ANNEXURE-VI

INDIAN COUNCIL OF AGRICULTURAL RESEARCH
CHECKLIST FOR SUBMISSION OF FINAL RESEARCH PROJECT REPORT (RPP-III)

1. Institute Project Code: IXX10451
2. Investigator as approved in RPP-1, If any change attach IRC proceedings:

Principal Investigator	Co-PI
Dr.(Mrs) Anupama Mukherjee (from July 2013 till 17.12.2014)	1. Dr. Sabyasachi Mukherjee 2. Dr. Nazrul Haque 3. Dr. Kezhavituo Vupru
Dr. Sabyasachi Mukherjee (18.12.2014 to 31.03.2015)	1. Dr.(Mrs) Anupama Mukherjee 2. Dr. Nazrul Haque 3. Dr. Kezhavituo Vupru

3. Any changes in objectives and activities: No
   (If yes, attach IRC proceedings)

4.	Date of Start and Date of Completion (Actual) if any extension granted enclose IRC proceedings			No
5.	Whether all objectives met		Yes	
6.	All activities completed		Yes	
7.	Salient achievements/major recommendations included		Yes	
8.	Annual Progress Reports (RPP-II) submitted	Yes	yes	
9.	Reprint of each publication attached	Yes	yes	
10.	Action for further pursuit of obtained results indicated	Yes	yes	
11.	Report presented in Divisional seminar (enclose proceedings & action taken repor)		Yes	
12.	Report presented in Institute seminar (enclose proceedings & action taken report)		Yes	
13.	IRC number in which the project was adopted		IRC No:	
14.	Any other Information			

15.Signature:

Project Leader

Co-PI

Co-Pi

Co-Pi…..
HOD/PD/I/c.

INDIAN COUNCIL OF AGRICULTURAL RESEARCH
FINAL RESEARCH PROJECT REPORT (RPP-III)

(For Guidelines Refer ANNEXURE-XI(G))

1. Institute project Code to be Provided by PME Cell) : IXX10451
2. Project Title: **"Genome Wide Association Study for growth and feed efficiency traits in Mithun"**

3. Key Words: **Genome Wide Association, quantitative trait loci, SNP genotyping, growth, mithun**
4. (a) Name of the lead Institute: **National Research Centre on Mithun**
   (b) Name of Section: **Animal Genetics and Breeding**

5. (a) Name of the Collaborating Institute(s), if any
   (b) Name of section of Collaborating Institute(s):
6. **Project Team (Name (s) and designation of PI and all project Co-PIs, with time spent)**

S. No	Name, designation and Institute	Status in the project (PI/CC-PI/Co-PI)	Time to be spent (%)	Work Components assigned to individual scientist
1.	Dr. Sabyasachi Mukherjee	PI	50%	1. Selection of animals for genotypic studies. 2. Association of whole genome with phenotypic traits. 3. Interpretation of result and report writing.
2.	Dr.(Mrs) Anupama Mukherjee	Co-PI	30%	1. Quality control of Genotypic data. 2. Analysis of Data
3.	Dr. Nazrul Haque	Co-Pi	10%	1. Selection of animals for genotypic studies. 2. Observation of phenotypic data.
4.	Dr. Kezhavituo Vupru	Co-PI	10%	1. Observation of phenotypic data 2. Compilation of phenotypic data and generation of secondary traits.

7. **Priority Area : Genome Resource Conservation**
8. **Project Duration : 02 Years (Two Years) and eight months**

Date of Start- July 2013 Date of Completion- 31st March 2015

9. (a) Objectives

1. To assess the genetic diversity and haplotype block structure for characterization Mithun Population structure using the IIIumina Bovine HD Genotyping Bead Chip Panel.
2. To determine the efficiency of genotyping and level of polymorphism and minor allele frequency distribution in Mithun population.
3. To identify putative SNP markers potentially contributing to variation observed in the mendalian trait and quantitative traits (growth related traits and feed efficiency traits **(ADG, FCR)** measured in mithun.

(b) Practical Utility

The findings from GWAS will accelerate the genome-scale measurement that will help: firstly in making the comprehension of the basic structure and function of mithun genome; secondly to unravel the history of mithun development and domesticated, thirdly in characterizing the cause of relatively simple phenotypes and genetic diseases; and finally explain the control of complex characteristic features. Finally the result of the investigation will help to close the gap between genetics and the traits that are observed, known as the "genotype/phenotype gap."

The casual relationship between genetic polymorphism within a species and the phenotypic differences observed between individuals is of fundamental biological interest. The ability to predict genetic risk factors for economically important traits like growth rate and carcass yield in mithun require an understanding of both the specific loci that underlie a phenotype, and the genetic architecture of a trait. Forward genetics, in which many individuals that differ in genotype are screened for phenotypes of interest. Any phenotype differences identified are connected back to the underlying causative loci via various mapping approaches including Quantitative Trait Locus (QTL) mapping in this perspective, Genome Wide Association Studies (GWAS) is a very complementary and powerful tool for connecting the genotype-phenotype map.

QTL mapping has proved an, and remains, a powerful method to identify regions of the genome that co-segregate with a given trait in F2 populations. Despite this success, QTL mapping suffers from two fundamental limitations; only allelic diversity that segregates between the parents of the particular F2 cross can be assayed, and second, the amount of recombination places a limit on the mapping resolution.

GWAS overcome the two main limitations of QTL analysis mentioned above. Generally, after identifying a phenotype of interest, GWAS can serve as a foundation experiment by providing insight into the genetic architecture of the trait, allowing informed choice of parents for QTL analysis. The implication of an 'association; between a marker and a trait is that it exist across the whole population, and so specially designed mapping families are not needed. In fact, a sample of unrelated individuals would be ideal.

The basic approach in GWAS is to evaluate the association between each genotyped marker and a phenotype of interest that has been scored across a large

number of individuals. This approach was pioneered nearly ten years ago in human genetics. GWAS are now widely used in dairy and beef cattle and more recently other species of Bos. This is the first attempt to uncover the association at genetic level of growth and carcass quality traits in mithun using hidh density SNP chip. The meaningful association may result.

10. Final Report on the Project (material and method used, results and discussion, objective wise achievements and conclusions)

– **Please see Annexure-A**

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11. Financial Implications (Rs in Lakhs)

(i) Budget

(ii) A. Non-Recurring

S. No	Item	1 year	II Year	III Year	Total
1.	High data computing system	500000	-	-	
2.	Renovation of Lab	200000	-	-	700000

(iii) B. Recurring

(iv) B.1 Manpower

S. No	Position No.	Consolidated Emolument	1 year	II Year	III Year	Total
1.	YP-I	Rs 16000 + HRA @ 10% 1st and 2nd year; Rs 18000 + HRA @ 10%	2,11,200	2,11,2000	237600	6,60,000
2	Lab attendent	3rd Year Rs 8000 per month	96,000	96,000	96,000	288000

B.2 Consumables

S. No	item	Quantity	1 year	II Year	III Year	Total
1.	Chemicals	As per need	200000	400000	200000	800000
2.	Glassware & Plastic ware		50000	50000	50000	150000

Other items	Consol Emol.	1 year	II Year	III Year	Total
B.3 Travel		50000	50000	50000	150000
B.4 Contingency		2000000	2000000	2000000	6000000
B.5 Overhead		20000	15000	12000	470000
Sub-total of B (B>!+B.2+B.3+B.4+B.5)		1627200	1822200	1645600	5095000
Grand Total (A+B)		**3327200**	**2822200**	**2645600**	**8795000**

Grand Total: Rs 5795000

12. Cumulative Output

a. Special attainments/innovations:
   - The transferability of 770k HD Bovine Bead Chip for presence of polymorphic loci and parameter for population study was assessed first time in the world for mithun genome.
   - The result indicated sufficient SNP loci to carry out genomic studies in this unique bovine species.

b. List of publications (0ne copy each to be submitted if not already submitted)
   i. Research Papers - Nil
   ii. Reports/Manuals - Nil
   iii. Working and Concept Papers - Nil
   iv. Popular Articles - Nil
   v. Books/Book Chapters - NIl
   vi. Extension Bulletins - Nil

c. Intellectual property Generation - Nil
(Patents- filled/obtained; Copyrights- filed/obtained; Designs- filled/obtained; Registration details of variety/germplasm/accession if any)

The genotypic data were generated based on high density chip in mithun

d. Presentation in Workshop/Seminars/Symposia/Conferences
(relevant to the project in which scientists have participated)

   - Mukherjee, Anupama: Mukherjee, Sabyasachi, Adebambo, A.O., Longkumer, Imsusosang and Mech, Moonmoon. (2014) **Genomic Information a tool for Assessment of Genetic Diversity in Mithun (Bos frontalis).** 2nd International Conference on Animal & Dairy Sciences" (Animal Science-2014) held from 15-17th Sept '2014 at Hyderabad, India.
   - Presented a poster at the XII Agricultural Science Congress on **"Genome wide scan and application of high density SNP arrays in mithun (Bos frontalis)** held at ICAR-NDRI, Karnel, February 3-6, 2015.

e. Details of technology developed
(Crop-based; Animal-based, including vaccines; Biological- biofertilizer, biopesticide, etc; IT based- database, software; Any other- please specify)

f. Trainings/demonstrations organized
   - Exhaustive hands-on training was imparted to one Post Doctoral fellow who came in our lab on a six-months C.V Raman African Researcher Scholarship to perform analysis of genomic data and genome wide association with the important economic traits of mithun.

g. Training received

h. Any other relevant information - NA

13. (a) Extent of achievement of objectives and outputs earmarked as per RPP-I

Ojective wise	**Activity**	**Envisaged output of monitorable target(s)**	**Output achieved**	**Extent of Achievement (%)**
1.To assess the genetic diversity and haplotype block structure for characterizing Mithun population structure using the IIIumina Bovine HD Genotyping Bead Chip panel.	1. Selection of experimental animal.	Generation wise information on parameters were collected	Phenomic data and pedigree was compiled	100%
	2. Isolation of DNA for generation of genotypic data	Genotypic data was generated	Quality control of genotypic data was done. Mithun population structure was characterized based on genetic diversity and haplotype block structure	100%
2. To determine the efficiency of genotyping and level of polymorphism and minor allele frequency distribution in Mithun population.	The geneotypic data was analysed using software	The transferrabili SNP chip was assessed	The MAF and polymorphism for important traits economic traits can be easily explained using bovine HD chip.	100%
3. To identify putative SNP markers potentially contributing to variation observed in the mendalian trait and quantitative traits (growth related traits and feed efficiency traits (ADG, RFI) measured in Mithun.	Genome wide association was carried out using software	Polymorphic SNP associated with various traits considered in the present study was established.	Novel SNP associated genome wide with body coat colour characteristics for mithun could established	100%

(b) Reasons of shortfall, if any – Nil

14. Efforts made for commercialization/ technology transfer

The study was the first attempt of this kind to use bovine HD Chip770k in mithun and needs to be validated in field samples with sufficient large number in order to transfer in the field for application.

15. (a) How the output is proposed to be utilized?

The output from a baseline information generated on genome wide association of SNPs with growth and feed efficiency traits. This can be further utilized for establishing the association with carcass quality and other important economic traits.

(b) How will it help in knowledge creation

The study of application of bovine SNP chip and genome wide association is first attempt in indigenous livestock. The information generated indicated that the bovine HD Bead SNP chip can be very convienetly utilized in mithun for generating the genomic information. The SNP chip is transferrable to other species of Bos also in generating sufficient polymorphic SNPs for genomic studies.

16. Expected benefits and economic impact. (If any)

Mithun is mainly reared for meat purpose and the genetic improvement for carcass quality traits with the traditional breeding strategies is not possible, the faster genetic gain and improvement in mithun could be achieved using genomic technology.

17. Future line of research work/other identifiable problems

- The research work in future can be taken up for validating the result on more population from field and the genome wide association can be established for all the economic traits of mithun.
- SNP Genotypic data of all the mithun herd can be attempted in future that can be base for effecting genomic selection in mithun for various carcass quality and meat, at the same time it will be an assest of the Institute**.**

18. Details on the research data (registers and records) generated out of the project deposited with the institute for future use.

- The soft copy of genotypic data generated is available with the incharge animal genetics and breeding section, NRC on mithun, Jharnapani.

- Records and other valuable documents related to the project is kept in proper condition in the Animal Genetics and Breeding section, NRC on Mithun, Jharnapani, Nagaland.
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19. Signature

(i) Dr. Sabyasachi Mukherjee (PI) : Sabyasachi Mukherjee

(ii) Dr. (Mrs) Anupama Mukherjee (Co-PI) :----------

(iii) Dr. Nazrul Haque (Co-PI) :----------

(iv) Dr. Kezhavituo Vupru (Co-PI) :----------

20. Signature of Head of Division

21. Observations of PME Cell based on Evaluation of Research Project after Completion

22. Signature (with comments if any along with rating of the project in the scale of 1 to 10 on the overall quality of the work) of JD ®/ Director.

Annexure-A

Final Report of the Project

SNP Quality Control Analysis for whole Population

Samples and Markers

For GWAS a total of 48 samples,51 males and 45 females, were used for the quality control check. All the samples exhibiting a call rate .90 will be included in further analysis.

1. Identity By descent (Detection of Duplicate of Duplicated Samples or Sample Swap): To Identify duplicate and related individuals, identity by state, IBS is calculated for each pair of individuals based on the average proportion of alleles shared in common at genotyped SNPs (excluding the sex chromosomes)

   Following the calculation of IBS between all pairs of individuals, duplicates are denoted as those with an IBS of

   1. Removed Samples

2. Minor allele frequency: This parameter generate a list of minor allele frequencies (MAF) for each SNP markers with minor allele frequency. 0.05 are considered for analysis rest filtered as monomorphic marker.

   Results: Total SNP Markers: 777962 MAF Filtration = 627686 SNP markers considered for further analysis: 150276 New

3. Hardy-Weinberg Equilibrium: SNP markers showing deviation from Hardy-Weinberg Equilibrium based on parental genotype data. The expected genotype frequencies within the parental genotype data are calculated based upon the proband genotype frequencies. Deviations from markers for potential genotyping error. SNP markers with P- Value < 0.05 are removed which deviating from HWE.

   Results: 10442 markers to be excluded based on HWE test (p <= 0.05) SNP markers considered for further analysis: 139834 New

   QC Performed after the filtration. No samples with IBS.>0.95 and markers failing MAF and HWE test retained

Frequency of Heterozygosity

Inbreeding Coefficient: Given a large number of SNPs, in a homogeneous sample, it is possible to calculate inbreeding coefficients (i.e. based on the observed versus expected number of homozygous genotypes).

Inbreeding Coefficient Frequency

Determination of Substructure

Linkage Disequilibrium: SNPs that are not more than 1000kb apart are considered for both r and r2 calculation

Frequency of LD r

Frequency of LD r2

Case Control SNP Association Analysis

Basic control case association test is a 2x3 chi square test performed by comparing allele frequencies between cases and controls to determine the degree of association of the SNP marker(s) with diseases trait. P-value < 0.05 represents highly associated SNP markers.

Adjustment for multiple testing Bonferroni, Sidak FDR, etc: Multiple testing correction refers to re-calculating probabilities obtained from a statistical test which was

repeated multiple times. Multiple testing corrections is performed to remove false positives obtained from P-value computation

Phenotype A

Phenotype B

Phenotype C

Phenotype D

Phenotype E

Results

Descriptive statistics

Since Mithun genome differs form cattle, 2 level of OC were run . First was done with 29 chromosomes, exempting X chromosome, while second run was done with 30 chromosomes, (X=30th Chromosome). Initial number of individuals and SNPs before quality check were 24 and 777,962, respectively. After quality check 23 individuals (95.82%) and 127,432 SNPs (16.387%) were used in the analysis. 584705 (79.52%) markers excluded as having low (<5%) minor allele frequency (least common alleles) and 64296 (8.744269%) markers and 1 individual excluded because of low (<955) call rate. In the second QC with chromosome=30, out of 774660 markers and 24 samples, 620581 (80.11011%) markers were excluded as having low (<5%) minor allele frequency, 67760 (8.7470663%) markers and one individual excluded because of low (<95%) call rate.

The MAF or percent monomorphic allele per population for each SNP calculated from the genotypic data is presented in Table 2. Mean MAF range from 22.4 (Manipur) to 27.7 (Nagaland). At MAF p>/0.05 (common allele), Nagaland mithun population markers exhibited lowest minor allele frequency of 85%, while all other populations had no MAF- Identity of by state (IBS) was least among Mizoram strain (0.8130+0.0207) and highest among Manipur mithun (0.9334+0.0574) Inbreeding coefficient range from 0.0865+0.1389 for Nagaland to 0.1858+0.0526 for Manipur mithun. Observed heterozygousity ranged between 0.2629+0.0400 (Nagaland) to 0.2995+0.0442 (Arunachal). The majority of polymorphic SNPs were found to be in HWE, percentage SNP deviation from HWE (P<0.05) was least among Manipur mithun (0.7151+0.0037) and highest among Nagaland mithun (1.1698+ 0.0014)

Table 1. Basic diversity indices across population based on 127,432 SNPS

Table 2. Minor allele frequency distribution of 770k BeadChip SNP in Bos frontalis

Fixation Indices and gene inflow

Analyses of global F_{ST} showed that deviations from HWE as a result of inbreeding coefficient (F_{IS}) and in total population was quite high. F_{IS} was 0.8705, while F_{IT} was0.8705, While F_{IT} was 0.8778. Overall due to population substructure (F_{ST}) on the other hand was 5.63%. Pairwise F_{ST} reveals highest values between Manipur and Mizoram (0.0808). While least was recorded between Manipur and Nagaland (0.0496).

Table 3: Global and pairwise fixation indices for the 4 mithun strains using 127,432 SNPs

Principle component analysis

The result of the PCA generated with Adegenet (Jombart, 2008) showed a clear non separation of the 4 populations with the first and second principal components (PC1 and PC2) explaining 9.59% and 88% of the total variation, respectively.

Figure 1. Population stratification of the 4 strains of mithun populations based on PCA across 127,432 SNPs. PC1 showing north-south orientation, while PC2 shows an east west orientation.

Genetic distances and Phylogenetic tree

Results of phylogenetic relationship and genetic distance between and within the four mithun populations, based on Nei's genetic distance is shown in Table 3. Within and between breed genetic distances were quite similar. Average genetic distance across all groups is 0.244. Within genetic distance does not vary much in each population. Nagaland had the least withing group genetic distance (0.227), While Mizoram had the highest (0.248). Between groups genetic distance shows Manipur and Mizoram exhibiting highest distance (0.255) and least value of 0.238 between Arunachal and Mizoram. Net genetic distance was also highest with value 0.0013 between Mizoram-Manipur and Mizoram-Nagaland, while least was Mizoram- Arunachal (-0.008). Figure 2. Show a picturesque summary of the genetic distance among the populations. The figure shows no specific clustering of the 4 populations which is also supported by the result sub-structure analysis by the STRUCTURE and ADMIX.

TABLE 4: Nei's genetic distance (lower diagonal) and average net genetic distance (upper diagonal) between groups from 127,432 among the six mithun populations.

Figure 2. Neighbour-joining tree reconstructed using MEGA 5.2 software from 127,432SNPs among the4 mithun populations.

Genetic sub-structuring

STRUCTURE analyses (Pritchard et al,2000) were performed on random subset of 127,432 SNPs with the admixture unlinked loci model set at 50000 burn-in followed by 20,000-100000 MCMC repetitions, assuming K=1-5, for all the mithun datasets.

A graphic representations of cluster structure analysis is depicted in Figure 2 at K=2-5 inferred ancestral populations. The result shows no population substructure as inferred from an increasing plot of cross validation error (Alexander et al., 2013). This depicts the mithun population exhibits no substructure.\

Figure 4. Estimated population Structure using 127,432 SNPs generated by ADMIX for K=2-5

Table 5. Most significant SNPs for individual trait measured

Figure5. Qtscore for individual trait showing -log10(P-value) level of association of SNPs across chromosomes.

Discussions

The world's animal genetics resources (AnGR) is depleting. The loss of a specific breeds means loss of specific attributes that characterizes and makes that breed adaptive to the prevailing changing environment and people need. Conservation of AnGR is as important as preserving the life and the culture of the people. Conservation is best sustained if the people are encouraged to profitably utilize the AnGR. A good conservation and the utilization program needs good information on the phenotypic and genotypic variation that exist within the AnGR.

The genetic variation existing in AnGR is a factor of geographical and human activities surrounding the AnGR. While mutation as a force of genetic change might appear at any period in the history of an AnGR, other forces affecting hardy-weinberg equilibrium are more under geographical and human activities.

Bos frontalis is an extant population of bovine species, historically located to a narrow geographical locations of the Himalayan strip. Its population is tending towards extinction. The preservation of such a species will preserve the culture and livelihood of the people in this region. Conservation and utilization programs need a priori information on diversity and variation within the population assessed using molecular markers. Among such markers SNPs are the most densely populated across the genome and easily assayed with reproducible results. Although a large number of SNPs have been identified from the bovine genome-sequencing project, this has not been validated at large in Bos frontalis. The level of polymorphism in mithun population has not been known and analysed. Prior to this study, no SNPs have been described for these populations. In this study, we report the first preliminary findings on SNP variation in the population of Bos frontalis (mithun) in north-east region of India. Determination of the population structure of the mithun based on the770k IIumina BovineHD chip more or less looks more a blind shot into thick darkness as the mithun genome was never sequenced nor included in any whole genome analysis project. The closed relative of mithun; gaur was included in developing the 770k chip (IIIumina 2012). The low number polymorphic loci (167,215) derived on outgroups (water buffalo, yak and gaur) corroborates our findings in this work (127,432).

The mithun population diversity was tested based on Wright's global fixation indices, population substructure and genetic distances within and between

populations were also evaluated. The farther populations are from each other geographically the less they mate or breed with other, resulting in less alleles shared among the population. With time the population differentiates from each other and becomes fixed to their separate allele frequency. As a result of inbreeding within the population it soon becomes homogeneous with and fixed to a theoretical single allele frequency with high observed homozygosity and low heterozygosity. The Wright overall fixation index (F_{ST}) recorded here showed an expected low value (0.0563). $F_{ST}$is reported to generate low value among high diverse, unselected populations viewed as substantially distinct and among biallelic single nucleotide polymorphic markers when compared to microsatellite or others markers (Jakobsson et al., 2013). On the other hand F_{IT} and F_{IS} showed high values signifying both high inbreeding and fixation of lots of loci, though this values cannot be verified due to exemption of mithun in the design of the IIIumina HD chip being used here. The paired F_{ST} value signifies level of shared alleles as a result of present or past within paired populations breeding. Values show more relatedness among the mithun populations which should more or less be expected most likely due to spatial distance. The variation reported is also supported by the values of observed (H_O) and expected (H_E) heterozygousity found in this study showing the panmitic nature of the populations. The populations also exhibit some level of inbreeding which might have been responsible or slight deviations from HWE. The results show that the mithun populations are considered to exhibit high within population heterozygousity. Between and net Nei's genetic distance showed low divergence between the mithun populations. Both within and between divergences were similar, which might more or less be result of no substructure due to geographical separation nor separate selection pressures on individual population.

ANNEXURE- VIII

INDIAN COUNCIL OF AGRICULTURAL RESEARCH

(For Guidelines Refer ANNEXURE- XI(H))

PROFORMA FOR RESEARCH PRFORMANCE EVALUATION OF INDIVIIDUAL SCIENTIST

1. Institute Project Code * - **1XX10451**

2. Evaluation by PI on the contribution of the team in the project including self

S. No	Name	Status in the project (PI/CC-PI/Co-PI)	*Rating in the scale of 1 to 10
1.	Sabyasachi Mukherjee	Co-PI	7
2.	Anupama Mukherjee	Co-PI	9
3.	Nazrul Haque	Co-PI	7
4.	Kezhavituo Vupru	Co-PI	7

3. Signature of PI

***** Individual scientist participating in the project would be assessed for their performance through an appraisal system in a scale of 1 to 10 for each of the following attributes:

S.No	Criteria	Marks
1.	Percentage of the assigned activity completed	**40**
2.	Quality of the completed activity	**10**
3.	Authenticity/reliability of the data generated	**10**
4.	Enthusiasm and sincerity to work	**10**
5.	Inferences made	**10**
6.	Collaboration and cooperation demonstrated in performing the task at hand	**10**
7.	Amenability to scientific/academic/laboratory discipline	**10**
	Total Score	**100**

ANNEXURE- IX

INDIAN COUNCIL OF AGRICULTURAL RESEARCH

(For Guidelines Refer ANNEXURE- XI(I))

PROFORMA FOR EVALUATION OF RESEARCH PROJECT AFTER COMPLETION BY PI

1. Institute Project Code *- **1XX10451**

2. Evaluation research project after completion by PI

S. No	Criteria	Methodology	Marks (output)	Self Evaluation by PI
1.	Achievements Against approved and stipulated outputs under project	**Qualitative and quantitative assessment of objectives and stipulated outputs under the project will be carried out**	75	
		a) Activity Input/Projected Output/Output Achieved	35	**35**
		b) Extent to which standard design methodology, experimental designs, test procedures, analytical methods followed	10	**09**
		c) Does the data justify the conclusions?	05	**04**
		d) Innovativeness and creating of new Knowledge	10	**10**
		e) Additional outputs over those stipulated under the project	05	**04**
		f) Creation of linkages for commercialization of technology developed under the project	05	**03**
		g) Is scientific input commensurate to output (manpower, Financial input and time	05	**04**

		duration)?		
2.	Publication/ awards	Assessment will be done in respect of : Research papers; Reports/Manuals; Working and concept Papers; Books/Book Chapters/Bulletins. Quality of publication (s) and Awards/Scientific recognitions received	**10**	**2**
3.	Additional facilities created	Facilities created in terms of laboratory. Research set-up, instrumentation, etc. during the project.	**05**	**04**
4.	Human Resource Development (Scientific and Technical)	Scientist trained in different areas	**05**	**04**
5.	Revenue generated under the project/avenues created for revenue generation	Resources and revenues generated	**05**	**0**
6.	Product/process/Technology/IPR/Commercial value of the technology developed	Details to be provided on a) Products b) Process c) Technology d) IPR e) Registration of the varieties	**10**	**0**
7.	Quality of available documents of the project dully authenticated	Research project Files, Data, Reports etc.	**05**	**05**
Total Marks			**115**	**84**
8.	Timelines of execution of the project	Marks will be deducted if extension sought over the approved project duration beyond recorded and officially granted extension with recorded reasons	Marks to be deducted	**0**
		Up to 5%	01	
		Up to 10%	02	

		Up to 30%	03		
		Beyond 30%	05		
Net score: Score obtained to be counted out of 100 to compensate for activities not relevant to the project				**100**	**73.04**

However, looking into the requirements of different research institute and disciplines, IRC may modify the indicators, their weights and total scores. The time gap for assessment of different indicators may also be decided by IRC

3. Signature of PI

ANNEXURE- X

INDIAN COUNCIL OF AGRICULTURAL RESEARCH

(For Guidelines Refer ANNEXURE- XI(j))

PROFORMA FOR EVALUATION OF ARESEARCH PROJECT AFTER COMPLETION BY EVALUATION COMMITTEE

1. Institute Project Code *- **1XX10451**

2. Evaluation research project after completion by Evaluation Committee

S. No	Criteria	Methodology	Marks (output)	Evaluation by Evaluation Committee
1.	Achievements Against approved and stipulated outputs under project	**Qualitative and quantitative assessment of objectives and stipulated outputs under the project will be carried out** a) Activity Input/Projected Output/Output Achieved b) Extent to which standard design methodology, experimental designs, test procedures, analytical methods followed c) Does the data justify the conclusions? d) Innovativeness and creating of new Knowledge e) Additional outputs over those stipulated under the project f) Creation of linkages for commercialization of technology developed under the project **g)** Is scientific input commensurate to output (manpower, Financial input and time duration)?	75 35 10 05 10 05 05 05	
2.	Publication/ awards	Assessment will be done in respect of : Research papers; Reports/Manuals; Working and concept Papers; Books/Book Chapters/Bulletins. Quality of publication (s) and Awards/Scientific recognitions received	**10**	
3.	Additional facilities created	Facilities created in terms of laboratory. Research set-up, instrumentation, etc. during the project.	**05**	
4.	Human Resource Development (Scientific and Technical)	Scientist trained in different areas	**05**	

5.	Revenue generated under the project/avenues created for revenue generation	Resources and revenues generated		**05**	
6.	Product/process /Technology/IPR/Commercial value of the technology developed	Details to be provided on h) Products i) Process j) Technology k) IPR l) Registration of the varieties		**10**	
7.	Quality of available documents of the project dully authenticated	Research project Files, Data, Reports etc.		**05**	
Total Marks				**115**	
8.	Timelines of execution of the project	Marks will be deducted if extension sought over the approved project duration beyond recorded and officially granted extension with recorded reasons	Marks to be deducted		
		Up to 5%	01		
		Up to 10%	02		
		Up to 30%	03		
		Beyond 30%	05		
Net score: Score obtained to be counted out of 100 to compensate for activities not relevant to the project				**100**	

4. Signature of Evaluation Committee