

Recommendations for scientific community (in brief with title) / Patent

Year 2015-16

1. **QTL Mapping and development of SCAR marker for Fusarium wilt (*Fusarium oxysporum f. sp. ricini*) in castor (*Ricinus communis*).**

The scientific community involved in castor improvement are recommended to use below mentioned JAUC series of primers to transfer resistance toward fusarium wilt into the new genotype through Marker Assisted Selection (MAS) or Marker Assisted Backcrossing (MAB).

Sr. No.	Primer name	Sequence	Product Length
1	JAUC1F	CAATGTCGAGCATAGCTGCC	312
	JAUC 1R	ACAATTGGCGAAGCAAGCTG	
2	JAUC 2F	GTCGAGCATAGCTGCCAACA	166
	JAUC 2R	ACGTTTCAGCCAACAAAAGCC	
3	JAUC 3F	TGTCGAGCATAGCTGCCAAC	853
	JAUC 3R	ATGCCACCTCCAGCATAAC	
4	JAUC 4F	GTCAATGTCGAGCATAGCTGC	389
	JAUC 4R	GGTCCCTGATTACCAGACGC	
5	JAUC 5F	AATGTCGAGCATAGCTGCCAA	864
	JAUC 5R	TCACTAGCAATGCCACCTCC	

2. **Sex determination of papaya (*Carica papaya*) through Molecular characterization.**

The scientific community involved in papaya improvement are recommended to use below mentioned JAUP series of primers to determine pre-flowering stage sexuality in 'Madubindu' variety of papaya.

Sr. No.	Name of Primer	Primer Sequence	Product Length
1	JAUP1F	GCGTTTCGAGGAGATGGTCA	410
	JAUP 1R	ACCTAACAACTTGGCTGGC	
2	JAUP 2F	TTTATTTCTTTCGGCTGCGGG	782
	JAUP 2R	AGCTGCTTCTTCACGCTCAT	
3	JAUP 3F	ACCCTCGGAAACAGGACAAG	427
	JAUP 3R	TTGGCATAACGGGTGTTGGA	
4	JAUP 4F	CCGCTCCCTCTTTTCTGGT	487
	JAUP 4R	ACATGCAAGAGTGTAGCGCA	

3. **QTL Mapping and development of SCAR marker for Macrophomina root rot in castor (*Ricinus communis*).**

The scientific community involved in castor improvement are recommended to use below mentioned JAUC series of primers to transfer resistance toward root rot into the new genotype through Marker Assisted Selection (MAS) or Marker Assisted Backcrossing (MAB).

Sr. No.	Primer	Sequence	Product Length
1	JAUC6F	TGGTATTCGCGGCAGGAATG	851
	JAUC 6R	GAAAGCCCTCTGCCATCCAT	
2	JAUC 7F	GTGGGCATGGGTGGTATAGG	622
	JAUC 7R	CGCTCACCAAGTCCCACATA	
3	JAUC 8F	GTCTATGGATGGCAGAGGGC	345
	JAUC 8R	TCCAGGAAGGCGAGCTATCA	
4	JAUC 9F	GATGCCCTTGGGCTAAGCAT	157
	JAUC 9R	AGCCATTGCAATCGGTCTGA	
5	JAUC 10F	GGGGCAGGAATGAGGACAAG	97
	JAUC 10R	CCTATACCACCCATGCCCAC	

Year 2016-17

1.	Biochemical and molecular characterization of phosphate solubilizing bacteria from different soil rhizosphere. It is informed to scientific community that among 17 PSBs, isolate derived from chickpea rhizosphere exhibited highest phosphate solubilizing index followed by isolates from pigeonpea rhizosphere and poultry farms. The best PSBs were confirmed as <i>Pseudomonas putida</i> and <i>Pseudomonas fulva</i> .																																																																																						
Year 2017-18																																																																																							
1.	Development of cultivar specific markers for the hybrids released by JAU in pearl millet. The scientific community involved in pearl millet improvement are recommended to use below mentioned JAUB series of primers for the identification of hybrids.																																																																																						
	<table><tr><th>Primer Name</th><th>Primer Sequence</th><th>Product Length</th><th>Hybrid</th></tr><tr><td>JAUB5F</td><td>CTGCTTCTTCTCGTAAT</td><td>941</td><td>GHB 538</td></tr><tr><td>JAUB5R</td><td>TTCGCCAGGAGGGCGT</td><td></td><td></td></tr><tr><td>JAUB7F</td><td>ATCGCTACGTCTACGATG</td><td>527</td><td>GHB 558</td></tr><tr><td>JAUB7R</td><td>TCTCCGATTAGGTCGTTG</td><td></td><td></td></tr><tr><td>JAUB17F</td><td>TACCTTTGTGTTGATGGTTT</td><td>415</td><td>GHB 577</td></tr><tr><td>JAUB17R</td><td>CTACTCTTGTTCTCTCTCT</td><td></td><td></td></tr><tr><td>JAUB10F</td><td>CAACATACCTCTCGTACGGT</td><td>1020</td><td>GHB 719</td></tr><tr><td>JAUB10R</td><td>TTTTCGGATAGTTCAAACAGT</td><td></td><td></td></tr><tr><td>JAUB1F</td><td>TAGCTGGGTAGAGGCTGACT</td><td>249</td><td>GHB 526</td></tr><tr><td>JAUB1R</td><td>GCCTGTTGACAGTCCGTAGA</td><td></td><td></td></tr><tr><td>JAUB22F</td><td>CGCAGTGGATTATCCCTCTC</td><td>354</td><td>GHB 732</td></tr><tr><td>JAUB22R</td><td>GGATGACCCTCGAAACCATA</td><td></td><td></td></tr><tr><td>JAUB24F</td><td>GGCATCTCGTTGTACCTCGT</td><td>339</td><td>GHB 744</td></tr><tr><td>JAUB24R</td><td>AACAGCATCAGAGCGGACTT</td><td></td><td></td></tr><tr><td>JAUB27F</td><td>CTTGTGCCTTGGAGCTGTTT</td><td>550</td><td>GHB 757</td></tr><tr><td>JAUB27R</td><td>GTGGCTGTTGTCATGAATGC</td><td></td><td></td></tr><tr><td>JAUB30F</td><td>TTAGCATTTTGCGCTTTGTG</td><td>250</td><td>GHB 905</td></tr><tr><td>JAUB30R</td><td>GCATGAATCAGCCCATACAA</td><td></td><td></td></tr><tr><td>JAUB15F</td><td>TGTGTTCTAATGTGCTATGTA</td><td>330</td><td>GHB 941</td></tr><tr><td>JAUB15R</td><td>CACTAAGCTTCATGACGTGAT</td><td></td><td></td></tr></table>	Primer Name	Primer Sequence	Product Length	Hybrid	JAUB5F	CTGCTTCTTCTCGTAAT	941	GHB 538	JAUB5R	TTCGCCAGGAGGGCGT			JAUB7F	ATCGCTACGTCTACGATG	527	GHB 558	JAUB7R	TCTCCGATTAGGTCGTTG			JAUB17F	TACCTTTGTGTTGATGGTTT	415	GHB 577	JAUB17R	CTACTCTTGTTCTCTCTCT			JAUB10F	CAACATACCTCTCGTACGGT	1020	GHB 719	JAUB10R	TTTTCGGATAGTTCAAACAGT			JAUB1F	TAGCTGGGTAGAGGCTGACT	249	GHB 526	JAUB1R	GCCTGTTGACAGTCCGTAGA			JAUB22F	CGCAGTGGATTATCCCTCTC	354	GHB 732	JAUB22R	GGATGACCCTCGAAACCATA			JAUB24F	GGCATCTCGTTGTACCTCGT	339	GHB 744	JAUB24R	AACAGCATCAGAGCGGACTT			JAUB27F	CTTGTGCCTTGGAGCTGTTT	550	GHB 757	JAUB27R	GTGGCTGTTGTCATGAATGC			JAUB30F	TTAGCATTTTGCGCTTTGTG	250	GHB 905	JAUB30R	GCATGAATCAGCCCATACAA			JAUB15F	TGTGTTCTAATGTGCTATGTA	330	GHB 941	JAUB15R	CACTAAGCTTCATGACGTGAT				
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2.	Development of cultivar specific markers for the varieties released by JAU in Groundnut The scientific community involved in Groundnut improvement are recommended to use below mentioned JAUG series of primers for the identification of groundnut varieties.																																																																																						
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	JAUG26F	TGAGGATTTGCCGTTTCTTT	405	GJG 7																													
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	JAUG8F	AAACCGCTGTGTCTCTCTGC	329	GG 11																													
	JAUG8R	GCCTGTTGACAGTCCGTAGA																															
3.	Biochemical and molecular characterization of brinjal varieties and promising genotypes It is recommended to the scientific community that the most diverse varieties were found to be GOB-1 and JBGR-1 compared to the other promising genotypes and varieties based biochemical, nutritional analysis. The diverse GOB-1 contained higher protein, total soluble solids, soluble sugars, phenols, ascorbic acid, PPO activity and flavanoid content and lower in glycoalkaloids and acidity. The clustering pattern on the basis of molecular analysis (SSR) depicting diverse varieties GOB-1 and GJB-3 out grouped from other genotypes with 48 % similarity.																																
4.	Genome sequencing of pathogenic <i>Macrophominaphaseolina</i> isolated from castor. It is recommended to the scientific community involved in castor improvement that the sequencing of plant pathogenic fungi <i>Macrophominaphaseolina</i> showed the size of genome is 98.6 Mb. The draft genome having 3061 contings, 30756 genes, 183303 exon, 28096 SSR and 13947 repeat region present in the genome. In genome 24.30 % of genes involve in molecular function, 34.27% of genes involve in cellular component and 41.43% of genes involve in biological process. pathogenicity related genes identified in this study have high relevance in future fungicide designing and following primers will be used for the specific identification of pathogenic fungi <i>Macrophominaphaseolina</i> .																																
	<table><tr><th>Name</th><th>Primer 3'-5'</th><th>Productlength</th><th>GC%</th><th>Tm</th></tr><tr><td>JAUMPF1</td><td>GGAGAGTTTGCGTCAAGTCC</td><td rowspan="2">202</td><td>55</td><td>59.85</td></tr><tr><td>JAUMPR1</td><td>ACTGTCTGGAGAAACCGAAGA</td><td>50</td><td>59.84</td></tr><tr><td>JAUMPF2</td><td>GCGAACTCAATCCCAACATC</td><td rowspan="2">226</td><td>50</td><td>60.47</td></tr><tr><td>JAUMPR2</td><td>TCGACCATGAGGGTTTTCTC</td><td>50</td><td>60.05</td></tr><tr><td>JAUMPF3</td><td>CGCACTAATAATCGGCCCTA</td><td rowspan="2">193</td><td>50</td><td>60.07</td></tr><tr><td>JAUMPR3</td><td>GTAAAAGTGCGTTGGCGTTT</td><td>45</td><td>60.17</td></tr></table>	Name	Primer 3'-5'	Productlength	GC%	Tm	JAUMPF1	GGAGAGTTTGCGTCAAGTCC	202	55	59.85	JAUMPR1	ACTGTCTGGAGAAACCGAAGA	50	59.84	JAUMPF2	GCGAACTCAATCCCAACATC	226	50	60.47	JAUMPR2	TCGACCATGAGGGTTTTCTC	50	60.05	JAUMPF3	CGCACTAATAATCGGCCCTA	193	50	60.07	JAUMPR3	GTAAAAGTGCGTTGGCGTTT	45	60.17
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JAUMPF1	GGAGAGTTTGCGTCAAGTCC	202	55	59.85																													
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JAUMPR2	TCGACCATGAGGGTTTTCTC		50	60.05																													
JAUMPF3	CGCACTAATAATCGGCCCTA	193	50	60.07																													
JAUMPR3	GTAAAAGTGCGTTGGCGTTT		45	60.17																													
5.	<i>In situ</i> detection of potassium status in cotton plants It is recommended to the scientific community that silver and carbon nanoparticles based nano-biosensor developed for detection of potassium deficiency directly from the leaf sap of plants. The nano-biosensor works on the basis of ion-selective mechanism to detect potassium ion in the range of 10 mM to 120 mM. The deficiency of potassium below threshold line of 40 mM from sap with the sensor display indicating the voltage output below (-ve) 15 mV will be signaled. The onetime cost of the developed nano-biosensor is about Rs. 2500-3000 and worked to detect potassium deficiency level at any growth stage of cotton crop.																																
Year 2018-19																																	
1.	Draft genome sequencing and analysis of fungal phytopathogen <i>Sclerotium rolfsii</i> to reveal insight into its genetic structure. It is recommended to the scientific community involved in Groundnut that the sequencing of plant pathogenic fungi <i>Sclerotium rolfsii</i> showed the size of genome is 73 Mb. The draft genome having 8919 contings, 16830 genes and 11171 SSR present in the genome. In genome 3507 and 261 genes involve in Transporter and catalytic function respectively , 1571 genes involve in cellular component and 709 of genes involve in biological process. pathogenicity related genes identified in this study have high relevance in future fungicide designing and following primers will be used for the specific identification of pathogenic fungi <i>Sclerotium rolfsii</i> .																																
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Name	Primer 3'-5'	Product length	GC%	Tm																													

	JAUSRF1	GAAGAGTTTGCCTCGAGTCC	250	55	59.85
	JAUSRR1	GCTGTCAGAGAAACCGAAGA		50	59.84
	JAUSRF2	ACGAACTCGATCCCAGCATC	170	50	60.47
	JAUSRR2	TCGATTATGAGGGTTTCCTC		50	60.05
	JAUSRF3	CGGACTAATAATCGACCCTA	230	50	60.07
	JAUSRR3	ATAAAGGTGCGTTGACGTTT		45	60.17

Year 2019-20

- Qualitative and nutritional evaluation of promising genotypes of groundnut.**

The scientific communities involved in groundnut improvement are recommended to use below mentioned groundnut genotypes for the qualitative and nutritional improvement of groundnut crop.

	Trait for improvement	Name of genotype
1	Total Carbohydrate	: GG-16, KDG-123, GG-4, RG-578
2	Total Soluble Sugar	: TG-51, ICGV-00440, JL-501
3	True Protein	: RG-510, TG-51, TG-37
4	Total Oil	: TLG-45, J SSP-35, ICGV-86156, GG-20
5	Iron	: JL-501, ICGV-91114, AG-2006-6
6	Calcium	: GJG-9, ICGV-02266, TPG-41, GJG-17
7	Oleic Acid	: ICGV-15055, ICGV-15050, ICGV-15035
8	O/L ratio	: ICGV-15035, ICGV-15033, Sunoleic
- Phytochemical, antioxidant and antidiabetic characterizations of custard apple (*Annona squamosa* L.) genotypes**

It is informed to the scientific community that fruit pulp of custard apple genotypes DS-1, Aml-10 and Aml-6 acquired higher antidiabetic potential (as α amylase inhibition) and antioxidant activity (as % DPPH free radical scavenging). The ascorbic acids and phenols contributed positively for both antidiabetic and antioxidant potentials in fruit pulp of custard apple. Phytochemicals analysis illustrated that terpenoids and flavonoids present in fruit pulp are positively correlated with antioxidant activity and that of alkaloids contributed significantly positive correlation for antidiabetic potential.

Year 2020-21

- Studies on Phytochemicals And Metabolomics Profiling of Seaweeds**

The seaweed resources viz., Green, Red and Brown seaweeds analyzed through MS/MS based platform showed presence of 375 unique compounds. These seaweeds were found to contain important oil content, vitamin D3 and many bioactive compounds that can be used as nutraceutical products. In case of ω -3 polyunsaturated fatty acids, eicosapentaenoic acid (EPA) was found in seaweed species, viz., *Sarconemafiliforme* (5.02%) and *Spatoglossum asperum* (4.04%). Vitamin D-3 was found in *Caulerpa Lenthilifolia* (16.7%), *Caulerpa sertulorioides* (8.5%), *Ulva fasciata* (10.7%), *Halimeda tuna* (12.7%), *Hydroclatharus clathratus* (18.9%), *Halymenia venusata* (6.5%), *H. porphyraeformis* (20.6%), *Dictyopteris marginatum*, *Gelidiopsisrepens* (18.2%) and *Heterosiphonia muelleri* (26.1%). Some species of seaweeds viz, *Dictyopterisdelicatula* (2.68%), *Heterosiphonia muelleri* (0.24%), *Dictyopterismarginatum* (*stoecosperrum*) (4.07%), *Spatoglossum asperum* (8.1%), *Padina gymnospora* (4.86%), *Caulerpa lenthilifolia* (0.96%) contained docosahexaenoic acid (DHA). These compounds are notfound in plants.
- Transcriptome and Proteomic Characterization for Identification of Candidate Genes Responsible for Pistillate Inflorescence and Its Reversion in Castor**

The scientific community involved in Castor improvement are recommended to use the set of 14 primers as mentioned below to distinguish the pistillate and

monoecious plants in castor. They are also advised to use the castor database developed (http://webtom.cabgrid.res.in/castdb/) for the identification of gene of interest and selection of SSRs and their primers to be used under Marker Assisted Selection and molecular breeding.																																																																															
<table><tr><th>Sr. No</th><th>Name of the gene</th><th>Forward primer</th><th>Reverse Primer</th><th>Gene Function</th></tr><tr><td>1</td><td>Dynamin-2A</td><td>GCTAAGCAAGGG T TC GTCAG</td><td>CTGGCAGGTCG ATCAA TTTT</td><td>Response to hormone stimulus</td></tr><tr><td>2</td><td>Auxin response factor</td><td>CACACATGGTGG G TT CTCAG</td><td>TGAGTTGGTGGTTGCA TTGT</td><td>Organ development; and post-embryonic development</td></tr><tr><td>3</td><td>ATP-binding protein</td><td>CATTGGACAGGT CCT CCACT</td><td>AAGCAAGGTGAAGCA AGGAA</td><td>Regulation of ARF protein signal transduction</td></tr><tr><td>4</td><td>Spermidine synthase</td><td>GGTGCTGCATTTT TC TCCTC</td><td>TGCCCTGGAATAAATC TTGC</td><td>Polyamine biosynthetic process</td></tr><tr><td>5</td><td>Xaa-pro amino peptidase</td><td>GGATGGAAGCTTT GG CATAA</td><td>GCCCTTCTCACCAAAA TTGA</td><td>Auxin transport</td></tr><tr><td>6</td><td>Conserved hypothetical protein</td><td>TCGAATGAAGAG GCC ATTCT</td><td>GTGAGAAGGGCAAAA GCAAG</td><td>Abscisic acid metabolic process</td></tr><tr><td>7</td><td>MADS box protein</td><td>AAAGGTTGGCCTG A GGAGTT</td><td>GTCACCTGCCTGTTGC TTGA</td><td>Transcription, DNA-dependent</td></tr><tr><td>8</td><td>RNA polymerase sigma factor rpoD1</td><td>GATCTTCAGGCAA G CACTCC</td><td>ATATCCTCCCCTTGGT C CAC</td><td>DNA-dependent transcription, initiation</td></tr><tr><td>9</td><td>Protein with unknown</td><td>TTGTCAAGGGCCA G TTCTTT</td><td>TTGACCTGCTGTGTCC C ATA</td><td>Guanylrribonucleoti de binding</td></tr><tr><td>10</td><td>Arginine/serine-rich splicing</td><td>CGGAAGCTTGATG A CACTGA</td><td>GGCTTCTACTTCGGCT C CTT</td><td>Sex differentiation</td></tr><tr><td>11</td><td>Acid phosphatase</td><td>TCCTGTAACCGTT CC TTTCG</td><td>TGTTTCAGGCTCGAAAC CTCT</td><td>Phosphatase activity</td></tr><tr><td>12</td><td>DNA replication helicase dna2</td><td>AGGCTGTGAATA ACC CAACG</td><td>CCCAATATCTTCGCCT T GAA</td><td>DNA metabolic process</td></tr><tr><td>13</td><td>Eukaryotic translation initiation</td><td>CACGACTTTTTCC CG TTGAT</td><td>GAACTCCCTCTGGTGG CATA</td><td>Translation</td></tr><tr><td>14</td><td>s-adenosyl-methyltransferase</td><td>TCTCCGTTCTTTC GT CGATT</td><td>GGGTCAACATCCATTC CAAC</td><td>rRNA methylation</td></tr></table>					Sr. No	Name of the gene	Forward primer	Reverse Primer	Gene Function	1	Dynamin-2A	GCTAAGCAAGGG T TC GTCAG	CTGGCAGGTCG ATCAA TTTT	Response to hormone stimulus	2	Auxin response factor	CACACATGGTGG G TT CTCAG	TGAGTTGGTGGTTGCA TTGT	Organ development; and post-embryonic development	3	ATP-binding protein	CATTGGACAGGT CCT CCACT	AAGCAAGGTGAAGCA AGGAA	Regulation of ARF protein signal transduction	4	Spermidine synthase	GGTGCTGCATTTT TC TCCTC	TGCCCTGGAATAAATC TTGC	Polyamine biosynthetic process	5	Xaa-pro amino peptidase	GGATGGAAGCTTT GG CATAA	GCCCTTCTCACCAAAA TTGA	Auxin transport	6	Conserved hypothetical protein	TCGAATGAAGAG GCC ATTCT	GTGAGAAGGGCAAAA GCAAG	Abscisic acid metabolic process	7	MADS box protein	AAAGGTTGGCCTG A GGAGTT	GTCACCTGCCTGTTGC TTGA	Transcription, DNA-dependent	8	RNA polymerase sigma factor rpoD1	GATCTTCAGGCAA G CACTCC	ATATCCTCCCCTTGGT C CAC	DNA-dependent transcription, initiation	9	Protein with unknown	TTGTCAAGGGCCA G TTCTTT	TTGACCTGCTGTGTCC C ATA	Guanylrribonucleoti de binding	10	Arginine/serine-rich splicing	CGGAAGCTTGATG A CACTGA	GGCTTCTACTTCGGCT C CTT	Sex differentiation	11	Acid phosphatase	TCCTGTAACCGTT CC TTTCG	TGTTTCAGGCTCGAAAC CTCT	Phosphatase activity	12	DNA replication helicase dna2	AGGCTGTGAATA ACC CAACG	CCCAATATCTTCGCCT T GAA	DNA metabolic process	13	Eukaryotic translation initiation	CACGACTTTTTCC CG TTGAT	GAACTCCCTCTGGTGG CATA	Translation	14	s-adenosyl-methyltransferase	TCTCCGTTCTTTC GT CGATT	GGGTCAACATCCATTC CAAC	rRNA methylation
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3.	Genome Sequencing of Cumin (<i>Cuminumcuminum</i>L.) to Reveal Insight of its Genomic Architecture The scientific community involved in Cumin improvement are recommended to use genomic information generated (https://drive.google.com/file/d/1ukln_R77lYWJcRlp8m40lLpmOP_ujqJz/view?usp=sharing) for cumin in Marker Assisted Selection for the improvement of cumin. They are also advised to use the genes identified as mentioned below and SSRs identified in Marker Assisted Selection. <table><tr><th>Sr. No.</th><th>Character</th><th>Number of genes</th><th>Gene identified</th></tr></table>				Sr. No.	Character	Number of genes	Gene identified																																																																							
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	1	Flavonoid	21	U78D2, C75A2, 75A4, C75B3, C93C F3PH, FAOMT, FL3H3, MOMT, SOMT SOT5, UFOG, UFOG1, UFOG2, UFOG UFOG4, UFOG5, UFOG6, FOG7, UGF and Y1103	
	2	Chalcone synthase	9	6DCS, CHS1, CHS2, CHSA, CHSB, CHS CHSL1, CHSY, PKS5	
	3	Chalconeisomerase	4	CFI, CFI1, CFI2B, CFI3	
	4	Flavanone synthase	3	C93C1, FNSI, C93B1	
	5	Terpenoid synthase	15	BAMS, GBIS1, GBIS2, HUMS, TPS TPS05, TPS07, TPS08, TPS09, TPS TPS18, TPS22, TPS26, TPS29, TPS30	
	6	Disease resistance	89	ADR2, CDR1, CHS1, CSA1, DF230, DR206, DRL12, DRL13, DRL14, DRL15, DRL16,DRL17, DRL18, DRL19, DRL2, DRL20,DRL21, DRL23, DRL24, DRL25, DRL26,DRL27, DRL28, DRL29, DRL3, DRL30,DRL31, DRL32, DRL33, DRL34, DRL36,DRL37, DRL38, DRL39, DRL4, DRL40,DRL41, DRL42, DRL43, DRL45, DRL5,DRL7, DRL8, DRL9, DSC1, DSC2, EDR1,EDR2, EDR2L, EDR4, LAZ5, LOV1A,NDR1, R13L1, R13L2, R13L3, R13L4,RFL1, RGA1, RGA2, RGA3, RGA4,RLM1B, RLM3, RP8HA, RP8L2, RP8L3,RP8L4, RPM1, RPP1, RPP13, RPP4, RPP5,RPP8, RPS2, RPS4C, RPS4L, RPS4W,RPS5, RPS6C, RPS6R, RPS6R, SUMM2,TAO1, WR52C, WR52N, WR52R, WR52W,Y4117	
	7	Antifungal	4	DEF1, DEF15, DEF2, DEF4	
	8	Early flowering	13	ASHH2, EFM, ELF3, ELF6, HD16N, PA PIE1, REF6, RUP1, RUP2, SKIP, SWC VIP6	
	9	Aromatic	11	5MAT, ANTA, AVT3A, AVT3B, AVT3 DDC, ISS1, PGL1, PGL2, PGL3, SOT16	
	10	Drought	8	AL7A1, DIS1, ERG14, HDG11, LSM5, SAD2, SDIR1, SSP1A	
	11	Nematodes	2	ELF3, HSPR2	
4.	Transcriptome Analysis in Coriander for Identification of Candidate Genes Against Stem Gall Disease The scientific community involved in Coriander improvement is recommended to use the following set of 7 primers in the process of marker assisted selection for the identification of disease defence genes in coriander genotypes				
	Sr. No	GeneName	ForwardPrimer	ReversePrimer	Function
	1.	RL31	GCCAAACCAAAAG GTGAGAA	CGGATACCCTTA GCCCAGAT	Jasmonicacid Mediated signalingpathway
	2.	A0A2Z5D8 54	CCACCGTTTCCAAT GCTAGT	GGAATCTCTCGG GCCTAAAC	Metal ion binding

3.	A0A166CJ74	ATTGGCTGAGCTTT GGATTG	GGCTTGATGCTC CATTGTTT	Regulation of Transcription DNA- template
4.	A0A166CJ74	CACGCATTTCTCCT CCTGAT	TCAGAGGGGGT TTTCTGATG	DNA-template
5.	Y1934	ACTCGGTGTCACGG TTTTTC	CAAAAGCCGAG ATTGTGGAT	Molecular function DNA- binding
6.	TGA10	CCCTGTTGGGAAAC TTCGTA	GCTGCAAAGGT CCAGCTATC	Nitrogen- activated protein kinasebinding
7.	A0A164XUZ0	GAGTTGGAGTTCAG GGAGGA	GATGAGCGGGA TATCTGGAA	Affects Fungal Development and Pathogenicityof <i>Fusarium</i> <i>graminearum</i>

5. Elemental, Nutritional and Microbiological Analysis of Panchagavya (Ancient Liquid Organic)

The Scientific community involved in Panchagavya research or microbial research are recommended to use 19th day old Panchagavya to study maximum microbial diversity. The higher proportion of α -proteobacteria was observed in 19th day of Panchagavya preparation while 21st Day Panchagavya formulation was found to be dominated by Firmibacteria, β -proteobacteria or Actinobacteria. The presence of unknown/novel microbes were higher in 21st day old Panchagavya on the basis of results of Metagenomic analysis.

a) Panchagavya contained dominant bacteria of nitrogen fixing, phosphate solubilizers and potash mobilizers. Moreover, it showed antagonism towards plant pathogenic fungi like *Helminthosporium* (47%), *A. flavus* (45%), *A. niger* (35%) and *Sclerotium rolfsii* (40%) *in vitro*. Elemental composition of Panchagavya showed higher concentration of Fe (158.94 ppm), Ca (2789.99 ppm), Mg (1553.76 ppm) and Mo (25.50 ppm). It also contained N-Methyl-2-pyrrolidinone used as insecticide, herbicide and fungicide. Phenylacetaldehyde is a second major compound found which has very important antibiotic compound.

b) Bijamruta elemental analysis revealed that it contains Cu (4.19 ppm), Fe (111.16 ppm), Mn (1.56 ppm), Zn (2.40), Ca (1211.63 ppm) and Mg (1084.65 ppm) which can provide immunity against various diseases and improve seed germination. It also contained important compound 5(6)-EpETrE-EA which has antagonist activity against pathogenic microbes. 17 β -Nitro-5 α -androstane is the aza-steroid which enhances the germination of plant seed.

c) Liquid organic preparation of Jivamruta has bacteria, fungi, actinomycetes, N-fixers and P-solubilizers and K-mobilizers. Jivamruta inhibited *Helminthosporium* (40%), *A. flavus* (30%), *A. niger* (25%) and *Sclerotium rolfsii* (35%), *Fusarium oxysporum* (35%). Jivamruta contains high concentration of Fe (115.09 ppm), Ca (1575.78 ppm), Mg (621.57 ppm) and Co (88.90 ppm). LC-QToF analysis showed Pyropheophorbide is an antioxidant found in Jivamruta.

d) Amrutpani is a good source of micronutrient which includes high concentration of Fe (208.44 ppm), Ca (2276.73 ppm), Mg (1119.15 ppm) and Ti (73.05 ppm). LC-QToF analysis revealed that Adouetine Z is an insecticidal cyclic peptide and (5 α , 8 β , 9 β)-5,9-Epoxy-3,6-megastigmadien-8-olisan antioxidant compound found in Amrutpani.

e) Sanjivak has antagonist activity and micronutrient content with important compound like Methyl jasmonate.

6.	Biochemical and Molecular Evaluation of A1 and A2 Casein Protein of Milk in Holstein Friesian Cow and Indigenous Gir Cow The scientific community involved in cow improvement is recommended to use DNA markers to detect or distinguish A1A2 and A2A2 genotypic frequency among the Gir Bulls and Cows using below mentioned marker. <table><tr><td>1</td><td>A1 Forward</td><td>5' CTTCCCTGGGCCCCATCCA 3'</td></tr><tr><td></td><td>A1 Reverse</td><td>5' AGACTGGAGCAGAGGCAGAG 3'</td></tr><tr><td>2</td><td>A2 Forward</td><td>5' CTTCCCTGGGCCCCATCCC 3'</td></tr><tr><td></td><td>A2 Reverse</td><td>5' AGACTGGAGCAGAGGCAGAG 3'</td></tr></table>	1	A1 Forward	5' CTTCCCTGGGCCCCATCCA 3'		A1 Reverse	5' AGACTGGAGCAGAGGCAGAG 3'	2	A2 Forward	5' CTTCCCTGGGCCCCATCCC 3'		A2 Reverse	5' AGACTGGAGCAGAGGCAGAG 3'
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7.	Studies on Phytochemicals And Metabolomics Profiling of Seaweeds The seaweed resources viz., Green, Red and Brown seaweeds analyzed through Ms/Ms based platform showed presence of 375 unique compounds. These seaweeds were found to contain important oil content, vitamin D3 and many bioactive compounds that can be used as nutraceutical products . In case of ω-3 polyunsaturated fatty acids, eicosapentaenoic acid (EPA) was found in seaweed species, viz., Sarconemafiliforme (5.02%) and Spatoglossum asperum(4.04%). Vitamin D-3 was found in Caulerpa Lenthilifolia (16.7%), Caulerpa sertulorioides (8.5%), Ulva fasciata (10.7%) , Halimeda tuna (12.7%) , Hydroclatharusclathratus (18.9%), Halymeniavenusata (6.5%), H. porphyraeformis (20.6%), Dictyopteris marginatum, Gelidiopsisrepens (18.2%) and Heterosiphoniamuelleri (26.1%). Some species of seaweeds viz, Dictyopterisdelicatula (2.68%), Heterosiphoniamuelleri (0.24%), Dictyopterismarginatum (stoeospermum) (4.07%), Spatoglossum asperum (8.1%), Padina gymnospora(4.86%), Caulerpa lenthilifolia (0.96%)contained docosaheaxaenoic acid (DHA). These compounds are not found in plants.												
Year 2021-22													
1.	Development and characterization of polymer based nanofertilizers and their response to wheat Chitosan nanoparticles (CS-NPs) were synthesized and examined greater than 40 mV zeta potential indicating good stability. The urea, tricalcium phosphate and muriate of potash were used as sources for incorporation of N, P and K elements individually onto the CS-NPs and the elevation of size of the nanofertilizers, without aggregation of nanoparticles, were observed. Scanning electron micrograph illustrated spherical shape of the CS-NPs and gave the idea about the morphology of incorporated NPK nanofertilizers. The FTIR study indicated that there is a electrostatic interaction occurs between the charges of CS-NPs and the N P K elements, resulted to stretching of spectra (peak) at specific wavelength confirming the incorporation of N P and K elements on to the CS-NPs. The application of 5% NPK nanofertilizers (10 time less) on wheat suggested higher nutritional seed quality and maintained yield equivalent to chemical fertilizers. The cost-effective NPK-nanofertilizers thus developed may save the forex (subsidy) about 38.22%. It has better controlled-release system in a liquid formulation to enhance nutrient use efficiency and sustained crop growth.												
2	Isolation and identification of entomopathogenic microorganisms from the soils of Junagadh district. The Scientific communities involved in microbial and entomological research are recommended to use native identified entomopathogenic microbes including 213 Pseudomonas putida (MK415028.1), P. monteilii (KT881478.1), P. knackmussii (KY324901.1), P. fulva (KC293832.1), Bacillus subtilis (MH141058.1), B. thuringiensis (KY003094.1), B. clausii (AB251924.1), Enterobacter asburiae (MK 467572.1), E. cloacae (JX514409.1), Beauveria bassiana (KC753382.1), Metarhiziumanisopliae (KJ573520.1) and Verticillium lecanii (AJ292383.1) for the production of biofertilizer and biocontrol												

	agent as they suppressed <i>Helicoverpa armigera</i> , and have PGPR activity
3	Isolation and identification salt tolerant strains of beneficial microorganisms from the coastal soils of Saurashtra region. Native halophilic bacterial strains isolated from agricultural soils of coastal regions of Saurashtra have potential for application in both industries and agriculture. The promising performance of these isolates in terms of plant growth promoting characteristics such as nitrogen fixing capacity, solubilization of phosphate and potash, production of IAA, siderophore along with production of biochemically important enzymes and bioactive compounds such as chitinase, cellulase, protease, carotene, ectoine, glycine betaine was observed. Halophilic bacterial isolates were <i>Halomonas pacifica</i> strain_JAU_7B (MK955347), <i>H. pacifica</i> strain_JAU_20A (MK575078), <i>H. pacifica</i> strain_JAU_22A (MK042491), <i>H. pacifica</i> strain_JAU_22C (MK043087), <i>H. pacifica</i> strain_JAU_25A (MK116946), <i>H. pacifica</i> strain_JAU_29A (MK114047), <i>H. pacifica</i> strain_JAU_36A (MK114047), <i>H. pacifica</i> strain_JAU_36B (MK114047), <i>H. stenophila</i> strain_JAU_37A (MK961217), <i>Oceanobacillus aidingsensis</i> strain_JAU_39B (MK148253), <i>H. pacifica</i> strain_JAU_40B (MK114047), <i>Bacillus haynesii</i> strain_JAU_41A (MK157609), <i>B. licheniformis</i> strain_JAU_43A (MK118996), <i>B. haynesii</i> strain_JAU_43B (MK157608) and <i>B. haynesii</i> strain_JAU_45A (MK157609) which confirmed through molecular characterization by 16srRNA
4	Biochemical appraisal of enzymatic activities from soils of permanent plot experiment at JAU, Junagadh The soil enzyme activity studied viz., urease, acid phosphatase, alkaline phosphatase, β-Galactosidase and nitrate reductase, from the plot having different fertilizer applications, remains higher during the mid-season and found to be lower before sowing and after harvest of the crop. Minimum variation of enzyme activity was observed in a plot of only FYM treatment (25 tons/ha). The activity of urease, β-Galactosidase and β-glucosidase as well as acid phosphatase and alkaline phosphatase was enhanced by balance fertilizer application (100 % NPK (25:50:50) as per soil test as well as 25 tons/ha FYM application. The pod yield of groundnut was remained highly positively correlated with urease, acid phosphatase and alkaline phosphatase enzyme activity.
5	Diversity analysis of fresh water diatoms through SEM-EDX from surfacemicroalgae of water bodies of Junagadh region The scientific community involved in diatom study of fresh water in context to climate change and environment are recommended to use cataloguing of fresh water diatoms collection images from water bodies in and around JAU, Junagadh. Total 46 species of diatoms were identified from water bodies of Junagadh, out of which eleven genera viz., <i>Cyclotella</i>, <i>Melosira</i>, <i>Navicula</i>, <i>Achnanthes</i>, <i>Amphora</i>, <i>Synedra</i>, <i>Nitzschia</i>, <i>Gomphonema</i>, <i>Hantzschia</i>, <i>Pinnularia</i> and <i>Fragillaria</i> were predominant. The sizeable variation among the elements presents on freshwater algae through SEM EDAX showed the presence of all macro elements except phosphorus and nitrogen. All species of diatoms had higher amount of diversity indices including Shannon-Wiener diversity index (3.57) and Berger Parker Dominance (30.57). Morphometric analysis showed wider variability in location and species wise according to length (7.049 μm to 43.08 μm) and width (2.53 μm to 23.44 μm) as well as diversity indices too. Willington dam site showed maximum spp. variation of diatoms than the other location.
Year 2022-23	
1	Development of biochemical and molecular markers for heat tolerance in chickpea The chickpea genotype namely ICC-4958 was identified highly tolerant when exposed to 42/37 °C temperature at germination stage. This genotype had high antioxidant activity, ascorbic acid, glutathione, super oxide dismutase, ascorbate peroxidase, glutathione reductase along with Quinone oxidoreductase, glutaredoxine and heat shock protein 70. SSR markers namely Cam1536, TA27, TR 58 could also reveal this genotype different at

	DNA level. Hence, this genotype can be exploited in breeding to develop heat tolerant lines/varieties of chickpea.																																																																																																																																				
2	Diversity analysis of marine diatoms through SEM-EDX from surfacemicroalgae of saurashtra coastal belt The scientific community working on diatoms of coastal belt of Saurashtra are recommended to use diatoms diversity analysis done through Scanning electron microscopy as ready references. The diatom analysis of marine samples from three locations (Okha, Veraval and Aadri) identified fifty diatom species and most of them are pennate types. The Cocconeis spp., Grammatophora spp., Fragilaria sp, Nitzschia spp., Achnanthes spp and Licmophora were found dominant diatoms on the surface of microalgae. Again, diatom abundance of Cocconeis scutellum was reported higher than 52% of total diatom considering three locations. The energy dispersive X-ray spectroscopy (EDS) graph prepared for individual species of diatoms from SEM images observed that the frustules of the diatoms were other than Si. It has many elements at various sites attached to them. The catalogue of diatoms and alpha-diversity index revealed many diverse rich populations in coastal belt of Saurashtra																																																																																																																																				
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4	Biochemical analysis based lipid indices of edible, non edible and medicinal herbs oils Scientific community involved in the essential oil research of the following crops are recommended to use marker bioactive compounds detected through GC MS platform <table><tr><th>Name of crops</th><th>Important Marker Bioactive compounds</th></tr><tr><td>Blackpepper (<i>Piper nigrum</i> L.)</td><td>Piperine (α-Phellandrene, 4.64%) cis-sabinene (23.21%) Caryophyllene (13.58%) Caryophyllene oxide (0.33%) 1,4-Cyclohexadiene, 1-methyl-4-(1-methylethyl) (20.84%)</td></tr></table>	Name of crops	Important Marker Bioactive compounds	Blackpepper (<i>Piper nigrum</i> L.)	Piperine (α -Phellandrene, 4.64%) cis-sabinene (23.21%) Caryophyllene (13.58%) Caryophyllene oxide (0.33%) 1,4-Cyclohexadiene, 1-methyl-4-(1-methylethyl) (20.84%)																																																																																																																																
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Volatileoil of Cardamom	α -Terpinylacetate(37.05%) Eucalyptol (25.79%) Sabinen (3.41%)
Volatileoil of Cinnamom	Cinnamaldehyde, (E) (77.55%) Copaene(2.98%)
Volatileoil from leavesof cinnamom	Phenol,2-methoxy-3-(2-propenyl)(79.17%),, Spathulenol(3.26%) gamma.-Elemene (3.66%),, Caryophyllene(1.24 %)
Volatileoil of cloves	Caryophyllene(37.5%)and Phenol,2-methoxy-3-(2-propenyl)-(44.04%)
Volatileoil of corianderleaves	LINALOOL (63.23%),2,6-Octadien-1-ol, 3,7-dimethyl-, acetate(7.78%),,1,6-Octadien-3-ol, 3,7-dimethyl(2.64%),,(1R)-2,6,6- Trimethylbicyclo[3.1.1]hept-2-ene (2.59%)
Volatileoilof cumin seeds	Beta.-Pinene(19.09%) Benzene, 1-methyl-4-(1-methylethyl) (12.4%) 1,4-Cyclohexadiene,1-methyl-4-(1-methylethyl) (10.69%)Benzaldehyde, 4-(1-methylethyl)(26.8%) TERPIN-7-AL <GAMMA->DB5-1106 (12.36%)
Volatileoil of curryleaves	Bicyclo[7.2.0]undec-4-ene, 4,11,11-trimethyl-8-methylene-, [1R-(1R@,4Z,9S@)] (29.28%) Caryophyllene(4.44%),,alpha.-Caryophyllene(4.88%) Azulene, 1,2,3,3a,4,5,6,7-octahydro-1,4-dimethyl-7-(1- methylethenyl)- (21.24%) [1R-.alpha.,3a.beta.,4.alpha.,7.beta.]-Caryophyllene oxide (4.05%).
Volatileoil ofDill seed	Tetrahydro carvone (19.82%) trans-dihydrocarvone(14.53%) cis-Carvylacetate (25.7%) Eugenol (0.01%) And Apiol(Abotiondrug) (17.59%)
Volatile oil ofDry ginger	CURCUMENE (16.56%) Zingiberene(21.03%); FARNESENE <(E,E)-ALPHA(15.26%) beta-Sesquiphellandrene (7.61%) VALERIANOL (5.91%)
Volatileoil of fennel seed	Fenchone(8.93%) Anisole, p-allyl(5.29%) (Estragole) cis-Anethol (68.56%)
VolatileofGarlic oil	1,3-Dithiane(6.7%) Dimethyltrisulfide(7.43%) Diallyl disulphide(17.72%) Hydroperoxide, 1,4-dioxan-2-yl (26.34%) Trisulfide, di-2-propenyl (31.49%)
Volatileoil ofholy basil	1,6-Octadien-3-ol, 3,7-dimethyl (18.47%)/(Linalool) METHYLCINNIMATE(8.48%) and METHYL CINNIMATE<(E)- (45.94%)
Volatileoil ofmint leaves	Limonene(5%) 2-Cyclohexen-1-ol, 2-methyl-5-(1-methylethenyl)-, trans- (35.63%) 2-Cyclohexen-1-one, 2-methyl-5-(1-methylethenyl) (31.59%) trans-Carveylacetate(5.19%)

	Volatileoil of nutmeg	1R)-2,6,6-Trimethylbicyclo[3.1.1]hept-2-ene/ (α-Pinene-14.64%) Bicyclo[3.1.0]hexane, 4-methylene-1-(1-methylethyl)- (cis-sabinene-18.5%) Cyclohexene, 1-methyl-4-(1-methylethenyl)-, (S)- (Limonene-5.84%) 1,4-Cyclohexadiene, 1-methyl-4-(1-methylethyl) -(α- Terpinene-5.13%) 3-Cyclohexen-1-ol, 4-methyl-1-(1- methylethyl)- (R)-(-)-; (-)-Terpinen-4-ol-8.05%) Benzene, 1,2-(methylenedioxy)-4-propenyl-, (E)- (β- Isosafrole-5.4%)																																																							
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	Turmericoil &Oleoresin	Caryophyllene(6.74 %and 0.29,%) ZINGIBERENE(18.86%and 4.59%) Benzene,1-(1,5-dimethyl-4-hexenyl)-4-methyl(9.49% and 0.45%) SESQUIPHELLANDRENE <BETA(14.25% and 1.17%) Tumerone(23.26% and 17.39%) Ar-tumerone(25.15% and8.93%)																																																							
5	Dr PJ.Rathod is the one of the inventor in Patent Granted on A PROCESS OF ENZYMATIC PRE-TREATMENT ON VARIETIES OF PIGEON PEA which was filled in 29/01/2020 and Granted on 21/12/2023. Application number: 202021004030																																																								
Year 2023-24																																																									
1.	Development of biochemical and molecular markers for heat tolerance in chickpea The chickpea genotype namely ICC-4958 was identified highly tolerant when exposed to 42/37 °C temperature at germination stage. This genotype had high antioxidant activity, ascorbic acid, glutathione, super oxide dismutase, ascorbate peroxidase, glutathione reductase along with Quinone oxidoreductase, glutaredoxine and heat shock protein 70. SSR markers namely Cam1536, TA27, TR 58 could also reveal this genotype different at DNA level. Hence, this genotype can be exploited in breeding to develop heat tolerant lines/varieties of chickpea.																																																								
2	Biochemical analysis based lipid indices of edible, non edible and medicinal herbs oils Recommendation-I Scientific community involved in lipid indices of edible oils research is recommended to use the sets of following biochemical based fatty acids calculation for the quality of oils and their lipid indices.																																																								
	<table><tr><th>Edible oils</th><th>DR</th><th>OD R</th><th>LD R</th><th>MUF A</th><th>PUF A</th><th>SF A</th><th>DU</th><th>UI</th><th>AI</th><th>TI</th></tr><tr><td>GG -20</td><td>0.009</td><td>0.247</td><td>0.001</td><td>63.72</td><td>20.64</td><td>15.64</td><td>105.0</td><td>590.5</td><td>0.14</td><td>10.32</td></tr><tr><td>GG-21</td><td>0.008</td><td>0.185</td><td>0.003</td><td>69.62</td><td>15.67</td><td>14.71</td><td>101.0</td><td>597.0</td><td>0.13</td><td>9.18</td></tr><tr><td>GG-3</td><td>0.009</td><td>0.451</td><td>0.001</td><td>44.47</td><td>35.93</td><td>19.6</td><td>116.3</td><td>562.8</td><td>0.19</td><td>13.30</td></tr><tr><td>Coconut seed oil</td><td>0.007</td><td>0.396</td><td>0.011</td><td>11.43</td><td>7.05</td><td>81.52</td><td>25.5</td><td>129.4</td><td>20.73</td><td>34.60</td></tr></table>	Edible oils	DR	OD R	LD R	MUF A	PUF A	SF A	DU	UI	AI	TI	GG -20	0.009	0.247	0.001	63.72	20.64	15.64	105.0	590.5	0.14	10.32	GG-21	0.008	0.185	0.003	69.62	15.67	14.71	101.0	597.0	0.13	9.18	GG-3	0.009	0.451	0.001	44.47	35.93	19.6	116.3	562.8	0.19	13.30	Coconut seed oil	0.007	0.396	0.011	11.43	7.05	81.52	25.5	129.4	20.73	34.60	
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Corn oil	0.01 2	0.56 3	0.00 5	33.24	41.4 3	25.3 3	116. 1	522. 7	0.67	23.1 7
Cotton seed oil	0.00 3	0.64 5	0.03 5	26.01	40.8 8	33.1 1	107. 8	468. 2	2.19	28.7 8
Soybean	0.02 2	0.61 2	0.02 5	23.5	53.8 8	22.6 2	131. 3	541. 7	0.36	14.3 0
Sunflower	0.00 7	0.63 0	0.01 9	30.71	47.0 9	22.2	124. 9	544. 6	4.32	17.6 0
Brown mustard seed	0.18 1	0.64 7	0.43 9	57.51	30.2 6	12.2 3	118. 0	614. 4	0.06	40.7 4
White sesame	0.00 1	0.55 8	0.01 1	39.17	48.1 9	12.6 4	135. 6	611. 5	0.09	10.0 0
Black sesame	0.00 1	0.57 4	0.00 7	38.07	50.4 7	11.4 6	139. 0	619. 8	0.08	8.34

DR= Desaturation ratio; **ODR**= Oleic desaturation ratio; **LDR**= Linoleic desaturation ratio; **MUFA** = Monounsaturated fatty acid; **PUFA** = Polyunsaturated fatty acid; **SFA** = Saturated fatty acid; **DU**= Degree of unsaturation; **UI**= Index of unsaturation; **AI**= Atherogenic index; **TI**= Thrombogenic index

Recommendation- II

Scientific community involved in the essential oil research of the following crops are recommended to use bioactive compounds detected through GC MS platform as a markers

Name of crops	Important Marker Bioactive compounds
Black pepper (<i>Piper nigrum</i> L.)	Piperine (α -Phellandrene, 4.64%) cis-sabinene (23.21%) Caryophyllene (13.58%) Caryophyllene oxide (0.33%) 1,4-Cyclohexadiene, 1-methyl-4-(1-methylethyl) (20.84%)
Volatile oil of Cardamom	α -Terpinyl acetate (37.05%) Eucalyptol (25.79%) Sabinen (3.41%)
Volatile oil of Cinnamom	Cinnamaldehyde, (E) (77.55%) Copaene (2.98%)
Volatile oil from leaves of cinnamom	Phenol, 2-methoxy-3-(2-propenyl) (79.17%), Spathulenol (3.26%) gamma.-Elemene (3.66%), Caryophyllene (1.24 %)
Volatile oil of cloves	Caryophyllene (37.5%) and Phenol, 2-methoxy-3-(2-propenyl)-(44.04%)
Volatile oil of coriander leaves	LINALOOL (63.23%), 2,6-Octadien-1-ol, 3,7-dimethyl-, acetate(7.78%), 1,6-Octadien-3-ol, 3,7-dimethyl(2.64%), (1R)-2,6,6-Trimethylbicyclo[3.1.1]hept-2-ene (2.59%)
Volatile oil of cumin seeds	Beta.-Pinene (19.09%) Benzene, 1-methyl-4-(1-methylethyl) (12.4%) 1,4-Cyclohexadiene, 1-methyl-4-(1-methylethyl) (10.69%) Benzaldehyde, 4-(1-methylethyl) (26.8%) TERPIN-7-AL <GAMMA-> DB5-1106 (12.36%)
Volatile oil of curry leaves	Bicyclo[7.2.0]undec-4-ene, 4,11,11-trimethyl-8-methylene-, [1R-(1R@,4Z,9S@)] (29.28%) Caryophyllene (4.44%), .alpha.-Caryophyllene(4.88%) Azulene, 1,2,3,3a,4,5,6,7-octahydro-1,4-dimethyl-7-(1-

		methylethenyl)-(21.24%) [1R-.alpha.,3a.beta.,4.alpha.,7.beta.)]-Caryophyllene oxide (4.05%).
	Volatile oil of Dill seed	Tetrahydro carvone (19.82%) trans-dihydrocarvone (14.53%) cis-Carvyl acetate (25.7%) Eugenol (0.01%) And Apiol (Abortion drug) (17.59%)
	Volatile oil of Dry ginger	CURCUMENE (16.56%) Zingiberene (21.03%); FARNESENE <(E,E)-ALPHA (15.26%) beta-Sesquiphellandrene (7.61%) VALERIANOL (5.91%)
	Volatile oil of fennel seed	Fenchone (8.93%) Anisole, p-allyl(5.29%) (Estragole) cis-Anethol (68.56%)
	Volatile of Garlic oil	1,3-Dithiane (6.7%) Dimethyl trisulfide (7.43%) Diallyl disulphide (17.72%) Hydroperoxide, 1,4-dioxan-2-yl (26.34%) Trisulfide, di-2-propenyl (31.49%)
	Volatile oil of holy basil	1,6-Octadien-3-ol, 3,7-dimethyl (18.47%)/(Linalool) METHYL CINNIMATE (8.48%) and METHYL CINNIMATE <(E)-(45.94%)
	Volatile oil of mint leaves	Limonene (5%) 2-Cyclohexen-1-ol, 2-methyl-5-(1-methylethenyl)-, trans- (35.63%) 2-Cyclohexen-1-one, 2-methyl-5-(1-methylethenyl) (31.59%) trans-Carveyl acetate (5.19%)
	Volatile oil of nutmeg	1R)-2,6,6-Trimethylbicyclo[3.1.1]hept-2-ene/ (α -Pinene-14.64%) Bicyclo[3.1.0]hexane, 4-methylene-1-(1-methylethyl)-(cis-sabinene-18.5%) Cyclohexene, 1-methyl-4-(1-methylethenyl)-, (S)- (Limonene-5.84%) 1,4-Cyclohexadiene, 1-methyl-4-(1-methylethyl)-(α -Terpinene-5.13%) 3-Cyclohexen-1-ol, 4-methyl-1-(1-methylethyl)-((R)-(-); (-)-Terpinen-4-ol-8.05%) Benzene, 1,2-(methylenedioxy)-4-propenyl-, (E)- (β -Isosafrole-5.4%)
	Volatile oil of nutmeg mace	α -Pinene-(15.97%);. cis-sabinene-(17.66%); α -Terpinene-(6.23%), L-4-terpineol-(9.11%)
	Turmeric oil & Oleoresin	Caryophyllene (6.74 %and 0.29,%) ZINGIBERENE (18.86% and 4.59%) Benzene, 1-(1,5-dimethyl-4-hexenyl)-4-methyl (9.49% and 0.45%) SESQUIPHELLANDRENE <BETA(14.25% and 1.17%) Tumerone (23.26% and 17.39%) Ar-tumerone (25.15% and 8.93%)
3.	Diversity analysis of marine diatoms through SEM-EDX from surface microalgae of saurashtra coastal belt The scientific community working on diatoms of coastal belt of Saurashtra are recommended to use diatoms diversity analysis done through Scanning electron	

	microscopy as ready references. The diatom analysis of marine samples from three locations (Okha, Veraval and Aadri) identified fifty diatom species and most of them are pennate types. The <i>Cocconeis</i> spp., <i>Grammatophora</i> spp., <i>Fragilariasp</i>, <i>Nitzschiasp</i>, <i>Navicula</i> sp., <i>Achnanthes</i> spp. and <i>Licmophora</i> were found dominant diatoms on the surface of microalgae. Again, diatom abundance of <i>Cocconeis scutellum</i> was reported higher than 52% of total diatom considering three locations. The energy dispersive X-ray spectroscopy (EDS) graph prepared for individual species of diatoms from SEM images observed that the frustules of the diatoms were other than Si. It has many elements at various sites attached to them. The catalogue of diatoms and alpha-diversity index revealed many diverse rich populations in coastal belt of Saurashtra.
Year 2024-25	
1.	Improvement of Groundnut oil quality for high oleic acid through CRISPR/Cas gene editing technology The scientific community involved in groundnut improvement through genome editing technology is recommended to use the optimized tissue culture protocol using de-embryonated cotyledone as explants (multiple shoot formation: MS + 25.0 mg/l 6-benzylaminopurine, shoot elongation: MS + 3.0 mg/l 6-benzylaminopurine, + 1.0 mg/l gibberellic acid, root induction: MS + 1.0 mg/l naphthalene acetic acid), CRISPR/Cas9 technology and binary vector for successfully editing the gene of interest (<i>AhFAD2B</i>) in groundnut for achieving high O/L ratio (8.52). A single guide RNA sequence (5'TGTGGTCTATGATCTGTTAATGG3'), designed by using CHOPCHOP, was utilized to guide the Cas nuclease for precise editing.
2.	Optimization of regeneration protocol using different plant growth regulator in pomegranate (<i>Punica granatum</i> L.) Cv.'Bhagwa' cultivar A regeneration protocol was successfully developed from using nodal explant for pomegranate (<i>Punica granatum</i> L.) cv. 'Bhagwa,' highlighting the following key findings: ❖ Surface sterilization with Carbendazim-50% @ 10 min + Cefotaxime @ 7 min + Kanamycin @ 5 min + Ketokenazol @ 10 min + 0.1% HgCl₂ @ 3 min was effectively prevented contamination in nodal explant. ❖ Transfer of explants every 24 hours reduces 90% polyphenol accumulation. ❖ Shoot initiation was achieved using MS +0.2 mg/L BAP + 0.1 mg/L NAA. ❖ The highest number of multiple shoots was observed using MS + 0.2 mg/L BAP + 0.1 mg/L KIN. ❖ Root induction was optimal with MS + 0.3 mg/L IBA using WPM media for root development. ❖ Hardening was most effective when plantlets were acclimatized in a 3:1 soil-to cocopeat ratio, with a 94% survival rate.
Year- 2025-26	
1.	Improvement of antioxidant and defense properties of Tomato using <i>Bacillus</i> spp. The consortium of <i>Bacillus</i> isolates, namely <i>Priestia endophytica</i> (T4), <i>Bacillus cereus</i> (L3), <i>Bacillus sonorensis</i> (L8), <i>Bacillus licheniformis</i> (TJ3) and <i>Bacillus endophytica</i> (TJ-6) as well as the individual isolate TJ3, demonstrated significant potential in enhancing antioxidant activity and reduced <i>Fusarium</i> wilt incidence in tomato (<i>Solanum lycopersicum</i>). Their application improved fruit quality parameters, including DPPH radical scavenging activity, total phenolics, total flavonoids and lycopene content. These positive effects were consistently observed in tomato varieties (JT-3 and GT-6).
2.	Molecular characterization of sesame genotypes using SRAP markers A total of 121 SRAP primer combinations (11F x 11R) were employed to screen

polymorphism among sesame genotypes/varieties comprising 18 white-, 4 black-, and 8 brown-seeded types. Out of these, 109 primer combinations exhibited polymorphism. Based on the polymorphic markers, genetic diversity analysis grouped the sesame genotypes into two major clusters: Cluster A (Table 1), representing genotypes collected from the Regional Research Station, TNAU, Vriddhachalam, and Cluster B (Table 2), representing genotypes/varieties collected from the Agricultural Research Station, JAU, Amreli. The following 10 highly polymorphic SRAP primer combinations are recommended for DNA fingerprinting of sesame genotypes/varieties.

Sr. No.	Name of Primer	Combination	Primer sequence (5'—3') Forward (Me) and reverse (Em) primers
1	SRAP-15	Me-02 Em-04	Me02 : TGAGTCCAAACCGGAGC Em04 : GACTGCGTACGAATTTGA
2	SRAP-16	Me-02 Em-05	Me02 : TGAGTCCAAACCGGAGC Em05 : GACTGCGTACGAATTAAC
3	SRAP-25	Me-03 Em-03	Me03 :TGAGTCCAAACCGGAAT Em03 : GACTGCGTACGAATTGAC
4	SRAP-33	Me-03 Em-11	Me03 :TGAGTCCAAACCGGAAT Em-11 :GACTGCGTACGAATTCCA
5	SRAP-57	Me-06 Em-03	Me06: TGAGTCCAAACCGGTAA Em03 :GACTGCGTACGAATTGAC
6	SRAP-58	Me-06 Em-04	Me06 :TGAGTCCAAACCGGTAA Em04 :GACTGCGTACGAATTTGA
7	SRAP-74	Me-07 Em-09	Me07 :TGAGTCCAAACCGGTCC Em09 :GACTGCGTACGAATTCTGA
8	SRAP-79	Me-08 Em-03	Me08 : TGAGTCCAAACCGGTGC Em03 :GACTGCGTACGAATTGAC
9	SRAP-81	Me-08 Em-05	Me08 : TGAGTCCAAACCGGTGC Em04 :GACTGCGTACGAATTTGA
10	SRAP-86	Me-08 Em-10	Me08 :TGAGTCCAAACCGGTGC Em-10:GACTGCGTACGAATTCTAG