Conservation Genetics Resources
https://doi.org/10.1007/s12686-021-01210-x

METHODS AND RESOURCES ARTICLE

SNPRBb: economically important trait specific SNP resources of buffalo (*Bubalus bubalis*)

D. C. Mishra[1] · Sunita Yadav[1] · Poonam Sikka[2] · A. Jerome[2] · S. S. Paul[2] · A. R. Rao[1] · Neeraj Budhlakoti[1] · Jyotika Bhati[1] · K. P. Singh[2] · A. K. Balhara[2] · I. Singh[2] · Anil Rai[1] · K. K. Chaturvedi[1]

Received: 11 October 2019 / Accepted: 29 April 2021

Abstract
Throughout Asian countries including India, water buffalo *(Bubalus bubalis)* plays a crucial role in socio-economic status of the farmers by providing nutritional security. The concept of genomic selection through genetic markers has been widely used in various livestock species and this is extended to buffalo species as well. Molecular markers have been extensively used in animal breeding for improvements of desirable animal traits. Single Nucleotide Polymorphism (SNP), one of the important molecular markers is widely used in animal breeding program. In this study, SNPs related to four important traits of buffalo i.e., milk volume, age at first calving, post-partum cyclicity and feed conversion efficiency have been identified based on genome sequence data generated using ddRAD (double digest Restriction-site Associated DNA) sequencing technology. These identified SNPs have been compiled as database accessible through Web and can be used in molecular breeding program of buffalo species. This database facilitates easy search of SNPs, Polymorphic Loci and Haplotypes along with their important features like minor and major allele frequencies, observed and expected heterozygosity, observed and expected homozygosity and nucleotide diversity. This database will help to accelerate the molecular breeding program for developing trait specific breeds of buffalo to meet the need of food and nutritional security of the world including India.

Keywords SNP · Database · DdRAD · Molecular breeding · Water buffalo

Background

Asia comprise of 97% of total world buffalo (*Bubalus bubalis*) population (Faostat 2014) and 56.5% of Asian buffalos are in India. Asian buffaloes contribute significantly to the agricultural economy and nutritional security of the country. India ranks highest in milk production with annual production of 216 million tonnes, and buffalo contributes 49% to India's milk production, which is higher than milk production by cattle (Hegde 2019). In addition, India has been world leader in meat exports till recently (Department of Animal Husbandry 2018–19) and out of total meat exports, buffalo meat contributes to 23% whereas 5% and 46% are contributed by cattle and poultry, respectively.

Cattle were domesticated around 8000–10,000 years ago (Lenstra and Felius 2015) whereas, buffaloes were around 1000–3000 years back i.e., later than cattle in *Bovidea* family (Bibi and Vrba 2010). Out of 16 registered breeds in India, Murrah is one the most important breed of buffalo (Borghese and Mazzi 2005) both in India and around the world. This breed's average milk production is as high as 5.76 kg/day as compared to average national milk production of 3.41 kg/day by cattle (Borghese and Mazzi 2005). Apart from this, it is an important resource to sustain livelihood of small and marginal farmers (Gogoi et al. 1985). This breed has been extensively used in India to upgrade the non-descript buffalo stock and improve the milk production (Dutt and Yadav 1988; Taneja and Bhat 1986). The home tract of Murrah buffaloes is a hot and dry climatic region of the north-western part of India (Thiruvenkadan 2011). The dairy industry in India has made significant progress in the last few decades (Seno et al. 2010). However, animal health and its wider adaptability to changing environment need attention, while planning breeding programs to retain India's contribution to world milk production.

✉ K. K. Chaturvedi
kkcchaturvedi@gmail.com; kk.chaturvedi@icar.gov.in

[1] ICAR-Indian Agricultural Statistics Research Institute, Library Avenue, New Delhi 110012, India

[2] ICAR-Central Institute for Research on Buffaloes, Hisar, India

Published online: 06 May 2021

Genetic markers, mainly Single Nucleotide Polymorphism (SNP), Simple Sequence Repeat (SSR), Copy Number Variant (CNV) have been widely used for selection of livestock animal for desired traits (Matukumalli et al. 2009; Surya et al. 2018). Genetic variants underlying complex phenomic traits like animal reproduction, health and its productivity is an outcome of interactive polygenic (pedigree) and genomic (SNP/SNV) additive effects, which can be characterized using structure nucleotide variant (SNV) arrays. Also, the relationship between the SNPs and the functional feasibility of the identified genes over the genome has significant role to measure the feed efficiency in cattle (Duarte et al. 2019). Phenotypic superiority of animal has been determined through 'breeding value' which is assigned to mating individuals. This cumulative measure based on genomic information of an individual holds the key to the success of any genetic improvement program in livestock species (Barker 1994; Notter 1999).

Traits having high heritability (>0.4) have scope of genetic improvement (Kiplagat et al. 2012). Thus, the use of molecular markers, unraveling polymorphism at the DNA level has important role in identification of high merit germplasm. Markers developed from single nucleotide polymorphisms (SNPs) are considered to be potential markers (Group 2001; Stickney et al. 2002; Vignal et al. 2002) due to its high prevalence near the locus of interest and its occurrence in approximately every 1000 bases as reported in human genome (Landegren et al. 1998).

In recent times, thousands of SNPs, distributed across the genome were identified using restriction site associated DNA sequencing (RAD-Seq)—Reduced Representational Sequencing approach (Hohenlohe et al. 2010; Malik et al. 2018). This technique reduces the complexity of the genome by sub-sampling only at the sites identified by restriction enzymes (Davey et al. 2011). RAD-Seq can be used to study the population genetics of a species with availability of very less or no sequence data contributing to the added advantage over other methods for SNP discovery.

Currently SNP database (dbSNP) of National Center for Biotechnology Information (NCBI) contains over 9.5 million bovine SNPs; however, number of SNPs identified in buffalo species is limited (Amaral et al. 2008; Michelizzi et al. 2010, 2011). As buffalo and cattle are closely related species, therefore, it was expected that large quantity of genomic resources developed for cattle might be helpful in characterizing the buffalo genome, and in the genomic selection of these species. However, transference of genomic information contained in the Illumina Bovine HD Bead Chip from cattle to buffaloes revealed only 16,580 polymorphic markers (MAF >0.05) out of 688,593 bovine SNPs which were successfully genotyped from the 384 buffalo samples (Borquis et al. 2014). Hence, identification of SNP markers for high throughput genetic analysis has great scope in buffaloes as well. Recently, Axiom buffalo genotyping array has been used to estimate molecular diversity in Swamp buffalo, describing population structure and its historic relationship with other population (Iamartino et al. 2013), confirming some genomic regions equivalent to BTA 3 and BTA 14 of *Bos taurus* in African buffaloes (*Syncerus caffer*) (Liu et al. 2018; Mokhber et al. 2019).

However, reports on trait based SNP information for Indian buffalo genome are scarce. SNPs from whole exome sequencing related to milk production performance level from buffalo breeds of Banni/Jaffrabadi and Mehsana were obtained (Han et al. 2018; Li et al. 2019; Menon et al. 2016). In this study, SNPs and Polymorphic Loci associated with ddRAD genomic data for four different traits (milk volume, age at first calving, post-partum cyclicity, and feed conversion efficiency) in Murrah buffalo have been identified. These SNPs are documented as a web based database for its wider access and application. This database aims to understand the influence of SNP markers related to four economically important traits of Murrah buffaloes.

Materials and methods

Animals, phenotypic resource and genotyping data generation

Murrah buffaloes used in the present study were from the progeny testing programme at ICAR-Central Institute for Research on Buffaloes, Hisar (Government of India) for genetic improvement of the buffalo breed. All the pedigree and performance records are maintained starting from birth to death/culling of every calf at farm. Selection of individual animals for implementing mating plans is based on specific performance criteria of mates for genetic improvement and productivity enhancement. These specific criteria are phenotype determinants for selective genotyping. Selective genotyping based on discrete levels of performance to harness true genetic variants as source of mapping nucleotide based markers to achieve higher gain in selection programmes have been followed.

Individual animals were selected from unrelated pedigree and extreme performance levels for traits as: milk volume (milk yield), age at first calving, post-partum cyclicity and feed conversion efficiency [Institutional Animal Ethics Committee (IAEC); Reg. No. 406/GO/RBI/L/01/CPCSEA]. Data search on phenotype records (for almost 25 years) were made while considering animals selection for genotyping, ensuring wide variation over sire, parity of animals, best milk yield in whole production span, milk constituents, lactation length subject to performance criteria is shown in Table 1.

Table 1 The performance criteria for measurement of phenotypic records

S.no	Traits	Phenotype determinant		
		Higher limit	Lower	Pre-determined/Experimented
1	Milk volume (milk yield) in kg per lactation (measured in 305 days lactation length)	> 3000 kg	< 1800 kg	Phenotype records available at Farm
2	Age at first calving (Records are kept for every heifer at farm under the Genetic Improvement Programme)	< 40 months	> 55 months	Phenotype records available at Farm
3	Post-partum cyclicity (It is taken as gestation period *i.e.,* period between two subsequent calvings)	< 70 days	> 200 days	Phenotype records available at Farm
4	Feed conversion efficiency trials	− 0.437	0.359	Based on feed trials

For generation of feed conversion efficiency, feeding trials for feed conversion efficiency were conducted for 90 days feed trial on 42 growing animals of age 10 to 12 months. Individual feeding of animals was conducted for 3 months period to identify efficient energy utilizing animals for growth. Data on feed (dry matter) intake and body weight gain was recorded respectively, daily, before and after trial for 90 days to determine high and low residual feed Intake [RFI] per unit daily weight gain, to estimate Feed Conversion Efficiency (FCE). RFI is determined as difference in actual and predicted dry matter intake (DMI) of individual heifer (Sikka et al. 2020). Average daily weight (g/day) gain was recorded for each of the animals under trial. Under this trial, eleven high and eleven low feed convergent animals out of 42 animals were selected for genotyping based on residual feed intake /daily intake. Actual dry matter intake per unit body weight gain was determined. High and low feed convergent were identified by determining residual feed intake variation for genotyping.

Selective genotypes were bled for isolation of nucleic acid (DNA and RNA) by Phenol-Chloroform method (Sambrook and Russell 2001) and further used for SNP genotyping. Study comprised of 85 buffaloes, out of these, 8 to 14 buffaloes were selected for each trait based on their contrasting phenotypic performance i.e., low and high performance as per records maintained at farm. However, in the current study, 25 animals for milk volume, 19 animals for age at first calving, 19 animals for post-partum cyclicity and 22 animals for feed conversion efficiency were selected. Individual sample-wise ddRADdata were generated by Hi-Seq Illumina sequencing platform (Peterson et al. 2012).

Data quality check, processing and analysis

The ddRAD sequencing of genome data generated over 85 animals were checked for quality parameters followed by trimming of these quality sequences using Trimmomatic tool (Bolger et al. 2014). These sequences were further aligned to the available reference genome i.e., *Bubalus bubalis* (UOA_WB_1) (Low et al. 2019) and indexing has been done by using Bowtie2 tool (Langmead and Salzberg 2012) with default parameter settings. Further, the resultant sequences were aligned and produced as Sequence Alignment Map (SAM) formatted files and then passed to STACKS pipeline (Catchen et al. 2013). The wrapper program *ref_map.pl* available in STACKS pipeline was used to create the catalog of loci for SNP identification using the standard parameters. First, the sequences were aligned to the same genomic location were stacked together and merged to form loci. These loci with a sequencing depth of three or more reads per individual were retained and catalog has been created. SNPs at each locus were selected using a maximum likelihood framework. Population program of STACKS pipeline (*populations*) was used to process all the SNP data across individuals to generate summary statistics. Genetic diversity was estimated using important genetic parameters such as major and minor allele frequency, observed and expected heterozygosity, observed and expected homozygosity and nucleotide diversity (π) (Fig. 1). Further, annotation of these SNPs was carried out with the help of SnpEff tool and related gene Ids were converted into UniProt gene Id using DAVID software. Moreover, the functional classification of the genes was carried out by using agriGo tool with FDR value ≤ 0.05 based on uniProt gene Ids. The agriGo tool maps genes to function according to GO categories: molecular function, cellular component and biological process (Young et al. 2019). The location of the uniProt gene Ids was retrieved from Ensemble genome browser.

Results and discussion

Data statistics

The total identified SNP by using group wise computational approach in all low and high performance groups of genotypes (animals) belonging to four traits and the trait wise minimum and maximum number of identified unique stacks, polymorphic loci and SNPs for all samples is shown in Tables 2, 3 and Fig. 2.

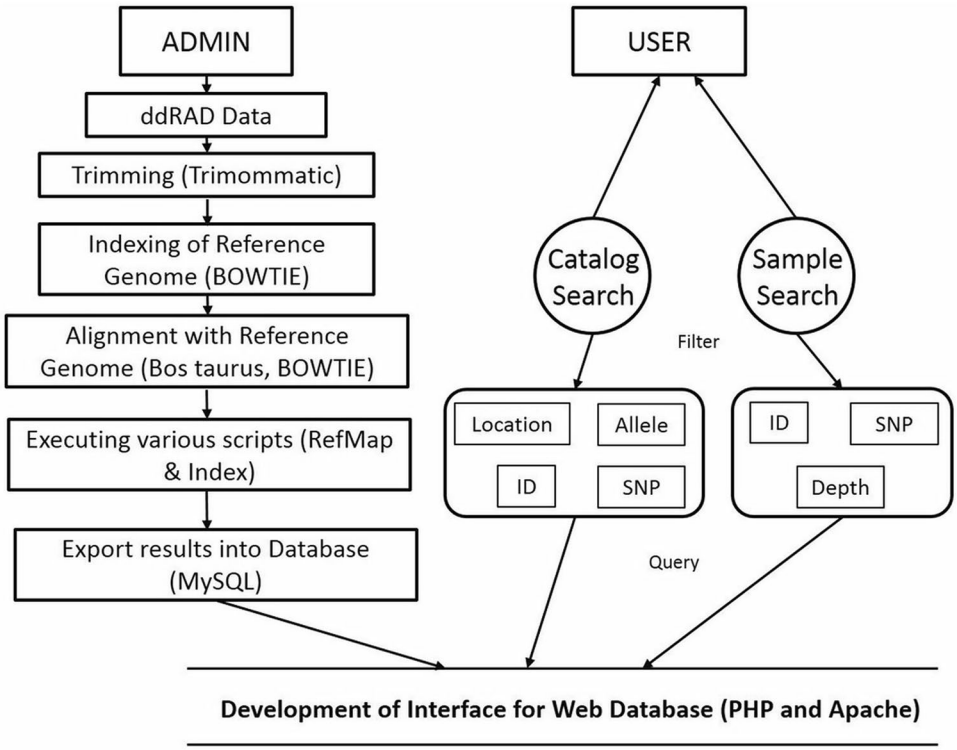


Fig. 1 The data and process flow architecture

Table 2 The total identified SNP by using group wise computational approach in all low and high performance groups of genotypes (Animals) belonging to four traits

S.no	Traits	Genotypes/ Samples (n)		SNPs (n)	
		High	Low	High	Low
1	Milk volume	11	14	119,755	127,227
2	Age at first calving	08	11	97,030	86,461
3	Post-partum cyclicity	11	08	42,144	44,232
4	Feed conversion efficiency	11	11	98,753	98,454

SNPRBb: design and implementation

The structure of the database has been designed by applying the normalization procedure of Relational Database Management System (RDBMS) to avoid the duplicate values of attributes and corresponding entities. The database was developed in MySQL. MySQL feature-rich database software that provides speedy data access, ease of use, portable etc. (Bowman et al. 1996). The identified SNPs and their characteristics from the different samples across the four traits of water buffalo has been integrated and assembled in this relational open source database i.e., MySQL. The accessibility of this data is provided to the end users by writing server side scripts in PHP language and hosted at Apache Web Server (Lee and Ware 2002). The Web based end user interface has been developed by using HTML5 and Java script language and dynamic Web interface has been created using PHP for quick and easy retrieval of SNPs and their associated information from the database. This web application has been hosted using an open source software Apache web Server to provide multi-user access of the developed interface. This database is named as SNP resources on *Bubalus bubalis* (SNPRBb) (Fig. 3).

Table 3 Trait wise minimum (Min) and maximum (Max) number of identified unique stacks, polymorphic loci and SNPs for all samples

S. no	Traits	Unique Stacks		SNPs (n)		Polymorphic loci	
		Min	Max	Min	Max	Min	Max
1	Milk volume	10,382	362,429	203	26,465	144	22,120
2	Age at first calving	38,440	329,562	771	26,778	673	21,415
3	Post-partum cyclicity	11,021	329,562	165	26,778	132	21,415
4	Feed conversion efficiency	25,873	329,262	434	22,505	373	18,832

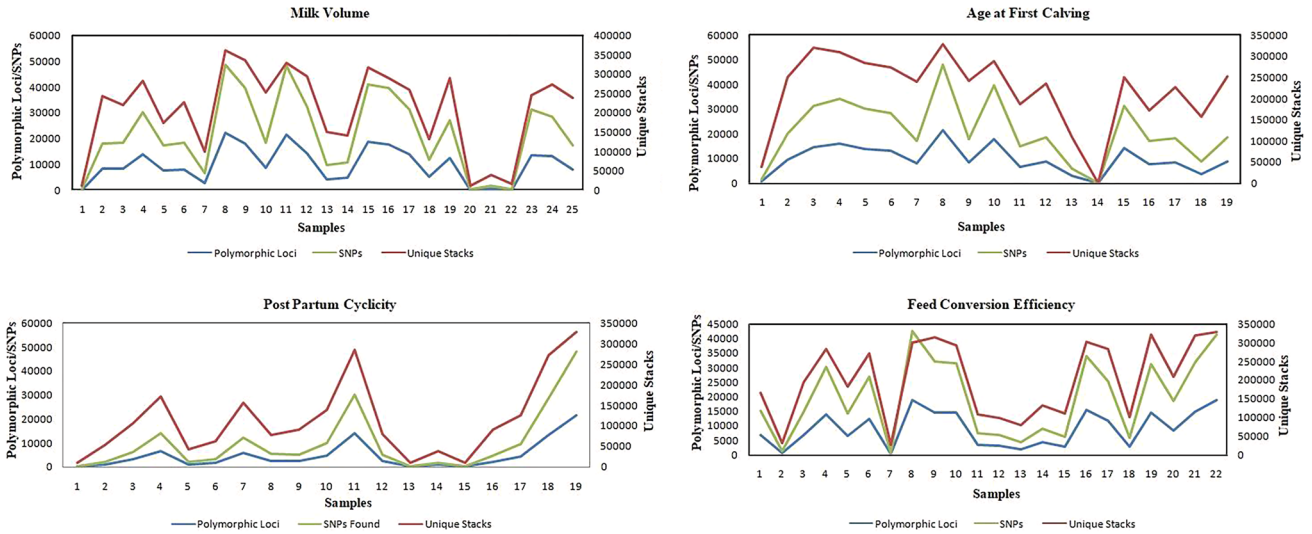


Fig. 2 Sample wise identified unique stacks, polymorphic loci and SNPs for all the selected traits

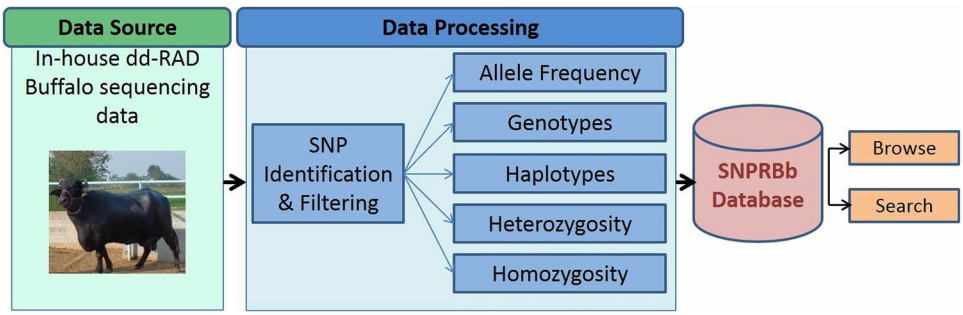


Fig. 3 Shows the Data Flow Diagram (DFD) of the SNPRBb, starting from data collection to upload the results in database including data processing and analysis

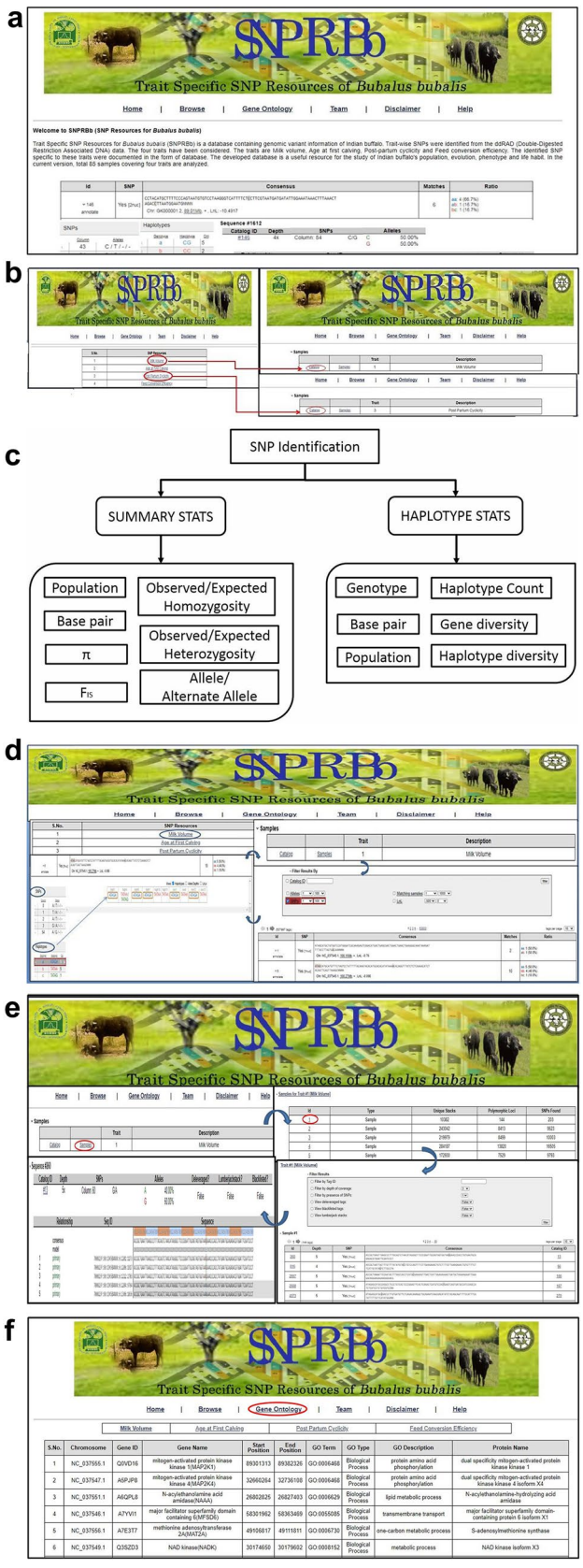
The Web access has been developed to provide seamless integration with the underlying database. The database is accessible from http://snprbb.icar.gov.in and home page (Fig. 4a).End users access the available options to click on any of the item i.e., Browse, Gene Ontology, Team, Disclaimer and Help to view the required information (Fig. 4b).

If any user wants to revert back to home page, the "Home" link is made available at every page. The identified SNP resources can be browsed or explored by clicking on the link "Browse". This option allows the users to search and explore SNP resources based on catalog and samples for selected trait. The current database contains the identified SNP resources for four traits of *Bubalus bubalis* i.e., milk volume, age at first carving, post-partum cyclicity and feed conversion efficiency.

Furthermore, the users have two choices to browse these SNPs i.e., either by catalog or samples for the selected trait. Catalog will provide identified Tags, SNPs, consensus sequence based on samples corresponding to chromosome number, position of base pair, matches and allele ratio of the selected trait. The user can even explore more details by choosing a specific Id to get the information related to the SNP position, haplotypes, genotypes and their count, allele depth and LnLs (Log Likelihood filter). In case of more SNPs, the summary statistics can be viewed by clicking on the SUMMARY STATISTICS. This will display population, base pair, column (position), allele, alternate allele, and other useful information related to the identified SNPs. Similarly, the information is also accessible for HAPLOTYPES STATS in a separate window. The features of the SNPs, stepwise procedure for selection of mentioned parameters and statistics are described in Fig. 4c–f.

Conclusion

SNPRBb documents the identified SNPs using ddRAD data for four important traits in *Bubalus bubalis* i.e., milk volume, age at first carving, post-partum cyclicity and feed conversion efficiency. These identified SNPs specific to these traits are assembled as database and available to end users through web browser. Detailed information of each SNP, including allele frequencies in buffalo populations, heterozygosity and homozygosity value, haplotypes statistics, F_{IS} and



◀ **Fig. 4** **a** Database is accessible source; **b** End users options (Browse, Gene Ontology, Team, Disclaimer and Help to view the required information); **c** Features of the SNPs; **d** & **e** Step-wise procedure for selection of mentioned parameters; and f: Gene Ontology

their position on reference chromosome are available in the database. SNPRBb mainly provides the information associated to SNP in two ways viz. Catalog and sample which will enable the researchers in the comparative analysis for quick comparison of SNPs in different samples. This developed database will be a useful resource for planning breeding program for genetic gain by studying the genetic variants associated with economically important traits buffalo.

Acknowledgements We acknowledge support from Network Project on Agricultural Bioinformatics and Computational Biology under Centre for Agricultural Bioinformatics Scheme, ICAR-IASRI, Indian Council for Agricultural Research (ICAR), New Delhi, India.

Funding The financial support for this study has been provided by Centre for Agricultural Bioinformatics (CABin) scheme of Indian Council of Agricultural Research (ICAR), New Delhi, India.

Data availability Database URL:http://snprbb.icar.gov.in/

Declarations

Conflict of interest The authors declare that they have no conflict interest.

Ethical approval The data and samples of buffaloes used in this study were provided by buffalo herd of ICAR-Central Institute for Research on Buffaloes Hisar (Haryana), India. Experiment design and animal treatments were approved by the Institutional Animal Ethics committee (IAEC) of the Institute.

References

Amaral MEJ, Grant JR, Riggs PK, Stafuzza NB, Rodrigues Filho EA, Goldammer T, Weikard R, Brunner RM, Kochan KJ, Greco AJ (2008) A first generation whole genome RH map of the river buffalo with comparison to domestic cattle. BMC Genomics 9:631

Barker J (1994) A global protocol for determining genetic distances among domestic livestock breeds. In: Proceedings of the 5th World congress on genetics applied to livestock production, Guelph, Ontario, Canada, pp 501–508

Bibi F, Vrba ES (2010) Unraveling bovin phylogeny: accomplishments and challenges. BMC Biology 8:50

Bolger AM, Lohse M, Usadel B (2014) Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120

Borghese A, Mazzi M (2005) Buffalo population and strategies in the world. Buffalo Product Res 67:1–39

Borquis R, Baldi F, de Camargo G, Cardoso D, Santos D, Lugo N, Sargolzaei M, Schenkel F, Albuquerque L, Tonhati H (2014) Water buffalo genome characterization by the Illumina BovineHD BeadChip. Genet Mol Res 13(2):4202–4215

Bowman JS, Emerson SL, Darnovsky M (1996) The practical SQL handbook: using structured query language, 3rd edn. Addison-Wesley

Catchen J, Hohenlohe PA, Bassham S, Amores A, Cresko WA (2013) Stacks: an analysis tool set for population genomics. Mol Ecol 22:3124–3140

Davey JW, Hohenlohe PA, Etter PD, Boone JQ, Catchen JM, Blaxter ML (2011) Genome-wide genetic marker discovery and genotyping using next-generation sequencing. Nat Rev Genet 12:499

Department of Animal Husbandry and Dairying, Annual Report (2018–19)

Duarte D, Newbold CJ, Detmann E, Silva F, Freitas PHF, Veroneze R, Duarte M (2019) Genome-wide association studies pathway-based meta-analysis for residual feed intake in beef cattle. Animal Genet 50(2):150–153

Dutt G, Yadav M (1988) A Genetic-Study of Milk-Yield in Nili Buffalos. Indian Veter J 65:512–515

Faostat (2014) Food and Agriculture Organization of the United Nations. http://www.fao.org/faostat/en/

Gogoi P, Johar K, Singh A (1985) Genetic analysis of milk yield in Murrah buffaloes Indian. Veter J 62:970–975

Group ISMW (2001) A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. Nature 409:928

Han B, Liang W, Liu L, Li Y, Sun D (2018) Genetic association of the ACACB gene with milk yield and composition traits in dairy cattle. Animal Genet 49:169–177

Hegde NG (2019) Buffalo husbandry for sustainable development of small farmers in India and other developing countries. Asian J Res Animal Vet Sci 3(1):1–20

Hohenlohe PA, Bassham S, Etter PD, Stiffler N, Johnson EA, Cresko WA (2010) Population genomics of parallel adaptation in three-spine stickleback using sequenced RAD tags. PLoS Genet 6:e1000862

Iamartino D, Williams JL, Sonstegard T, Reecy J, Tassell CV, Nicolazzi EL, Biffani S, Biscarini F, Schroeder S, de Oliveira DA (2013) The buffalo genome and the application of genomics in animal management and improvement buffalo. Bulletin 32:151–158

Kiplagat SK, Limo MK, Kosgey IS (2012) Genetic improvement of livestock for milk production. In: Chaiyabutr N (ed) Milk production-advanced genetic traits, cellular mechanism. Animal Management and Health. InTechOpen

Landegren U, Nilsson M, Kwok P-Y (1998) Reading bits of genetic information: methods for single-nucleotide polymorphism analysis. Genome Res 8:769–776

Langmead B, Salzberg SL (2012) Fast gapped-read alignment with Bowtie 2. Nat Methods 9(4):357

Lee J, Ware B (2002) Open source development with LAMP: using Linux, Apache, MySQL and PHP. Addison-Wesley Professional

Lenstra JA, Felius M (2015) Genetic aspects of domestication. In: Garrick DJ, Ruvinski A (eds) The genetics of cattle. CAB International

Li Y, Han B, Liu L, Zhao F, Liang W, Jiang J, Yang Y, Ma Z, Sun D (2019) Genetic association of DDIT 3, RPL 23A, SESN 2 and NR 4A1 genes with milk yield and composition in dairy cattle. Animal Genet 50(2):123–135

Liu J, Liang A, Campanile G, Plastow G, Zhang C, Wang Z, Salzano A, Gasparrini B, Cassandro M, Yang L (2018) Genome-wide association studies to identify quantitative trait loci affecting milk production traits in water buffalo. J Dairy Sci 101:433–444

Low WY, Tearle R, Bickhart DM, Rosen BD, Kingan SB, Swale T, Thibaud-Nissen F, Murphy TD, Young R, Lefevre L (2019) Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. Nat Commun 10:260

Malik A, Sharma R, Ahlawat S, Deb R, Negi M, Tripathi S (2018) Analysis of genetic relatedness among Indian cattle (Bos indicus) using genotyping-by-sequencing markers. Animal Genet 49:242–245

Matukumalli LK, Lawley CT, Schnabel RD, Taylor JF, Allan MF, Heaton MP, O'Connell J, Moore SS, Smith TP, Sonstegard TS (2009) Development and characterization of a high density SNP genotyping assay for cattle. PloS One 4:e5350

Menon R, Patel AB, Joshi C (2016) Comparative analysis of SNP candidates in disparate milk yielding river buffaloes using targeted sequencing. PeerJ 4:e2147

Michelizzi VN, Dodson MV, Pan Z, Amaral MEJ, Michal JJ, McLean DJ, Womack JE, Jiang Z (2010) Water buffalo genome science comes of age international. J Biol Sci 6:333

Michelizzi VN, Wu X, Dodson MV, Michal JJ, Zambrano-Varon J, McLean DJ, Jiang Z (2011) A global view of 54,001 single nucleotide polymorphisms (SNPs) on the Illumina BovineSNP50 BeadChip and their transferability to water buffalo. Int J Biol Sci 7:18

Mokhber M, Shahrbabak MM, Sadeghi M, Shahrbabak HM, Stella A, Nicolzzi E, Williams JL (2019) Study of whole genome linkage disequilibrium patterns of Iranian water buffalo breeds using the Axiom Buffalo Genotyping 90K Array. PloS One 14:e0217687

Notter DR (1999) The importance of genetic diversity in livestock populations of the future. J Anim Sci 77:61–69

Peterson BK, Weber JN, Kay EH, Fisher HS, Hoekstra HE (2012) Double digest RADseq: an inexpensive method for de novo SNP discovery and genotyping in model and non-model species. PloS One 7:e37135

Sambrook J, Russell DW (2001) Molecular cloning: a laboratory manual (3-volume set). Immunol 49:895–909

Seno L, Cardoso V, El Faro L, Sesana R, Aspilcueta-Borquis R, De Camargo G, Tonhati H (2010) Genetic parameters for milk yield, age at first calving and interval between first and second calving in milk Murrah buffaloes. Livestock Res Rural Dev 22:1–8

Sikka P, Nath A, Paul SS, Andonissamy J, Mishra DC, Rao AR, Balhara AK, Chaturvedi KK, Yadav KK, Balhara S (2020) Inferring relationship of blood metabolic changes and average daily gain with feed conversion efficiency in murrah heifers: machine learning approach. Front Vet Sci 7:518

Stickney HL, Schmutz J, Woods IG, Holtzer CC, Dickson MC, Kelly PD, Myers RM, Talbot WS (2002) Rapid mapping of zebrafish mutations with SNPs and oligonucleotide microarrays. Genome Res 12:1929–1934

Surya T, Vineeth M, Sivalingam J, Tantia MS, Dixit SP, Niranjan SK, Gupta ID (2018) Genomewide identification and annotation of SNPs in Bubalus bubalis. Genomics 111(6):1695–1698

Taneja VK, Bhat PN (1986) Milk and beef production in tropical environments. In: Dickerson GE, Johnson RK (eds) 3rd world congress on genetics applied to livestock production, 4 vols. University of Nebraska Institute of Agriculture and Natural Resources, Lincoln

Thiruvenkadan A (2011) Performances of Murrah buffaloes at coastal region of Tamil Nadu. India Indian J Animal Sci 81:1080

Vignal A, Milan D, SanCristobal M, Eggen A (2002) A review on SNP and other types of molecular markers and their use in animal genetics. Genet Sel Evol 34:275

Young R, Lefevre L, Bush SJ, Joshi A, Singh SH, Jadhav SK, Dhanikachalam V, Lisowski ZM, Iamartino D, Summers KM (2019) A gene expression atlas of the domestic water buffalo (Bubalus bubalis). Front Genet 10:668

Terms and Conditions

Springer Nature journal content, brought to you courtesy of Springer Nature Customer Service Center GmbH (“Springer Nature”).
Springer Nature supports a reasonable amount of sharing of research papers by authors, subscribers and authorised users (“Users”), for small-scale personal, non-commercial use provided that all copyright, trade and service marks and other proprietary notices are maintained. By accessing, sharing, receiving or otherwise using the Springer Nature journal content you agree to these terms of use (“Terms”). For these purposes, Springer Nature considers academic use (by researchers and students) to be non-commercial.
These Terms are supplementary and will apply in addition to any applicable website terms and conditions, a relevant site licence or a personal subscription. These Terms will prevail over any conflict or ambiguity with regards to the relevant terms, a site licence or a personal subscription (to the extent of the conflict or ambiguity only). For Creative Commons-licensed articles, the terms of the Creative Commons license used will apply.
We collect and use personal data to provide access to the Springer Nature journal content. We may also use these personal data internally within ResearchGate and Springer Nature and as agreed share it, in an anonymised way, for purposes of tracking, analysis and reporting. We will not otherwise disclose your personal data outside the ResearchGate or the Springer Nature group of companies unless we have your permission as detailed in the Privacy Policy.
While Users may use the Springer Nature journal content for small scale, personal non-commercial use, it is important to note that Users may not:

1. use such content for the purpose of providing other users with access on a regular or large scale basis or as a means to circumvent access control;
2. use such content where to do so would be considered a criminal or statutory offence in any jurisdiction, or gives rise to civil liability, or is otherwise unlawful;
3. falsely or misleadingly imply or suggest endorsement, approval , sponsorship, or association unless explicitly agreed to by Springer Nature in writing;
4. use bots or other automated methods to access the content or redirect messages
5. override any security feature or exclusionary protocol; or
6. share the content in order to create substitute for Springer Nature products or services or a systematic database of Springer Nature journal content.

In line with the restriction against commercial use, Springer Nature does not permit the creation of a product or service that creates revenue, royalties, rent or income from our content or its inclusion as part of a paid for service or for other commercial gain. Springer Nature journal content cannot be used for inter-library loans and librarians may not upload Springer Nature journal content on a large scale into their, or any other, institutional repository.
These terms of use are reviewed regularly and may be amended at any time. Springer Nature is not obligated to publish any information or content on this website and may remove it or features or functionality at our sole discretion, at any time with or without notice. Springer Nature may revoke this licence to you at any time and remove access to any copies of the Springer Nature journal content which have been saved.
To the fullest extent permitted by law, Springer Nature makes no warranties, representations or guarantees to Users, either express or implied with respect to the Springer nature journal content and all parties disclaim and waive any implied warranties or warranties imposed by law, including merchantability or fitness for any particular purpose.
Please note that these rights do not automatically extend to content, data or other material published by Springer Nature that may be licensed from third parties.
If you would like to use or distribute our Springer Nature journal content to a wider audience or on a regular basis or in any other manner not expressly permitted by these Terms, please contact Springer Nature at

onlineservice@springernature.com