Final progress report on

Collection, conservation and characterization of Appemidi (pickling mango) types from Yellapura, Kumta and Honnavara talukas

Submitted to

Karnataka Biodiversity Board, Bengaluru

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The Western Ghats region in Karnataka is considered to be one of richest Biodiversity centers for mango. Most of the pickling type mangoes which are locally called "Appemidi" are present in this region. Mango has been cultivated over the thousands of years in India (Mukherjee 1951). Generally, mango genotypes are classified into two broad categories, the polyembryonic types and the monoembryonic types. Very few polyembryonic types are cultivated and are concentrated mostly in the west coast regions and forest areas of India. These are inferior in fruit quality. However, they may have other desirable agronomic characters like disease resistance and regular bearing. The varieties that produce the best quality of fruits are monoembryonic types. Most of the commercial cultivars of mango have predominantly originated from the Indian subcontinent and are distributed throughout the tropical and subtropical regions of the world. However, there are not much studies on Appemidi mango types. They are characterized by highly acidic, generally bunch bearing types. Raw immature whole mango fruits are used for pickling. They have a typical aroma of cumin or sour orange. The consumer like these Appemidis for its aroma and acidic nature. Another important property of Appemidi pickles is long shelf life. Keeping this in view, Appemidis have been given GI (Geographical indicator) tag in Karnataka.

Need for collection and Characterization

A large variation exists even among the popular commercial cultivars and some indigenous cultivars grown in different parts of the Karnataka especially in western ghats regions. Many of them cannot be easily distinguished morphologically. The same cultivars distributed in different regions are referred to by different names (Ravishankar et al 2000). Recently, due to urbanization and deforestation, a lot of genetic erosion has occurred in many important local Appemidi types. In Appemidi types most of the gene pools have remained unexplored with regard to extent of variability, identification, collection and conservation of germplasm. There is considerable confusion regarding cultivar nomenclature. Many similar cultivars grown in different areas are known by different names (Lakshminarayana 1980). This necessitates collection of appemidi types and characterization programme, which is the first step towards its conservation and improvement. In the era where the free and open exchange of germplasm is moving towards controlling and facilitated exchange, management of germplasm information is essential and also in light of IPR issues the cataloging of germplasm is essential.

Karnataka state has a unique position with respect to the mango diversity. The state is famous for its tender mango fruits, which is used for pickling known as "Appemidi". This "Appemidi" (tender mango) market is valued around Rs 12 crore (on the minimum side) per annum in Karnataka alone. This is not a very organised market compared to others. This commodity, which has high potential for marketing, needs attention for conservation. It is to be noted here that tender mango is mainly grown near forests and also on the riversides. "Appe midi" (midi means tender mango in Kannada) is the king of all tender mangoes as far as its use in pickle industry is concerned.

However, there are many problems associated with "Appemidi" types. In these types the fruits are harvested from forests, farm lands and river/stream sides in Western Ghats of Karnataka, and many of the good trees are old and are on the verge of death. In a few places they are over harvested and branches are cut to harvest fruits. Therefore, there is an urgent need for identifying these trees and conserve them. Realising "Appemidis" economic importance, many private nurseries have started grafting and selling mango grafts with their own names. This has added to confusion about their nomenclature. There are no systematic study about their growth, yield and other agronomic parameters. Keeping this in view, IIHR has made an attempt to collect a few appemidi types from Shimoga, Uttara kannada and Coorg districts and characterize them molecularly. But there is an urgent need to conduct a systematic study on Appemidi diversity and plan for conservation develop both *in situ* and *Ex situ* conservation sites and cataloguing.

Keeping this in view, the present study was conducted with the following objectives:

I To collect indigenous Appemidi mango types from Kumta, Honnavar and Yellapur area.

ii. To characterize these types through morphological, molecular and biochemical tools.

iii. To document and print a Appemidi catalogue with these characters in Kannada.

iv. To propagate a selected unique types thro'grafting.

Work done:

Objective 1. To collect indigenous Appemidi mango types from Kumta, Honnavar and Yellapura areas.

We have done surveys for local pickling types in Yellapura, Kumta and Honnavar Taluk of Uttara Kannada district of Karnataka. We have met farmers, local enthusiasts, horticultural officers and appemidi lovers in these areas to identify appemidi types. We have collected leaves, twigs small branches of 62 different appemidi types from these talukas (Table 1). The locations of collection were recorded using GPS. The details of collected samples and place of collection is given below in the table.

Sl. No	Variety name	Place	Taluk	Elevation (MSL)	Longitude	Latitude
1.	Bhaskar Appe	Biscur	Yellapura	502	077^{0}29’28.0”	13^{0}08’01.7”
2.	Ganesh Appe	Sava Gadde	Yellapura	464	077^{0}29’28.0”	13^{0}08’01.7”
3.	Hoovappe	Magodu,	Yellapura	444	074^{0}34’38.4”	14^{0}44’19.8”
4.	Jeerige appe	Magodu,	Yellapura	446	074^{0}34’38.4”	14^{0}44’19.8”
5.	Kanakodlu jeerige	Kanakodlu	Yellapura	483	074^{0}50’59.0”	14^{0}45’13.4”
6.	Ananthabhatta appe (sada)	Kanakodlu	Yellapura	483	074^{0}51’00.5”	14^{0}45’15.3”
7.	Kanakodlu hole appe	Kanakodlu	Yellapura	472	074^{0}50’53.7”	14^{0}45’09.9”
8.	Kanakodlu hole jeerige	Kanakodlu	Yellapura	472	074^{0}50’53.7”	14^{0}45’09.9”
9.	Kanakodlu hole gundappe	Kanakodlu	Yellapura	472	074^{0}50’53.7”	14^{0}45’09.9”
10	Mango spp	Biscur	Yellapura	409	077^{0}29’28.0”	13^{0}08’01.7”
11	Purandaraappe 1	Magodu,	Yellapura	441	074^{0}34’38.4”	14^{0}44’19.8”
12	Purandaraappe 2	Magodu,	Yellapura	441	074^{0}34’38.4”	14^{0}44’19.8”
13	Aanegundi Appe 1	Aanegundi	Kumta	48	074°30'58.5"	14^{0}19'25.5"
14	Aanegundi Appe 2	Aanegundi	Kumta	48	074°30'58.5"	14^{0}19'25.5"
15	Appemidi	Kumta	Kumta	9	074^{0}28'49.9"	14^{0}19'06.8"
16	Aremale Appe	Aremale	Kumta	60	074^{0}27'58.6"	14^{0}30'06.6"
17	Ashok appe1	Yellavalli	Kumta	100	074^{0}27'55.3"	14^{0}30'11.3"
18	Ashok appe2	Yellavalli	Kumta	100	074^{0}27'55.3"	14^{0}30'11.3"
19	Ashok appe3	Yellavalli	Kumta	100	074^{0}27'55.3"	14^{0}30'11.3"
20	Attimane Jeerige Appe	Attimane	Kumta	82	074°27'09.8"	14^{0}27'39.9"
21	Bhoothana midi	Konare	Kumta	15	074^{0}27'15.6"	14^{0}25'58.3"
22	Dinesh Bhat Appe1	Bellangi (Bank of River Chandika)	Kumta	39	074°30'43.9"	14^{0}30'28.5"
23	Doddahithalalli Appe	Konare	Kumta	15	074^{0}27'15.6"	14^{0}25'58.3"
24	Doddahithalalli midi	Konare	Kumta	15	074^{0}27'15.6"	14^{0}25'58.3"
25	Gangadhar appe	Yellavalli	Kumta	232	074^{0}27'55.4"	14^{0}30'11.3"
26	Gopal Appe	Haladipura	Kumta	50	074^{0}27'29.7"	14^{0}21'34.7"
27	Gundappe	Antralli	Kumta	115	074^{0}27'30.5"	14^{0}28'02.3"
28	Jeerige Appe	Bellangi (Bank of River Chandika)	Kumta	39	074^{0}30'43.9"	14^{0}30'28.5"
29	Jeerige appe	Kumta	Kumta	9	074^{0}28'49.9"	14^{0}19'06.8"
30	Kudle Appe	Kudle ,	Kumta	358	077^{0}29'28.1"	13^{0}08'01.6
31	Malavalli Appe 1	Konare	Kumta	15	074^{0}27'15.6"	14^{0}25'58.3"
32	Manjunath Appe1	Dharmashala	Kumta	50	074^{0}27'14.7"	14^{0}23'22.6"
33	Pikale Appe	Hondadakla	Kumta	9	074°28'18.9"	14^{0}27'43.2
34	Raghavendra Appe1	Aremale	Kumta	61	074^{0}27'58.6"	14^{0}30'06.6"
35	Raghavendra Appe2	Aremale	Kumta	61	074^{0}27'58.6"	14^{0}30'06.6"
36	Rajappe	Yellavalli	Kumta	64	074^{0}28'20.7"	14^{0}30'41.8"
37	Subhray Appe	Dharmashala	Kumta	71	074^{0}25'03.9"	14^{0}23'02.2"
38	Subhray Appe 1	Dharmashala	Kumta	49	074^{0}27'45.0"	14^{0}21'29.0"
39	Vivek appe	Yellavalli	Kumta	106	074^{0}25'59.9"	14^{0}21'13.0"
40	Eshwar Appe	Kadatoka	Honnavar	23	074^{0}27'00.5"	14^{0}22'46.2"
41	Hulimane appe 1	Hulimane	Honnavar	38	074^{0}28'49.0"	14^{0}26'28.3"
42	Hulimane appe 2	Hulimane	Honnavar	38	074^{0}28'49.0"	14^{0}26'28.3"
43	Jeerige appe	Kadatoka	Honnavar	23	074^{0}27'00.5"	14^{0}22'46.2"
44	Kelaginur appe	kelaginanura	Honnavar	4	074^{0}27'45.6"	14^{0}13'52.5"
45	Krishna Bhatta Appe	Kekkar	Honnavar	8	074^{0}28'11.2"	14^{0}23'09.5"
46	Madigeri Jeerige Appe	Madigeri	Honnavar	12	074^{0}26'46.2"	14^{0}22'29.9"
47	Manjunath Appe2	Kundgoni	Honnavar	71	074^{0}25'03.9"	14^{0}23'02.2"

48.	Manjunath Appe2	Kundgoni	Honnavar	71	074^{0}25'03.9"	14^{0}23'02.2"
49.	Prakash Appe	Chandavara	Honnavar	20	074^{0}27'09.9"	14^{0}27'89.9"
50.	Santeguli appe	Santeguli (Near H.P.S, Santeguli)	Honnavar	86	074^{0}26'14.6"	14^{0}22'26.5"
51.	Shanbhag appe	Kekkar	Honnavar	20	074^{0}28'08.8"	14^{0}23'09.9"
52.	Shankar Appe	Hebble keri(Kadatoka)	Honnavar	12	074^{0}28'48.9"	14^{0}21'53.0"
53.	Thimmanna Appe	Honnavar	Honnavar	12	074^{0}27'28.7"	14^{0}14'22.4"
54.	Ganesh	Haluvalli	Ankola	59	074^{0}40’58.1”	15^{0}02’09.0”
55.	Hasehalla hole Appe	Haluvalli,	Ankola	62	074^{0}34’38.4”	14^{0}45’08.5”
56.	Hebhar mane appe	Haluvalli,	Ankola	62	074^{0}34’38.4”	14^{0}45’08.5”
57.	Hebhar mane appe 1	Haluvalli,	Ankola	62	074^{0}34’38.4”	14^{0}45’08.5”
58.	Hebhar mane appe 2	Haluvalli,	Ankola	62	074^{0}34’38.4”	14^{0}45’08.5”
59.	Madevkotteappemane	Haluvalli,	Ankola	62	074^{0}34’38.4”	14^{0}45’08.5”
60.	Prasad Appe	Haluvalli	Ankola	30	074^{0}40’58.1”	15^{0}02’09.0”
61.	Prasad Appe 1	Haluvalli	Ankola	34	074^{0}40’58.1”	15^{0}02’09.0”
62.	Siddappe	Malgao	Ankola	51	074^{0}34’28.2”	14^{0}45’14.5”

Objective 2: To characterize these types through morphological, molecular and biochemical tools.

Considering the difficulties involved in the traditional divergence studies based on morphological characterization (Rajan *et al*., 1999 and Dinesh and Vasugi, 2002), new methods based on studies at the DNA level are incorporated into fruit breeding programmes in order to accelerate and optimize genotype fingerprinting and to study genetic relationships among cultivars.DNA markers have become powerful tools in discriminating variation among germplasm and characterization of genotypes and they have been used for mango (Ravishankar et al, 2011, 2015). The use of DNA markers has several advantages over morphometric and isozyme analysis. They are reproducible and more efficient. Sequence Tagged sites (STS) or SSR (simple sequence repeats) or microsatellite markers are now developed as an alternative to RAPD and RFLP markers. These PCR based markers amplify the regions containing a microsatellite repeat sequence (Schnell et al 2005; Tautz 1989). These markers are also referred as Simple Sequence Repeats (SSR) and Sequence Tagged Microsatellite Sites (STMS). Microsatellites are tandemly repeated motifs of less than four nucleotides. These regions are highly interspersed throughout the eukaryotic genome. The flanking sequence of the micro satellites is unique. The designing of primers to these regions produce STMS. An advantage of STS marker is codominant inheritance and results are expressed as allele length. These markers are successfully used in genotyping of individuals and studying genetic variation in both mammals and plants. Under the DBT funded project entitled “Characterization and Assessment of genetic diversity in Indian mango cultivars using DNA markers: Sequence Tagged Microsatellite Site markers microsatellite markers have been developed at the Institute for characterization of mango cultivars. We have employed a total of eight SSR markers to characterize 51 appemidi types collected from these three talukas.

Methodology: We have isolated total genomic DNA using modified CTAB method (Ravishankar et al 2000). Selected eight SSR markers from previous study (Ravishankar et al 2015) were employed for molecular characterization. The PCR conditions followed for amplification of mango DNA is given below.

PCR Conditions

Step 1	Initial denaturation	94° C for 4 minutes
Step 2	Denaturation	94° C for 30 seconds
Step 3	Annealing	55° C for 30 seconds
Step 4	Extension	72° C for 1 minute
Step 5	Repeat step 2 to step 4 for 35 cycles	
Step 6	Final extension	72° C for 7 minutes

Table 2 Genetic analysis of SSR markers used for appemidi

Locus	Sequence	HObs	HExp	PIC	Pi
MiIIHR_31	F: TTCTGTAGTGGCGGTGTTG R: CACCTCCTCCTCCTCCTCTT	0.990	0.984	0.972	0.0014
MiIIHR _26	F: GCGAAAGAGGAGAGTGCA R: TCTATAAGTGCCCCCTCACG	1	0.989	0.979	0.0008
MiIIHR_34	F: CTGAGTTTGGCAAGGGAG R: TTGATCCTTCACCACCATCA	1	0.989	0.979	0.0008
MiIIHR _36	F: TCTATAAGTGCCCCCTCACG R: ACTGCCACCGTGAAAGTAG	1	0.982	0.972	0.0015
MiIIHR _23	F: TCTGACCAACAAAGAACCA R: TCCTCCTCGTCCTCATCATC	1	0.979	0.969	0.0018
MiIIHR _17	F: GCTTGCTTCCAACTGAGACC R: GCAAAATGCTCGCAGAAGAC	0.978	0.970	0.961	0.0026
MiIIHR _18	F: TCTGACGTCACCTCCTTTCA R: ATACTCGTGCCTCGTCCTGT	0.978	0.968	0.959	0.0028
MiIIHR _30	F: AGCTATCGCCACAGCAAATC R: GTCTTCTTCTGGCTGCCAAC	0.976	0.975	0.965	0.0021

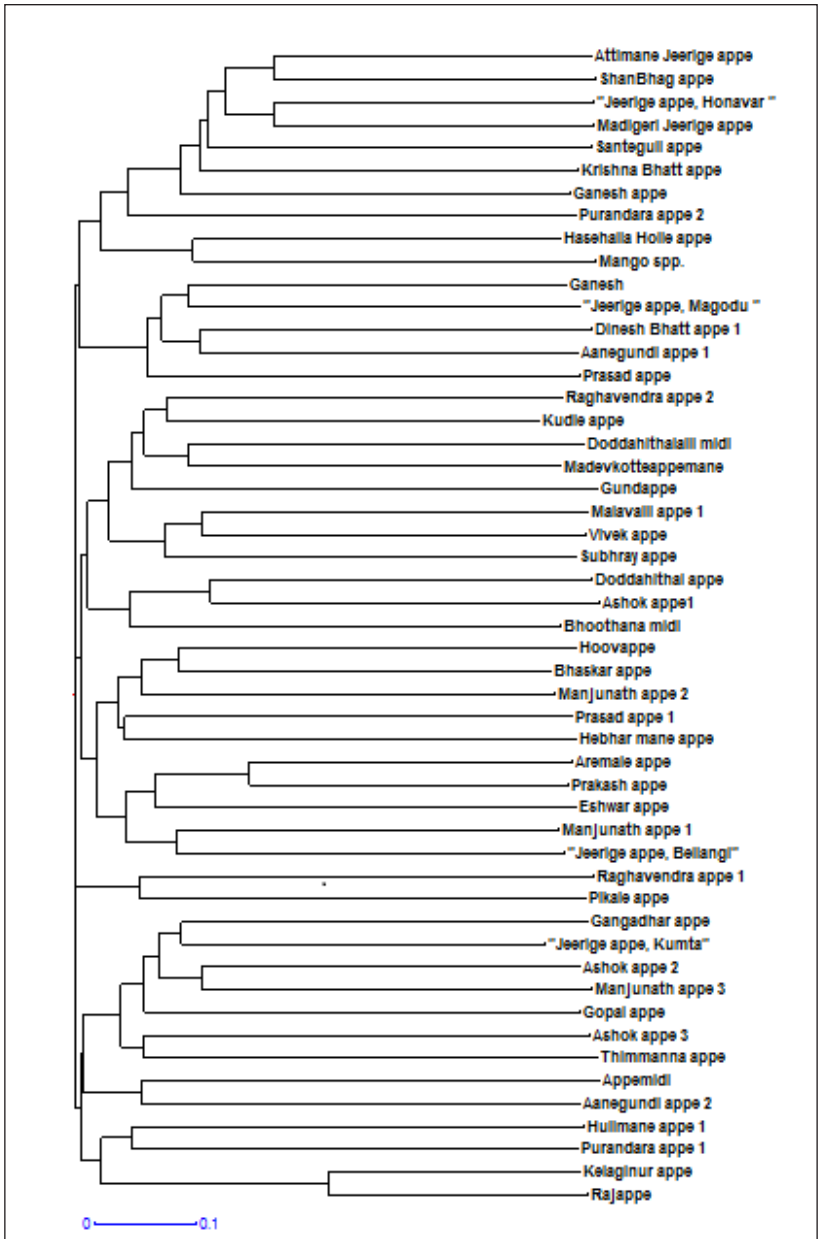
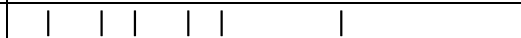
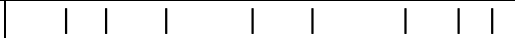
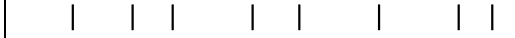
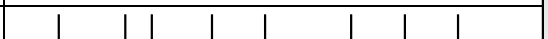
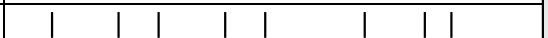
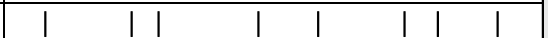
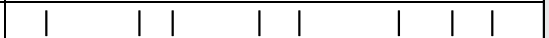
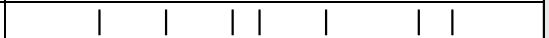


Fig 1. Dendrogram analysis of Appemidi mango genotypes collected from Yellapura, Honnavara and Kumta taluks

Table 3. Molecular barcodes developed for Appemidi genotypes

Sl. No.	Variety	Barcode
1	Bhaskar Appe	
2	Ganesh Appe	
3	Hoovappe	
4	Jeerige appe	
5	Mango spp	
6	Purandaraappe 1	
7	Purandaraappe 2	
8	Aanegundi Appe 1	
9	Aanegundi Appe 2	
10	Appemidi	
11	Aremale Appe	
12	Ashok appe1	
13	Ashok appe2	
14	Ashok appe3	
15	Attimane Jeerige Appe	
16	Bhoothana midi	
17	Dinesh Bhat Appe1	
18	Doddahithalalli Appe	
19	Doddahithalalli midi	
20	Gangadhar appe	
21	Gopal Appe	
22	Gundappe	
23	Jeerige Appe, Bellangi	
24	Jeerige appe, Kumta	
25	Kudle Appe	
26	Malavalli Appe 1	
27	Manjunath Appe1	
28	Pikale Appe	
29	Raghavendra Appe1	
30	Raghavendra Appe2	
31	Rajappe	
32	Subhray Appe	
33	Vivek appe	
34	Eshwar Appe	
35	Hulimane appe 1	
36	Jeerige appe, Kadatoka	
37	Kelaginur appe	

38	Krishna Bhatta Appe		45	Thimmanna Appe	
39	Madigeri Jeerige Appe		46	Ganesh	
40	Manjunath Appe2		47	Hasehalla hole Appe	
41	Manjunath Appe 3		48	Hebhar mane appe	
42	Prakash Appe		49	Madevkotteappemane	
43	Santeguli appe		50	Prasad Appe	
44	Shanbhag appe		51	Prasad Appe 1	

Eight SSR loci, which showed high PIC values in our previous study (Ravishankar et al., 2015), were employed for genotyping (Table 2). Polymerase chain reaction (PCR) amplification was performed using labelled primers with fluorophores FAM, NIC, TET and PET and at their 5' end. PCRs were carried out according to Ravishankar et al. (2011). Amplification products were initially checked on 3% agarose gel electrophoresis. PCR products sizes were determined by using automated ABI 3730 DNA analyzer (Applied Biosystems, Foster City, CA) at Bioserve technologies Ltd, Hyderabad facility. Fragment sizes in bp determined using the Peak Scanner programme

Genetic diversity Analysis

The allelic composition of each accession and the number of total alleles were determined for each SSR locus. Putative alleles were indicated by the estimated size in bp. The genetic information was assessed by estimating the following parameters: number of alleles per locus (A), observed heterozygosity (H_o, direct count), expected heterozygosity (H_e=1 (pi^2 where pi is the frequency of the i^{th} allele; Nei, 1973)), PIC (Botstein et al., 1980). The computation has been performed using CERVUS 3.0.3 software (Kalinowski et al., 2007). Genetic relationships among the genotypes were calculated by computing the dissimilarities through simple matching co-efficient. A dendrogram was constructed through Wards Minimum Variance method using DARWin 5 software (Perrier et al., 2003) .

The observed heterozygosity (H_0) ranged from 0.976 to 1.00; expected heterozygosity (H_e) ranged from 0.968 to 0.989. PIC values ranged from 0.959 to 0.979. The genetic parameters for the 8 SSR loci are presented in Table 2. The Probability of Identity (PI), maximum value (0.0028) was observed for MiIIHR18 loci and the minimum value (0.0008) was observed for MiIIHR26 and MiIIHR34 locus. The dendrogram analysis (Fig. 1) classified the mango cultivars into three main groups, mainly based on their geographical origin. Within these main groups there are many sub-groups and sub-clusters based on their genetic similarity.

Objective 3: To document and print a Appemidi catalogue with these characters in Kannada.

Even though the Karanataka harbors a wide diversity for appemidi types, there are no written documentation of these types for reference. And also, the success of a crop improvement program depends on the choice of parental cultivars/varieties for crossing. To choose varieties, with all the desirable characters in a crop like mango, that is highly heterozygous and in which inheritance patterns and genetics are not clearly worked out, a thorough evaluation is required. Therefore, morphological and molecular information are important and very useful in mango breeding program. Cataloguing of morphological and molecular characterization together helps in parental selection with desirable traits. If the mango catalogue is made available, the breeder can choose the parents for a hybridization program very easily. In a perennial crop like mango, this helps in reducing the time and cost of the breeding program. At present, there is no comprehensive Appemidi mango catalogue available for Karnataka in kannada. Therefore, the catalogue will become a valuable reference book for farmers, collector, geneticist, plant-breeder and molecular biologist.

Keeping this in view, we have prepared Appemidi catalogue in Kannada language. It has nine chapters, including four essays from well known kannada writers Dr. Rahamath Tarikere, Mr. Sushrutha Dodderi, Mr. Poornaprajna Beluru, and Mr. MVS Prasad about cultural and culinary aspects local mango types and Appemidi. The writers have described different Appemidi types available and their local uses. Mr. MVS Prasad has written an exclusive chapter on Mr. BV Subba Rao alias Beluru Heggade Subbana, who is one of the pioneers in conservation and collection of mango types. His collection and his experiences with Appemidi grafting and conservation has been vividly documented. Then we have a chapter on morphological characters, photos, molecular barcodes of 48 appemidi types. We have also documented different aromatic compounds present in the sap of appemidi. Finally, we have presented the list of 188 appemidi genotypes available in IIHR germplasm collection. Overall, this book forms first documentation of Appemidi types in Karnataka in kannada language.

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Figure 2.
Glimpse of Appemidi Book in Kannada published by ICAR-IIHR, Bengaluru

Objective V: To propagate a selected unique types thro'grafting.

The scion sticks were brought from the different sites were grafted to root stocks. They were initially maintained at green house for 30-45 days. Later shifted to field. The success of grafts mainly depends on scion material.

The successful grafts will be planted in the field during next season.

Field view of Appe midi grafted plants

Shan bhag Appe

Ganesh Appe

Dinesh Bhat

Purandaraappe 1

Aanegundi Appe 1

Attimane Jeerige

Krishna Bhatta Appe

Aanegundi Appe 2

Aremale Appe

Ashok Appe2

Appemidi

Ganesh

Hebhar mane appe

Siddappe

Hebhar mane appe 1

Bhaskar

Jeerige

Kanakodlu hole

Kanakodlu hole

midiEshwar

AppeJeerige

Appe 1Manjunath

Santeguli

Subhrav

Raghavendra

Doddahithalalli

Gopal

Bhoothana

Doddahithalalli

Malavalli

Subhrav

Shankar Appe

Krishna Bhatta Appe

Thimmanna Appe

Madigeri Jeerige Appe

Hoovappe

Kanakodlu hole jeerige

Raghavendra Appe2

Gangadhar appe

Summary:

In this project, we have extensively surveyed Kumata, Yellapura and Honnavara areas for appemidi mango types. We could identify 62 appemidi types and collected leave and twigs. These twigs were used for grafting. From leaf samples, we have isolated total genomic DNA. The DNA was used for developing molecular barcodes and assessing genetic diversity using microsatellite markers. From the PIC (polymorphic information content) values, we can conclude that there is a wide diversity exists for Appemidi mangoes in this area. Another major objective of this study is to bring out an Appemidi catalogue in Kannada. This was successfully published with nine chapters including four essays from well known kannada writers Dr. Rahamath Tarikere, Mr. Sushrutha Dodderi, Mr. Poornaprajna Beluru, and Mr. MVS Prasad about cultural and culinary aspects local mango types and appemidi. The writers have described different appemidi types available and their local uses. Mr. MVS Prasad has written an exclusive chapter on Mr. BV Subba rao alias Beluru Heggade Subbana, who is one of the pioneer in conservation and collection of mango types. Overall, it is the first documentation on Appemidi in Kannada which now has GI tag. The successful grafts would be transplanted to our germplasm field bank.

References

Botstein D, White RL, Skolnick M, Davis RW (1980) Construction of a genetic linkage map in man using restriction fragment length polymorphism. American Journal of Human Genetics 32:314-331.

Kalinowski ST, Taper ML, Marshall, TC (2007) Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Mol Ecol 16:1099-1006.

Lakshminarayana, S., 1980. Mango. Tropical and subtropical fruits, pp.184-257.

Mukherjee SK (1951) Origin of mango. Indian Journal of Genetics and Plant Breeding 11: 49-56.

Nei M (1973) Analysis of gene diversity in subdivided populations. Proc Natl Acad Sci USA 70: 3321–3323.

Perrier X, Flori A, Bonnot F (2003). Data analysis methods. In: Hamon, P, Seguin M, Perrier X, Glaszmann JC Ed, Genetic diversity of cultivated tropical plants. Enfield, Science Publishers. Montpellier. pp 43 - 76.

Ravishankar, K.V., Bommisetty, P., Bajpai, A., Srivastava, N., Mani, B.H., Vasugi, C., Rajan, S. and Dinesh, M.R., 2015. Genetic diversity and population structure analysis of mango (Mangiferaindica) cultivars assessed by microsatellite markers. Trees, 29(3), pp.775-783.

Ravishankar KV, Anand L, Dinesh MR (2000) Assessment of genetic relatedness among mango cultivars of India using RAPD markers. J Hortic Sci Biotech 75:198– 201.

Ravishankar KV, Mani BH, Anand L, Dinesh MR (2011) Development of new microsatellite markers from Mango (*Mangifera indica*) and cross-species amplification. Am J of Bot 98:e96-e99.

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