy fleece weight. The least-squares means of second greasy fleece weight was lowest in the period P1 (2000-2002) as 540.08 ± 13.070 g and highest in period P3 (2006-2008) as 931.34 ± 11.489 g. Differences in second greasy fleece weight in different periods could be attributed to the variation in rainfall affecting availability of pasture grasses and environmental conditions over the periods. Lower second greasy fleece yield during P4 (2009-2011) and P5 (2012-2014) was due to the practice of three shearing per year, adopted after 2009. The second greasy fleece weight was significantly affected by the year as reported by Gopal and Singh (2001) and Dass *et al.* (2008) in Marwari; and Dixit *et al.* (2011) in Bharat Merino sheep. However, the non-significant effect of year on greasy fleece yield at second clip was reported by Mehta *et al.* (2004) in Magra sheep.

4.1.1.2.3 Effect of sex

The least-squares means for greasy fleece yield at second clip was estimated as 820.72 \pm 7.037 and 688.93 \pm 6.699 g in males and females, respectively. The effect of sex on second greasy fleece yield was found to be highly significant (P≤ 0.01). This could be attributed to the fact that males are always heavier than females, thereby providing more surface area of their skin for production of wool fibre. Similar results were reported by Mandal *et al.* (2002), Mehta *et al.* (2004), Dass (2007) and Dass *et al.* (2008) in Muzaffarnagri, Magra, Pugal and Marwari breed of sheep. However, non-significant effect of sex of lamb on second greasy fleece yield was reported by Gopal and Singh (2001) and Dixit *et al.* (2011) in Marwari and Bharat Merino sheep, respectively.

4.1.1.2.4 Effect of season of birth

The effect of season of birth on greasy fleece yield at second clip was found to be highly significant (P \leq 0.01). The least-squares means for greasy fleece yield at second clip in season 1st and 2nd was estimated as 810.80 ± 4.745 and 698.85 ± 10.104 g, respectively. Higher fleece weight at season 1st might be due to better nutrition and favourable environmental conditions. The greasy fleece yield at second clip was significantly affected by season of birth as reported by Mehta *et al.* (2004) in Magra. However, Mandal *et al.* (2002) and Poonia (2006) reported non-significant effect of season of birth on first greasy fleece yield in Muzaffarnagri and Munjal breed of sheep, respectively.

4.1.1.2.5 Regression of age at shearing

Regression of age at shearing on greasy fleece yield at second clip was found to be significantly (P \leq 0.01). The regression coefficient of second greasy fleece yield was 1.473 ± 0.1546. Positive regression coefficient indicates that the more second greasy fleece yield was produced by lambs whose age at second shearing was higher. Dixit *et al.* (2009) and Dixit *et al.* (2011) reported non-significant effect of age at shearing on second greasy fleece yield in Bharat Merino sheep.

4.1.1.3 Greasy fleece yield at third shearing

The least-squares means of greasy fleece yield at third clip for different periods, sex and season along with the regression on age at shearing are presented in Table 4.1. The overall least-squares means of third greasy fleece yield was estimated to be 670.93 ± 5.386 g.

The lower estimates for third greasy fleece yield were reported as 549 and 549.23 \pm 6.46 g by Dass (2006) and Dass (2007) in Pugal sheep, respectively. However, Sharma *et al.* (1999) reported higher estimates of third greasy fleece yield as 875 \pm 0.03 g in Nali sheep.

4.1.1.3.1 Effect of sire

The effect of sire on greasy fleece yield at third clip was estimated to be significant ($P \le 0.05$). This shows that if fleece weight of sire is higher, then their lamb's fleece weight at third clip will also be higher.

4.1.1.3.2 Effect of period

The effect of period on third greasy fleece yield was found to be non-significant. The least-squares means for greasy fleece yield at third clip was estimated as 667.34 ± 7.822 and 674.53 ± 8.445 g in period 4th and 5th, respectively. Contrary to our result, significant effect of period on third greasy fleece yield was reported by Sharma *et al.* (1999) in Nali sheep.

4.1.1.3.3 Effect of sex

The least-squares means for third greasy fleece yield was estimated as 746.95 \pm 7.985 and 594.91 \pm 7.248 g in males and females, respectively. The effect of sex on greasy fleece yield at third clip was found to be highly significant (P≤ 0.01). The males being heavier than the females at the time of third shearing could attribute to more body surface area in males which resulted in higher greasy fleece yield at third clip. Similar results were reported by Dass (2007) in Pugal breed of sheep. However, non-significant effect of sex of lamb on third greasy fleece yield was reported by Sharma *et al.* (1999) in Nali breed of sheep.

4.1.1.3.4 Effect of season of birth

The least-squares means for greasy fleece yield at third clip was estimated as 613.46 ± 8.329 and 728.41 ± 7.894 g in season 1st and 2nd, respectively. The effect of season of birth on greasy fleece yield at third clip was found to be highly significant (P≤ 0.01). This might be due to the fact that usually, the animals were reared throughout the year facing all seasonal variability within year and then, reached to third shearing stage.

4.1.1.3.5 Effect of age at shearing

Age at shearing had highly significant influence ($P \le 0.01$) on the greasy fleece yield at third clip. The regression coefficient of third greasy fleece yield was found to be negative and the estimated value was -0.893 ± 0.2961.

4.1.2 Performance of wool quality traits

The overall least-squares means for staple length, crimp frequency and fibre diameter have been shown in Table 4.2. The overall least-squares means were observed to be 6.26 ± 0.039 cm, 0.92 ± 0.010 per cm and $33.31 \pm 0.131 \mu$ for staple length, crimp frequency and fibre diameter respectively. The least-squares means for proportions of different fibres in wool have been shown in Table 4.3. The per centage of pure, hetro, hairy and medullated fibres in total

wool fibres were estimated as 54.74 ± 0.593 , 33.25 ± 0.416 , 12.01 ± 0.291 and 45.26 ± 0.593 %, respectively. The estimated values of wool quality traits clearly indicate the suitability of Magra wool for carpet wool production.

4.1.2.1 Staple length

The least-squares means of staple length for different periods, sex and season along with the regression on age at shearing are presented in Table 4.2. The overall least-squares means for staple length was estimated as 6.26 ± 0.039 cm.

The lower estimates for staple length were reported by Mehta *et al.* (1998) as 4.26 ± 0.16 cm in Magra sheep; Gopal and Singh (2001) and Dass *et al.* (2008) as 4.69 ± 0.05 and 5.16 ± 0.04 cm, respectively, in Marwari sheep; and Chopra *et al.* (2010), Gowane *et al.* (2010b) and Dixit *et al.* (2011) as 3.30 ± 0.04 , 1.25 ± 0.07 and 3.32 ± 0.07 cm, respectively, in Bharat Merino sheep.

However, Naidoo *et al.* (2004) and Ciappesoni *et al.* (2013) reported slightly higher estimates of staple length as 8.32 ± 0.27 and 7.89 cm, respectively, in Merino sheep. The present findings were in close agreement with the reports of Nimbalkar *et al.* (2005), Dass (2007) and Narula *et al.* (2011) as 6.64 ± 0.16 , 6.07 ± 0.13 and 6.81 ± 0.04 cm, respectively in Deccani, Pugal and Magra breed of sheep, respectively.

4.1.2.1.1 Effect of sire

The effect of sire on staple length was estimated to be highly significant ($P \le 0.01$). This might be due to the fact that the genes affecting staple length are being transmitted from the sire to the progeny. Thus, if a lamb has good staple length, it might have attained this trait from the sire. Similar result was also found by Dixit *et al.* (2009) in Bharat Merino sheep.

4.1.2.1.2 Effect of period

The effect of period on staple length was estimated to be highly significant (P≤ 0.01). Highest staple length was found in period 2^{nd} (2003-2005) as 6.73 ± 0.080 cm, while lowest staple length was reported in period 1^{st} (2006-2009) as 5.94 ± 0.077 cm. The staple length varied from 5.94 to 6.73 cm, which suits best to carpet industry for carpet manufacturing. Usually wool carding machines at carpet industries utilize only those fibres which are above 5 cm length for yarn making. Similar results were reported by Dass *et al.* (2008), Chopra *et al.* (2010) and Narula *et al.* (2011) in Marwari, Bharat Merino and Magra sheep, respectively. However, non- significant effect of year on staple length was reported by Dass *et al.* (2014) in Kashmir Merino sheep.

4.1.2.1.3 Effect of sex

The effect of sex on staple length of wool fibre was found to be non-significant. Dass (2007), Devendran *et al.* (2008), Chopra *et al.* (2010) and Narula *et al.* (2011) also reported non-significant effect of sex on staple length in Pugal, Coimbatore, Bharat Merino and Magra breed of sheep, respectively.

4.1.2.1.4 Effect of season of birth

The effect of season of birth on staple length of wool was found to be highly significant (P≤ 0.01). The least-squares means for staple length in season 1st and 2nd were estimated as 6.08 ± 0.035 and 6.43 ± 0.073 cm, respectively. The sheep born in the season 2nd had longer staple length than those born in season 1st. This may be due to favourable environmental conditions in season 2nd. The staple length was significantly affected by season as reported by Chopra *et al.* (2010) and Dixit *et al.* (2011) in Bharat Merino and Das *et al.* (2014) in Kashmir Merino sheep. However, non-significant effect of season on staple length was reported by Khan *et al.* (2015) in Rambouillet breed of sheep.

4.1.2.1.5 Regression of age at shearing

The regression of age at shearing on staple length of wool in Magra sheep was found to be non-significant. The regression coefficient of staple length was found to be positive and the estimated value was 0.003 ± 0.0016 . This might be due to the fact that the estimation of staple length is usually done at the time of first shearing when all the animals are younger and of approximately same age.

Non- significant effect of age at shearing on the staple length was also found by Tabbaa *et al.* (2001) in Awassi sheep. Contrary to our results, Devendran *et al.* (2008) found significant effect of lamb's age at shearing on staple length in Coimbatore breed of sheep.

4.1.2.2 Crimp frequency

The least-squares means for crimp frequency for different periods, sex and season along with the regression on age at shearing are presented in Table 4.2. The overall least-squares means for crimp frequency was estimated as 0.92 ± 0.010 per cm of wool fibre.

Similar estimate of crimp frequency was reported by Narula *et al.* (2011) as 0.80 ± 0.01 per cm, in Magra sheep. Lower estimates than the present study were reported by Gopal and Singh (2001) and Dass *et al.* (2008) as 0.56 ± 0.01 and 0.49 ± 0.01 per cm of wool fibre, respectively, in Marwari sheep; and Devendran *et al.* (2008) as 0.20 ± 0.02 per cm of wool fibre in Coimbatore sheep.

However, Mehta *et al.* (1998) reported higher estimates of crimp frequency as 1.05 ± 0.06 in Magra sheep. The present finding was in close agreement with the reports of Dass *et al.* (2003) as 0.86 ± 0.02 in Magra breed of sheep.

4.1.2.2.1 Effect of sire

The effect of sire on crimp frequency was found to be highly significant ($P \le 0.01$). This shows that if crimp frequency of sire is more, then their lamb's crimp frequency will also be on the higher side.

4.1.2.2.2 Effect of period

The effect of the period was found highly significant (P \leq 0.01) on crimp frequency. The crimp frequency was lowest in the period P5 (2012-2014) as 0.78 ± 0.018 per cm of wool fibre and highest in the period P4 (2009-2011) as 1.06 ± 0.015 per cm of wool fibre.

Similar results were also reported by Dass *et al.* (2008) and Narula *et al.* (2012) in Marwari; and Narula *et al.* (2011) in Magra sheep.

Table 4.2: Least-squares means (± S.E) of staple length (cm), crimp frequency (per cm) and fiber diameter (µ) of wool in Magra lambs.

TRAITS/	STAPLE	CRIMP	FIBER
FACTORS	LENGTH	FREQUENCY	DIAMETER
Overall Mean	6.26 ± 0.039	0.92 ± 0.010	33.31 ± 0.131
(µ)	(2073)	(2073)	(2073)
SIRE	**	**	**
PERIOD	**	**	NS
P1 (2000-2002)	6.16 ± 0.082 ^b	0.81 ± 0.021ª	32.50 ± 0.279
	(309)	(309)	(309)
P2 (2003-2005)	6.73 ± 0.080 ^c	0.95 ± 0.021 ^b	33.62 ± 0.271
	(378)	(378)	(378)
P3 (2006-2008)	5.94 ± 0.077 ^a	1.02 ± 0.020 ^c	33.32 ± 0.262
	(421)	(421)	(421)
P4 (2009-2011)	6.03 ± 0.057 ^b	1.06 ± 0.015 ^d	33.16 ± 0.195
	(576)	(576)	(576)
P5 (2012-2014)	6.42 ± 0.068 ^c	0.78 ± 0.018 ^a	33.95 ± 0.230
	(389)	(389)	(389)
SEX	NS	**	*
Male	6.33 ± 0.046	0.89 ± 0.012 ^a	33.12 ± 0.156 ^a
	(1142)	(1142)	(1142)
Female	6.18 ± 0.051	0.96 ± 0.013 ^b	33.51 ± 0.173 ^b
	(931)	(931)	(931)
SEASON	**	**	**
1 st (Jan- June)	6.08 ± 0.035 ^a	0.87 ± 0.009 ^a	31.68 ± 0.117ª
	(1617)	(1617)	(1617)
2 nd (July- Dec)	6.43 ± 0.073 ^b	0.98 ± 0.019 ^b	34.94 ± 0.249 ^b
	(456)	(456)	(456)
AGE AT SHEARING	NS	**	NS
Regression coefficient	0.003 ± 0.0016	-0.002 ± 0.0004	0.005 ± 0.0057

No. of observations are given in parenthesis. Figure with different superscripts differ significantly. ** - Highly significant ($P \le 0.01$); * - Significant ($P \le 0.05$); NS - Non-significant

4.1.2.2.3 Effect of sex

The least-squares means for crimp frequencies were estimated as 0.89 ± 0.012 and 0.96 ± 0.013 per cm of wool in males and females, respectively. The effect of sex on crimp frequency of wool fibre was found to be highly significant (P ≤ 0.01). The crimp frequency of females was on the higher side than males. crimp frequency is usually affected by fibre diameter and greasy fleece yields. Differences in Fibre diameter and GFY for male and female could be attributed to differences in crimp frequencies in different sex.

Similar results were reported by Gopal and Singh (2001), Dass *et al.* (2008) and Narula *et al.* (2012) in Marwari sheep; and Narula *et al.* (2011) in Magra sheep. However, non-significant effect of sex of lamb on crimp frequency was reported by Dass *et al.* (2003) and Dass (2007) in Magra and Pugal breed of sheep, respectively.

4.1.2.2.4 Effect of season of birth

The effect of the season of birth was found to be highly significant (P \leq 0.01) on crimp frequency. The least-squares means for crimp frequency was estimated as 0.87 ± 0.009 and 0.98 ± 0.019 per cm of wool fibre in season 1st and 2nd, respectively. Better nutrition, management and favourable climatic conditions might be the reason for better crimp frequency in 2nd season.

4.1.2.2.5 Regression of age at shearing

The regression of age at shearing had highly significant influence ($P \le 0.01$) on the crimp frequency. The regression coefficient of crimp frequency was found to be negative and the estimated value was -0.002 ± 0.0004. Contrary to our results, Devendran *et al.* (2008) reported non-significant effect of age at shearing on crimp frequency in Bharat Merino sheep.

4.1.2.3 Fibre diameter

The least-squares means of fibre diameter for different periods, sex and season along with the regression on age at shearing are presented in Table 4.2. The overall least-squares means for fibre diameter was estimated as $33.31 \pm 0.131 \mu$. The quality of wool produced is well within the range (30-35 μ fiber diameter) desired by the carpet industry. Gopal and Singh (2001), Tabbaa *et al.* (2001), Poonia (2006) and Devendran *et al.* (2008) reported slightly higher estimates of fibre diameter as 36.15 ± 0.27 , 36 ± 0.33 , 38.70 ± 0.51 and $45.8\pm2.20 \mu$ in Marwari, Awassi, Munjal and Coimbatore breed of sheep, respectively.

The lower estimates for fibre diameter were reported by Sharma *et al.* (2000) as $28.34 \pm 0.46 \mu$ in Nali sheep; and Chopra *et al.* (2010), Gowane *et al.* (2010b) and Dixit *et al.* (2011) as 18.34 ± 0.09 , 18.08 ± 0.04 and $18.89 \pm 0.15 \mu$, respectively, in Bharat Merino sheep. The present findings were in close agreement with the reports of Dass *et al.* (2003), Mehta *et al.* (2004) and Narula *et al.* (2011) as 32.31 ± 0.17 , 32.41 ± 0.28 and $31.80 \pm 0.18 \mu$, respectively, in Magra sheep; and Dass *et al.* (2008) and Narula *et al.* (2012) as 33.66 ± 0.28 and $33.38 \pm 0.18 \mu$, respectively, in Marwari sheep.

4.1.2.3.1 Effect of sire

The effect of sire on fibre diameter was estimated to be highly significant ($P \le 0.01$). This indicates that selection of superior sires for fibre diameter can bring further genetic improvement in the trait. Similar result was also reported by Dixit *et al.* (2009) in Bharat Merino sheep.

4.1.2.3.2 Effect of period

The effect of period on fibre diameter was found to be nonsignificant. Lowest fiber diameter was found in P1 (2000-2002) as 32.50 ± 0.279 and highest was observed in P5 (2011-2014) as $33.95 \pm$ 0.230. Mehta *et al.* (2004), Poonia (2006) and Dass *et al.* (2014) also found non- significant effect of period on Magra, Munjal and Kashmir Merino sheep.

4.1.2.3.3 Effect of sex

The effect of sex was found to be significant ($P \le 0.05$) on fibre diameter of wool. The least-squares means for fibre diameter were

estimated as 33.12 ± 0.156 and $33.51 \pm 0.173 \mu$ in males and females, respectively. The differences in fibre diameter of the male and female lambs may be due to differences in their physiological processes.

Devendran *et al.* (2008) and Dixit *et al.* (2011) also reported significant effect of sex on fibre diameter in Coimbatore and Bharat Merino sheep, respectively. However, non-significant effect of sex on fibre diameter were observed by Dass *et al.* (2003), Mehta *et al.* (2004) and Narula *et al.* (2011) in Magra sheep; Dass *et al.* (2008) and Narula *et al.* (2012) in Marwari sheep; and Chopra *et al.* (2010) in Bharat Merino sheep.

4.1.2.3.4 Effect of season of birth

The effect of the season of birth was found to be highly significant (P \leq 0.01) on fibre diameter in the present study. The least-squares means for fibre diameter was estimated as 31.68 ± 0.117 and 34.94 ± 0.249 µ in season 1st and 2nd, respectively. Lambs born in season 1 showed lower fibre diameter than those during season 2. Similar results were observed by Nehra *et al.* (2005) and Dixit *et al.* (2011) in Marwari and Bharat merino sheep. However, Mehta *et al.* (2004) reported non- significant effect of season on fibre diameter in Magra sheep.

4.1.2.3.5 Regression of age at shearing

Regression of age at shearing had non- significant effect on the fibre diameter. The regression coefficient of fibre diameter was found to be positive and the estimated value was 0.005 ± 0.0057 . This might be due to the reason that fibre diameter is a life time trait and is not affected by the age of the animal at shearing.

Similar to our result, non- significant effect of age at shearing on the fibre diameter was found by Tabbaa *et al.* (2001) in Awassi sheep. Contrary to our result, Devendran *et al.* (2008) reported significant effect of age at shearing on fibre diameter in Bharat Merino sheep.

4.1.2.3 Pure fibres

The least-squares means for pure fibres of wool for different periods, sex and season along with the regression on age at shearing are presented in Table 4.3. The overall least-squares means for pure fibres was estimated as 54.74 ± 0.593 %. Higher values than the present study were estimated by Mehta *et al.* (1998) and Mehta *et al.* (2004) as 57.75 ± 2.67 and 63.31 ± 1.58 %, respectively in Magra sheep. However, Nehra *et al.* (2005) and Poonia (2006) observed lower estimates as 40.39 ± 0.72 and 36.84 ± 1.24 %, in Marwari and Munjal breed of sheep, respectively.

4.1.2.3.1 Effect of sire

The effect of sire on pure fibres was observed to be highly significant (P \leq 0.01). This indicates that superior sires can be used effectively for bringing further genetic improvement in the trait.

4.1.2.3.2 Effect of period

The effect of period on pure fibres was found to be highly significant (P \leq 0.01). However, highest per centage of pure fibres was found in P4 (2009-2011) as 59.95 ± 0.879 %, while lowest was reported in P2 (2003-2005) as 51.28 ± 1.222 %. This may be due to the reason that in 2007 and 2011, some purchased animals, with higher percentage of pure fibres, were included in the flock. Selective breeding by using these superior rams and their lambs might have increased the percentage of pure fibres during the P4 and P5.

Significant effect of period on pure fibres was also reported by Nehra *et al.* (2005) and Dass *et al.* (2008) in Marwari sheep. Contrary to our results, Mehta *et al.* (2004) and Poonia (2006) found non-significant effect of period on pure fibres in Magra and Munjal sheep, respectively.

4.1.2.3.3 Effect of sex

The effect of sex was found to be non- significant on pure fibres of wool. The least-squares means for pure fibres were estimated as 54.36 ± 0.704 and 55.12 ± 0.780 % in males and females, respectively, which didn't vary statistically.

Nehra *et al.* (2005) and Narula *et al.* (2011) also reported nonsignificant effect of sex on pure fibres in Marwari and Magra sheep, respectively. However, significant effect of sex on fibre diameter was observed by Mehta *et al.* (2004) in Magra sheep.

4.1.2.3.4 Effect of season of birth

The effect of season of birth on pure fibres was found to be nonsignificant. The least-squares means for pure fibres in season 1st and 2nd were estimated as 55.69 \pm 0.528 and 53.79 \pm 1.126 %, respectively. Lambs born in season 1st showed higher pure fibres than those during season 2nd. However, the difference didn't vary statistically. Mehta *et al.* (2004) also found non-significant effect of season on pure fibres in Magra sheep.

4.1.2.3.5 Regression of age at shearing

The regression of age at shearing had non- significant effect on the pure fibres. The regression coefficient of pure fibres was found to be positive and the estimated value was 0.048 ± 0.0252 . Contrary to our result, Behdad *et al.* (2013) observed significant effect of age at shearing on per centage of pure fibres in an exotic breed of sheep.

4.1.2.4 Hetro fibres

The least-squares means for per centage of hetro fibres of wool for different periods, sex and seasons along with the regression on age at shearing are presented in Table 4.3. The overall least-squares means for hetro fibres was estimated as 33.25 ± 0.416 %. The quality of wool produced is well within the range (30-35 % hetro fibres) desired

by the carpet industry. Quality carpets require hetro fibres to be in this range in order to provide proper bulkiness, durability and appearance retention to the carpets.

Lower values than the present study were estimated by Mehta *et al.* (1998) and Nehra *et al.* (2005) as 8.68 ± 0.91 and 23.06 ± 0.42 % in Magra and Marwari sheep, respectively. The present findings are in close agreement with the reports of Dass *et al.* (2003) and Narula *et al.* (2011) as 31.32 ± 0.72 and 33.29 ± 0.50 %, respectively, in Magra sheep; and Dass *et al.* (2008) as 30.46 ± 0.68 % in Marwari breed of sheep. Narula *et al.* (2012) reported higher estimates as 37.81 ± 0.49 % in Marwari breed of sheep.

4.1.2.4.1 Effect of sire

The effect of sire on hetro fibres was found to be highly significant (P \leq 0.01). This indicates that this trait can be further improved effectively by using superior sires in the flock.

4.1.2.4.2 Effect of period

The effect of the period on hetro fibres was found to be highly significant ($P \le 0.01$). The estimate was lowest in the period P4 (2009-2011) as 30.75 ± 0.616 % and highest in the period P3 (2006-2008) as 36.71 ± 0.830 %. The variability in hetro fibres due to periods may be due to variations in physical environmental conditions, feeding, forage availability prevailing in different periods for grazing resources and selection of rams. Selective breeding of the rams and ewes, purchased from the field in 2007 and 2011, having low hetro fibres and using their progenies as future parents might also have affected the number of hetro fibres in later periods.

Similar results were also reported by Poonia (2006), Narula *et al.* (2011) and Narula *et al.* (2012) in Munjal, Magra and Marwari breed of sheep, respectively.

4.1.2.4.3 Effect of sex

The effect of sex was found to be non- significant on hetro fibres of wool. The least-squares means for hetro fibres were estimated as 33.47 ± 0.493 and 33.03 ± 0.547 % in males and females, respectively.

Dass (2007), Dass *et al.* (2008) and Narula *et al.* (2011) also reported non- significant effect of sex on hetro fibres in Pugal, Marwari and Magra sheep, respectively. However, significant effect of sex on per centage of hetro fibres was observed by Behdad *et al.* (2013) in an exotic breed of sheep.

4.1.2.4.4 Effect of season of birth

The effect of season of birth on hetro fibres was found to be non-significant. The least-squares means for hetro fibres were estimated as 33.26 ± 0.370 and 33.23 ± 0.789 % in season 1st and 2nd, respectively, which didn't differ statistically. Similar report was observed by Nehra *et al.* (2005) in Marwari sheep.

4.1.2.4.5 Regression of age at shearing

The regression of age at shearing on the hetro fibres of wool was found to be highly significant ($P \le 0.01$). The regression coefficient of hetro fibres was found to be negative and the estimated value was - 0.061 ± 0.0176. Similar to the present findings, Behdad *et al.* (2013) also found significant effect of age at shearing on per centage of hetro fibres in an exotic breed of sheep.

4.1.2.5 Hairy fibres

The least-squares means for hairy fibres of wool for different periods, sex and season along with the regression on age at shearing are presented in Table 4.3. The overall least-squares means for hairy fibres was estimated as 12.01 ± 0.291 %, which is well within the range (10-15 %) desired by the carpet industry. Hairy fibres should not be more than 15 % as it may reduce the quality and life of the carpets.

Higher values than the present study were estimated by Mehta *et al.* (1998), Dass (2007) and Dass *et al.* (2008) as 33.63 ± 2.44 , 30.94 ± 1.22 and 20.27 ± 0.52 % in Magra, Pugal and Marwari sheep, respectively. The present finding was in close agreement with the reports of Dass *et al.* (2003) and Narula *et al.* (2011) as 12.46 ± 0.47 and 16.03 ± 0.42 %, in Magra breed of sheep.

4.1.2.5.1 Effect of sire

The effect of sire on hairy fibres of wool was observed to be highly significant ($P \le 0.01$). This indicates that superior sires can be used effectively for bringing further genetic improvement in the trait.

4.1.2.5.2 Effect of period

The effect of period was found to be highly significant (P \le 0.01) on hairy fibres of wool. The least squares means was found lowest in the period P4 (2009-2011) as 9.30 ± 0.431 % and highest in the period P2 (2003-2005) as 16.93 ± 0.599 %.

Similar to the present findings, Dass *et al.* (2003) and Narula *et al.* (2011) in Magra sheep; and Dass *et al.* (2008) and Narula *et al.* (2012) in Marwari sheep, reported significant effect of period on hairy fibres.

4.1.2.5.3 Effect of sex

The effect of sex was found to be non- significant on hairy fibres of wool. The least-squares means for hairy fibres were estimated as 12.17 ± 0.345 and 11.85 ± 0.382 % in males and females, respectively.

Dass (2007), Narula *et al.* (2011) and Narula *et al.* (2012) also reported non- significant effect of sex on hairy fibres of Pugal, Magra and Marwari breed of sheep, respectively. However, significant effect of sex on per centage of hairy fibres was observed by Gopal and Singh (2001) and Dass *et al.* (2008) in Marwari sheep.

4.1.2.5.4 Effect of season of birth

The effect of the season of birth was found to be highly significant (P \leq 0.01) on hairy fibres. The least-squares means for hairy fibres were estimated as 11.05 ± 0.259 and 12.97 ± 0.552 % in season 1st and 2nd, respectively. Lambs born in season 1 showed lower hairy fibres than those during season 2.

4.1.2.5.5 Regression of age at shearing

Non- significant regression of age at shearing was observed on the hairy fibres of wool. The regression coefficient of hairy fibres was found to be positive and the estimated value was 0.008 ± 0.0124 . This indicates that the per centage of hairy fibres in total wool sample is independent of lamb's age at shearing. Usually, such traits are not age specific and they remain same in the lifetime of the animal with slight variations due to the content of fodder. Similar to our result, Behdad *et al.* (2013) observed significant effect of age at shearing on hairy fibres in an exotic breed of sheep.

4.1.2.6 Medullated fibres

The least-squares means for medullation per centage of wool for different periods, sex and season along with the regression on age at shearing are presented in Table 4.3. The overall least-squares means for medullation per centage was estimated as 45.26 ± 0.593 %. The quality of wool produced is well within the range (40- 46 % medullated fibres) desired by the carpet industry.

Lower values than the present study were estimated by Mehta *et al.* (2004), Nehra *et al.* (2005) and Arora *et al.* (2007) as 36.68 ± 1.59 , 39.33 ± 0.67 and 39.75 % in Magra, Marwari and Jaisalmeri sheep, respectively. However, Dass *et al.* (2008), Devendran *et al.* (2008) and Narula *et al.* (2011) reported higher estimates as 50.72 ± 0.90 , 48.76 ± 2.85 and 49.32 ± 0.79 % in Marwari, Coimbatore and Magra sheep, respectively.

4.1.2.6.1 Effect of sire

The effect of sire was found to be highly significant ($P \le 0.01$) on medullation per centage. This suggests that sires can be used effectively for bringing further genetic improvement in the trait. Similar result was also found by Dixit *et al.* (2009) in Bharat Merino sheep.

TRAITS/ FACTORS	Pure	Hetro	Hairy	Medullation
Overall Mean	54.74 ± 0.593	33.25 ± 0.416	12.01 ± 0.291	45.26 ± 0.593
(µ)	(2073)	(2073)	(2073)	(2073)
SIRE	**	**	**	**
PERIOD	**	**	**	**
D4 (2000 2002)	53.67 ± 1.259 ^{ab}	33.60 ± 0.882 ^b	12.73 ± 0.617°	46.33 ± 1.259 ^{bc}
PT (2000-2002)	(309)	(309)	(309)	(309)
D2 (2002 2005)	51.28 ± 1.222ª	31.79 ± 0.857 ^{ab}	16.93 ± 0.599^{d}	48.72 ± 1.222°
P2 (2003-2005)	(378)	(378)	(378)	(378)
D2 (2006 2008)	52.52 ± 1.184 ^{ab}	36.71 ± 0.830°	10.77 ± 0.580 ^b	47.48 ± 1.184 ^{bc}
F3 (2000-2008)	(421)	(421)	(421)	(421)
D4 (2000 2011)	59.95 ± 0.879°	30.75 ± 0.616 ^a	9.30 ± 0.431 ^a	40.05 ± 0.879^{a}
P4 (2009-2011)	(576)	(576)	(576)	(576)
DE (2012 2014)	56.28 ± 1.040 ^b	33.39 ± 0.729 ^b	10.33 ± 0.510^{ab}	43.72 ± 1.040 ^b
P5 (2012-2014)	(389)	(389)	(389)	(389)
SEX	NS	NS	NS	NS
Mala	54.36 ± 0.704	33.47 ± 0.493	12.17 ± 0.345	$45.64 \pm 0.704(1142)$
Iviale	(1142)	(1142)	(1142)	$45.04 \pm 0.704 (1142)$
Fomolo	55.12 ± 0.780	33.03 ± 0.547	11.85 ± 0.382	44.88 + 0.780 (021)
remale	(931)	(931)	(931)	$44.00 \pm 0.700 (931)$
SEASON	NS	NS	**	NS
1st (lon Juno)	55.69 ± 0.528	33.26 ± 0.370	11.05 ± 0.259^{a}	44.31 ± 0.528
(Jan- June)	(1617)	(1617)	(1617)	(1617)
2nd (July Doo)	53.79 ± 1.126	33.23 ± 0.789	12.97 ± 0.552 ^b	46.21 ± 1.126
Z ^{ria} (July- Dec)	(456)	(456)	(456)	(456)
AGE AT SHEARING	NS	**	NS	*
Regression coefficient	0.048 ± 0.0252	-0.061 ± 0.0176	0.008 ± 0.0124	-0.056 ± 0.0255

Table 4.3: Least-squares means (± S.E) for pure (%), hetro (%), hairy (%) and medullation per centage (%) of wool in Magra lambs.

No. of observations are given in parenthesis. Figure with different superscripts differ significantly.

** - Highly significant (P≤ 0.01) ; * - Significant (P≤0.05); NS - Non-significant

4.1.2.6.2 Effect of period

The effect of period was found to be highly significant on medullation per centage. However, there was no definite trend over the periods. Highest medullation per centage was found in P2 (2003-2005) as 48.72 ± 1.222 %, while lowest was reported in P4 (2009-2012) as 40.05 ± 0.879 %. This may be due to the reason that in 2007 and 2011, some animals with lower medullation per centage were purchased from the field and included in the flock. Selective breeding by using these superior rams and their lambs might have reduced the medullation percentage during the P4 and P5.

Significant effect of period on medullation per centage was also reported by Dass *et al.* (2003), Dass *et al.* (2008), and Dixit *et al.* (2011) in in Magra, Marwari and Bharat Merino sheep, respectively. Contrary to our results, Mehta *et al.* (2004) and Narula *et al.* (2011) in Magra sheep; and Poonia (2006) and Narula *et al.* (2012) in Munjal and Marwari breed of sheep, respectively, found non- significant effect of period on medullated fibres.

4.1.2.6.3 Effect of sex

The effect of sex was found to be non- significant on medullation per centage. The least-squares means for medullation per centage were estimated as 45.64 ± 0.704 and 44.88 ± 0.780 % in males and females, respectively.

Dass *et al.* (2008), Narula *et al.* (2011) and Dixit *et al.* (2011) also reported non- significant effect of sex on medullation per centage in Marwari, Magra and Bharat Merino breed of sheep, respectively. However, significant effect of sex on medullation per centage was observed by Mehta *et al.* (2004) and Chopra *et al.* (2010) in Magra and Bharat Merino sheep, respectively.
4.1.2.6.4 Effect of season of birth

The effect of season of birth on medullation per centage was found to be non-significant. The least-squares means for medullation per centage in season 1^{st} and 2^{nd} were estimated as 44.31 ± 0.528 and 46.21 ± 1.126 %, respectively.

Similar to the present findings, Dixit *et al.* (2009), Chopra *et al.* (2010) and Dixit *et al.* (2011) also found non-significant effect of season on medullation per centage in Bharat Merino sheep. However, Nehra *et al.* (2005) observed significant effect of season on medullated fibres in Marwari sheep.

4.1.2.6.5 Regression of age at shearing

The regression of age at shearing on medullation per centage was found to be significant (P \leq 0.05). The regression coefficient of medullation per centage was found to be negative and the estimated value was -0.056 ±0.0255. Contrary to the present findings, Devendran *et al.* (2008) reported non-significant effect of age at shearing on medullation per centage in Bharat Merino sheep.

4.2 Genetic and phenotypic parameters for wool traits

The genetic and phenotypic parameters *viz.,* heritability, genetic correlation and phenotypic correlation were estimated both by sire model i.e., model 2 of LSMLMW programmes (Harvey, 1990) and by animal model i.e., WOMBAT programme (Meyer, 2007). The results have been presented and discussed under the following subheadings:

4.2.1 Genetic and phenotypic parameters by sire model

4.2.2 Genetic and phenotypic parameters by animal model

4.2.1 Genetic and phenotypic parameters by sire model

Estimation of genetic and phenotypic parameters was done using model 2 of LSMLMW programmes (Harvey, 1990). The heritability, genetic and phenotypic correlations for different traits under study has been discussed under the following heads:

4.2.1.1 Heritability estimates by sire model

Heritability estimates for wool production and quality traits in Magra sheep have been presented in Table 4.4(a) and Table 4.4(b), respectively

Heritability of greasy fleece yield at first clip (GFY I) was found to be 0.68 \pm 0.083. High heritability estimate for greasy fleece yield at first clip indicates the presence of high genetic variability for this trait in the flock which can be utilized through selection. Lower estimates were reported by Mandal *et al.* (2002), Nehra *et al.* (2005), Kumar *et al.* (2005), Dixit *et al.* (2011) and Khan *et al.* (2015) as 0.23 \pm 0.05, 0.16 \pm 0.12, 0.24 \pm 0.08, 0.54 \pm 0.13 and 0.49 \pm 0.08 in Muzaffarnagri, Marwari, Chokla, Bharat Merino and Rambouillet breed of sheep respectively. Higher estimates were reported by Joshi (2001) as 0.70 \pm 0.15 in Marwari sheep.

Heritability of greasy fleece yield at second clip (GFY II) was estimated to be 0.81 \pm 0.095. Heritability for greasy fleece yield at second clip was more than first clip indicating that population was exhibiting more genetic variability than first greasy fleece weight. Lower estimates were reported by Sharma *et al.* (1999) as 0.02 \pm 0.14, Mandal *et al.* (2002) as 0.38 \pm 0.06 and Dixit *et al.* (2011) as 0.54 \pm 0.13 in Nali, Muzaffarnagri and Bharat Merino sheep, respectively.

The heritability of greasy fleece yield at third clip (GFY III) was estimated to be 0.66 \pm 0.150. High estimate of heritability for GFY III

suggested that most of the variation in this trait is genetic rather than environmental.

Heritability estimate for staple length was found as 0.52 ± 0.085 . High heritability estimate for staple length indicates that the trait can be improved through selection. Lower heritability values than the present study were estimated by Nimbalkar *et al.* (2005) as 0.18 ± 0.15 and Khan *et al.* (2015) as 0.15 ± 0.05 in Deccani and Rambouillet sheep, respectively. However, Dixit *et al.* (2011) reported higher estimate for heritability of staple length as 0.76 ± 0.15 in Bharat Merino sheep.

Heritability for crimp frequency was estimated as 0.20 ± 0.055 . Safari *et al.* (2005) found higher estimates for crimps per cm of wool fibre as 0.41 ± 0.03 in different exotic breeds of sheep. Low heritability estimate for crimp frequency indicated that most of the variation in this trait was non-genetic in nature. Thus, this trait could be improved through managemental intervention.

Heritability for fibre diameter of wool was estimated as 0.18 \pm 0.052. Higher estimates than the present study were reported by Nehra *et al.* (2005), Dixit *et al.* (2011) and Khan *et al.* (2015) as 0.22 \pm 0.12, 0.46 \pm 0.13 and 0.55 \pm 0.09 in Marwari, Bharat Merino and Rambouillet breed of sheep, respectively.

The heritability of pure fibres was estimated as 0.41 ± 0.073 . Higher estimate than the present study was reported by Dashab *et al.* (2012) as 0.65 ± 0.44 in an exotic sheep breed. Lower estimate was reported by Nehra *et al.* (2005) as 0.03 ± 0.10 in Marwari breed of sheep.

Heritability estimate for hetro fibres was found as 0.33 ± 0.066 . Lower values than the present study was estimated by Nehra *et al.* (2005) as 0.18 ± 0.15 in Marwari sheep. The heritability of hairy fibres was estimated to be 0.53 ± 0.082 . Dashab *et al.* (2012) reported lower estimate of heritability for hairy fibres as 0.20 ± 0.08 in an exotic breed of sheep.

Heritability estimate for medullation per centage was found as 0.44 ± 0.075 . Higher heritability than the present study was reported by Sharma *et al.* (2000) as 0.75 ± 0.35 in Marwari and Nali breed of sheep. However, Dixit *et al.* (2011) reported lower estimate as 0.15 ± 0.10 in Bharat Merino sheep.

Moderate to high heritability estimates for pure, hetro, hairy and medullated fibres suggested that the direct selection for fibre quality traits could be successful if environmental conditions are more tightly controlled or accounted for the selection programme.

The estimates of heritability for wool production and wool quality traits (except that of crimp frequency and fibre diameter) indicated the existence of considerable additive genetic variance in these traits. The genetic differences in these traits can, therefore, be exploited through selection for genetic improvement in these traits of Magra sheep. Though genetic variation is present in the animals, but the environmental conditions like high humidity and higher ambient temperature also affects the wool production and quality. It has thus, suggested that a more critical and careful selection of breeding stock be adopted in order to control these environmental conditions.

4.2.1.2 Genetic and phenotypic correlations by sire model

Estimates of genetic and phenotypic correlations among wool traits were estimated by LSMLMW programme (Harvey, 1990) under model 2 and are presented in Table 4.4(a) and Table 4.4(b).

4.2.1.2.1 Genetic correlations

The genetic correlations of first greasy fleece yield with greasy fleece yield at second and third clip were estimated as 0.33 ± 0.248 and 0.55 ± 0.261 , respectively. The positive and moderate genetic correlation between GFY I and GFY II indicates that lambs with heavier fleece at first clip might have heavier fleece at second clip also. The result was in accordance with the findings of Mandal *et al.* (2002) and Dixit *et al.* (2011) in Muzaffarnagri and Bharat Merino sheep, respectively.

The genetic correlation of greasy fleece yield at second clip with greasy fleece yield at third clip was estimated as 0.87 ± 0.256 . The positive and high genetic correlation between GFY II and GFY III indicates that if selection is practiced for high greasy fleece yield at second clip, it will subsequently improves yield at third clip also.

The genetic correlations of staple length with crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres were estimated as -0.15 ± 0.168 , -0.11 ± 0.171 , -0.15 ± 0.139 , -0.05 ± 0.145 , 0.41 ± 0.129 and 0.15 ± 0.137 , respectively. The result was in accordance with the findings of Safari *et al.* (2005) in different wool breeds; Di *et al.* (2011) and Ciappesoni *et al.* (2013) in Merino; and Khan *et al.* (2015) in Rambouillet breed of sheep.

The genetic correlations of crimp frequency with fibre diameter, pure, hetro, hairy and medullated fibres were estimated as -0.72 \pm 0.246, 0.49 \pm 0.156, -0.59 \pm 0.190, -0.24 \pm 0.194 and -0.49 \pm 0.187, respectively.

	GFYI	GFYII	GFYIII
GFYI	0.68 ± 0.083	0.33 ± 0.248	0.55 ± 0.261
GFYII	0.09 ± 0.021	0.81 ± 0.095	0.87 ± 0.256
GFYIII	0.07 ± 0.036	- 0.007 ± 0.036	0.66 ± 0.150

 Table 4.4 (a): Estimates of heritability, genetic and phenotypic

 correlation using sire model for wool yield in Magra sheep

Values at the diagonal are heritability estimates, and values above and below the diagonal are genetic and phenotypic correlations, respectively.

	SL	CF	FD	PURE	HET	HAIRY	MED
SI	0.52 ±	-0.15 ±	-0.11 ±	-0.15 ±	-0.05 ±	0.41 ±	0.15 ±
U L	0.085	0.168	0.171	0.139	0.145	0.129	0.137
CE.	0.04 ±	0.20 ±	-0.72 ±	0.49 ±	-0.59 ±	-0.24 ±	-0.49 ±
	0.022	0.055	0.246	0.156	0.190	0.194	0.187
ED	0.06 ±	-0.20 ±	0.18 ±	-0.81 ±	0.93 ±	0.44 ±	0.81 ±
FD	0.022	0.022	0.052	0.227	0.117	0.147	0.098
DIIDE	-0.06 ±	0.20 ±	-0.52 ±	0.41 ±	-0.93 ±	-0.86 ±	-1.00 ±
FURL	0.022	0.022	0.019	0.073	0.202	0.188	0.197
ЦЕТ	0.003 ±	-0.15 ±	0.32 ±	-0.89 ±	0.33 ±	0.62 ±	0.93 ±
1161	0.022	0.022	0.021	0.010	0.066	0.111	0.024
	0.12 ±	-0.20 ±	0.59 ±	-0.76 ±	0.39 ±	0.53 ±	0.86 ±
	0.022	0.022	0.018	0.014	0.020	0.082	0.046
MED	0.06 ±	-0.20 ±	0.52 ±	-1.00 ±	0.89 ±	0.76 ±	0.44 ±
	0.022	0.022	0.019	0.000	0.010	0.014	0.075

 Table 4.4 (b): Estimates of heritability, genetic and phenotypic

 correlation using sire model for wool quality traits in Magra sheep

Values at the diagonal are heritability estimates, and values above and below the diagonal are genetic and phenotypic correlations, respectively.

The genetic correlations of fibre diameter with pure, hetro, hairy and medullated fibres were estimated as -0.81 ± 0.227 , 0.93 ± 0.117 , 0.44 ± 0.147 and 0.81 ± 0.098 , respectively. The result was in accordance with the findings of Nehra *et al.* (2005) in Marwari sheep.

The genetic correlations of pure fibres with hetro, hairy and medullated fibres were estimated as -0.93 ± 0.202 , -0.86 ± 0.188 and -1.00 ± 0.197 , respectively. The result was in accordance with the findings of Nehra *et al.* (2005) in Marwari sheep.

The genetic correlations of hetro fibres with hairy and medullated fibres were estimated as 0.62 ± 0.111 and 0.93 ± 0.024 , respectively; and between hairy and medullated fibres was estimated as 0.86 ± 0.046 .

Results clearly indicate that selection may be practiced for heavier fleeces giving negative weightage to fibre diameter and medullation percentage. Moreover, giving negative weightage to fibre diameter will increase the percentage of pure fibres of wool and decrease the medullation percentage which may result in further improvement of the wool quality.

4.2.1.2.2 Phenotypic correlations

The phenotypic correlations of first greasy fleece yield with greasy fleece yield at second and third clip were estimated as 0.09 ± 0.021 and 0.07 ± 0.036 , respectively. The result was in accordance with the findings of Sharma *et al.* (1999), Mandal *et al.* (2002) and Dixit *et al.* (2011) in Nali, Muzaffarnagri and Bharat Merino sheep, respectively.

The phenotypic correlation of greasy fleece yield at second clip with greasy fleece yield at third clip was estimated as - 0.007 ± 0.036 .

The phenotypic correlations of staple length with crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres were estimated as 0.04 ± 0.022 , 0.06 ± 0.022 , -0.06 ± 0.022 , 0.003 ± 0.022 , 0.12 ± 0.022 and 0.06 ± 0.022 , respectively. The result was in accordance with the findings of Mehta *et al.* (1998) in Magra sheep, Safari *et al.* (2005) in different wool breeds; Di *et al.* (2011) and Ciappesoni *et al.* (2013) in Merino; and Khan *et al.* (2015) in Rambouillet breed of sheep.

The phenotypic correlations of crimp frequency with fibre diameter, pure, hetro, hairy and medullated fibres were estimated as - 0.20 ± 0.022 , 0.20 ± 0.022 , -0.15 ± 0.022 , -0.20 ± 0.022 and -0.20 ± 0.022 , respectively. The result was in accordance with the findings of Mehta *et al.* (1998) in Magra sheep.

The phenotypic correlations of fibre diameter with pure, hetro, hairy and medullated fibres were estimated as -0.52 ± 0.019 , 0.32 ± 0.021 , 0.59 ± 0.018 and 0.52 ± 0.019 , respectively. The result was in accordance with the findings of Mehta *et al.* (1998) and Nehra *et al.* (2005) in Magra and Marwari sheep, respectively.

The phenotypic correlations of pure fibres with hetro, hairy and medullated fibres were estimated as -0.89 ± 0.010 , -0.76 ± 0.014 and -1.00 ± 0.000 , respectively. The result was in accordance with the findings of Mehta *et al.* (1998) and Nehra *et al.* (2005) in Magra and Marwari sheep, respectively.

The phenotypic correlation of hetro fibres with hairy and medullated fibres were estimated as 0.39 ± 0.020 and 0.89 ± 0.010 , respectively; and between hairy and medullated fibres was estimated as 0.76 ± 0.014 . The result was in accordance with the findings of Mehta *et al.* (1998) and Nehra *et al.* (2005) in Magra and Marwari sheep, respectively.

4.2.2 Genetic and phenotypic parameters by animal model

For different wool traits, (co) variance components along with the genetic and phenotypic parameters i.e. heritability (h²), genetic correlation (r_g) and phenotypic correlation (r_p) were also estimated using the WOMBAT programme (Meyer, 2007) by fitting an animal model throughout. Animal model partitions the total heritability estimates into direct. maternal and permanent environment components. (Co) variance components along with the heritability and maternal components were estimated by univariate animal model analysis while a series of bivariate animal model analysis was carried out in order to estimate genetic and phenotypic correlations between the traits.

Least square means along with the standard deviation as estimated by the animal model for various traits under study are given in Table 4.5. Least square means for greasy fleece yield at first, second and third clips were estimated as 689.57 ± 3.898 , 788.56 ± 5.104 and 665.15 ± 6.277 g, respectively. The least-squares means were observed to be 6.14 ± 0.030 cm, 0.91 ± 0.008 per cm and $32.39 \pm 0.104 \mu$ for staple length, crimp frequency and fibre diameter, respectively. The least-squares means for per centage of pure, hetro, hairy and medullated fibres in total wool fibres were estimated as 55.71 ± 0.450 , 33.10 ± 0.315 , 11.19 ± 0.225 and 44.29 ± 0.450 , respectively. The estimated values of wool quality traits clearly indicate that the Magra wool is suitable for carpet production.

(Co)variance components and genetic parameters estimated by most appropriate model in univariate analysis by WOMBAT for various wool traits of Magra sheep are presented in Table 4.6, 4.7 and 4.8. The log-L values did not differ significantly in all the six models in any of the traits under study. However, addition of σ_{am} in model 3 and 6 brought

Table 4.5 Descriptive statistics and data structure for wool traitsby WOMBAT in Magra sheep

TRAIT	NO OF RECORDS	MEAN	STANDARD DEVIATION	SIRES WITH PROGENY RECORDS	DAMS WITH PROGENY RECORDS
GFY I	2873	689.57	208.92	112	701
GFY II	2342	788.56	247.01	120	691
GFY III	779	665.15	175.19	27	129
STAPLE LENGTH	2073	6.14	1.36	99	440
CRIMP FREQUENCY	2073	0.91	0.36	99	440
FIBRE DIAMETER	2073	32.39	4.74	99	440
PURE FIBRES	2073	55.71	20.50	99	440
HETRO FIBRES	2073	33.10	14.36	99	440
HAIRY FIBRES	2073	11.19	10.26	99	440
MEDULLATED FIBRES	2073	44.29	20.50	99	440

Table 4.6 Estimated parameters and their standard errors for
greasy fleece yield at different clips from the best model
by univariate analysis of WOMBAT in Magra sheep

ITEMS ^a	GFYI	GFYII	GFYIII
MODEL	1	1	1
σ^2_a	8216.95	8323.29	6815.74
σ^2_m	-	-	-
σ_{am}	-	-	-
σ^2_c	-	-	-
σ²e	25292.70	26144.90	14557.80
σ² _p	33509.65	34468.19	21373.50
h²	0.25 ± 0.037	0.24 ± 0.039	0.32 ± 0.075
m²	-	-	-
r _{am}	-	-	-
C ²	-	-	-
h ² t	0.25	0.24	0.32
t _m	0.06	0.06	0.08

^a σ_{a}^{2} , σ_{m}^{2} , σ_{c}^{2} , σ_{e}^{2} and σ_{p}^{2} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma_{c}^{2}/\sigma_{p}^{2}$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT(Meyer, 2006). Table 4.7 Estimated parameters and their standard errors for staple length, crimp frequency and fibre diameter from the best model by univariate analysis of WOMBAT in Magra sheep

ITEMS ^a	STAPLE LENGTH	CRIMP FREQUENCY	FIBRE DIAMETER
MODEL	1	1	1
σ^{2}_{a}	0.56	0.01	2.77
σ^2_m	-	-	-
σ_{am}	-	-	-
σ^2_c	-	-	-
σ^2_{e}	1.24	0.11	17.66
$\sigma^{2}{}_{p}$	1.80	0.12	20.43
h²	0.31 ± 0.046	0.09 ± 0.033	0.14 ± 0.035
m²	-	-	-
r _{am}	-	-	-
C ²	-	-	-
h ² t	0.31	0.09	0.14
t _m	0.08	0.02	0.03

^a σ_{a}^{2} , σ_{r}^{2} , σ_{c}^{2} , σ_{e}^{2} and σ_{p}^{2} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h^{2} is heritability; c^{2} is $\sigma_{c}^{2}/\sigma_{p}^{2}$; t_{m} is maternal across year repeatability for ewe performance; h^{2}_{t} is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT(Meyer, 2006).

Table 4.8 Estimated parameters and their standard errors for pure, hetro, hairy and medullated fibres from the best model by univariate analysis of WOMBAT in Magra sheep

ITEMS ^a	PURE	HETRO	HAIRY	MEDULLATED
MODEL	1	1	1	1
σ^2_a	170.65	55.99	43.79	172.40
σ^2_m	-	-	-	-
σ_{am}	-	-	-	-
σ^2_c	-	-	-	-
σ^2_{e}	253.27	147.37	62.14	251.54
σ^2_p	423.92	203.35	105.93	423.93
h²	0.40 ± 0.046	0.28 ± 0.044	0.41 ± 0.045	0.41 ± 0.046
m²	-	-	-	-
r _{am}	-	-	-	-
C ²	-	-	-	-
h ² t	0.40	0.28	0.41	0.41
t _m	0.10	0.07	0.10	0.10

^a σ_{a}^{2} , σ_{r}^{2} , σ_{c}^{2} , σ_{e}^{2} and σ_{p}^{2} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h^{2} is heritability; c^{2} is $\sigma_{c}^{2}/\sigma_{p}^{2}$; t_m is maternal across year repeatability for ewe performance; h^{2}_{t} is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT(Meyer, 2006).

significant change in log likelihood but inflated the heritability estimate due to very high negative covariance between direct and maternal effects. It might be due to some hidden mechanism underlying phenotypic relation, which restricts genetic covariance at higher negative magnitude (Prince *et al.*, 2010). The antagonism between direct and maternal genetic effect was generally supported by several authors (Maria et al., 1993; Tosh and Kemp, 1994; Ligda et al., 2000; Ozcan et al., 2005; Safari et al., 2005), and the positive estimates of direct-maternal genetic correlations were also reported (Nasholm and Danell, 1996; Yazdi et al., 1997; Neser et al., 2001). The antagonism between the effects of an individual's genes for growth and those of its dam for a maternal ability might be due to natural selection for an intermediate optimum (Tosh and Kemp, 1994), however, the small amount of data and the structure of data could induce the antagonism too (Maria et al., 1993).

Thus, Model 1- the model with fewest random terms was chosen as the best model as per Likelihood ratio test (LRT) for all the wool traits under study.

4.2.2.1 Heritability estimates by animal model

The (co)variance components and genetic parameter estimates for different wool traits under study has been discussed as under the following heads:

4.2.2.1.1 Greasy fleece yield at first shearing

(Co)variance components along with the genetic parameters for greasy fleece yield at first clip (GFY I) from six different models are given in Table 4.9. The model including only direct additive effect (model 1) was sufficient to explain the variation in the first greasy fleece yield of lambs. In the model 1, the heritability for GFY I was 0.25 \pm 0.037. This moderate heritability estimate suggests further scope for improvement due to selection in the flock for higher fleece yield at first

clip. The estimate was in agreement with the findings of Safari *et al.* (2005), Gowane *et al.* (2010a) and Ciappesoni *et al.* (2013) as 0.25 ± 0.06 , 0.30 ± 0.00 and 0.29 in different wool breeds, Malpura and Merino sheep, respectively. Higher estimates than the present study were reported by Swan *et al.* (2008) as 0.43 ± 0.04 in Merino sheep. However, Gowane *et al.* (2010c) and Di *et al.* (2011) reported lower heritability estimates as 0.05 ± 0.03 and 0.14 ± 0.02 in Bharat Merino and Merino sheep, respectively.

The estimates of repeatability of ewe performance (t_m) and total heritability (h^2_t) were estimated as 0.06 and 0.25, respectively.

Addition of maternal genetic effect (m²) and maternal permanent environmental effect (c²) in model 2 and 4 respectively didn't change the heritability estimates. This indicates that all the genetic variation was due additive genetic effect. Addition of covariance between direct and maternal effects in model 3 and model 6 has shown negative and high estimate of r_{am} (-0.99), which resulted in highly inflated values of heritability and maternal effect in these models. In a more comprehensive model, i.e., model 5, we found h²= 0.25 ± 0.038, m²= 0.00 ± 0.019 and c² = 0.00 ± 0.022. However, all these models (2, 4 and 5) did not increase the likelihood and model 1 was considered best for studying variation in first greasy fleece yield.

4.2.2.1.2 Greasy fleece yield at second shearing

(Co)variance components along with the genetic parameters for greasy fleece yield at second clip (GFY II) from six different models are given in Table 4.10. The direct heritability estimate for GFY II from the best model (model 1) was found as 0.24 ± 0.039 . The moderate heritability estimate for GFY II in Magra sheep indicates further scope of genetic improvement in the trait through selection. Higher estimates than the present study were reported by Mandal *et al.* (2002) and Dixit *et al.* (2011) as 0.38 ± 0.06 and 0.54 ± 0.13 in Muzaffarnagri

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	8216.95	8230.46	26001.60	8232.94	8235.14	26054.70
σ^2_m	-	0.02	8938.80	-	0.004	8791.00
σ_{am}	-	-	-15072.00	-	-	-15039.70
σ²c	-	-	-	0.001	0.001	224.935
σ^2_e	25292.70	25283.10	15618.20	25281.40	25280.00	15468.20
σ^{2}_{p}	33509.65	33513.58	35486.60	33514.40	33515.10	35499.20
h ²	0.25 ± 0.037	0.25 ± 0.038	0.73 ± 0.078	0.25 ± 0.037	0.25 ± 0.038	0.73 ± 0.078
m²	-	0.00 ± 0.015	0.25 ± 0.038	-	0.00 ± 0.019	0.25 ± 0.040
r _{am}	-	-	-0.99 ± 0.019	-	-	-0.99 ± 0.023
C ²	-	-	-	0.00 ± 0.018	0.00 ± 0.022	0.006 ± 0.019
h ² t	0.25	0.25	0.22	0.25	0.25	0.22
t _m	0.06	0.06	0.01	0.06	0.06	0.01
Log L	-16308.75	-16308.75	16260.13	-16308.75	-16308.75	-16260.07

Table 4.9: Estimates of (co)variance components (g²) and genetic parameters for greasy fleece yield at first clip inMagra sheep

Column in bold represents estimates from best model as per LRT.

 $\sigma^{2}_{a}, \sigma^{2}_{m}, \sigma^{2}_{c}, \sigma^{2}_{e}$ and σ^{2}_{p} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma^{2}_{c}, \sigma^{2}_{p}$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT(Meyer, 2006).

6.10 5.67 5.16 35
5.67 5.16 \$5
5.16
ì5
4.30
1.50
0.069
0.042
0.052
0.026
5
)1
2.31

Table 4.10: Estimates of (co)variance components (g²) and genetic parameters for greasy fleece yield at second clip in Magra sheep

Column in bold represents estimates from best model as per LRT. ^a σ^2_{a} , σ^2_{n} , σ^2_{c} , σ^2_{c} , σ^2_{e} and σ^2_{p} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h^2 is heritability; c^2 is σ_c^2/σ_p^2 ; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006). and Bharat Merino sheep, respectively. However, Singh and Kushwaha (1995) and Sharma et al. (1999) estimated lower heritability as 0.18 ± 0.13 and 0.02 ± 0.14 in Bharat Merino and Nali sheep, respectively.

Estimate of repeatability of ewe performance (t_m) for GFY II was low in magnitude as 0.06 in Magra sheep. In the current study, moderate estimate of total heritability (h^2_t) was found as 0.24.

No evidence of maternal genetic effect (m^2) and maternal permanent environmental effect (c^2) was found in the present study. However, inclusion of covariance between direct and maternal effects in model 3 and model 6 increased the logarithm of the likelihood function, but due to negative and high values of r_{am} (-0.97), the inflated values of direct and maternal genetic heritability can't be accepted. Thus, model 1 was considered best for studying variation in second greasy fleece yield.

4.2.2.1.3 Greasy fleece yield at third shearing

(Co)variance components along with the genetic parameters for greasy fleece yield at third clip (GFY III) from six different models are given in Table 4.11. The log-L values did not change significantly in all the six models for GFY III. Thus, the model with fewest random terms i.e., model 1 was chosen as the best model as per Likelihood ratio test (LRT). The direct heritability estimate for GFY III from model 1 was estimated as 0.32 ± 0.075 . The moderate estimate of heritability for GFY III in Magra sheep indicates the presence of additive genetic variance in the flock which can be exploited through selection for further genetic improvement of the trait.

The estimates of repeatability of ewe performance (t_m) and total heritability (h^2_t) were estimated as 0.08 and 0.32, respectively.

Addition of maternal genetic effect to direct additive effect in model 2 didn't increase the likelihood over model 1. Estimate of

maternal additive effect (m²) for GFY III in model 2 was also found to be very low (0.01 ± 0.036). In model 3, an inflated h² estimate was observed (0.53), probably due to a very high negative covariance between direct and maternal effect, which resulted in -0.90 estimate of r_{am}. Similar results were found in model 6. In the more comprehensive model, i.e., Model 5, we found h²= 0.31 ± 0.079, m²=0.01 ± 0.045 and c²= 0.00 ± 0.062. No evidence of maternal permanent environmental effect (c²) was found in the present study. Also, these models were not superior to model 1 due to no significant increment in log-likelihood value.

4.2.2.1.4 Staple length

Estimates of (co)variance components along with the genetic parameters for staple length from six different models are given in Table 4.12. For staple length, model 1 explained 31% variance through direct heritability. Addition of m² in model 2 and c² in model 4 did not influence the heritability estimate. However, addition of σ_{am} in model 3 inflated the heritability estimate due to very high negative covariance between direct and maternal effects (ram = -0.91). Similar finding was seen in model 6 where σ_{am} was included in the analysis. Thus, model 1- the model with the fewest random terms was studied for genetic parameter estimates of staple length.

The direct heritability estimate for staple length from model 1 was estimated as 0.31 ± 0.046 . Higher estimates than the present study were reported by Swan *et al.* (2008) and Ciappesoni *et al.* (2013) as 0.54 ± 0.03 and 0.40, respectively, in Merino sheep. However, Naidoo *et al.* (2004) and Di *et al.* (2011) found lower estimates as 0.25 ± 0.04 and 0.22 ± 0.04 , respectively, in Merino sheep.

The estimates of repeatability of ewe performance (t_m) and total heritability (h^2_t) were estimated as 0.08 and 0.31, respectively.

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	6815.74	6704.40	11507.20	6815.85	6714.50	11511.70
σ^2_m	-	206.16	3432.99	-	201.46	3437.64
σ _{am}	-	-	-5669.60	-	-	- 5673.95
σ^2_c	-	-	-	0.01	0.35	0.02
σ^2_{e}	14557.80	14469.10	12293.60	14557.90	14466.60	12289.70
σ^2_p	21373.50	21379.70	21564.10	21373.70	21382.90	21565.10
h²	0.32 ± 0.075	0.31 ± 0.079	0.53 ± 0.137	0.32 ± 0.078	0.31 ± 0.079	0.53 ± 0.137
m²	-	0.01 ± 0.036	0.16 ± 0.082	-	0.01 ± 0.045	0.16 ± 0.088
r _{am}	-	-	-0.90 ± 0.103	-	-	- 0.90 ± 0.128
C ²	-	-	-	0.00 ± 0.048	0.00 ± 0.062	0.00 ± 0.058
h ² t	0.32	0.32	0.22	0.32	0.32	0.22
t _m	0.08	0.09	0.03	0.08	0.09	0.03
Log L	- 4133.65	- 4133.60	- 4127.73	- 4133.65	- 4133.60	- 4127.73

Table 4.11: Estimates of (co)variance components (g²) and genetic parameters for greasy fleece yield at third clip inMagra sheep

Column in bold represents estimates from best model as per LRT.

 $^{a}\sigma_{a}^{2}, \sigma_{m}^{2}, \sigma_{c}^{2}, \sigma_{e}^{2}$ and σ_{p}^{2} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma_{c}^{2}/\sigma_{p}^{2}$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006).

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	0.56	0.56	1.19	0.56	0.56	1.19
σ^2_m	-	0.002	0.35	-	0.00	0.35
σ _{am}	-	-	- 0.58	-	-	- 0.58
σ^2_c	-	-	-	0.02	0.02	0.001
σ^2_{e}	1.24	1.24	0.90	1.22	1.22	0.90
σ^{2}_{p}	1.80	1.80	1.85	1.80	1.80	1.85
h²	0.31 ± 0.046	0.31 ± 0.048	0.64 ± 0.088	0.31 ± 0.047	0.31 ± 0.048	0.64 ± 0.088
m²	-	0.001 ± 0.020	0.19 ± 0.047	-	0.00 ± 0.025	0.19 ± 0.053
r _{am}	-	-	-0.91 ± 0.046	-	-	- 0.91 ± 0.059
C ²	-	-	-	0.01 ± 0.024	0.01 ± 0.030	0.00 ± 0.030
h ² t	0.31	0.31	0.26	0.32	0.31	0.26
t _m	0.08	0.08	0.03	0.09	0.09	0.03
Log L	-1584.96	-1584.96	-1563.94	-1584.87	-1584.87	-1563.94

Table 4.12: Estimates of (co)variance components (cm²) and genetic parameters for staple length in Magra sheep

Column in bold represents estimates from best model as per LRT.

^a σ^2_{a} , σ^2_{c} , σ^2_{e} , σ^2_{e} , σ^2_{e} and σ^2_{p} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma^2_{c}/\sigma^2_{p}$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006)

4.2.2.1.5 Crimp frequency

(Co)variance components along with the genetic parameters for crimp frequency from six different models have been presented in Table 4.13. The log-L values did not change significantly in all the six models for crimp frequency. Thus, the model with lowest parameters fitted i.e., model 1 was chosen as the best model as per Likelihood ratio test (LRT). The direct heritability estimate from model 1 was estimated as 0.09 ± 0.033 . The low estimate of heritability for crimp frequency in Magra sheep indicates little scope of genetic improvement in the trait through selection. There is very little information about the estimation of genetic parameters for crimp frequency in the literature. However, Safari *et al.* (2005) estimated higher estimates of heritability for crimp frequency as 0.41 ± 0.03 in different wool breeds of sheep.

The estimates of repeatability of ewe performance (t_m) and total heritability (h^2_T) were estimated as 0.02 and 0.09, respectively.

Addition of maternal genetic effect to direct additive effect in model 2 didn't increase the likelihood over model 1. In model 3, an inflated h^2 estimate was observed as 0.16 ± 0.056, probably due to a very high negative covariance between direct and maternal effect, which resulted in r_{am} converging to zero. Similar results were found in model 6. In the more comprehensive model, i.e., Model 5, we found no change in the heritability estimate. Thus, it can be concluded that direct maternal genetic (m²) and maternal permanent environmental effect (c²) didn't affect crimp frequency in the present study.

4.2.2.1.6 Fibre diameter

(Co)variance components along with the genetic parameters for fibre diameter from six different models have been presented in Table 4.14.

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	0.01	0.01	0.02	0.01	0.01	0.02
σ^2_m	-	0.00	0.002	-	0.00	0.002
σ _{am}	-		-0.006	-	-	-0.006
σ^2_c	-		-	0.00	0.00	0.00
σ²e	0.11	0.11	0.10	0.11	0.11	0.10
$\sigma^{2}{}_{p}$	0.12	0.12	0.12	0.12	0.12	0.12
h ²	0.09 ± 0.033	0.09 ± 0.034	0.16 ± 0.056	0.09 ± 0.033	0.09 ± 0.034	0.16 ± 0.056
m ²	-	0.00 ± 0.019	0.02 ± 0.030	-	0.00 ± 0.025	0.02 ± 0.032
r _{am}	-	-	-1.00 ± 0.529	-	-	-1.00 ± 0.696
C ²	-	-	-	0.00 ± 0.023	0.00 ± 0.029	0.00 ± 0.028
h ² t	0.09	0.09	0.09	0.09	0.09	0.09
t _m	0.02	0.02	0.01	0.02	0.02	0.01
Log L	1147.79	1147.79	1150.26	1147.79	1147.79	1150.26

Table 4.13: Estimates of (co)variance components (per cm²) and genetic parameters for crimp frequency in Magra sheep

Column in bold represents estimates from best model as per LRT.

 ${}^{a}\sigma_{a}^{2}, \sigma_{p}^{2}, \sigma_{e}^{2}$ and σ_{p}^{2} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma_{c}^{2}/\sigma_{p}^{2}$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006).

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	2.77	2.70	3.65	2.77	2.70	3.65
σ^2_m	-	0.10	0.69	-	0.10	0.69
σ_{am}	-		- 0.86	-	-	- 0.86
σ²c	-		-	0.00	0.00	0.00
σ²e	17.67	17.63	17.02	17.67	17.63	17.02
σ^2_p	20.43	20.43	20.50	20.43	20.43	20.50
h²	0.14 ± 0.035	0.13 ± 0.038	0.18 ± 0.057	0.14 ± 0.036	0.13 ± 0.038	0.18 ± 0.057
m ²	-	0.01 ± 0.018	0.03 ± 0.032	-	0.01 ± 0.023	0.03 ± 0.036
r _{am}	-	-	-0.54 ± 0.251	-	-	-0.54 ± 0.274
C ²	-	-	-	0.00 ± 0.023	0.00 ± 0.030	0.00 ± 0.030
h ² t	0.14	0.13	0.13	0.14	0.13	0.13
t _m	0.03	0.04	0.04	0.03	0.04	0.04
Log L	- 4180.69	- 4180.65	- 4179.98	- 4180.69	- 4180.65	- 4179.98

Table 4.14: Estimates of (co)variance components (μ^2) and genetic parameters for fibre diameter in Magra sheep

Column in bold represents estimates from best model as per LRT.

 $^{a}\sigma_{a}^{2}, \sigma_{m}^{2}, \sigma_{c}^{2}, \sigma_{e}^{2}$ and σ_{p}^{2} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma_{c}^{2}/\sigma_{p}^{2}$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006).

The direct heritability estimate from the best model (Model 1) was estimated as 0.14 ± 0.035 . Low heritability estimate indicates the presence of low additive genetic variance which hampers the selection procedure for the trait. Higher heritability estimates than the present study were reported by Naidoo *et al.* (2004), Swan *et al.* (2008) and Ciappesoni *et al.* (2013) as 0.61 ± 0.04 , 0.66 ± 0.02 and 0.74 in Merino breed of sheep. However, the estimate was slightly in agreement with the findings of Di *et al.* (2011) as 0.26 ± 0.05 in Merino sheep.

Addition of direct maternal genetic effect (m²) in model 2 showed that maternal genetic variance has contributed to only 1% of the total phenotypic variance. Maternal permanent environmental effect was not evident at all in model 4. Similar values were also observed in model 5 that fitted the direct additive, maternal genetic and maternal environmental effect separately in one model. Addition of σ_{am} in model 3 and model 6 didn't increased the heritability estimate to a greater extent as the covariance between direct and maternal effects ($r_{am} = -$ 0.54) wasn't very high as compared to other traits studied earlier. However, Model 1 was used because it was not significantly different from other models and also because it was less complex.

4.2.2.1.7 Pure fibres

(Co)variance components along with the genetic parameters for pure fibres from six different models have been presented in Table 4.15. The model including only direct additive effect (model 1) was sufficient to explain the variation in the pure fibres. In the model 1, the heritability estimate was 0.40 ± 0.046 . There is little information about the estimation of genetic parameters for pure fibres by animal model in the literature. Thus, the estimated value of heritability has been compared with the heritability estimated by various workers by paternal half sib method. The estimate was in agreement with the findings of Behdad *et al.* (2013) as 0.34 ± 0.38 in Bakhtiari sheep. Higher estimates than the present study were reported by Dashab *et al.* (2012) as 0.65 ± 0.44 in Baluchi sheep. However, Nehra *et al.* (2005) found lower estimates than the present study as 0.02 ± 0.10 in Marwari sheep.

The estimates of repeatability of ewe performance (t_m) and total heritability (h^2_t) were estimated as 0.10 and 0.40, respectively. This high heritability estimate suggests further scope for improvement due to selection in the flock for higher percentage of pure fibres.

Addition of maternal genetic effect (m²) and maternal permanent environmental effect (c²) in model 2 and 4, respectively, didn't brought significant change in heritability estimates. However, m² and c² account 1% and 2% proportion of total phenotypic variance in model 2 and 4, respectively. Estimates from the comprehensive model, Model 5, which attempted independent estimation of m² and c² were found as: h²= 0.39 \pm 0.050, m²= 0.00 \pm 0.023 and c² = 0.02 \pm 0.027. It suggested that all the maternal effects were environmental in origin, and there was no evidence for direct maternal effect as variance converged to zero. Addition of σ_{am} in model 3 and model 6 didn't inflate the heritability estimate to a greater extent as the covariance between direct and maternal effects (r_{am} = -0.54) wasn't very high as compared to most of the traits under study. However, all these models did not increase the likelihood and the model with the fewest random terms (model 1) was considered best for studying variation in pure fibres.

4.2.2.1.8 Hetro fibres

(Co)variance components along with the genetic parameters for hetro fibres from six different models have been presented in Table 4.16. The heritability estimate for hetro fibres from model 1 was estimated as 0.28 ± 0.044 . Moderate heritability estimate indicates that the trait can be improved through selection. Nehra *et al.* (2005) and

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	170.65	165.62	216.22	165.96	165.96	219.80
σ^2_m	-	4.55	23.66	-	0.005	15.40
σ_{am}	-	-	- 38.07	-	-	- 37.86
σ^2_c	-	-	-	8.97	8.97	11.94
σ²e	253.27	253.16	226.17	248.36	248.36	219.18
σ^{2}_{p}	423.92	423.33	427.98	423.30	423.30	428.46
h²	0.40 ± 0.046	0.39 ± 0.050	0.51 ± 0.080	0.39 ± 0.048	0.39 ± 0.050	0.51 ± 0.080
m²	-	0.01 ± 0.020	0.06 ± 0.034	-	0.00 ± 0.023	0.04 ± 0.034
r _{am}	-	-	-0.53 ± 0.151	-	-	- 0.65 ± 0.231
C ²	-	-	-	0.02 ± 0.022	0.02 ± 0.027	0.03 ± 0.027
h ² t	0.40	0.40	0.40	0.39	0.39	0.40
t _m	0.10	0.11	0.09	0.12	0.12	0.10
Log L	- 7257.29	- 7257.14	- 7254.51	- 7256.76	- 7256.76	- 7253.96

Table 4.15: Estimates of (co)variance components (%²) and genetic parameters for pure fibres in Magra sheep

Column in bold represents estimates from best model as per LRT.

^a $\sigma^2_{a}, \sigma^2_{m}, \sigma^2_{c}, \sigma^2_{e}$ and σ^2_{p} are additive genetic, maternal across year repeatability for ewe performance; h²_i is total heritability; c² is σ^2_c/σ^2_p ; t_m is maternal across year repeatability for ewe performance; h²_i is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006).

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	55.99	53.30	72.49	54.30	53.51	73.05
σ^2_m	-	2.53	11.89	-	1.06	9.75
σ _{am}	-	-	-16.13	-	-	-15.85
σ^2_c	-	-	-	3.59	2.86	3.14
σ²e	147.37	147.23	136.41	145.26	145.63	134.64
σ^2_p	203.35	203.06	204.66	203.15	203.07	204.74
h²	0.28 ± 0.044	0.26 ± 0.048	0.35 ± 0.075	0.27 ± 0.046	0.26 ± 0.048	0.36 ± 0.075
m ²	-	0.01 ± 0.020	0.06 ± 0.035	-	0.01 ± 0.023	0.05 ± 0.038
r _{am}	-	-	-0.55 ± 0.163	-	-	-0.59 ± 0.194
C ²	-	-	-	0.02 ± 0.023	0.01 ± 0.028	0.02 ± 0.028
h ² t	0.28	0.27	0.27	0.27	0.27	0.26
t _m	0.07	0.08	0.07	0.08	0.09	0.07
Log L	- 6546.79	-6546.57	-6544.58	-6546.46	-6546.43	-6544.43

Table 4.16: Estimates of (co)variance components (%²) and genetic parameters for hetro fibres in Magra sheep

Column in bold represents estimates from best model as per LRT.

 $^{a}\sigma_{a}^{2}, \sigma_{m}^{2}, \sigma_{c}^{2}, \sigma_{e}^{2}$ and σ_{p}^{2} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma_{c}^{2}/\sigma_{p}^{2}$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006).

Dashab *et al.* (2012) found lower estimates than the present study as 0.03 ± 0.10 and 0.16 ± 0.09 in Marwari and Baluchi breed of sheep.

The estimates of repeatability of ewe performance (t_m) and total heritability (h²t) were estimated as 0.07 and 0.28, respectively. Addition of maternal genetic and maternal permanent environmental effect in model 2 and 4, respectively, didn't cause any significant change in the heritability estimate and the log- likelihood values. The estimated values for m² and c² in model 2 and 4, respectively, were estimated as 0.01 ± 0.020 and 0.02 ± 0.023. In model 5, the estimates of h², m² and c² were 0.26 ± 0.048, 0.01 ± 0.023 and 0.01 ± 0.028, respectively. Inclusion of covariance between animal and maternal effect also resulted in very low estimate of maternal genetic and permanent environmental heritability. Hence, it was concluded that for genetic (m²) and maternal permanent environmental effects (c²) are not important and selection process should be focused on only additive genetic effect of the animal.

4.2.2.1.9 Hairy fibres

(Co)variance components along with the genetic parameters for hairy fibres from six different models have been presented in Table 4.17. The heritability estimate for hairy fibres from the best model was estimated as 0.28 ± 0.044 . Lower estimates of heritability than the present study was reported by Dashab *et al.* (2012) as 0.20 ± 0.08 in Baluchi sheep. The estimates of repeatability of ewe performance (t_m) and total heritability (h²_t) were estimated as 0.10 and 0.41, respectively.

As the log- likelihood values were not significantly different among the six models, model 1, simple univariate model with the fewest parameters fitted was chosen best for studying the genetic parameters of hairy fibres in Magra sheep. Maternal genetic and maternal permanent environmental effects were not observed to affect the trait.

4.2.2.1.9 Medullated fibres

(Co)variance components along with the genetic parameters for medullation percentage from six different models have been presented in Table 4.18. The heritability estimate for hetro fibres from model 1 was estimated as 0.41 ± 0.046 . High estimate of heritability indicates that the trait can be improved through selection. Higher heritability than the present study was reported by Sharma *et al.* (2000) as 0.75 ± 0.35 in Marwari and Nali breed of sheep. However, Dixit *et al.* (2011) reported lower estimate as 0.15 ± 0.10 in Bharat Merino sheep.

The estimates of repeatability of ewe performance (t_m) and total heritability (h²t) were estimated as 0.10 and 0.41, respectively. Addition of maternal genetic and maternal permanent environmental effect in model 2 and 4, respectively, didn't cause any significant change in the heritability estimate and the log- likelihood values. The estimated values for m² and c² in model 2 and 4, respectively, were estimated as 0.01 \pm 0.020 and 0.02 \pm 0.022. In a more comprehensive model i.e., model 5, the estimates of h², m² and c² were 0.40 \pm 0.050, 0.00 \pm 0.023 and 0.021 \pm 0.027, respectively. Inclusion of covariance between animal and maternal effect in model 3 and model 6 also resulted in very low estimate of maternal genetic and permanent environmental heritability.

This clearly indicates that maternal effects were not important and thus, may not be considered while formulating breeding plans for improvement of this trait in Magra sheep population under study.

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	43.80	42.91	59.60	43.80	42.92	59.60
σ^2_m	-	0.90	7.32	-	0.90	7.31
σ_{am}	-	-	-13.00	-	-	-13.00
σ^2_c	-	-	-	0.00	0.00	0.00
σ²e	62.14	62.03	53.27	62.14	62.03	53.27
σ^{2}_{p}	105.93	105.85	107.18	105.93	105.85	107.18
h²	0.41 ± 0.045	0.41 ± 0.049	0.56 ± 0.079	0.41 ± 0.046	0.41 ± 0.049	0.56 ± 0.080
m²	-	0.01 ± 0.019	0.07 ± 0.035	-	0.01 ± 0.023	0.07 ± 0.039
r _{am}	-	-	-0.62 ± 0.119	-	-	-0.62 ± 0.141
C ²	-	-	-	0.00 ± 0.021	0.00 ± 0.026	0.00 ± 0.027
h ² t	0.41	0.41	0.41	0.41	0.41	0.41
t _m	0.10	0.11	0.09	0.10	0.11	0.09
Log L	-5803.34	-5803.22	-5798.08	-5803.34	-5803.22	-5798.08

Table 4.17: Estimates of (co)variance components (%²) and genetic parameters for hairy fibres in Magra sheep

Column in bold represents estimates from best model as per LRT.

 $^{a}\sigma_{a}^{2}, \sigma_{m}^{2}, \sigma_{c}^{2}, \sigma_{e}^{2}$ and σ_{p}^{2} are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma_{c}^{2}/\sigma_{p}^{2}$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006).

ITEMS ^a	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
σ^2_a	172.40	166.91	219.32	167.64	167.64	222.33
σ^2_m	-	5.00	25.42	-	0.01	17.28
σ_{am}	-	-	- 40.00	-	-	-39.54
σ²c	-	-	-	9.01	9.00	11.38
σ²e	251.54	251.39	223.31	246.64	246.64	216.94
σ^{2}_{p}	423.93	423.30	428.04	423.29	423.29	428.40
h²	0.41 ± 0.046	0.39 ± 0.050	0.51 ± 0.080	0.40 ± 0.048	0.40 ± 0.050	0.52 ± 0.080
m²	-	0.01 ± 0.020	0.06 ± 0.034	-	0.00 ± 0.023	0.04 ± 0.035
r _{am}	-	-	-0.54 ± 0.145	-	-	-0.64 ± 0.210
C ²	-	-	-	0.02 ± 0.022	0.02 ± 0.027	0.03 ± 0.027
h ² t	0.41	0.40	0.40	0.40	0.40	0.40
t _m	0.10	0.11	0.09	0.12	0.12	0.10
Log L	-7266.05	-7265.87	-7263.02	-7265.52	-7265.52	-7262.52

Table 4.18: Estimates of (co)variance components (%²) and genetic parameters for medulated fibres in Magra sheep

Column in bold represents estimates from best model as per LRT.

 $a \sigma_{a}^2, \sigma_{m}^2, \sigma_{c}^2, \sigma_{e}^2$ and σ_{p}^2 are additive genetic, maternal additive genetic, maternal permanent environmental, residual variance and phenotypic variance, respectively; h² is heritability; c² is $\sigma_{c}^2/\sigma_{p}^2$; t_m is maternal across year repeatability for ewe performance; h²_t is total heritability and log-L is log-likelihood for the best model obtained from WOMBAT (Meyer, 2006).

4.2.2.2 Genetic correlations by animal model

The genetic correlations of first greasy fleece yield with greasy fleece yield at second and third clip were estimated as 0.32 ± 0.116 and 0.67 ± 0.131 , respectively. The positive and moderate to high genetic correlations between GFY at different clips indicate that lambs with heavier fleece at first clip might have heavier fleece at subsequent clips also. The result was in accordance with the findings of Mandal *et al.* (2002) and Dixit *et al.* (2011) in Muzaffarnagri and Bharat Merino sheep, respectively.

The genetic correlation of greasy fleece yield at second clip with greasy fleece yield at third clip was estimated as 0.94 ± 0.108 . The positive and high genetic correlation between GFY II and GFY III indicates that if selection is practiced for high greasy fleece yield at second clip, it will subsequently improves yield at third clip also.

The genetic correlations of staple length with crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres were estimated as -0.06 ± 0.187 , -0.33 ± 0.146 , -0.24 ± 0.103 , 0.15 ± 0.121 , 0.34 ± 0.098 and 0.22 ± 0.103 , respectively. Desirable genetic correlation was found between staple length and fiber diameter which indicates that if selection is practiced to improve staple length, it might improve fibre diameter also. However, such a selection process might cause slight increase in medullation percentage. It is due to antagonism among these traits. However, the standard error for the estimates of genetic correlations were found high which clearly indicates that more number of observations are required to arrive at these conclusions. The result was in accordance with the findings of Safari *et al.* (2005) in different wool breeds; Di *et al.* (2011) and Ciappesoni *et al.* (2013) in Merino; and Khan *et al.* (2015) in Rambouillet breed of sheep.

The genetic correlations of crimp frequency with fibre diameter, pure, hetro, hairy and medullated fibres were estimated as -0.68 \pm 0.166, 0.58 \pm 0.138, -0.51 \pm 0.163, -0.61 \pm 0.133 and -0.58 \pm 0.136, respectively.

The genetic correlations of fibre diameter with pure, hetro, hairy and medullated fibres were estimated as -0.92 ± 0.054 , 0.90 ± 0.074 , 0.69 ± 0.081 and 0.85 ± 0.067 , respectively. The result was in accordance with the findings of Nehra *et al.* (2005) in Marwari sheep.

The genetic correlations of pure fibres with hetro, hairy and medullated fibres were estimated as -0.97 ± 0.011 , -0.91 ± 0.025 and -1.00 ± 0.010 respectively. The result was in accordance with the findings of Nehra *et al.* (2005) in Marwari sheep.

The genetic correlation of hetro fibres with hairy and medullated fibres was estimated as 0.85 ± 0.057 and 0.97 ± 0.011 , respectively; and between hairy and medullated fibres was estimated as 0.91 ± 0.025 .

Results clearly indicate that the estimates of genetic correlations by bivariate animal model for most of the traits under study are in same range with those estimated by paternal half sib method. So, for the estimation of genetic correlations between these traits, either of the two methods can be used. However, large variations were found in genetic correlation estimates between certain traits viz. staple length- fibre diameter, crimp frequency- hairy fibres, fibre diameter- hairy fibres and hetro-hairy fibres.

4.2.2.3 Phenotypic correlations by animal model

The phenotypic correlations of first greasy fleece yield with greasy fleece yield at second and third clip were estimated as 0.12 ± 0.023 and 0.12 ± 0.037 , respectively. The result was similar with the

findings of Sharma *et al.* (1999), Mandal *et al.* (2002) and Dixit *et al.* (2011) in Nali, Muzaffarnagri and Bharat Merino sheep, respectively.

The phenotypic correlation of greasy fleece yield at second clip with greasy fleece yield at third clip was estimated as 0.31 ± 0.035 .

The phenotypic correlations of staple length with crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres was estimated as 0.03 ± 0.023 , 0.05 ± 0.024 , -0.07 ± 0.025 , 0.01 ± 0.025 , 0.12 ± 0.025 and 0.06 ± 0.025 , respectively. The result was in accordance with the findings of Mehta *et al.* (1998) in Magra sheep, Safari *et al.* (2005) in different wool breeds; Di *et al.* (2011) and Ciappesoni *et al.* (2013) in Merino; and Khan *et al.* (2015) in Rambouillet breed of sheep.

The phenotypic correlations of crimp frequency with fibre diameter, pure, hetro, hairy and medullated fibres was estimated as - 0.19 ± 0.022 , 0.20 ± 0.022 , -0.15 ± 0.022 , -0.20 ± 0.023 and -0.20 ± 0.022 , respectively. The result was in accordance with the findings of Mehta *et al.* (1998) in Magra sheep.

The phenotypic correlations of fibre diameter with pure, hetro, hairy and medullated fibres was estimated as -0.51 ± 0.017 , 0.32 ± 0.021 , 0.57 ± 0.016 and 0.50 ± 0.017 , respectively. The result was in accordance with the findings of Mehta *et al.* (1998) and Nehra *et al.* (2005) in Magra and Marwari sheep, respectively.

The phenotypic correlations of pure fibres with hetro, hairy and medullated fibres was estimated as -0.89 ± 0.005 , -0.76 ± 0.010 and -1.00 ± 0.013 , respectively. The result was in accordance with the findings of Mehta *et al.* (1998) and Nehra *et al.* (2005) in Magra and Marwari sheep, respectively.

Table 4.19 (a): Estimates of genetic and phenotypic correlation for wool yield in Magra sheep by multivariate model of WOMBAT

	GFY I	GFY II	GFY III	
GFY I -		0.32 ± 0.116	0.67 ± 0.131	
GFY II 0.12 ± 0.023		-	0.94 ± 0.108	
GFY III	0.12 ± 0.037	0.31 ± 0.035	-	

Values above and below the diagonal are genetic and phenotypic correlations, respectively.

Table 4.19 (b): Estimates of genetic and phenotypic correlation forwoolqualitytraitsinMagrasheepbymultivariate model of WOMBAT

	S.L	C.F	F.D	PURE	HETRO	HAIRY	MED
S.L	-	-0.06 ±0.187	0.33 ±0.146	-0.24 ±0.103	0.15 ±0.121	0.34 ±0.098	0.22 ±0.103
C.F	0.03 ±0.023	-	-0.68 ±0.166	0.58 ±0.138	-0.51 ±0.163	-0.61 ±0.133	-0.58 ±0.136
F.D	0.05 ±0.024	-0.19 ±0.022	-	-0.92 ±0.054	0.90 ±0.074	0.69 ±0.081	0.85 ±0.067
PURE	-0.07 ±0.025	0.20 ±0.022	-0.51 ±0.017	-	-0.97 ±0.011	-0.91 ±0.025	-1.00 ±0.010
HETRO	0.01 ±0.025	-0.15 ±0.022	0.32 ±0.021	-0.89 ±0.005	-	0.85 ±0.057	0.97 ±0.011
HAIRY	0.12 ±0.025	-0.20 ±0.023	0.57 ±0.016	-0.76 ±0.010	0.41 ±0.020	-	0.91 ±0.025
MED	0.06 ±0.025	-0.20 ±0.022	0.50 ±0.017	-1.00 ±0.013	0.89 ±0.005	0.76 ±0.010	-

Values above and below the diagonal are genetic and phenotypic correlations, respectively.

The phenotypic correlation of hetro fibres with hairy and medullated fibres was estimated as 0.41 ± 0.020 and 0.89 ± 0.005 , respectively; and between hairy and medullated fibres was estimated as 0.76 ± 0.010 . The result was in accordance with the findings of Mehta *et al.* (1998) and Nehra *et al.* (2005) in Magra and Marwari sheep, respectively.

Phenotypic correlations between all the traits estimated by animal model were same as were estimated by sire model. This clearly indicated that either of the two methods can be used for estimation of phenotypic correlations between wool production and quality traits.

4.3 Polymorphism of keratin genes (KIF- I and KAP 11-1 genes)

Variations at DNA level play important role in the genetic characterization of livestock populations. This may also help in identification of possible hybridization events as well as past evolutionary trends. Variation in the exonic region of a gene may lead to changes in amino acid sequences which can alter the structure of expressed protein. In livestock, such variations in DNA may also be associated with, or linked to, economic traits, which are governed by polygenes, each having a small effect (Gelderman, 1997). However, the major gene model suggests that only a few genes may account for relatively large proportion of the genetic variation (Lande, 1981). Such major genes are usually involved in the biology of a trait and are candidate genes for marker identification.

Among the candidate genes responsible for wool production and quality, keratin genes were investigated in the present study to characterize the genetic variation in Magra sheep breed of Rajasthan. The results regarding polymorphism of keratin genes have been discussed under the following heads:

- 4.3.1 Polymorphism of keratin intermediate filament type I gene (KIF- I)
- 4.3.2 Polymorphism of keratin associated protein 11-1 gene (KAP- 11-1)

4.3.1 Polymorphism of keratin intermediate filament type I gene (KIF- I)

The present investigation was undertaken to study the polymorphism of KIF- I gene at locus KRT1.2 using PCR-RFLP technique in Magra sheep and the results have been discussed below:

4.3.1.1 Genomic DNA isolation and Quality check up

Genomic DNA was extracted from 162 blood samples using Blood Genomic DNA Isolation Kit (HIMEDIA Ltd). The extracted DNA from each sample was stored in a deep freezer at -20°C till further use.

The quality of genomic DNA was checked on 1.2% agarose gel electrophoresis and visualized with ethidium bromide under UV transilluminator. Only the samples that showed clear distinct bands were selected for further investigation. Concentration and purity of DNA was also checked by nano-spectrophotometer. Samples showing absorbance ratio between 1.7-1.9 at 360/380 nm wavelength and concentration above 30 ng/ μ L were considered for further analysis.

Agarose gel electrophoretograms for different DNA samples have been presented in Fig. 3.

4.3.1.2 PCR amplification of KIF- I gene
A PCR gradient was tried at different annealing temperatures to optimize the annealing temperature at which amplification of the KIF gene is to be done. The best results were obtained at 58°C.

After optimization of PCR, amplification of the KIF gene was done from genomic DNA isolated from blood samples of Magra sheep. The standardized programme followed for amplification of KIF type I gene is shown in Table 3.7. PCR products were resolved on 2% agarose gel and visualized with ethidium bromide under U.V transilluminator. PCR products (amplicon) containing the segment of KRT 1.2 locus were of approximately 480 bp size. Agarose gel electrophoretograms for PCR product of KIF gene along with 100 bp DNA Ladder have been presented in Fig. 4.

4.3.1.3 Detection of genetic variation in KIF- I gene by Restriction Fragment Length Polymorphism (RFLP)

The PCR amplified product of KIF type I gene was cleaved by MspI restriction enzyme at 37 °C for 16 hours. The RE digested products were electrophoresed in 8 % Polyacrylamide gel electrophoresis.

The genotypic patterns were visualised by ethidium bromide staining and presented in Fig. 5. Following PCR-RFLP were generated by the KRT 1.2 Msp I RFLP polymorphisms : 159, 126, 100 and 95 bp for AA genotype ; 259, 126 and 95 for BB genotype ; and 259, 159, 126, 100 and 95 bp for AB genotype. Similar banding patterns for the three genotypes were also found by Arora *et al.* (2008) in Indian sheep breeds, and Ahlawat *et al.* (2014) in Patanwari, Marwari and Dumba breeds of sheep.

4.3.1.4 Analysis of genotypic and allelic frequencies of KIF- I gene

Estimated genotypic and allelic frequencies of the KIF-I gene at

KRT 1.2 locus in Magra sheep has been presented in Table 4.20. Restriction Fragment Length Polymorphism of KRT1.2 locus revealed three genotypes, viz. AA, AB and BB with genotypic frequencies 0.49, 0.43 and 0.08, respectively in Magra sheep. The allelic frequencies for A and B allele were estimated as 0.71 and 0.29, respectively. The estimated genotypic and allelic frequencies are in close agreement with the findings of Arora *et al.* (2008) in native Indian sheep breeds and Ahlawat *et al.* (2014) in Marwari, Patanwadi and Dumba sheep.

The observed and expected genotypic frequencies along with the Chi- square values have been presented in Table 4.21. The Chisquare test for Hardy Weinberg equilibrium indicated non-significant differences (P>0.05) among the genotypic and gene frequencies with respect to KIF-I gene (χ^2 = 0.3427). Hence, it was inferred that Magra population was in Hardy Weinberg equilibrium with respect to KIF-I gene. Arora *et al.* (2008) in native Indian sheep breeds and Ahlawat *et al.* (2014) in Marwari, Patanwadi and Dumba sheep also reported that allelic frequencies differences for both alleles were non- significant.

Table 4.20: Estimated genotypic and allelic frequencies of the KIF-I gene at KRT 1.2 locus in Magra sheep

Genotype	Observations	Frequency
AA	80	0.4938
AB	70	0.4320
BB	12	0.0741

Allele Frequency

A	0.7099
В	0.2901

Table 4.21: Estimates of Chi-square values for Hardy-Weinbergequilibrium KIF-I gene at KRT 1.2 locus in Magrasheep

Genotypes	Observed (O)	Expected (E)	(O-E)²/E
AA	80	81.5325	0.0288
AB	70	66.9350	0.1403
BB	12	13.5325	0.1736
	•	Total	0.342706*

*Chi square value (df=1) at probability : 0.558271

4.3.2 Polymorphism of keratin associated protein 11-1 gene (KAP-11-1)

Results regarding polymorphism of KAP-11-1 gene using PCR-SSCP technique in Magra sheep have been presented and discussed below:

4.3.2.1 PCR amplification of KAP 11-1 gene

The PCR parameters, viz. annealing temperature and cycling conditions were optimized to obtain a specific amplified product in sufficient quantity and best quality. The best results were obtained at 53.5°C.

After optimization of PCR, amplification of the KAP11-1 gene was done from genomic DNA isolated from blood samples of Magra sheep. The standardized PCR programme followed for amplification of KAP11-1 gene is shown in Table 3.8. The PCR products were resolved on 1% agarose gel and visualized with ethidium bromide under U.V transilluminator. Amplicons of approximately 532bp were obtained from all the blood samples. Agarose gel electrophoretograms for PCR product of KAP11-1 gene along with 100 bp DNA Ladder have been presented in Fig. 6.

4.3.2.2 Detection of genetic variation in KAP11-1 gene by Single Strand Conformational Polymorphism

The amplicons exhibited different banding patterns upon SSCP analysis, and three unique patterns could be identified and are presented in Fig. 7. The identification of three alleles of ovine KAP11-1 was consistent with the trend of many ovine KAP's being polymorphic. Gong *et al.* (2011b), Gong *et al.* (2011c) and Zhou *et al.* (2016) identified six, five and six sequence variants in ovine KRTAP11-1, KRTAP13-3 and KRTAP6-2 gene, respectively.

The identification of three patterns in 162 sheep indicates that the KAP11-1 gene is polymorphic and as more sheep from more sire lines and breeds are investigated, it could be expected that more alleles may be found.

4.3.2.3 Analysis of genotypic and allelic frequencies of KAP11-1 gene

Estimated genotypic and allelic frequencies of the KAP11-1 gene in Magra sheep has been presented in Table 4.22. Single Strand Conformational Polymorphism of the different PCR amplicon revealed three genotypes, viz. AA, AB and AC with genotypic frequencies 0.38, 0.51 and 0.11, respectively in Magra sheep. Genotypes BB, BC and CC were not observed in the present samples. The allelic frequencies for A, B and C allele were estimated as 0.69, 0.26 and 0.05, respectively. Gong *et al.* (2011b) reported six alleles for KAP11-1 gene with allelic frequency of A, B and C alleles as 39.8, 36.4 and 5.7 in

Merino; 51.6, 40.3 and 3.2 in Romney; 49.3, 43.5 and 3.6 in Coopworth and 36.2, 31.9 and 12.5 in Romney-cross breed of sheep, respectively.

The observed and expected genotypic frequencies along with the Chi- square values have been presented in Table 4.23. The chisquare test for Hardy Weinberg equilibrium indicated significant differences (P>0.05) among the genotypic and gene frequencies with respect to KAP11-1 gene (χ^2 = 32.8465). Hence, it was inferred that Magra population was not in Hardy Weinberg equilibrium with respect to KAP11-1 gene. Table 4.22: Estimated genotypic and allelic frequencies of theKAP11-1 gene in Magra sheep

Genotype	Observations	Frequency
AA	61	0.3765
AB	83	0.5123
AC	18	0.1111

Allele	Frequency	
A	0.6883	
В	0.2562	
C	0.0556	

Table 4.23: Estimates of Chi-square values for Hardy-Weinbergequilibrium for KAP11-1 gene in Magra sheep

Genotypes	Observed (O)	Expected (E)	(O-E)²/E
AA	61	76.6347	3.1897
AB	83	57.3034	11.5231
BB	0	10.5356	10.5356
AC	18	12.4272	2.4990
BC	0	4.6254	4.6254
CC	0	0.4737	0.4737
		Total	32.8465*

*Chi square value (df=3) at probability : 0.00000

4.4 Association of polymorphism of keratin genes with wool traits

The results associating variation in the Keratin genes with variation in the wool production and quality traits have been discussed under the following heads:

- 4.4.1 Association of KIF- I gene with wool traits
- 4.4.1 Association of KAP11-1 gene with wool traits

4.4.1 Association of KIF- I gene with wool traits

The association of KIF-I gene was studied with wool production traits *viz* greasy fleece yield at first, second and third clip; and wool quality traits *viz* staple length, crimp frequency, fibre diameter and proportion of pure, hetro, hairy and medullated fibres. The least-squares means along with the effects of observed genotypes have been discussed below:

4.4.1.1 Association of KIF- I gene with wool production

The overall least-squares means along with the impact of the different genotypes at KRT 1.2 locus for wool yield have been presented in Table 4.24.

Least squares means for greasy fleece yield at first clip was estimated as 620.08 \pm 25.075 g. Variation due to the genotypes was found significant (P≤0.05) on greasy fleece yield at first clip. This indicates that KIF-I gene affects first greasy fleece yield. Genotype AA had a higher first greasy fleece yield as 740.24 \pm 26.996 g as compared to AB and BB as 620.00 \pm 27.194 and 500.00 \pm 64.735 g, respectively. Results also indicate that allele A might be associated with increase in first greasy fleece yield in Magra sheep population under study. Least squares means for greasy fleece yield at second clip was estimated as 645.59 ± 18.756 g. The effect of genotypic patterns was found non-significant (P≤0.05) on greasy fleece yield at second clip. It might be due to the fact that as the age of the animal advances, environmental factors superimpose on the effect of the genotype. The least squares means of greasy fleece yield at second clip for AA, AB and BB genotypes were found as 696.76 ± 19.077 , 660.00 ± 22.572 and 580.00 ± 47.882 g, respectively.

Least squares means for greasy fleece yield at third clip was estimated as 636.87 ± 16.212 g. It was observed that greasy fleece yield at third clip didn't vary significantly in different genotypic patterns. The least squares means of greasy fleece yield at third clip for AA, AB and BB genotypes were found as 628.95 ± 16.490 , 641.67 ± 19.511 and 640.00 ± 41.388 g, respectively.

Table 4.24: Association of greasy fleece yield (g) at first, secondand third shearing with KIF-I gene at KRT 1.2 locus inMagra sheep.

Traits/ Factors	GFYI	GFYII	GFYIII
Overall Mean	620.08 ± 25.075	645.59 ± 18.756	636.87 ± 16.212
(µ)	(162)	(162)	(162)
GENOTYPES	*	NS	NS
AA	740.24 ± 26.996 ^b	696.76 ± 19.077	628.95 ± 16.490
	(80)	(80)	(80)
AB	620.00 ± 27.194 ^{ab} (70)	660.00 ± 22.572 (70)	641.67 ± 19.511 (70)
BB	500.00 ± 64.735 ^a	580.00 ± 47.882	640.00 ± 41.388
	(12)	(12)	(12)

No. of observations are given in parenthesis. Figure with different superscripts differ significantly.

* - Significant (P≤0.05); NS - Non-significant

Itenge-Mweza (2007a), Roldan *et al.* (2010) and Gong *et al.* (2015) also found significant association of KAP genes with greasy fleece weights in Merino sheep.

These results suggest that ovine KIF- I gene should be considered while developing breeding programs based on greasy wool yield.

4.4.1.2 Association of KIF- I gene with wool quality

The least-squares means along with the effect of the genotypes at KRT 1.2 locus for wool quality traits have been presented in Table 4.25 and 4.26.

Overall Least squares means for staple length was estimated as 6.19 ± 0.156 cm. The least squares means for staple length were found as 6.56 ± 0.163 , 6.41 ± 0.169 and 5.60 ± 0.404 cm for AA, AB and BB genotypes, respectively. However, variation due to the genotypes was found statistically non-significant on staple length. It indicated that staple length is not influenced by KIF-I gene in Magra sheep. Similar to our results, non-significant association of staple length with KIF gene was observed by Ahlawat *et al.* (2014) in Marwari, Patanwadi and Dumba breeds of sheep. Contrary to our results, Itenge- Mweza (2007a) reported significant association of staple length with keratin genes in Merino sheep.

The least squares means for crimp frequency was estimated as 0.87 ± 0.032 per cm of the wool fibre. It was observed that crimp frequency didn't vary significantly in different genotypic patterns. The least squares means of crimp frequency for AA, AB and BB genotypes were found as 0.88 ± 0.034 , 0.86 ± 0.035 and 0.87 ± 0.084 per cm, respectively. Contrary to our results, Roldan *et al.* (2010) and Wang *et al.* (2014) observed significant association of crimp frequency with keratin genes in Merino sheep.

Least squares means for fibre diameter was estimated as 36.43 \pm 0.587 μ . Significant differences (P≤ 0.05) among the three genotypes, as per the DNMRT, confirms the association of the KIF gene with fibre diameter in Magra sheep. Mean fiber diameter of AA genotype was lesser than BB genotype which further demonstrates the influence of this gene on fibre fineness. The least squares means of fibre diameter for AA, AB and BB genotypes were found as 35.35 \pm 0.587, 34.46 \pm 0.668 and 39.50 \pm 1.521 μ , respectively. Similar significant association of fibre diameter with Keratin genotypes was found by Beh *et al.* (2001), Wang *et al.* (2014) and Zhou *et al.* (2015) in Merino sheep. Contrary to our result, Ahlawat *et al.* (2014) observed non-significant association of fibre diameter with KIF gene in Marwari, Patanwadi and Dumba breeds of sheep.

The least squares means for pure fibres was estimated as 50.85 \pm 2.224 %. It was observed that pure fibres didn't vary significantly in different genotypic patterns. However, The least squares means for hetrozygote was found higher than both the homozygotes. The estimated means were 51.06 \pm 2.220, 55.40 \pm 2.530 and 46.12 \pm 5.759 % for AA, AB and BB genotypes respectively.

Overall Least squares means for hetro fibres was estimated as 34.83 ± 1.509 %. The least squares means of hetro fibres for AA, AB and BB genotypes were found as 35.84 ± 1.507 , 34.10 ± 1.717 and 34.55 ± 3.909 %, respectively. However, variation due to the genotypes was found statistically non-significant. It indicated that percentage of hetro fibres among total wool fibres are not influenced by KIF-I gene in Magra sheep.

Least squares means for hairy fibres was estimated as 14.17 \pm 1.068 %. Differences among the three genotypes were found significant (P \leq 0.05) statistically. It confirms the association of the KIF gene with hairy fibres in Magra sheep. The least squares means for

AA, AB and BB genotypes were found as 12.69 ± 1.066 , 10.50 ± 1.215 and 19.33 ± 2.766 %, respectively.

Overall Least squares means for medullation per centage was estimated as 49.00 ± 2.207 %. The least squares means were estimated as 48.53 ± 2.203 , 44.60 ± 2.511 and 53.88 ± 5.715 % for AA, AB and BB genotypes, respectively. However, variation due to the genotypes was found non-significant. It indicated that medullation per centage is not influenced by KIF-I gene in Magra sheep. Similar to our results, non-significant association of medullation per centage with KIF gene was observed by Ahlawat *et al.* (2014) in Marwari, Patanwadi and Dumba breeds of sheep.

Table 4.25: Association of staple length (cm), crimp frequency (per cm) and fiber diameter (μ) of wool with KIF-I gene at KRT 1.2 locus in Magra sheep.

Traits/ Factors	Staple Length	Crimp	Fiber Diameter
Overall Mean	6.19 ± 0.156	0.87 ± 0.032	36.43 ± 0.587
(µ)	(162)	(162)	(162)
GENOTYPES	NS	NS	*
AA	6.56 ± 0.163	0.88 ± 0.034	35.35 ± 0.587 ^a
	(80)	(80)	(80)
AB	6.41 ± 0.169	0.86 ± 0.035	34.46 ± 0.668 ^a
	(70)	(70)	(70)
BB	5.60 ± 0.404	0.87 ± 0.084	39.50 ± 1.521 ^b
	(12)	(12)	(12)

No. of observations are given in parenthesis. Figure with different superscripts differ significantly. * - Significant (P≤0.05); NS - Non-significant

Table 4.26: Association of pure (%), hetro (%), hairy (%) and
medullation per centage (%) of wool with KIF-I gene
at KRT 1.2 locus in Magra sheep.

Traits/ Factors	Pure	Hetro	Hairy	Medullation
Overall Mean	50.85 ± 2.224	34.83 ± 1.509	14.17 ± 1.068	49.00 ± 2.207
(µ)	(162)	(162)	(162)	(162)
GENOTYPES	NS	NS	*	NS
AA	51.06 ± 2.220	35.84 ± 1.507	12.69 ± 1.066 ^{ab}	48.53 ± 2.203
	(80)	(80)	(80)	(80)
AB	55.40 ± 2.530	34.10 ± 1.717	10.50 ± 1.215ª	44.60 ± 2.511
	(70)	(70)	(70)	(70)
BB	46.12 ± 5.759	34.55 ± 3.909	19.33 ± 2.766 ^b	53.88 ± 5.715
	(12)	(12)	(12)	(12)

No. of observations are given in parenthesis. Figure with different superscripts differ significantly. * - Significant ($P \le 0.05$); NS - Non-significant

4.4.1 Association of KAP11-1 gene with wool traits

The association of KAP11-1 gene was also analysed with different wool traits under study. The least-squares means along with the effects of observed genotypes have been discussed below:

4.4.1.1 Association of KAP11-1 gene with wool production

The overall least-squares means along with the effect of different genotypes of KAP11-1 gene on wool yield have been presented in Table 4.27.

Least squares means for greasy fleece yield at first clip was estimated as 658.45 ± 23.694 g. The effect of different genotypes was found non-significant (P≤0.05) on greasy fleece yield at first clip. However, genotype AA had a slightly higher first greasy fleece yield as 690.68 ± 29.721 g as compared to AB and AC as 638.00 ± 26.361 and 646.67 ± 58.95 g, respectively. Least squares means for greasy fleece yield at second clip was estimated as 700.32 \pm 22.476 g. The effect of genotypic patterns was found significant (P≤0.05) on greasy fleece yield at second clip. This indicates that KAP11-1 gene affects second greasy fleece yield. The least squares means of greasy fleece yield at second clip for AA, AB and AC genotypes were found as 672.39 \pm 23.434, 650.00 \pm 19.714 and 778.57 \pm 60.074 g, respectively. Results also indicate that allele C might be associated with increase in second greasy fleece yield in Magra sheep population under study.

Least squares means for greasy fleece yield at third clip was estimated as 635.51 ± 18.633 g. It was observed that greasy fleece yield at third clip didn't vary significantly in different genotypic patterns. The least squares means for greasy fleece yield at third clip for AA, AB and AC genotypes were found as 625.00 ± 19.428 , 631.54 ± 16.343 and 650.00 ± 49.802 g, respectively.

Significant association of KAP genes with greasy fleece weights were also reported by Itenge-Mweza (2007a), Roldan *et al.* (2010) and Gong *et al.* (2015) in Merino sheep. The significant ($P \le 0.05$) effect of genotypic patterns on second greasy fleece yield suggests that ovine KAP11-1 gene might be considered while selecting the animals on the basis of greasy fleece yield. However, association study with more number of samples is required to come to any conclusions.

Traits/ Factors	GFYI	GFYII	GFYIII
Overall Mean	658.45 ± 23.694	700.32 ± 22.476	635.51 ± 18.633
(µ)	(162)	(162)	(162)
GENOTYPES	NS	*	NS
AA	690.68 ± 29.721	672.39 ± 23.434^{ab}	625.00 ± 19.428
	(61)	(61)	(61)
AB	638.00 ± 26.361	650.00 ± 19.714ª	631.54 ± 16.343
	(83)	(83)	(83)
AC	646.67 ± 58.95	778.57 ± 60.074 ^b	650.00 ± 49.802
	(18)	(18)	(18)

Table 4.27: Association of greasy fleece yield (g) at first, secondand third shearing with KAP11-1 gene in Magra sheep

No. of observations are given in parenthesis. Figure with different superscripts differ significantly.

* - Significant (P≤0.05); NS - Non-significant

4.4.1.2 Association of KAP11-1 gene with wool quality

The least-squares means along with the impact of the different genotypes for wool quality traits have been presented in Table 4.28 and 4.29.

Least squares means for staple length was estimated as 6.53 ± 0.134 cm. Significant differences (P ≤ 0.05) among the three genotypes, as per the DNMRT, confirms the association of the KAP11-1 gene with staple length in Magra sheep. The least squares means of staple length for AA, AB and AC genotypes were found as 6.45 ± 0.179 , 6.06 ± 0.156 and 7.09 ± 0.324 cm, respectively. As per the results, we may conclude that the presence of C allele increased and B allele decreased the mean staple length of Magra wool. Similar significant association of staple length with keratin genotypes was found by Itenge-Mweza (2007a) in Merino sheep.

The least squares means for crimp frequency was estimated as 0.88 ± 0.029 per cm of the wool fibre. It was observed that crimp frequency didn't vary significantly in different genotypic patterns. The least squares means of crimp frequency for AA, AB and AC genotypes were found as 0.82 ± 0.039 , 0.93 ± 0.034 and 0.88 ± 0.070 per cm, respectively. Contrary to our results, Roldan *et al.* (2010) and Wang *et al.* (2014) observed significant association of crimp frequency with keratin genes in Merino sheep.

Overall least squares means for fibre diameter was estimated as $34.78 \pm 0.509 \mu$. The least squares means for fibre diameter were found as 34.01 ± 0.751 , 35.79 ± 0.576 and $34.55 \pm 1.200 \mu$ for AA, AB and AC genotypes, respectively. However, variation due to the genotypes was found statistically non-significant on fibre diameter. It indicated that fibre diameter is not influenced by KAP11-1 gene in Magra sheep population under study. Contrary to our results, significant association of fibre diameter with Keratin genes was found by Beh *et al.* (2001), Wang *et al.* (2014) and Zhou *et al.* (2015) in Merino sheep.

The least squares means for pure fibres was estimated as 55.66 \pm 1.913 %. It was observed that pure fibres didn't vary significantly in different genotypic patterns. The estimated means were 52.92 \pm 2.818, 53.09 \pm 2.164 and 60.99 \pm 4.506 % for AA, AB and AC genotypes respectively. However, The least squares means for CC genotype was found higher than both the other genotypes which clearly indicate that presence of C allele is increasing the proportion of pure fibres in wool.

Least squares means for hetro fibres was estimated as 32.89 ± 1.281 %. Differences among the three genotypes were found significant (P ≤ 0.05) statistically. It confirms the association of the KAP11-1 gene with hetro fibres in Magra sheep. The least squares means for AA, AB and AC genotypes were found as 36.34 ± 1.888 ,

 34.15 ± 1.450 and 28.16 ± 3.017 %, respectively. Results again indicate the superiority of C allele over A and B allele.

Overall least squares means for hairy fibres was estimated as 11.37 ± 0.929 %. The least squares mean of hairy fibres for AA, AB and AC genotypes were found as 10.74 ± 1.369 , 12.51 ± 1.051 and 10.86 ± 2.188 %, respectively. However, variation due to the genotypes was found statistically non-significant. It indicated that percentage of hairy fibres among total wool fibres were not influenced by KAP11-1 gene in Magra sheep population under study.

Table 4.28: Association of staple length (cm), crimp frequency (per cm) and fiber diameter (μ) of wool with KAP11-1 gene in Magra sheep.

Traits/ Factors	Staple Length Crimp		Fiber Diameter	
Overall Mean	6.53 ± 0.134	0.88 ± 0.029	34.78 ± 0.509	
(µ)	(162)	(162)	(162)	
GENOTYPES	*	NS	NS	
AA	6.45 ± 0.179 ^{ab}	0.82 ± 0.039	34.01 ± 0.751	
	(61)	(61)	(61)	
AB	6.06 ± 0.156 ^a	0.93 ± 0.034	35.79 ± 0.576	
	(83)	(83)	(83)	
AC	7.09 ± 0.324 ^b	0.88 ± 0.070	34.55 ± 1.200	
	(18)	(18)	(18)	

No. of observations are given in parenthesis. Figure with different superscripts differ significantly.

* - Significant (P≤0.05); NS - Non-significant

Table 4.29: Association of p	ure (%), hetro (%), hairy (%	%) and medullation	per centage (%) of wool with KAP1	1-1 gene
in Magra sheep.					

Traits/ Factors	Pure	Hetro	Hairy	Medullation
Overall Mean (µ)	55.66 ± 1.913 (162)	32.89 ± 1.281 (162)	11.37 ± 0.929 (162)	44.25 ± 1.898 (162)
GENOTYPES	NS	*	NS	NS
AA	52.92 ± 2.818	36.34 ± 1.888 ^b	10.74 ± 1.369	47.08 ± 2.796
	(61)	(61)	(61)	(61)
AB	53.09 ± 2.164	34.15 ± 1.450 ^{ab}	12.51 ± 1.051	46.66 ± 2.147
	(83)	(83)	(83)	(83)
AC	60.99 ± 4.506	28.16 ± 3.017 ^a	10.86 ± 2.188	39.02 ± 4.470
	(18)	(18)	(18)	(18)

No. of observations are given in parenthesis. Figure with different superscripts differ significantly. * - Significant (P≤0.05); NS - Non-significant

Overall Least squares means for medullation per centage was estimated as 44.25 ± 1.898 %. The least squares means were estimated as 47.08 ± 2.796 , 46.66 ± 2.147 and 39.02 ± 4.470 % for AA, AB and AC genotypes, respectively. However, variation due to the genotypes was found non-significant. It indicated that medullation per centage is not influenced by KAP11-1 gene in present samples of Magra sheep.

5. SUMMARY AND CONCLUSIONS

The present research involved study of wool traits in Magra sheep both at the phenotypic and molecular level. Data regarding wool traits, over a period from 2000 to 2014, were collected from the database of Magra sheep, maintained at arid region campus of ICAR-Central Sheep and Wool Research Institute, Bikaner, Rajasthan. Blood samples from 162 unrelated animals were also collected from the animals included in the same database. The phenotypic study was undertaken with objectives to find out the mean performance of wool traits along with the effect of genetic and non-genetic factors affecting them and estimation of genetic and phenotypic parameters both by sire and animal models. Molecular aspect of the study was to identify the polymorphism of keratin genes (KIF- I and KAP 11-1 genes) in Magra sheep and to find association of keratin genes with wool traits.

The wool performance of Magra sheep was evaluated in terms of wool production *viz* greasy fleece yield at first, second and third clip; and wool quality *viz* staple length, crimp frequency, fibre diameter and proportion of pure, hetro, hairy and medullated fibres. The data was first analyzed by least square analysis of variance (LSMLMW; Harvey, 1990) to estimate the mean performance and effect of genetic and nongenetic factors on wool traits. Genetic and phenotypic parameters were estimated both by model 2 of LSMLMW (Harvey, 1990) and WOMBAT programme (Meyer, 2007). The polymorphism of KIF- I gene was identified by Restriction Fragment Length Polymorphism (RFLP) using Msp1 enzyme; and of KAP11-1 was identified by Single Strand Conformational Polymorphism technique (SSCP). Finally, the study on association of these keratin genes with wool traits was done using model 1 of LSMLMW programme (Harvey, 1990). The overall least-squares means were observed to be 690.50 ± 4.713, 754.83 ± 5.571 and 670.93 ± 5.386 g for greasy fleece yield at first, second and third clip, respectively. The overall least-squares means were observed to be 6.26 ± 0.039 cm, 0.92 ± 0.010 per cm and $33.31 \pm 0.131 \mu$ for staple length, crimp frequency and fibre diameter respectively; and 54.74 ± 0.593, 33.25 ± 0.416 , 12.01 ± 0.291 and 45.26 ± 0.593 % for pure, hetro, hairy and medullated fibres, respectively. The estimated values of wool quality traits clearly indicate the suitability of Magra wool for carpet wool production.

The random effect of sire was observed to be highly significant $(P \le 0.01)$ on all the wool traits under study. Significant effect of sire indicated that sire selection for these traits can bring further genetic improvement in these traits. The fixed effect of period of shearing was found highly significant ($P \le 0.01$) for all the wool traits except at greasy fleece yield at third clip and fibre diameter. This might be due to differences in the climatic and managemental conditions prevailing over the different periods. The fixed effect of sex of lamb was found highly significant ($P \le 0.01$) on greasy fleece yield at different clips and crimp frequency; and significant (P≤ 0.05) on fibre diameter. No significant variation among males and females was observed with respect to percentage of pure, hetro, hairy and medullated fibres in Magra sheep population under study. The fixed effect of season of birth was found highly significant (P \leq 0.01) for all the wool traits except for pure, hetro and medullation percentage. The regression of lamb's age at shearing had highly significant (P≤ 0.01) effect on all wool production traits under study. However, among wool quality traits, highly significant ($P \le 0.01$) regression of age at shearing was observed only at crimp frequency and hetro fibres; and significant ($P \le 0.05$) effect was found on medullation percentage.

Genetic and phenotypic parameters were estimated by sire model using model 2 of LSMLMW (Harvey, 1990). Heritability

estimates for greasy fleece yield at first, second and third clip were estimated as 0.68 ± 0.083 , 0.81 ± 0.095 and 0.66 ± 0.150 , respectively. The estimates of heritability for staple length, crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres were estimated as 0.52 ± 0.085 , 0.20 ± 0.055 , 0.18 ± 0.052 , 0.41 ± 0.073 , 0.33 ± 0.066 , 0.53 ± 0.082 and 0.44 ± 0.075 , respectively. Moderate to high heritability estimates suggested that the direct selection for wool traits could be successful if environmental conditions are more tightly controlled or accounted for in the selection programme.

Using sire model, the genetic correlations of first greasy fleece yield with greasy fleece yield at second and third clip were estimated as 0.33 ± 0.248 and 0.55 ± 0.261 , respectively. The genetic correlation of greasy fleece yield at second clip with greasy fleece yield at third clip was estimated as 0.87 ± 0.256 . The positive and high genetic correlation among wool production traits indicates that lambs with heavier fleece at first clip might have heavier fleece at subsequent clips also. The genetic correlations of staple length with crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres were estimated as -0.15 ± 0.168 , -0.11 ± 0.171 , -0.15 ± 0.139 , -0.05 ± 0.145 , 0.41 ± 0.171 , -0.15 ± 0.139 , -0.05 ± 0.145 , -0.145, -0.0.129 and 0.15 \pm 0.137, respectively. The genetic correlations of crimp frequency with fibre diameter, pure, hetro, hairy and medullated fibres was estimated as -0.72 ± 0.246 , 0.49 ± 0.156 , -0.59 ± 0.190 , $-0.24 \pm$ 0.194 and -0.49 \pm 0.187, respectively. The genetic correlations of fibre diameter with pure, hetro, hairy and medullated fibres was estimated as -0.81 ± 0.227 , 0.93 ± 0.117 , 0.44 ± 0.147 and 0.81 ± 0.098 , respectively. The genetic correlations of pure fibres with hetro, hairy and medullated fibres was estimated as -0.93 ± 0.202 , -0.86 ± 0.188 and -1.00 ± 0.197 , respectively. The genetic correlation of hetro fibres with hairy and medullated fibres was estimated as 0.62 ± 0.111 and 0.93 ± 0.024 , respectively; and between hairy and medullated fibres was estimated as 0.86 ± 0.046. Results clearly indicate that the selection may be practiced for heavier fleeces giving negative weightage to fibre diameter and medullation percentage. Moreover, giving negative weightage to fibre diameter will increase the percentage of pure fibres of wool and decrease the medullation percentage which may result in further improvement of the wool quality.

Using sire model, the phenotypic correlations of first greasy fleece yield with greasy fleece yield at second and third clip were estimated as 0.09 ± 0.021 and 0.07 ± 0.036 , respectively; and greasy fleece yield at second clip with greasy fleece yield at third clip was estimated as - 0.01 \pm 0.036. The phenotypic correlations of staple length with crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres was estimated as 0.04 ± 0.022 , 0.06 ± 0.022 , $-0.06 \pm$ $0.022, 0.003 \pm 0.022, 0.12 \pm 0.022$ and 0.06 ± 0.022 , respectively. The phenotypic correlations of crimp frequency with fibre diameter, pure, hetro, hairy and medullated fibres was estimated as -0.20 ± 0.022 , 0.20 \pm 0.022, -0.15 \pm 0.022, -0.20 \pm 0.022 and -0.20 \pm 0.022, respectively. The phenotypic correlations of fibre diameter with pure, hetro, hairy and medullated fibres was estimated as -0.52 ± 0.019 , 0.32 ± 0.021 , 0.59 ± 0.018 and 0.52 ± 0.019 , respectively. The phenotypic correlations of pure fibres with hetro, hairy and medullated fibres was estimated as -0.89 ± 0.010 , -0.76 ± 0.014 and -1.00 ± 0.000 , respectively. The phenotypic correlation of hetro fibres with hairy and medullated fibres was estimated as 0.39 ± 0.020 and 0.89 ± 0.010 , respectively; and between hairy and medullated fibres was estimated as 0.76 ± 0.014 . It indicates that these traits are genetically related and governed by some common genes.

(Co)variance components along with the genetic and phenotypic parameters were also estimated by WOMBAT programme (Meyer, 2007), fitting six animal models with various combinations of direct and maternal effects. The log-L values did not differ significantly in all the six models in any of the traits under study. However, addition of σ_{am} in

model 3 and 6 brought significant change in log likelihood but inflated the heritability estimate due to very high negative covariance between direct and maternal effects. Thus, Model 1- the model with fewest random terms was chosen as the best model as per Likelihood ratio test (LRT) for all the wool traits under study. Direct heritability estimates from the best model for greasy fleece weight at first, second and third clip were estimated as 0.25 ± 0.037 , 0.24 ± 0.039 and $0.32 \pm$ 0.075, respectively. The heritability estimates for staple length, crimp frequency, fibre diameter, pure fibres, hetro fibres, hairy fibres and medullation percentage were 0.31 ± 0.046 , 0.09 ± 0.033 , 0.14 ± 0.035 , 0.40 ± 0.046 , 0.28 ± 0.044 , 0.41 ± 0.045 and 0.41 ± 0.046 , respectively. Moderate to high heritability estimates (except for crimp frequency and fibre diameter) indicate further scope of improvement in these traits through selection. There was either no or very low evidence of the maternal genetic and maternal permanent effect for all the wool traits under study. Also, the heritability estimated by sire model was biased upwards as compared to the heritability estimated by animal model. Subsequently, a series of bivariate animal model analysis was carried out in order to estimate genetic and phenotypic correlations among the traits. The genetic and phenotypic correlations as estimated by animal model were approximately in the same range as were estimated by sire models.

Molecular aspect of the present study involved three stepsisolation of the DNA from the blood samples; amplification of the genomic DNA using species specific primers under appropriate PCR conditions; and identification of polymorphism of Keratin genes among the selected individuals. Genomic DNA was isolated from 162 blood samples using Blood DNA isolation kit (Himedia Ltd.). The quality of genomic DNA was checked on 1.2% agarose gel electrophoresis and visualized with ethidium bromide under gel documentation system. Quality was also checked under nano-spectrophotometer. Samples showing absorbance ratio between 1.7-1.9 at 360/380 nm wavelength and concentration above 30 ng/ μ L were considered for further analysis. The extracted DNA from each sample was stored in a deep freezer at - 20°C till further use.

The polymorphism of KIF- I gene at locus KRT1.2 in Magra sheep was studied using PCR-RFLP technique. Polymerase chain reactions (PCR) were performed with one set of primers to amplify exon 1 (480bp) of KIF-I gene at KRT1.2 locus. PCR reactions were performed with an initial denaturation at 95°C for 5 minutes, then 40 cycles of reaction comprising of denaturation at 94°C for 45 seconds, annealing at 58 °C for 45 seconds and extension at 72 °C for one minute. The final extension was performed at 72 ° C for 10 minutes for the KIF loci. Amplified PCR products were electrophoresed on 2% agarose gel and visualized by using gel documentation system. The PCR amplified product of KIF type I gene was cleaved by MspI restriction enzyme at 37 °C for 16 hours. The RE digested products were electrophoresed in Non-denaturing 8 % Polyacrylamide gel electrophoresis (PAGE). Three genotypic patterns were generated by Mspl digestion of the amplicons as : 159, 126, 100 and 95 bp for AA genotype; 259, 126 and 95 for BB genotype; and 259, 159, 126, 100 and 95 bp for AB genotype. The genotypic frequencies of the genotypes AA, AB and BB were estimated as 0.49, 0.43 and 0.08, respectively. The allelic frequencies for A and B allele were estimated as 0.71 and 0.29, respectively. Greater frequencies of allele A and genotypes AA and AB suggests that selection for higher wool yield and wool quality favoured AA homozygote and AB heterozygote. The chisquare test for Hardy Weinberg equilibrium indicated non-significant differences (P>0.05) among the genotypic and gene frequencies with respect to KIF-I gene. Hence, it was inferred that Magra population was in Hardy Weinberg equilibrium with respect to KIF-I gene.

The polymorphism of KAP11-1 gene in Magra sheep was

studied using PCR-SSCP technique. Polymerase chain reactions (PCR) were performed with one set of primers to amplify 532bp region of KAP11-1 gene. PCR reactions were performed with an initial denaturation at 95°C for 5 minutes, then 40 cycles of reaction comprising of denaturation at 94°C for 45 seconds, annealing at 53.5 °C for 45 seconds and extension at 72 °C for one minute. The final extension was performed at 72 ° C for 10 minutes. Amplified PCR products were electrophoresed on 1.5% agarose gel and visualized by using gel documentation system. Non-denaturing 7% Polyacrylamide gel electrophoresis was carried out at 200 volt for 10-12 hours at 10°C in 0.5 X TBE buffer. The polyacrylamide gels were stained with ethidium bromide dye to visualize the SSCP patterns under UV transilluminator. SSCP of the different PCR amplicon revealed three genotypes, viz. AA, AB and AC with genotypic frequencies 0.38, 0.51 and 0.11, respectively in Magra sheep. Genotypes BB, BC and CC were not observed in the present samples. The allelic frequencies for A, B and C allele were estimated as 0.69, 0.26 and 0.05, respectively. The chi-square test for Hardy Weinberg equilibrium indicated significant differences (P>0.05) among the genotypic and gene frequencies with respect to KAP11-1 gene. Hence, it was inferred that Magra population was not in Hardy Weinberg equilibrium with respect to KAP11-1 gene.

Association of the keratin genes with wool traits was also studied in Magra sheep. Significant ($P \le 0.01$) variation in the first greasy fleece yield, fibre diameter and hairy fibres was found due to the observed genotypes of KIF-I gene. It indicates that KIF-I gene is associated with variation in these characters. Also, variation due to the three genotypes associated with KAP11-1 gene significantly affected second greasy fleece yield, staple length and hetro fibres in Magra sheep. It indicates that KAP11-1 gene is associated with variations in certain wool traits. Thus, these genes can be regarded as candidate genes for marking variations in wool production and quality traits.

One of the purified PCR products for KAP11-1 gene was sequenced and the sequence was submitted in GenBank database with the accession number KX863744.

The recommendations of the present study are as follows:

- The effect of sire was observed to be highly significant ($P \le 0.01$) ٠ on all the wool traits under study. The effect of period of shearing was found highly significant ($P \le 0.01$) for all the wool traits except at greasy fleece yield at third clip and fibre diameter. The effect of sex was found highly significant (P≤ 0.01) on greasy fleece yield at different clips and crimp frequency; and significant ($P \le 0.05$) on fibre diameter. The effect of season of birth was found highly significant (P≤ 0.01) for all the wool traits except for pure, hetro and medullation percentage. The regression of lamb's age at shearing had highly significant (P≤ 0.01) effect on greasy fleece yield at different clips, crimp frequency and hetro fibres; and significant (P≤ 0.05) effect was found on medullation percentage. The significant factors should be given due importance in general management in order to obtain higher wool production and better wool quality.
- Moderate to high estimates of heritability was found for all the traits except crimp frequency. No evidence of direct maternal genetic (m²) and maternal permanent environmental effects (c²) was found on all the wool traits under study. Thus, selection process should be focused on additive genetic effect of the animal.

- The polymorphic patterns for *KIF-I* gene (exon 1) and *KAP11-1* gene in Magra breed of sheep revealed by PCR-SSCP method may be characteristic for Magra breed and could be used to differentiate it with other breed of sheep. However; a definitive conclusion requires a larger number of sheep to be studied.
- Variation in wool traits due to different genotypes was found significant for GFYI, Fibre diameter and Hairy fibres for *KIF-I* gene. Variation in wool traits due to different genotypes was found significant for GFYII, Staple length and Hetero fibres for *KAP11-1* gene. It indicates that these genes may be regarded as candidate genes for marking variations in wool production and quality traits. However, association study with more number of samples is required to come to any conclusions.

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GENETIC ANALYSIS OF WOOL TRAITS AND ITS ASSOCIATION WITH KERATIN GENES IN MAGRA SHEEP

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ABSTRACT

The objectives of the present study were to estimate the mean performance of wool traits along with the effect of genetic and nongenetic factors affecting them, estimation of genetic and phenotypic parameters both by sire and animal models, to identify the polymorphism of keratin genes (KIF- I and KAP 11-1 genes) in Magra sheep and to find association of keratin genes with wool traits. Data and blood samples for the present study were collected from the farm of Magra sheep, maintained at arid region campus, Central Sheep and Wool Research Institute (ICAR- CSWRI), Bikaner, Rajasthan.

The overall least-squares means were observed to be 690.50 ± 4.713, 754.83 ± 5.571 and 670.93 ± 5.386 g for greasy fleece yield at first, second and third clip, respectively. The overall least-squares mean for staple length, crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres were estimated as 6.26 ± 0.039 cm, $0.92 \pm$ 0.010 per cm, 33.31 \pm 0.131 μ , 54.74 \pm 0.593 %, 33.25 \pm 0.416 %, 12.01 \pm 0.291 % and 45.26 \pm 0.593 %, respectively. The effect of sire was observed to be highly significant ($P \le 0.01$) on all the wool traits under study. The effect of period of shearing was found highly significant ($P \le 0.01$) for all the wool traits except at greasy fleece yield at third clip and fibre diameter. The effect of sex was found highly significant ($P \le 0.01$) on greasy fleece yield at different clips and crimp frequency; and significant (P≤ 0.05) on fibre diameter. The effect of season of birth was found highly significant ($P \le 0.01$) for all the wool traits except for pure, hetro and medullation percentage. The regression of lamb's age at shearing had highly significant ($P \le 0.01$) effect on greasy fleece yield at different clips, crimp frequency and hetro fibres; and significant (P≤ 0.05) effect was found on medullation percentage.

Heritability estimates for greasy fleece yield at first, second and third clip were estimated as 0.68 ± 0.083 , 0.81 ± 0.095 and 0.66 ± 0.150 , respectively, using sire model and 0.25 ± 0.037 , 0.24 ± 0.039 and 0.32 ± 0.075 , respectively, using animal model. The estimates of heritability for staple length, crimp frequency, fibre diameter, pure, hetro, hairy and medullated fibres were estimated as 0.52 ± 0.085 , 0.20 ± 0.055 , 0.18 ± 0.052 , 0.41 ± 0.073 , 0.33 ± 0.066 , 0.53 ± 0.082 and 0.44 ± 0.075 , respectively, using sire model and 0.31 ± 0.046 , 0.09 ± 0.033 , 0.14 ± 0.035 , 0.40 ± 0.046 , 0.28 ± 0.044 , 0.41 ± 0.045 and 0.41 ± 0.046 , respectively, using animal model. Fitting six different animal models with various combinations of direct and maternal effects showed that there was no or very low evidence of the maternal genetic and maternal permanent effect for all the wool traits under study.

Using sire model, genetic correlations among different wool production traits ranged from 0.33 to 0.87, and that of wool quality traits ranged from -1.00 to 0.93; and phenotypic correlations ranged from - 0.01 to 0.09 and -1.00 to 0.89, respectively for wool production and wool quality traits, respectively. Using animal model, genetic correlations among different wool production traits ranged from 0.32 to 0.94, and that of wool quality traits ranged from 0.12 to 0.31 and -1.00 to 0.89, respectively for wool production traits, respectively for wool production traits ranged from 0.32 to 0.94, and that of wool quality traits ranged from 0.12 to 0.31 and -1.00 to 0.89, respectively for wool production and wool quality traits, respectively.

For the molecular aspect of the present study, genomic DNA was isolated from 162 blood samples of Magra sheep. The genotyping of KIF-I gene and KAP11-1 gene was done with the help of PCR-RFLP and PCR-SSCP, respectively.

The PCR-RFLP of KIF- I gene at locus KRT1.2 in Magra sheep generated three genotypic patterns by MspI digestion of the 480 bp amplicons as: 159, 126, 100 and 95 bp for AA genotype; 259, 126 and 95 bp for BB genotype; and 259, 159, 126, 100 and 95 bp for AB genotype. The genotypic frequencies of the genotypes AA, AB and BB were estimated as 0.49, 0.43 and 0.08, respectively. The allelic frequencies for A and B allele were estimated as 0.71 and 0.29, respectively. Greater frequencies of allele A and genotypes AA and AB suggests that selection for higher wool yield and wool quality favoured AA homozygote and AB heterozygote. The chi-square test for Hardy Weinberg equilibrium indicated non-significant differences (P>0.05) among the genotypic and gene frequencies with respect to KIF-I gene. Hence, it was inferred that Magra population was in Hardy Weinberg equilibrium with respect to KIF-I gene.

The PCR-SSCP of KAP11-1 gene in Magra sheep revealed three unique banding patterns forming three genotypes, viz. AA, AB and AC with genotypic frequencies 0.38, 0.51 and 0.11, respectively in Magra sheep. Genotypes BB, BC and CC were not observed in the

present samples. The allelic frequencies for A, B and C allele were estimated as 0.69, 0.26 and 0.05, respectively. The chi-square test for Hardy Weinberg equilibrium indicated significant differences ($P \le 0.05$) among the genotypic and gene frequencies with respect to KAP11-1 gene. Hence, it was inferred that Magra population was not in Hardy Weinberg equilibrium with respect to KAP11-1 gene.

Association study of the keratin genes and wool traits revealed significant ($P \le 0.05$) variation in the first greasy fleece yield, fibre diameter and hairy fibres due to the observed genotypes of KIF-I gene. Also, variation due to the three genotypes associated with KAP11-1 gene significantly ($P \le 0.05$) affected second greasy fleece yield, staple length and hetro fibres in Magra sheep. It indicates that these genes may be regarded as candidate genes for marking variations in wool production and quality traits.

One of the purified PCR product for KAP11-1 gene was sequenced and the sequence was submitted in GenBank database with the accession number KX863744.

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exjk HksM+ esa izFke] f $\$ rh; ,oa r $\$ rh; drZu ds Åu Hkkj dk vkSlr dze'k% 690-50 \pm 4-713] 754-83 \pm 5-571 rFkk 670-93 \pm 5-386 xzke ik;k x;k A LVsiy yEckbZ] fdzEi vko`fr] Qkbcj O;kl] 'kq}] gsVjks] gs;jh o esMqysfVM+ Qkbcj dk vkSlr dze'k% 6-26 ± 0-039 Iseh-] 0-92 ± 0-010 izfr Iseh-] 33-31 ± 0-131 µ] 54-74 ± 0-593%] 33-25 ± 0-416%] 12-01 ± 0-291% rFkk 45-26 ± 0-593% ik;k x;k A IHkh Åu y{k.kksa ij iztud dk izHkko vR;kf/kd eqRoiw.kZ (P≤ 0.01) ik;k x;k A r`rh; drZu ds Åu Hkkj] o Qkbcj O;kl ds vfrfjDr lHkh Åu y{kkksa ij drZu dh vof/k dk izHkko vR;kf/kd egRoiw.kZ ik;k ($P \le 0.01$) x;k A HksM+ ds fyax dk izHkko IHkh drZuksa ij vR;kf/kd egRoiw.kZ ($P \le 0.01$) o Qkbcj O;kl ij egRoiw.kZ ($P \le 0.01$) ik;k x;k A tUe ds ekSle dk izHkko 'kq} gsVjks o esMqys'ku izfr'kr ds vfrfjDr IHkh y{k.kksa ij vR;kf/kd eqRoiw.kZ ($P \le 0.01$) ik;k x;k A drZu ds le; eseus dh mez dk izHkko IHkh drZuksa ds Åu Hkkj] fdzEi vko`fr o gsVjks Qkbcj ij vR;kf/kd egRoiw.kZ (P≤ 0.01) rFkk esMqys'ku izfr'kr ij egRoiw.kZ (P≤ 0.05) ik;k x;k A

izFke] f~rh; ,oa r`rh; drZu ds Åu Hkkj ds fy, vkuqokaf'kdrk dk eku iztud ekWMy }kjk dze'k% 0-68 \pm 0-083] 0-81 \pm 0-095 o 0-66 \pm 0-150; rFkk ,fuey ekWMy }kjk dze'k% 0-25 \pm 0-037] 0-24 \pm 0-039 o 0-32 \pm 0-075] Kkr fd;k x;k A LVsiy yEckbZ] fdzEi vko`fr] Qkbcj O;kl] 'kq} gsVjks] gs;jh o esMqysfVM+ Qkbcj ds fy, vuqokaf'kdrk dk eku iztud ekWMy }kjk dze'k% 0-52 \pm 0-085] 0-20 \pm 0-055] 0-18 \pm 0-052] 0-41 \pm 0-073] 0-33 \pm 0-066] 0-53 \pm 0-082] o 0-44 \pm 0-075; rFkk ,fuey ekWMy }kjk dze'k% 0-31 \pm 0-046] 0-09 \pm 0-033] 0-14 \pm 0-035] 0-40 \pm 0-046] 0-28 \pm 0-044] 0-41 \pm 0-045] o 0-41 \pm 0-046 Kkr fd;k x;k A ekr` vkuqokaf'kd ,oa ekr` LFkk;h i;kZoj.kh; izHkko Ifgr vFkok budh vogsyuk djrs gq, Ng fofHkUu ,fuey ekWMy dk izkDdyu fd;k x;k] ftlesa Åu y{k.kksa ij ekr` vuqokaf'kd ,oa ekr` LFkk;h izHkkoksa dk 'kwU; vFkok cgqr de lk{; feyk A

iztud ekWMy }kjk fofHkUu Åu mRiknu y{k.kksa ds e/; o fofHkUu Åu xq.kork y{k.kksa ds e/; vkuqokaf'kd lg IEcU/k dk ijkl dze'k% 0-33 ls 0-87 ,oa] &1-00 ls 0-93; rFkk izk:ih lg IEcU/k dk ijkl dze'k% &0-01 ls 0-09 ,oa &1-00 ls 0-89] Kkr fd;k x;k A ,uhey ekWMy }kjk fofHkUu Åu mRiknu y{k.kksa ds e/; o fofHkUu Åu xq.kork y{k.kksa ds e/; vuqokaf'kd lg IEcU/k dk ijkl dze'k% 0-32 ls 0-94 ,oa &1-00 ls 0-97; rFkk izk:ih lg IEcU/k dk ijkl dze'k% 0-12 ls 0-31 ,oa &1-00 ls 0-89] Kkr fd;k x;k A

orZeku v/;;u ds vk.kfod igyw ds fy, 162 exjk HksM+ksa ds jDr uewuksa Is thuksfed Mh,u, i`Fkd fd, x, A ĸıF-ı rFkk ĸapıı-ı thu dh thuksVkbfix dze'k% ihlhvkj&vkj,Q,yih rFkk ihlhvkj& ,I,IIhih fof/k }kjk dh xbZ A

exjk HksM+ esa ihlhvkj&vkj,Q,yih fof/k }kjk KRT1.2 yksdl ij 480 bp ,EifydkWu ds Mspl ikpu }kjk rhu thuizk:lk mRiUu gq, ftudh fLFkfr; 159] 126] 100 ,oa 95 bp AA thuizk:i ds fy,; 259] 126 ,oa 95 bp BB thuizk:i ds fy,; rFkk 259] 159] 126] 100 ,oa 95 bp AB thuizk:i ds fy, Kkr dh xbZ A AA, AB rFkk BB thuizk:lk dh thuizk:lk vko`fr dze'k% 0-49] 0-43 rFkk 0-01 Kkr dh xbZ A ,yhy A rFkk B ds fy, ,yhy vko`fr;ka dze'k% 0-71 rFkk 0-29 Kkr dh xbZ A A,yhy rFkk AA o AB thuizk:lk dh vf/kd vko`fr ;g iznf'kZr djrh gSa fd mPp Åu mRiknu rFkk mPp Åu xq.kork gsrq fd;k x;k p;u AA rFkk AB thuizk:lk lanHkZ esa ph&oxZ ijh{k.k fd;k x;k] ftlls ;g ldsar feyk fd κιF-ι thu ds IEcU/k esa thuizk:lk vkSj thu vko`fr;ksa ds e/; vUrj xSj egRoiw.kZ (P>0.05) gS A vr% ;g vuqeku yxk;k x;k fd exjk vkcknh κιF-ι thu ds lanHkZ esa gkMhZ osucxZ larqyu esa Fkh A

Ekxjk HksM+ esa κAP11-1 thu esa ihlhvkj& ,I,Ilhih fof/k }kjk rhu vfn`rh; cSfMx iSVuZ dk irk pyk tks rhu thuizk:Ik AA, AB o AC dk fuekZ.k dj jgs Fks rFkk ftudh thuizk:Ik vko`fr dze'k% 0-38] 0-51 rFkk 0-11 Kkr dh xbZA orZeku uewuksa esa BB, BC rFkk CC thuizk:Ik ugha feyk A A, B rFkk C ,yhy dh ,yhy vko`fr dze'k% 0-69] 0-26 rFkk 0-05 Kkr dh xbZ A gkMhZ osucxZ larqyu ds lanHkZ esa fd;s x;s ph&oxZ ijh{k.k ls ;g Idsar feyk fd κAP11-1 ds IEcU/k esa thu rFkk thuizk:Ik vko`fr;ksa ds e/; vUrj egRoiw.kZ (P≤ 0.05) gS A vr% ;g vuqeku yxk;k x;k fd exjk vkcknh ds lanHkZ esa gkMhZ osucxZ larqyu esa ugh gSa A

dsjsfVu thu rFkk Åu y{k.kksa ds lg IEcU/k dk v/;;u djus ij ik;k x;k fd KAP11-1 thu ds thuizk:iksa esa fofHkUurkvksa dk izHkko izFke drZu ds Åu Hkkj] Qkbcj O;kl rFkk gs;jh Qkbcj ij egRoiw.kZ (P≤ 0.05) gSa A blds vfrfjDr KAP11-1 thu ds rhuksa thuizk:Ik] fn`rh; drZu ds Åu Hkkj] LVsiy yEckbZ rFkk gsVjks Qkbcj dks egRoiw.kZ (P≤ 0.05) :Ik ls izHkkfor dj jgs gSa A ;g bafxr djrk gS fd bUgsa Åu mRiknu ,oa xq.kork ds y{k.kksa ds vadu ds fy, mEehnokj thu ds :Ik esa ekuk tk ldrk gSa A KAP11-1 thu ds ,d 'kq} ihlhvkj mRikn dk vuqdze.k fd;k x;k o vuqdze dks thucSad esa tek dj ifjxzg.k la[;k KX863744 izklr dh xbZ A

APPENDIX – I

1. Ag	1. Agarose Gel Electrophoresis buffer		
1.1 1	TAE buffer (50X) 50	0 ml	
Stoc	k solution:		
	Tris base		141 gm
	EDTA acid (.5M)		20 ml
	Glacial Acetic Aci	t	28.55 ml
Wor	Working concentration of TAE buffer (1x) 500 ml		
	TAE buffer (50x)		10 ml
	Water		490 ml
Wor	Working concentration of TAE buffer (0.5x) 500 ml		
	TAE buffer (50x)		5 ml
	Water		495 ml
1.2 1	E Buffer		
Stoc	k solution: (10x)		
	Tris-CI (pH to 8.5)		100 mM
	EDTA		10 mM

(sodium salt, adjust the pH to 7.2 with NaOH)

Autoclaved and stored at room temperature.

Working solution: (1x) 10 ml

Tris-Cl	1 ml (10 mM)
EDTA	5 ml (10 mM)
Distilled water	4 ml

1.3 TBE Buffer (10X) 1000 ml

Tris base	108	gm
EDTA acid (.5M)	40	ml

Boric Acid	55 gm
Boric Acid	55

Working concentration of TBE buffer (1x) 500 ml

TBE buffer (50X)	50 ml
Water	450 ml

Working concentration of TBE buffer (0.5x) 500 ml

TBE buffer (50X)	25 ml
------------------	-------

5 ml

2. PCR assay buffer for Taq DNA polymerase (10X)

Tris HCI (pH – 9.0) 1000 mM

MgCl₂ 15 mM

KCI

500 mM

Triton X 100

1.0 %

APPENDIX –II

1. 6X loading dye

Bromophenol blue	0.25%	
Xylene cyanol	0.25%	
Glycerol	50%	
EDTA	2mM	
2. Ethidium bromide solution (10 mg/ ml)		
Ethidium bromide	0.2gm	
Sterile Water	20 ml	
3. Agarose (1%)		
Agarose	1.00 g	
TAE buffer	100 ml	
4. Agarose (1.2%)		
Agarose	1.2 gm	
TAE buffer	100 ml	
5. Agarose (2%)		
Agarose	2 gm	
TAE buffer	100 ml	
6. 2X denaturing loading dye		

Bromophenol blue 25 mg

Xylene cyanol	25 mg
Formamide	9.5 ml
10 mM EDTA	400 µL
dd H ₂ O	100 µL
7. 10% APS	
APS	1 g
Water	10 ml

APPENDIX III

LIST OF ABBREVIATION

Abbreviation

Meaning

APS	Ammonium per sulphate
bp	base pair
DNA	Deoxyribonucleic acid
dNTP's	Di-nitro tri phosphate
DW	Distilled water
EDTA	Ethylene diamine tetra acetic acid
Etbr	Ethidium bromide
ml	Milliliter (s)
Μ	Molar
mM	Milimolar
ng	Nanogram (s)
TEMED N	I,N,N',N'-tetramethylethylenediamine
PAGE	Polyacrylamide gel electrophoresis
PBS	Phosphate buffer saline
pmole	Picomole(s)
PCR	Polymerase chain reaction

R.T.	Room temperature
rpm	Revolution per minute
TAE	Tris- Acetate EDTA
ТВЕ	Tris Borate EDTA buffer
TBE	Tris Borate EDTA buffer
TE	Tris- EDTA
UV	Ultra violet

APPENDIX – IV

UNITS OF MEASUREMENTS

<u>S. No.</u>	<u>Units</u>	<u>Meaning</u>
1.	%	Percentage
2.	ug	Micro-gram
3.	ul	Micro-litre
4.	cm	Centimeter
5.	°C	Degree centigrade
6.	Kg	Kilogram
7.	gm	Gram
8.	hr.	Hour
9.	IU	International unit
10.	mg	Milligram
11.	ml	milliliter
12.	min.	Minute
13.	bp	Base pair
14.	М	Molar
15.	U	Unit
16.	V	Volt
17.	mM	Millimolar

APPENDIX – V

Chi-Square Distribution Table



The shaded area is equal to α for $\chi^2=\chi^2_\alpha.$

ďf	X.995	χ ² .990	χ ² .975	$\chi^{2}_{.950}$	X ² .900	$\chi^{2}_{.100}$	$\chi^{2}_{.050}$	$\chi^{2}_{.025}$	$\chi^{2}_{.010}$	$\chi^{2}_{.006}$
1	0.000	0.000	0.001	0.004	0.016	2.706	3.841	5.024	6.635	7.879
2	0.010	0.020	0.051	0.103	0.211	4.605	5.991	7.378	9.210	10.597
3	0.072	0.115	0.216	0.352	0.584	6.251	7.815	9.348	11.345	12.838
4	0.207	0.297	0.484	0.711	1.064	7.779	9.488	11.143	13.277	14.860
5	0.412	0.554	0.831	1.145	1.610	9.236	11.070	12.833	15.086	16.750
6	0.676	0.872	1.237	1.635	2.204	10.645	12.592	14.449	16.812	18.548
7	0.989	1.239	1.690	2.167	2.833	12.017	14.067	16.013	18.475	20.278
8	1.344	1.646	2.180	2.733	3.490	13.362	15.507	17.535	20.090	21.955
9	1.735	2.088	2.700	3.325	4.168	14.684	16.919	19.023	21.666	23.589
10	2.156	2.558	3.247	3.940	4.865	15.987	18.307	20.483	23.209	25.188
11	2.603	3.053	3.816	4.575	5.578	17.275	19.675	21.920	24.725	26.757
12	3.074	3.571	4.404	5.226	6.304	18.549	21.026	23.337	26.217	28.300
13	3.565	4.107	5.009	5.892	7.042	19.812	22.362	24.736	27.688	29.819
14	4.075	4.660	5.629	6.571	7.790	21.064	23.685	26.119	29.141	31.319
15	4.601	5.229	6.262	7.261	8.547	22.307	24.996	27.488	30.578	32.801
16	5.142	5.812	6.908	7.962	9.312	23.542	26.296	28.845	32.000	34.267
17	5.697	6.408	7.564	8.672	10.085	24.769	27.587	30.191	33.409	35.718
18	6.265	7.015	8.231	9.390	10.865	25.989	28.869	31.526	34.805	37.156
19	6.844	7.633	8.907	10.117	11.651	27.204	30.144	32.852	36.191	38.582
20	7.434	8.260	9.591	10.851	12.443	28.412	31.410	34.170	37.566	39.997
21	8.034	8.897	10.283	11.591	13.240	29.615	32.671	35.479	38.932	41.401
22	8.643	9.542	10.982	12.338	14.041	30.813	33.924	36.781	40.289	42.796
23	9.260	10.196	11.689	13.091	14.848	32.007	35.172	38.076	41.638	44.181
24	9.886	10.856	12.401	13.848	15.659	33.196	36.415	39.364	42.980	45.559
25	10.520	11.524	13.120	14.611	16.473	34.382	37.652	40.646	44.314	46.928
26	11.160	12.198	13.844	15.379	17.292	35.563	38.885	41.923	45.642	48.290
27	11.808	12.879	14.573	16.151	18.114	36.741	40.113	43.195	46.963	49.645
28	12.461	13.565	15.308	16.928	18.939	37.916	41.337	44.461	48.278	50.993
29	13.121	14.256	16.047	17.708	19.768	39.087	42.557	45.722	49.588	52.336
30	13.787	14.953	16.791	18.493	20.599	40.256	43.773	46.979	50.892	53.672
40	20.707	22.164	24.433	26.509	29.051	51.805	55.758	59.342	63.691	66.766
50	27.991	29.707	32.357	34.764	37.689	63.167	67.505	71.420	76.154	79.490
60	35.534	37.485	40.482	43.188	46.459	74.397	79.082	83.298	88.379	91.952
70	43.275	45.442	48.758	51.739	55.329	85.527	90.531	95.023	100.425	104.215
80	51.172	53.540	57.153	60.391	64.278	96.578	101.879	106.629	112.329	116.321
90	59.196	61.754	65.647	69.126	73.291	107.565	113.145	118.136	124.116	128.299
100	67.328	70.065	74.222	77.929	82.358	118.498	124.342	129.561	135.807	140.169