# Unlocking the Genomic Potential in Indian Goats: Toward Enhanced Production



ICAR-National Bureau of Animal Genetic Resources



#### TOTAL GOAT POPULATION-148.88 Million (10.14% increase)

GOATS IN INDIA 2022-23 Share 2050 1.4 million 14.47% 2.03 million MEAT 39 registered breeds + several tonnes tonnes lesser known populations MILK 7.6 million 3.3% increasing **Highly diverse breeds** tonnes best dairy goat of Pashmina South East Asia **Traits of interest** fibre and is tallest goat Milk production breed of the -12 μ) country. Fibre quality Prolificacy **Chevon production** Prolificacy Growth rate & skin Disease resistance LAV litter size-1.75)

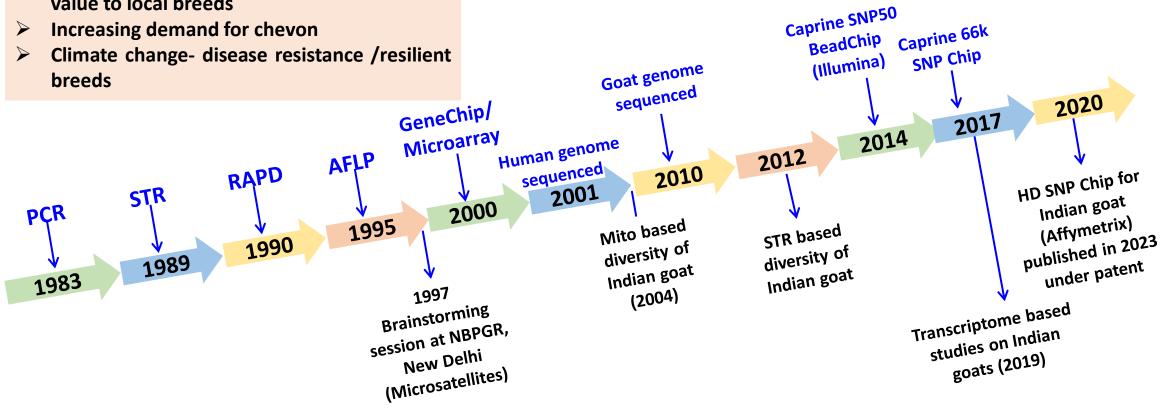
> Unlocking the hidden genetic potential of these breeds will provide an understanding of their adaptability and productivity traits, leading to more targeted and effective breeding strategies to boost production.

#### **THREATS AND CHALLENGES**

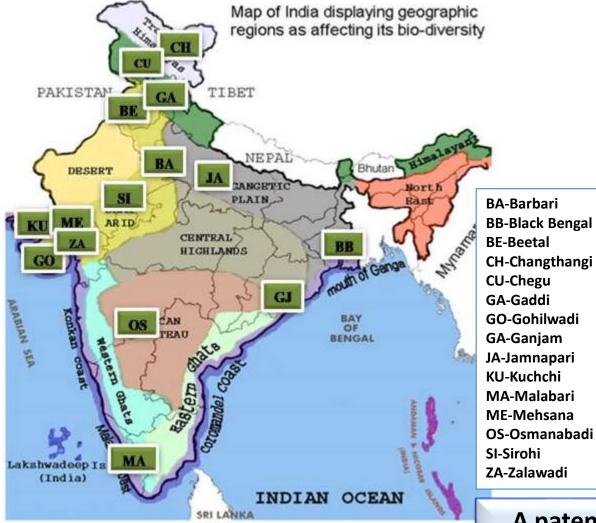
- Low productivity of indigenous breeds
- Admixture/Breed composition
- Identifying selection traits
- Identifying logical breeding objectives
- Maximizing genetic gain at an acceptable inbreeding rate (selection within breeds).
- Economic sustainability Adding market value to local breeds

### **OPPORTUNUTIES AND STRENGTHS**

- Vast caprine biodiversity
- Genetic potential unexplored
- Phenotype recording
- Omics to fast track genetic information
- Informed breeding strategies based on integrated data (phenotypic and genomic)



### Design and development of HD SNP Chip for Indian goats



• WGS data of 15 breeds from diverse agro-ecological regions was generated at 10X coverage using Illumina platform

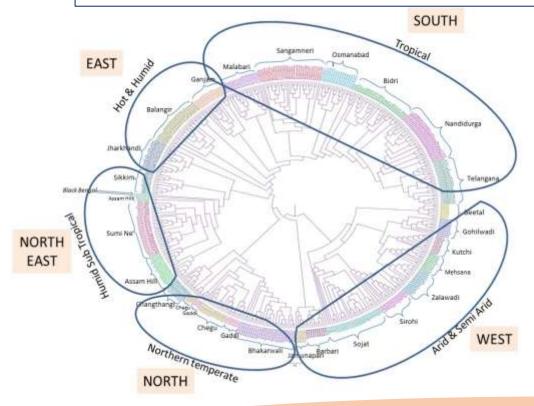
•626,975 informative SNPs were identified.

• A high density SNP array for Indian goat breeds was designed using the informative SNPs.

A patent application has been filed for the High density chip of *Capra hircus* (Application No. 202011057422; Dt. 31.12.2020)

# Goat SNP Chip validation - Whole genome SNP based diversity in indigenous goat breeds

- 480 samples of 26 goat breeds/populations genotyped.
- All samples passed the SNP QC thresholds.
- Average call rate for QC passing samples was 99.831 and 96.5% markers were best recommended.



#### **SALIENT FEATURES**

- High call rate (99.831%).
- >600K markers-increased marker density.
- Genome wide coverage.



Gene Volume 885, 15 November 2023, 147691



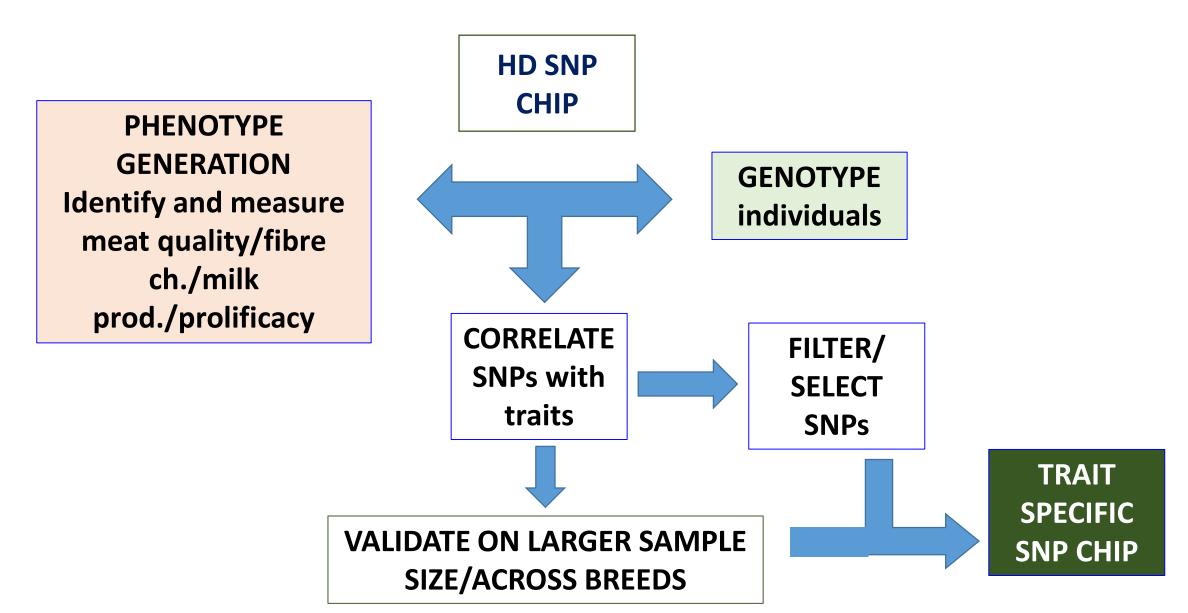
Research paper

Design and validation of high-density SNP array of goats and population stratification of Indian goat breeds

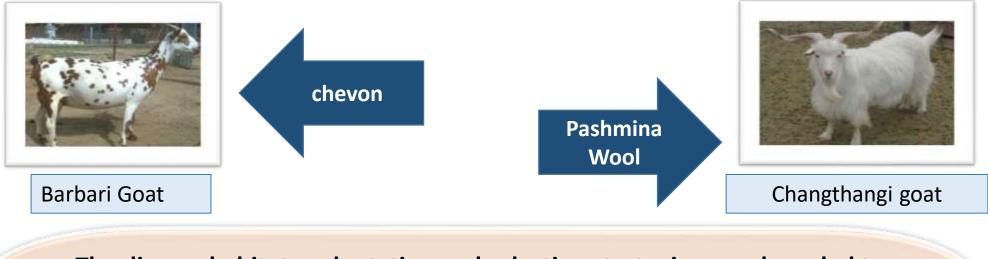
Ramesh Kumar Vijh 은 回, Upasna Sharma, Prerna Kapoor, Meenal Raheja, Reena Arora, Sonika Ahlawat, Vandana Dureja

The HD SNP chip for Indian goat can be utilized for selection and diversity analysis of indigenous goats.

## **TRAIT SPECIFIC SNP CHIP**



## Identification of genes associated with economically important traits in goat breeds of contrasting agro-ecological zones using comparative functional genomics



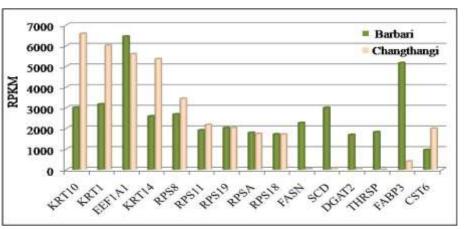
The diverse habitats, adaptation and selection strategies may have led to selection of specific traits in these breeds.

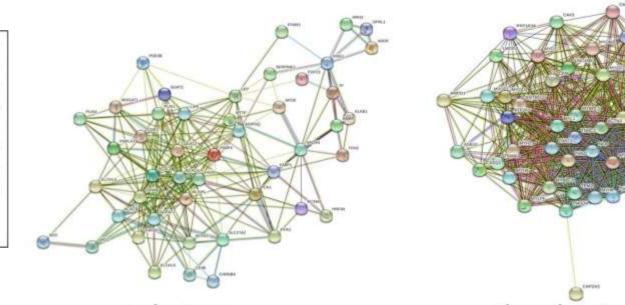
RNA Sequencing ,4 biological replicates of LD muscles

Identification of differentially expressed genes may help in understanding the genomic basis of diversity in these breeds.

#### Top 15 highest expressed genes in Barbari and Changthangi goats

Gene-protein interaction network of highly connected differentially expressed genes in Barbari and Changthangi goats







Ashish Kumai <sup>5,\*</sup>, Mandeep Kaui <sup>5,\*</sup>, Sonika Ahlawat<sup>4</sup>, Upasna Sharma<sup>4</sup>, Manoj Kumai Singli<sup>4</sup>, Kuran Veer Singli<sup>4</sup>, Pooja Chhabra<sup>4</sup>, Ramesh Kumar Vijli<sup>4</sup>, Anita Yadav<sup>5</sup>, Reena Arora<sup>6,\*</sup>

\* EAA-Netional Bornes: of Ambed Genetic Researces, Samuel 252801, Ranyons, Judie

\* Andrarge April and Links Constitution of Benefits (2016), Control Patitizes for Assessed on Links, Makhalune, Patrik, 2011;22 Adobum, 1100 Probability, 2010; 2 Anathranis Microbiology 114(114), American Index. Barbari goat FASN, DGAT2, ACACA, LIPE, ACSL1, GPAM, MLXIPL, AGPAT2, LEP and KNG1

Fatty acid content, backfat thickness, meat quality

Changthangi goat ACTN2, MYL1, TNNT3, TCAP, ACTN3, MYL3, MYOZ2, TNNI2, CAV3 and TNNC2

Muscle fibre type Acclimatization to Hypoxia

Gene expression differences underscore the selection objectives of the two breeds

#### Pashmina fiber from Changthangi goat

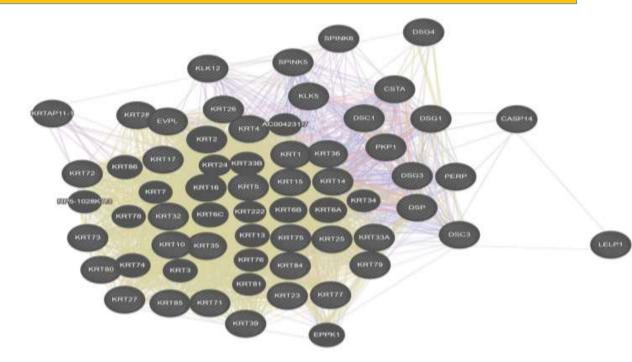


Barbari goat



Changthangi goat

# Co-expression network of DEGs involved in the keratinization pathway



www.nature.com/scientificreports

SCIENTIFIC REPORTS natureresearch

OPEN Skin transcriptome profiling of Changthangi goats highlights the relevance of genes involved in Pashmina production

> Sonika Ahlawat<sup>17</sup>, Reena Arora<sup>5</sup>, Rekha Sharma<sup>1</sup>, Upasna Sharma<sup>1</sup>, Mandeep Kaur<sup>3</sup>, Ashish Kumar<sup>1</sup>, Karan Veer Singh<sup>1</sup>, Manoj Kumar Singh<sup>2</sup> & Ramesh Kumar Vijh<sup>5</sup>

> Positive regulation of Wnt signaling pathway

Negative regulation of Oncostatin M signaling pathway

### **Molecular insights into Pashmina fiber production**



Skin transcriptome profiles of Changthangi goats and Changthangi sheep

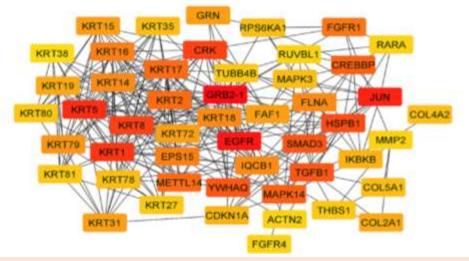
Discern the molecular drivers that underpin the recognition of Changthangi goats as the source of Pashmina

A total of 7155 genes were differentially expressed between the two species investigated in this study.

Drawing upon previously conducted studies, a collective of 225 genes correlated with fiber characteristics were extracted from the differentially expressed genes between the two species( $p_{adj}$  of  $\leq 0.05$  and a Log<sub>2</sub> fold change of  $\geq 1.5$ )

These genes were up-regulated in Changthangi goats as compared to Changthangi sheep.

Sub-network was constructed for the top 50 genes based on degree of interactions of up-regulated genes in Changthangi goats



Identified nodal genes of following pathways:- *MAPK* (JUN, HSPB1, TGFB1, FGFR1, FGFR4, FLNA, *RPS6KA1*) *PI3K-Akt* (COL2A1, COL4A2, CDKN1A) *Wnt* (RUVBL1) which are crucial for hair follicle formation and fiber characteristics.

Possible molecular determinants responsible for the superior quality of Pashmina fiber in Changthangi goats

RP GENOMICS REVIEW MEE

### THE PATH FORWARD......

- Generation of well annotated genome reference assemblies for goat.
- Breed/trait specific genomic mapping-GWAS.
- Development of trait specific SNP arrays for indigenous breeds, to be used for genomic selection.
- Epigenetic modifications and gene-environment interactions to understand adaption to different environments without permanent genetic changes.
  By utilizing advanced genomic tools, precision breeding programs can achieve higher productivity while preserving the rich genetic diversity unique to Indian goat breeds.



The future of Indian goat production lies not only in higher yields but also in the careful stewardship of genetic resources, ensuring the resilience and adaptability of these animals for generations to come.

