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Bioinformatics – A novel approach for crop improvement

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Abstract

The increasing role of bio-informatics in data mining and public databases of model organisms, presents a new opportunity as well as a challenge to researchers to develop more focused molecular tools for gene discovery and their analysis. The complete genome sequences of *Arabidopsis*, rice, sorghum and poplar as well as an enormous number of plant expressed sequence tags (ESTs) have become available in many databases like NCBI. In the next few years, the entire genomes or at least gene space will likely be sequenced for most major crops. However, improved varieties, not sequences *per se*, contribute to improved economic return to the farmer. Functional genomics and systems biology research are facilitating the identification of gene networks that are involved in controlling genetic variation for agronomically valuable traits in elite breeding populations. Furthermore, combining the new knowledge from genomic research with conventional breeding methods is essential for enhancing response to selection, hence crop improvement. Superior varieties can result from the discovery of novel genetic variations, improved selection techniques, and/or the identification of genotypes with improved attributes due to superior combinations of alleles at multiple loci assembled through marker-assisted selection. The goal of plant genomics is to understand the genetic and molecular basis of all biological processes in plants that are relevant to the species. This understanding is fundamental to allow efficient exploitation of crop plants as biological resources in the development of new cultivars of improved quality and reduced economic and environmental costs. This knowledge is also vital for the development of new diagnostic tools. Traits considered of primary interest are yield, resistance to biotic and abiotic stress and quality of crop plants. A genome program can now be envisioned as a highly important tool for plant breeding. Identifying key genes and understanding their function will result in a "quantum leap" in quality improvement. Additionally, the ability to examine gene expression will allow us to understand how plants respond to and interact with the physical environment and management practices. This information, in conjunction with appropriate technology, may provide predictive measures of plant health and quality and become part of future breeding decision management systems. Current genome programs generate a large amount of data that will require processing, storage and distribution to the international research community. The data include not only sequence information, but also information on mutations, markers, maps and functional discoveries.

The key objectives for plant bioinformatics include:

- **encouraging submission of all sequence data into the public domain, through repositories,**
- **providing rational annotation of genes, proteins and phenotypes, and**
- **elaborating relationships both within the data on individual crops and between Crop plants and other organisms.**

Keywords: Crop plants, bioinformatics, genomics, ESTs, QTL, MAS

Abbreviations : EST – Expressed Sequence Tag, BLAST–Basic Local Alignment Search Tool, NCBI –National Center for Biotechnology Information, cDNA – complementary DNA, dbEST– data base EST, TIGR – The Institute of Genomic Research, QTL–Quantitative Trait Loci, MAS –Marker Assisted Selection.

Introduction

Feeding the increasing world population is a challenge for modern plant biotechnology especially in the country like China and India. Genomics research has great potential to revolutionize the discipline of plant breeding in order to realize the future needs of an ever growing human population(1). Crop scientists are committed to generating improved crop species to meet the ever increasing demand for high yielding plants of cereals, pulses, vegetables and fruits with good quality. Crop yields have been increased during the last century and will continue to improve with the aid of enhanced breeding technology and new biotechnological-engineered strategies. The success of this research has resulted from collaborative efforts of researchers in a number of fields including: plant breeding, crop modeling, molecular biology and bioinformatics. Bioinformatics is a scientific and emerging discipline lying at the intersection of biology, mathematics, computing science, and information technology. The biotechnological interventions like molecular breeding, transgenics, bioreactor plants, genetic engineering, antisense technology, microarray analysis and RNA interference have made a dream true for the crop scientists to break the genetic barriers not only between the distant species but also the genera. Further, in order to facilitate this job, bioinformatics has revolutionized by *insilico* / computational management and retrieval of the enormous data, protein prediction, comparative and structural genomics and drug discovery. The data regarding the genome and protein sequences are stored in databanks which can be accessed and utilized by any of the scientists or researchers throughout the globe. This application has reduced the cost of the wet laboratory researches bypassing otherwise the long and cumbersome steps. In bioinformatics, the word "omics" has a vast relevance which refers to a field of study in biology ending in the suffix *–omics*. The most important in today's molecular era are Genomics , Proteomics, Transcriptomics, Metabolomics and Phenomics which include the field of study as below:

Genomics : Study of sequence, gene organization and mutations at the DNA level.

Proteomics: Large scale study of proteins, particularly their structure and their function.

Transcriptomics: Study of the sets of all the messenger RNA (mRNA) molecules that are produced in a population of cells.

Metabolomics: The quantitative measurement of the dynamic multiparametic metabolic response of a living organism to pathophysiological stimuli or genetic modifications.

Phenomics: The study of the phenome, or the set of all phenotypes expressed by a cell up to species.

Modules under Bioinformatics:

- **Applications:** What kind of research problems can be answered using bioinformatics ?
- **Databases:** What data sources and applicable semantic standards are pertinent to answer the research questions ?
- **Protocols, algorithms, and tools:** What analysis protocols, computing algorithms, and software tools can be applied ?
- **Infrastructure:** What hardware, operating system, software, and networking systems are required to support the required problem ?

The ultimate goal of genomics is to improve the yield and quality of the crop plants as well as conferring upon resistance against various biotic and abiotic stresses. Genomics research is generating new tools, such as functional and structural molecular markers using bioinformatics (2). It has also developed new knowledge about statistics and inheritance phenomena that could increase the efficiency and precision of crop improvement. In particular, the elucidation of the fundamental mechanisms of heterosis, gene action, combining ability and epigenetics and their manipulation, has great potential. Consequently, knowledge of the relative values of alleles at all loci segregating in a population could allow the breeder to design a genotype *in silico* and to practice whole genome selection. As a need of the hour, marker-assisted breeding and selection will gradually evolve into 'genomics-assisted breeding' for crop improvement.

Software tools and methods for genomics and proteomics

Crop plant networks, collection of databases and bioinformatics resources for crop plants genomics have been built to harness the extensive work in genome mapping. This resource facilitates the identification of agronomically important genes, by comparative analysis between crop plants and model species. It allows the genetic engineering of crop plants selected by the quality of the resulting products. Bioinformatics resources have evolved new nutritional genomics and biotechnology tools to genetically modify and improve food supply, for an ever-increasing world population. Multiple Alignment provides a method to estimate the number of genes in gene families allowing the identification of previously undescribed genes. This

information enables new strategies to study gene expression patterns in plants. DNA arrays contain the secrets of the gene expressions, which describe the genotype and determine the phenotype in a given environment. DNA arrays and other high-throughput technologies will continue to generate huge amount of data and even more powerful software tools will be required to process, analysis, visualize, interpret and present the genomic data. The existing data and tools facilitate gene mapping and QTL estimation, molecular data for biodiversity and phylogenetic analysis, SNP detection etc. It is required to target the identification of genes for various stress factors (drought, cold and biotic stresses), gene sequences, the proteins they produce and their biochemical pathways and their functions. Expressed sequence tags (ESTs) also provide an easy access to the coding part of total genome of a species unraveling initial clues toward unknown regulatory phenomena. This information is publicly available for large scale analysis from GenBank at NCBI and European Molecular Biology Laboratory (EMBL). DbEST is a division of GenBank that contains sequence data and other information on "single-pass" cDNA sequences, or Expressed Sequence Tags, from a number of organisms. The Institute for Genomic Research (TIGR) defines TC as Tentative Consensi (assemblies from ESTs) and ET as Expressed Transcripts (both non-human) when building TIGR Gene Indices (TGI).

BLAST algorithm is used for large sequence similarity search(3). For Genome Comparison , MegaBlast is an algorithm based on NCBI. Jim Kent's BLAT (BLAST-Like Alignment Tool) is a tool which performs rapid mRNA/DNA and cross-species protein alignments. BLAT is more accurate, 500 times faster than popular existing algorithms for mRNA/DNA alignments, and 50 times faster for protein alignments at sensitivity settings typically used when comparing vertebrate sequences. Some of the softwares for genome analysis are listed below:

Sequence analyses :

DnaSP: estimates several measures of DNA sequence variation within and between populations, linkage disequilibrium, recombination, gene flow and gene conversion.

GenScan: an online program to identify complete gene structures in genomic DNA.

FLUCTUATE: estimates the effective population size and an exponential growth rate of a single growing population using non-recombining sequences.

GENETREE: allows ancestral inference from DNA sequences from single or subdivided populations which conform to the infinite sites model.

ProSeq: PROcessor of SEQuences- aligns, edits, and analyzes sequence data.

SITES: analysis of comparative DNA sequence data.

Allelic analyses :

Arlequin: population genetics software environment able to handle large samples of molecular data (RFLPs, DNA sequences, microsatellites), while retaining the capacity of analyzing conventional genetic data (standard multi-locus data or mere allele frequency data).

GDA: Software for the Analysis of Discrete Genetic Data. Presents basic population genetic parameters, F-statistics, and tests for disequilibrium.

GeneClass: Identifies whether specific populations can be source populations for an observed founder population.

FSTAT: A computer package for PCs which estimates and tests gene diversities and differentiation statistics from codominant genetic markers

Quantitative genetics (compiled by B. Walsh) :

EQTL EXPLORER: An eQTL visualization tool that allows users to mine and understand data from a repository of genetical genomics experiments

Phylogenetics:

DAMBE: integrated software package for comparative molecular data.

HY-PHY: hypothesis testing using phylogenies.

PUZZLE: reconstruct trees from sequence by maximum likelihood.

PHYLIP. Reconstruct phylogenetic tree

Instructional software:

PopBio: population biology simulation package written for the Macintosh; contains components for population growth, population genetics, predator/prey interactions, and inter- specific competition.

Population genetic applets : that can be run from the web, including genetic drift, Wahlund effect, etc.

Populus: simulation software for population biology and evolutionary ecology.

The software developers, biometricians and end users of the technology, are a wide array of partners engaging in plant genomic research projects. Examples of partners include: IRRI, CIMMYT, CIP, IPGRI, ICRISAT, ICARDA,CIAT, IITA, Agropolis, ACTG, WUR, NIAS, Embrapa, and Cornell University (within the Consortium); and University of California, Hitachi Software Engineering Co. Ltd., CSIRO, Keygene, ILRI, NCGR, Universidad Autónoma Chapingo (Mexico), and INIA (Uruguay) (outside the Consortium). As more and more genomes are sequenced completely, the

analysis of raw genome data has become a more important task. The accumulation of sequence data allows detailed genome analysis by using-friendly database access and information retrieval. As more genetic and sequence information become available for model organisms, more specific genome databases are generating that could be queried to retrieve different informations. Presently, there is a large number of publicly available databases, few of them are enlisted below in Table 1.

Table 1. List of public available databases

Subject	Source	Link
Biomedical literature	PubMed	http://www.ncbi.nlm.nih.gov/entrez/query.fcgi
Nucleic acid sequence	GenBank	http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi ? db= Nucleotide
	SRS at EMBL	http://srs.ebi.ac.uk
Genome sequence	Entrez Genome	http://www.ncbi.nlm.nih.gov:80/entrez/ query.fcgi ? db=Genome
	TIGR database	http://www.tigr.org/tdb/
Protein sequence	GenBank	http://www.ncbi.nlm.nih.gov:80/entrez/ query.fcgi ? db=Protein
	SWISS-PROT at ExPASy	http://www.expasy.ch.spro/
	PIR	http://www.nbrf.georgetown.edu
Protein structure	Protein Data Bank	http://www.rcsb.org/pdb/
Entrez structure db		
Protein and peptide mass spectroscopy	PROWL	http://prowl.rockefeller.edu
Post-translational modifications	RESID	http://www.nbrf.georgetown.edu/pirwww/ search/textresid.html
Biochemical and Biophysical informations	ENZYME	http://www.expasy.ch./énzyme/
	BIND	http://www.ncbi.nlm.nih.gov:80/entrez/ query.fcgi?db=Structure
Biochemical pathways	PathDB	http://www.ncrg.org/software/pathdb/
	KEGG	http://www.genome.ad.jp/kegg/
	WIT	http://wit.mcs.anl.gov/WIT2/
Microarray	GeneExpression Links	http://industry.ebi.ac.uk/~alan/MicroArray/
2D-PAGE	SWISS-2DPAGE	http://www.expasy.ch./ch2d/ch2d-top.html
Web Recourses	The EBI Biocatalog	http://www.ebi.ac.uk/biocat/
	IUBio Archieve	http://iubio.bio.indiana.edu

The functional and structural genomics of model organisms provide the comparative information about crop plants. Generally, most of the plant species are closely related, the complete sequencing of all the genes in a single representative plant species will provide a lot of knowledge about all higher plants. Similarly, discovering the functions of the proteins produced by a model species will provide a lot of information on protein function in all higher related plants(4). A large amount of information can then be derived from these organisms, providing valuable data for the analysis of gene regulation, genetic resistance, biochemical pathways, physiology and evolutionary processes in crop plants alike(5). There are several databases on proteins, from plants, animals, humans, bacteria and other forms of life(6). The databases of some of the model organisms are listed in Table 2.

Table 2. Database including genome size, number of genes, genes shared with human and their websites

Organism	Approximate size of Genome (Date completed)	Number of Genes	Approximate % of Genes shared With human	Web access to Genome db
Bacteria (*Escherichia coli*)	4.6 million bp (1997)	4,300	Not determined	http://www.genome.wisc.edu/
Fruit fly (*Drosophila melanogaster*)	165 million bp (2000)	~13,300	50%	http://www.fruitfly.org/sequence/index.html http://Flybase.bio.indiana.edu
Human (*Homo sapiens*) (feb 2001)	3,200 million bp	25,000- 30,000	100%	http://www.ornl.gov/hgmis/
Mouse (*Mus musculus*)	3,000 million bp (2001)	~30,000	~90%	http://www.information.jax.org
Plant (*Arabidopsis thaliana*)	120 million bp	~20,000	Not determined	http://www.arabdopsis.org
Round worm (*Caenorhabditis elegans*)	97 million bp (1998)	19,000	40%	http://www.genome.wus/edu/projects/celegans
Yeast (*Saccharomyces cerevisiae*)	12 million bp (1996)	~6,000	31%	http://www.yeastgenomes.org

Application of Bioinformatics in crop research

The uprising in life sciences brought on by genomics dramatically increases the scale and scope of our experimental enquiry and applications in plant breeding(7). Methods of crop improvement have also changed dramatically throughout this century. Mass and pure line selection in landraces, consisting of genotype mixtures, were the popular breeding techniques until the 1930s for most crops. In the 1930s maize breeders started the commercial development of double cross hybrids that was followed by the extensive utilization of single crop hybrids since the 1960s(8). Pedigree, bulk, backcross and other selection methods were also developed especially for self-pollinating crop species. Such scientific advances in plant breeding led to the so-called 'Green Revolution', one of the greatest achievements to feed the world in the years of the Cold War(9). Owing to this agricultural betterment, cereal production, which accounts for more than 50% of the total energy intake

of the world's poor, kept in pace with the high average population growth rate of 1.8 % since 1950(10). Today, 370 kg of cereals per person are harvested as compared to only 275 kg in the 1950s; i.e., in excess of 33% per capita gain. Similar progress in other food crops resulted in 20% per capita gains since the early 1960s, according to FAO(11). There are 150 million fewer hungry people in the world today than 40 years ago, though there are twice as many human beings. Despite this splendid progress in crop productivity, even greater progress must be made in order to feed an additional two billion people by the early part of the 21st century(12) . Around 800 million people are hungry today and another 185 million pre-school children are still malnourished owing to lack of food and water, or disease(13). Hence as suggested by the Nobel Peace Laureate Bourlag(14), new biotechniques, in addition to conventional plant breeding, are needed to boost yields of the crops that feed the world. Bioinformatics for crop improvement revolves around to create a global crop information platform and network to share genetic resources, genomics, proteomics and crop improvement information. Hence, it covers germplasm, genotype, phenotype, functional genomics and geographical information data.

The fundamental scientific question underlying germplasm research is- What is the causal relationship between genotype and phenotype? DNA is transcribed into RNA, which is either bioactive itself (as noncoding RNA gene products) or is translated into peptides that form part of protein gene products. Ultimately, these products act as structural elements, genetic regulatory control factors, or modulators of the biochemical fluxes within metabolic and physiological pathways, at the subcellular, tissue, organ, and whole organism level. This sum total of molecular expression integrates to give the overall structural and behavioral features of the plant i.e. its "phenotype." The unfolding of this story, includes biotic (ecosystem) and abiotic (geophysical) factors modulating expression in a variety of ways via diverse sensory and regulatory mechanisms in the plant. Various classes of experimental data associated with this tapestry of germplasm function are summarized in Figure 1.

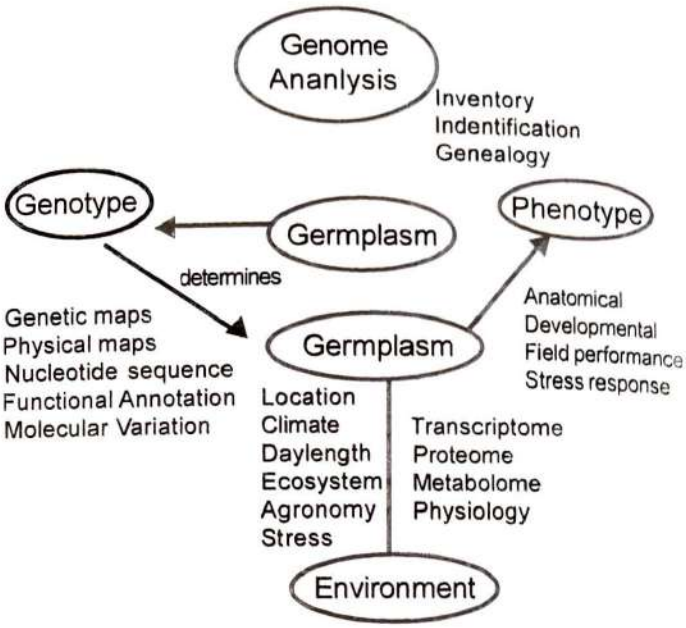

Fig.1 Germplasm research showing biological and information relationships.

Germplasm

Proper management of germplasm information is essential for the elucidation of genotype-expression phenotype associations. Management goals of germplasm information include systematic tracking of germplasm origin (passport and genealogy information), recording of alternate germplasm names, accurate linkage of experimental results to applicable genotypes, and proper material management of germplasm inventories. An important aspect of any good germplasm information system is the separation of the management of nomenclature from identification. Users must be free to name germplasm as they like, and the system must make sure that the names are bonded to the right germplasm. A key to effective management of such variable germplasm information is the assignment of a unique germplasm identifier (GID) to each distinct germplasm sample (seed package or clone) that needs to be tracked ("bar coded"). The essential reference point for managing all meta-data about the germplasm is the GID and the example is the parents (sources) and progeny of the given sample, including membership of the sample in global "management neighborhoods". In this manner, historical information about germplasm may be efficiently integrated with information about extant descendants of that germplasm.

Genotypes

The characterization of genotypes can be done by taking the various DNA markers including RFLP's,

SNP's, STS, EST's, minnisatellites and microsatellites. Such identification is attributed directly or indirectly by the nucleotide variation in the DNA of the organisms. Experimental systems conceived to make those measurements are designated as markers. Markers can be any selectable or scoreable feature to observe a biological process usually associated with the molecular variation of interest. This broad definition includes laboratory measurements of DNA (e.g., polymerase chain reactions or DNA-DNA hybridization events) and simple observations of visible phenotypes (e.g., classical visible genetic markers such as morphological variants). The molecular variation measured by genotyping can be neutral or biologically significant. Neutral molecular variation generally involves markers that simply exhibit DNA structural polymorphism which is usefully applied to answer the following basic questions :

- To what extent are germplasm samples similar to or different from one another (i.e., "fingerprinting" experiments)?
- What is the chromosome location of a marker (i.e., "mapping" experiments)?

Answering such questions will often lead to deeper exploration of germplasm, such as evolutionary studies, practical management of plant crosses, and genetic resource management. Molecular variation that is biologically significant is that postulated to be causally correlated with differences in structure (i.e., genome content or arrangement), biochemical function (resulting from critical functional changes in RNA bases or amino acid residues), or regulation of gene products (by affecting promoter or enhancer sequences). Whatever the nature of genotype measurements, the primary task of bioinformatics is to completely capture and accurately codify the raw and derived genotype data. Bioinformatics also applies statistical algorithms to raw genotype measurements to make useful inferences such as locus assignments on genetic and physical maps, assessments of germplasm relatedness and biodiversity, or assays of the impact of molecular variation on the biological system. Bioinformatics methodology assists in all stages of genotyping experiments and in the interpretation of results: from raw data capture (e.g., gel image processing), documentation, and storage to semiautomated analysis of raw data into inferences (i.e., germplasm fingerprinting and mapping, alignments of DNA variation to RNA and protein structures to elucidate functional variance, etc.) through visualization and publication of the information.

A growing foundation for modern genotyping is, of course, the sequence-level structural characterization of plant genomic DNA, an activity within which bioinformatics has played an enormous technical role. The publication of the *Arabidopsis thaliana* genome(15), gave plant biologists a major information resource for indexing current and future understanding of plant genotypes. Since that time, a complete survey of the rice genome sequence has also become available(16). Several other Species Specific Databases are listed as follows:

- Arabidopsis Swiss-Prot list - Links to A.thaliana WWW sites and to Swiss-Prot entries
- TAIR - The Arabidopsis Information Resource
- MATDB - MIPS Arabidopsis thaliana db
- TIGR At - TIGR Arabidopsis thaliana db
- Arabidopsis ABC transporters
- AMPL - Arabidopsis Membrane Protein Library
- Arabidopsis at PlaCe - Site with info on P450, glucosyltransferases, etc.
- Gramene - A comparative mapping resource for grains
- KOMUGI (Japan)
- GrainGenes , a genome database for Triticeae and related species.
- RiceGenes a genome database for rice.
- RGP - Rice Genome Research Program
- Oryzabase - Japanese rice genome db
- RiceGAAS: Rice Genome Annotation Database. A rice genome automated annotation system; integrates programs for prediction and analysis of protein-coding gene structure.
- Rice genome project at Wisconsin
- Rice-research.org - Monsanto rice genome site
- TIGR OsGI - TIGR Rice Genome project
- BeanGenes - Beans genome db
- BeanRef-Links and references from literature to different aspects of research on beans (Phaseolus and Vigna) - Beans genome db and other resources
- Chlamydomonas resource center
- ChlamyDB - Chlamydomonas reinhardtii genome db
- CottonDB - Cotton genome db
- MaizeDb - Maize genome db
- Mendel Bioinformatics Group , UK
- Mendel-ESTS , contains all of the plant EST and STS sequences currently in dbEST and dbSTS (>94,000) related to the sequences, grouped by gene family, in the Gene Family Database .
- Mendel-GFDb Database of Genes Organized by Families. Now with Pfam, Prosite & TRANSFAC domain information

- Mendel-CPGN : developinging a common nomenclature for sequenced plant genes
- INRA Maize - INRA Maize genome db
- Plant Chromatin Database
  Database for chromatin proteins in plants, including functions and molecular phylogenetic relationships, with initial emphasis on Arabidopsis and maize.]
- Pisum sativum (pea) web site
- TIGR Potato - TIGR Potato Functional Genomics project.
- TIGR GmGI - TIGR Soybean Gene Index
- Snapdragon (A.majus) web site
- SolGenes — Genome Database for the Solanaceae. A U.S.D.A.-funded Genome Database for the Solanaceae, containing information about potatoes, tomatoes, peppers, and related species.
- SorghumDB - Sorghum genome db
- SIU-C Soy Phytoestrogen Gene Mapping
- SoyBase - Soybean genome db
- SoyBase metabolic db - Metabolic subset of the soybean genome db
- TIGR LeGI - TIGR Tomato Gene Index
- Dendrome - Forest trees genome db
- ZmDB Maize Genome Database

Goals include discovering maize genes using EST sequencing and engineered Mu (RescueMu) tagging, and developing new tools to facilitate gene mapping and phenotypic analysis.

Phenotypes

Bioinformatics management of phenotype data primarily focuses on cataloging simple phenotypes. Bioinformatics researchers, such as in the Open Biomedical Ontologies initiative (http://obo.sourceforge. net), are cataloging controlled vocabulary and ontology to formalize phenotype descriptions by cross-linking concepts of "observable," "attribute," and "value." A simple application of this paradigm is the following phenotype specification i.e. leaf (observable) color (attribute) is red (value). Observables for plants can be modified using plant anatomy and developmental process terms being defined by the Plant Ontology Consortium (POC)(17). The expected dramatic improvement in phenotypes of commercial interest include both the improvement of factors that traditionally limit agronomic performance (input traits) and the alteration of the amount and kinds of materials that crops produce (output traits). Examples include:

1. biotic stress tolerance (bacteria, fungi, viruses)
2. abiotic stress tolerance (drought,heat, cold, salt)
3. nutrient use efficiency
4. manipulation of plant architecture and development (size, organ shape, number and position , timing of development and senescence).
5. metabolic partitioning (redirecting of carbon flow among existing pathways, or shunting into new pathways).

Molecular expression

Moving beyond the map characterization of genomic DNA highlighted above, the task of functional genomics (and other "-omics" fields such as proteomics and metabolomics) is to characterize the dynamic picture of molecular expression within the living organism at the level of RNA, protein, and metabolites. The rice genome contains thousands of predicted genes. The primary motivation of functional genomics research is to narrow down the list of candidate genes implicated in specified biological processes, for example, as contributors to specified agronomic traits of interest. The overall strategy is that of intersecting evidence from positional, functional, expression, selection, and crop modeling information sources (Fig. 2).

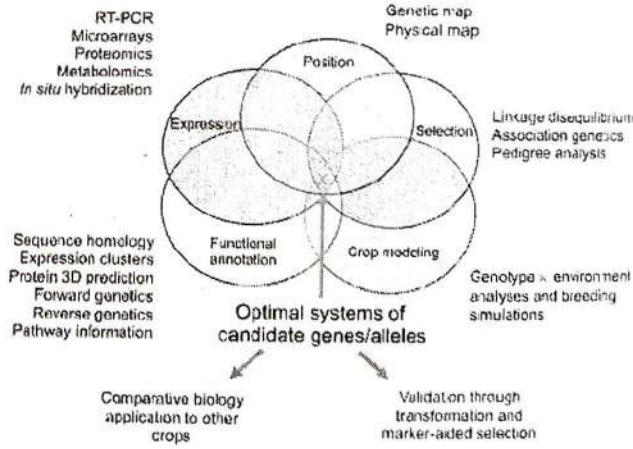

Fig. 2 Intersecting evidence for candidate genes

Protocols for crop research

Bioinformatics analysis requires a very broad range of protocols and algorithms. Many freely available tools can be used to apply such protocols and algorithms to crop research problems. A few representative tools will be mentioned here. The European Molecular Biology Open Software Suite (EMBOSS; www.emboss.org) is an opensource sequence-analysis package that provides more than 200 sequence analysis utilities, including wrappers for most publicly available algorithms such as pairwise

and multiple sequence alignments, primer design, and sequence feature recognition algorithms. EMBOSS also reads and writes a wide variety of sequence and annotation formats. The Open-Bio community (www.open-bio.org) is host to a series of computer language-specific bioinformatics tool kits useful for bioinformatics data transformation scripts and Web site development. The Generic Model Organism Database project (GMOD; www.gmod.org) is a clearinghouse of many freely available, open-source software tools for managing and manipulating biological information in databases. Another good source of freely available, open-source tools is the TIGR software site (www. tigr.org/software), which has various software systems useful in particular experimental contexts. For proteomics tools, the Expasy Web site at the Swiss Institute of Bioinformatics (www.expasy.ch) is a valuable resource. For metabolomics tools, the Systems Biology Markup Language site (SBML; www.sbml.org) is a good starting point. A principal limitation of many online databases is their dependence on regular Web server interfaces for data publication, interfaces solely searchable using standard Web browsers. Technologies such as semantic Web languages and Web services protocols are being explored as a means of creating frameworks for "computer program-friendly Web surfing," such that more powerful client software than Web browsers can be designed, implemented, and deployed on the biologist's desktop. One such protocol is BioCASE (www.biocase.org). Another notable protocol is the BioMOBY project(18), that is striving to apply biological semantics in a formal manner to integrate bioinformatics data sources and computational services into complex workflows that can be managed and visualized by sophisticated clients, such as the Taverna workflow tool (http://taverna. sourceforge.net/).

Conclusion

The large-scale quantification and identification of biological molecules has become possible with combined advances in biotechniques and computer technology . A very common bioinformatics strategy for sequence alignment is the comparison of cDNA/ EST and genomic sequences and annotation. The internet has made available large volumes of biological data that scientists can access from their desktops. By the time the human genome sequence was published in 2001, the rate of DNA sequencing had increased 2,000-fold since the inception of the technology in 1986(19). The increase was achieved by automation, miniaturization and integration of technologies. Applying this approach to other biological molecules including mRNA, proteins and metabolites has massively accelerated the accumulation of biological data. This data has been made readily accessible, in part due to publications such as the Molecular Biology Database Collection, an annual listing of the best databases publicly available to the biological community. A major aim of most genome projects is to determine the DNA sequence either of the genome or of a larger number of transcripts. These both lead to the identification of all or most genes and to the characterization of various structural features of the genome. The research agenda for Generation Challenge Programme is shown in Fig.3.

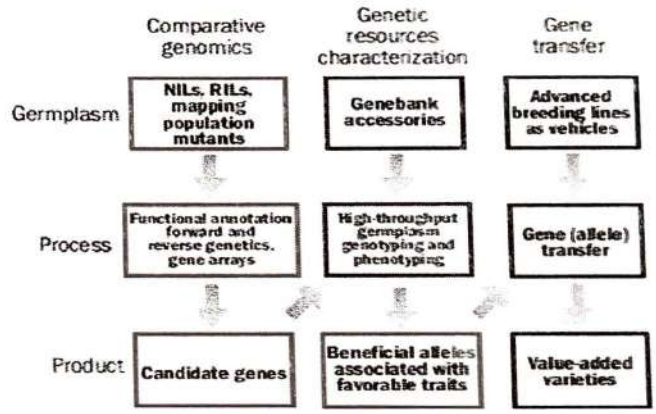

Fig.3 Research agenda for Generation Challenge Programme.

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Commercial exploitation of heterosis through cytoplasmic genic male sterility system in pigeonpea-Gujarat Tur Hybrid-1

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Abstract

The heterosis breeding has paid rich dividends over conventional breeding techniques in many crops that include both auto and allogamous crops ever since the phenomenon of heterosis was observed. The yield enhancements in pigeonpea through heterosis breeding were contemplated about three decades ago after the diverse genetic male sterility (GMS) conditioned independently by ms1 was reported, followed by identification of other genes (ms2 and ms3) for male sterility. These diverse sources of GMS system were exploited in breeding hybrids like ICPH 8, PPH 4, CoH 1, CoH 2, AKPH 4104 and AKPH 2022 with reasonably good heterosis up to 35 per cent, yet they could not become commercially viable due to nagging seed production problem inherent with the GMS system. The inherent problems of the GMS system was over come by developing stable cytoplasmic genic male sterile lines CMS GT 288 A using *Cajanus scarabaeoides* as source of sterile cytoplasm and identifying the perfectly stable restorer lines GTR-11 consummated with ideal commercial seed production protocols. The first cytoplasmic genic sterility based hybrid of pigeonpea was developed using GT 288 A as female and GTR 11 as male. The hybrid was tested in *Kharif* 2000 followed by extensive testing for another three years till 2003 over different locations in Gujarat against two latest varieties viz., GT 100 (determinate), GT 101 (indeterminate) and the best GMS based released hybrid i.e. AKPH 4101. The extensive testing over locations evinced clear superiority of GTH 1 over AKPH 4101, GT 100 and GT 101 by 42, 59 and 32 per cent, respectively. The hybrid was used as check in hybrid pigeonpea trials in central zone during *Kharif* 2007 and out yielded the best checks GT 101 and UPAS 120 by 44 and 52 per cent, respectively, there by maintaining its superiority in central zone too. The hybrid exhibited lesser incidence of wilt, SMD, *helicoverpa* and pod fly. The quality parameters viz protein content (%), cooking time, water absorption and *dhal* recovery (%) of the hybrid were at par with AKPH-4101 and GT-101. Thus hybrid programme in pigeonpea has become potent with lot of attention being given on diversification of parental materials. The crux of the programme can be gauged from the fact that in Gujarat alone there are 55 R and 53 A well established lines that have been characterized, documented and grouped according to different core characters like maturity, seed colour, seed weight and growth habit.

Key words: Cytoplasmic genetic male sterility, genetic male sterility, heterosis, pigeonpea

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp] still the characters of wild plant despite under cultivation since long. The early maturity with low spread of the plant, determinate growth habit, resistance to biotic and abiotic stresses are some the characters that have been improved in cultivated plant type. As such the country has been harvesting almost the same production of pigeonpea in lesser number of days than what it used to harvest earlier making lot of land available for other crops. The plateau and stagnation in pigeonpea productivity has become a national concern and was discussed in many brain storming sessions at different levels with little success. This is because the crop has indispensable place in all

regional food habits of the country. The crop has a unique place in Indian agriculture, as it is grown in diverse cropping system both as solo and intercrop due to wide flexibility in crop duration (140 - 300 plus days). The crop has diverse uses varying from vegetables, food grains, fodder, fuel, soil enriching and construction of shelters. As such the crop has wide potential for expansion under both subsistence farming and intensive agriculture. Several reasons for low productivity have been suggested (1) among which conventional breeding procedures with narrow genetic base have been the major bottlenecks for genetic improvement. Even today, most of the cultivars grown are land races or selections from them. Recent release and adoption of cytoplasmic genic male sterility based pigeonpea hybrid in India has set a perfect stage for addressing these issues of yield stagnation.

The heterosis breeding has paid rich dividends over conventional breeding techniques in many crops that include both auto and allogamous crops ever since the phenomenon of heterosis was observed by Shull (2). The manifestation of heterosis has been found to be independent of pollination system of the crop. Pigeonpea is an often cross pollinated crop. As such many useful dominant genes have been preserved in the cross pollinated land races and cultivars while the useful recessive genes have been fixed by breeders in pure lines through pedigree selection / breeding. These gene constellations can be used as advantage for realizing higher heterosis in pigeonpea. The important economic characters in pigeonpea like grain yield, pod plant -1, seeds pod-1, seed size and plant height are controlled by both additive and nonadditive gene action and that the level of heterosis is comparable with any other crop that has been exploited through heterosis breeding (3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15).

For commercial exploitation of heterosis in any crop, it is pertinent to have an economically viable mass pollen transfer mechanism in place. Pigeonpea is an often cross pollinated crop up to 70 per cent (16, 17) that primarily occurs due to insect visitations. The natural out crossing varies from location to location that could be due to number of factors among which number and types of pollinating vectors are the most important ones. The availability of male sterility system, occurrence of reasonably good out crossing and existence of heterosis has set a perfect milieu for addressing the yield stagnation through heterosis breeding.

The yield enhancements in pigeonpea through heterosis breeding were contemplated about three decades ago after the diverse genetic male sterility (GMS) conditioned independently by ms1 was reported (17). This followed identification of other genes (ms2 and ms3) for male sterility. These diverse sources of GMS system were exploited in breeding hybrids like ICPH 8, PPH 4, CoH 1, CoH 2, AKPH 4104 and AKPH 2022 with reasonably good heterosis up to 35 per cent, yet they could not become commercially viable due to nagging seed production problem inherent with the GMS system. Unwillingness of the farmers to remove fertile segregants from seed production plot, high seed rate, shortage of parental seed stocks, *Helicoverpa* havoc, problems of grow out test, low remuneration to seed growers, competition with other crops and lack of training to seed growers were some of the major reasons for failure of GMS based hybrids.

Results and discussion

Identification of Cytoplasmic Male Sterility System

The inherent problems of the GMS system can be over come by developing pure breeding and stable cytoplasmic genic male sterile lines consummated with perfect commercial seed production protocols. The aborted attempt to develop cytoplasmic male sterility in pigeonpea using wild relatives was done earlier using *Cajanus scarabaeoides* that is a secondary species of pigeonpea often used in breeding for yield improvement through donor characters like insect resistance, drought resistance and quality attributes (18, 19). The cross between *Cajanus scarabaeoides* and Cajanus cajan was attempted in *Kharif* 1992 and F_1 seeds were grown in the following year. The F1 plants were partially male sterile, erect, dwarf and small podded with 2 to 3 small seeds per pod. The F_2 population was raised in Kharif 1994 and was screened for identification of stable cytoplasmic genic male sterility. The pollen sterility was confirmed by microscopic studies using acetocarmine staining technique. The F_2 population was characterized for male sterile and male fertile

Table 1. Performance of CGMS based pigeonpea hybrid GTH-1 in Gujarat state

Year	Name of Trial	Location	Grain Yield (kg/ha)				C.D. at 5%	CV %
			GHT-1 (SKNPCH-10)	AKPH-4101 (C)	GT-100 (C)	GT-101 (C)		
Kharif-2000	PHT	Sardarkrushinagar	2827	1224	1218	-	161	4
		Mean	2827	1224	1218	-		
Kharif-2001	SSHT	Sardarkrushinagar	1852	1219	1431	-	242	10
		Ladol	644	679	707	-	NS	15
		Anand	450	825	770	-	266	35*
		Mean	1774	1041	1119	-		
Kharif-2002	LSHT	Sardarkrushinagar	2057	1543	-	1381	111	14
		Anand	2106	1759	-	1562	290	10
		Bharuch	1906	1662	-	1759	378	11
		Vadodara	849	548	-	540	238	21
		Derol	2547	1666	-	1782	369	11
		Navsari	2346	1698	-	2022	158	5
		Mean	1969	1479	-	1508		
Kharif-2003	LSHT	Sardarkrushinagar	2537	1444	-	1620	236	9
		Bharuch	1144	1130	-	1017	139	7
		Vadodara	1111	868	-	910	205	9
		Junagadh	2516	2161	-	2344	218	6
		Derol	938	608	-	573	212	19
		Navsari	1013	390	-	448	158	19
		Mean	1543	1100	-	1152		
		Mean (2002, 03)	1756	-	-	1330		
		Overall Mean	1760	1240	-	-		
		% increase		42	59	32		

* Results not considered due to high CV %

Table 2. Performance of GTH 1 in Central Zone during *Kharif* 2007

Sr. No.	Name of Trial	Locations	Variety/hybrid		
			GTH 1	GT 101	UPAS 120
1.	IHT (E)	Sardarkrushinagar	1167	1427	1177
		Rahuri	3912	1933	2271
		Navsari	816	625	348
		Khargone	878	447	339
		Mean	1693	1108	1033
		*Mean	2539	1680	1724
2.	AHT (E)	Sardarkrushinagar	1566	1487	986
		Rahuri	2520	1788	2034
		Navsari	1389	798	486
		Khargone	1623	1031	1038
		Mean	1775	1276	1136
		*Mean	2030	1411	1332
		% increase over		44	52

plants by splitting opening the flower and observing for pollen viability. It was inspiring to observe that unlike earlier studies of Reddy and Faris, (17), Ariyanayagam *et al.* (19), most of the male sterile plants were similar to *Cajanus cajan* and that could easily be divided in to two categories, (i) some plants were consummately devoid of pollens while (ii) others produced sterile pollens. The second category was utilized and maintained through recurrent mating with GT 100, ICPL 87, GT 288 F (having gms_1 gene) and QMS 2F (having gms_2 gene) as recurrent parents. Sibs of male sterile and male fertile plants were also developed besides collecting open pollinated seeds on the sterile plants for studying inheritance and genetic variability. The systematic studies indicated that male sterility was ascribed to cytoplasm and was maintained by plant to plant mating with GT 100, ICPL 87, GT 288 F and QMS 2F as recurrent parents. Wide range of variation in male sterility was observed in different recurrent. Cent percent sterility was aimed through out the selection process during the growing period of the plants. Further, it was enticing to observe that BC_1F_2 of GT 288F was fully sterile and did not evinced variation in pollen sterility at any stage of flower development. As such there was no pollen production on these BC_1F_2 of GT 288F plants through out the growing period of the plants. In BC_1F_2 of other three parents viz. ICPL 87, GT 100 and QMS 2F were also sterile but the male sterility varied a lot. This palpably indicated that the sterility maintained by GT 288F was convincingly different than that maintained by ICPL 87, GT 100 and QMS 2F. Further, the reversion of male sterile plants to male fertile plants was more in ICPL 87, GT 100 and QMS 2F under low temperature and high humidity where as GT 288 F maintained stability of male sterility over different range of temperature and humidity. The male sterile plants of GT 288F evinced cent percent male sterile plants in subsequent generations unlike maintainers of GT 288 F and QMS 2F (carrier of ms_1 and ms_2 genes for sterility) indicating that that the system is different from the genetic male sterility governed by ms1 and ms_2 genes. The stability of the lines for male sterility was studied after BC_4F_2 over different locations and line was found to be completely male sterile conditioned by cytoplasm. As such the cytoplasmic genic male sterile line was identified by Tikka *et al.*(20) that was registered as cytoplasmic genic male sterile line (CMS GT-288A) with INGR No.0012 with the NBPGR, New Delhi in 2003. The line is proving its versatility in propping up national pigeonpea hybrid programme as this is the most extensively used line in diversification of the female parents countrywide.

Identification of male fertility restoration system

The F_1 of the cross between Cajanus scarabaeoides and Cajanus cajan was partially male sterile and segregated for male fertility in F_2 population. The fertile plants were crossed with GT 100 as recurrent parent and selected for fertility restoration with GT 288 A through plant to plant mating and selfing under insect proof net house conditions. The male fertility restoration was confirmed by growing F_1 crossed seed and scoring for male fertile plants by splitting opening the flower, observing the pollen, seed setting and autogamous seed setting under net house conditions. The selection for strict male fertility restoration culminated in the development of stable and consummate fertility restoration system that was named as GTR 11. The line was registered as GTR-11 (R Line) with INGR No. 03102 (IC 296589) with the NBPGR, New Delhi in 2004.

Development and performance of GTH-1

The first cytoplasmic genic sterility based hybrid of pigeonpea was developed using GT 288 A as female and GTR 11 as male. As discussed above, GT 288 A has lineage to the maintainer i.e B line designated as GT 288F while GTR 11 was the released white seeded determinate early variety of pigeonpea GT 100. The female parent was early by about a week but the seed production was not bogged due to this difference as the female had indeterminate profuse flowering habit. The hybrid was preliminarily tested in Kharif 2000 followed by extensive testing for another three years till 2003 over different locations in Gujarat against two latest varieties viz., GT 100 (determinate), GT 101 (indeterminate) and the best GMS based released hybrid i.e. AKPH 4101. The extensive testing over locations evinced clear superiority of GTH 1 over AKPH 4101, GT 100 and GT 101 by 42, 59 and 32 per cent, respectively (Table 1). The hybrid was used as check in hybrid pigeonpea trials in central zone during Kharif 2007 and out yielded the best checks GT 101 and UPAS 120 by 44 and 52 per cent, respectively, there by maintaining its superiority in central zone too (Table 2). The hybrid exhibited lesser incidence of wilt, SMD, helicoverpa and pod fly (Table 3 & 4). The quality parameters i.e. with protein content (%), cooking time, water absorption and dhal recovery (%) of the hybrids were at par with AKPH-4101 and GT-101 (Table 5)

Table 3. Disease reaction of GTH 1 to major diseases in wilt sick plot

Year under testing	Variety	Percent damage	
		Wilt (%)	SMD (%)
Kharif 2003	GTH-1	1.00	0.00
	AKPH-4101	2.00	0.00
	GT-101	0.00	0.00
Kharif 2004	GTH 1	0.90	0.00
	AKPH 4101	2.10	1.20
	GT 101	0.00	0.40
Kharif 2005	GTH 1	0.95	0.00
	AKPH 4101	1.90	0.80
	GT 101	0.10	1.00
Kharif 2006	GTH 1	1.00	0.00
	AKPH 4101	1.70	1.00
	GT 101	0.15	0.60

Table 4. Reaction to major pests during *Kharif* 2003-04.

Sr. No.	Variety	Per cent damage	
		Helicoverpa	Podfly
1.	GTH-1 (SKNPCH-10)	11.05 (19.1)*	5.4 (13.5)
2.	AKPH-4101	30.8 (33.7)	20.8 (27.1)
3.	GT-101	25.3 (30.0)	16.0 (23.5)

* Value in parentheses are Arc sin

Standardization of Seed Production Protocol for Hybrids

Isolation distance

The natural out pollination in pigeonpea occurs primarily due to insect visitations among which honey bees are major. It can not fly more than 200 meters from one specific plot to another. This has been experimentally proved at Sardarkrushinagar. Hence 200 m isolation distance is recommended. There should not be any other pigeonpea in the 200m range surrounding parental / hybrid seed production plot to get genetically pure seed.

Rouging

Five rouging are recommended at different stages of plant growth to remove off type plants as follows.

- One at seedling stage
- Two at flowering stage
- One at podding stage
- One at physiological maturity

Parental seed production

Physical and genetic purity of the seed of parental lines is the hallmark of any successful hybrid programme. For this the authentic source of seed and precise production there of is the prerequisite for maintaining the purity. There are two types of parental seed production (i) seed production of female parent and (ii) seed production of male parent that are discussed here as under:

Female parent i.e. (A / B Lines)

Cytoplasmic Genetic Male Sterile line i.e. A line is used as female parent for the hybrid seed production plot. It is maintained separately for maintenance and production of bulk seed. It is maintained by its fertile counterpart. i. e. maintainer (B line). Morphologically A and B lines are same, except for cytoplasm i.e. male sterility. The sterility is confirmed at flowering i.e. anthesis. Anthers of A line are white and translucent type, while of B line are full of pollen grains and can be distinguished with eye observation in the form of pollen mass.

Maintenance of A/B Lines

- Sow A and B lines alternately in a single row plot of 4m length
- Cover the plot with insect proof net to ward off cross pollination
- Select the required number of true to type plants in each row of A and pollinate with selected plants of B line in plant-to-plant fashion. The crossed seed on A line will be the seed of A line.
- Since the B line is in insect proof net house, the seed on selected plants of B line is selfed seed of B lines.
- Harvest the crossed seed plant wise on A line and selfed seed of B line separately
- Grow the crossed seed (A line) with B line and observe the sterility. The pairs of A and B line that evince the satisfactory sterility are retained separately as A and B line for further maintenance and seed production.

Table 5. Comparative quality attributes of GTH 1

Sr. No.	Variety	Protein content (%)		Cooking time (Minutes)		Water absorption (g/g.seeds)	*Dhal* recovery (%)
		Seed	Dhal	Seed	Dhal		
1	GTH-1	22.75	22.92	33	19	1.74	87.2
2	AKPH-4101	21.90	21.97	34	18	1.69	86.1
3	GT-101	22.80	22.90	35	20	1.74	86.8

Breeder seed production of A/B Lines

Experiments conducted for seed production of GT 288 A at Deesa, Bharuch, Navasari and Aseda confirmed higher seed production with 4 : 1 row ratio (Fig. 3). Therefore, it is recommended that bulk breeder seed production of A lines may be taken in 4A : 1B row ratio with planting of 2 to 3 B lines all around the seed plot for easy availability of pollen.

Seed production of male parent i.e. R line

Seed production of male line (R line) requires genetically pure basic seed. Timely sowing and rouging at different stages as mentioned in female seed production will produce genetically pure seed.

Maintenance of R lines

- Grow the individual selected R plants in plant to row progenies og 4 m length
- Select required number of true to type plants in each R line and cross with A line in plant to plant fashion.
- Harvest the crossed seed and selfed seed of individual plants separately.
- Plant the crossed / hybrid seed along with its respective self-progeny of R plant in insect proof net house.
- Observe the seed setting on the hybrid plants. Select only those R plants that evince better fertility restoration as exhibited by seed setting on hybrids.

Nucleus seed stage II

For hybrid programme A and R line can be maintained in isolation. For this A and B lines can be planted in 4:1 ratio for production of A line seed while the R line can straight way be maintained in net house or in isolation. The size of the plots can vary depending upon the nucleus seed requirement and the availability of NSS I seed stock. These plots are once again subjected to critical examinations to eliminate any off type plants that might have escaped detection during NSS I. In case of detection of any off types, the entire row-to-plot should be discarded. Only those plots that meet the stringent physical and genetic purity standards are selected, harvested and threshed separately. The harvested seed are once again examined for size, colour and shape and uniformity. The plots that possess uniform seed and are true to type are bulked to form the NSS II for raising breeder seed.

Breeder seed

The seed harvested from NSS II is used for raising breeder seed of parental lines. The breeder seed of R line is produced in isolation while that of A line is also raised in isolation or net house conditions in 4:1 lines ratio of A and B lines. Strict seed production measures are taken to maintain seed purity. Five rouging at different stages as mentioned in parental seed production should be followed. Other morphological characteristics are also used for removing off type plants.

Hybrid seed production

For hybrid seed production programme, genetically pure seed of A and R lines must be procured. Experiments conducted at Deesa and Aseda in Gujarat confirmed higher seed production with 4 : 1 row ratio (Fig. 3). Five rouging at different stages as mentioned in parental seed production should be followed. Other morphological characteristics are also used for removing off type plants.

The diagnosis features of parents and the hybrid GTH-1 are given here as under for easy identificatio of parents and hybrids at different growth stages:

S. N.	Characters	Observation Stage	Hybrid	Parents	
			GHT-1	GT-288A	GTR-11
1.	Color of base petiole	Cotyledons unfolded	Purple	Green	Purple
2.	Growth habit	About 60 % flowers open	Semi erect	Erect	Bushy
3.	Growth type	About 60% flowers open	Indeterminate	Indeterminate	Determinate
4.	Shape of terminal leaf	About 60 % flowers open	Elliptical	Elliptical	Elliptical
5.	Leaf color	About 60% flowers open	Green	Green	Dark green
6.	Pubescence on leaf	About 60% flowers open	Sparse pubescence	Dense pubescence	Sparse pubescence
7.	Outer surface of flower standard (banner petal)	Full flowering	Yellow with few red streaks	Yellow with few red streaks	Yellow
8.	Standard color	Full flowering	Yellow	Yellow	Yellow
9.	Patterns of streaks	Full flowering	Parallel	Parallel	-
10.	Pod color (Pre-mature)	Podding (Pre-mature)	Green with black streaks	Green with on base	Green black streaks
11.	Pubescences on pods	Pods are green and pre-mature	Sparse	Sparse	Sparse
12.	Seed color	Maturity	White	White	White
13.	Seed shape	Maturity	Ovate	Ovate	Ovate

Grow-out tests for pigeonpea hybrid GTH-1

Hybrid seed crop sown in the month of July will be ready by the end of November. Samples for G.O.T. may be drawn and tested for G.O.T. in December in off season nursery that can be easily raised in states like Gujarat or Tamil Nadu. Results of G.O.T. will be available by the end of February.

Sr. No.	Characters	Hybrids / Parents			Maximum time / duration
		GTH-1	GT-288-A (Female)	GTR-11 (Male)	
1.	Growth habit	Semi-erect	Erect	Bushy	80 days
2.	Growth type	NDT	NDT	DT	80 days
3.	Flower colour (standard)	Yellow with few red streaks	Yellow with few red streaks	Yellow	85 days
4.	Pod colour (pre-mature)	Green with black basal streaks	Green	Green with black streaks on entire pod	90 days

Economics of commercial seed production

The general expenditure and income from a unit seed plot is calculated on the prevailing market rates and is reproduced here as under :

Expenditure

Sr. No.	Particulars	Rates	Cost (Rs.)
1.	Seed cost	Female 18 kg @ Rs.50	900
		Male 3kg @ Rs.50	150
2.	Cultivation	3 hrs @ Rs.400	1200
3.	Sowing	2 hrs @ Rs.400	800
4.	Fertilizer	Dose 25:50:00 NPK kg/ha	1000
5.	Irrigation (Five)	5 @ Rs.600	3000
6.	Insecticides and Pesticides	As required	2000
7.	Rouging charges	3 @ Rs.400	1200
8.	Harvesting	12 labour @ Rs. 100	1200
9.	Thrashing	a. 2 labour @ Rs. 100	200
		b. 3 hrs thrasher @ Rs. 400	1200
10.	Grading	5 labour @ Rs. 100	500
11.	Packing charges	380 bag @Rs. 10	3800
	Total Expenditure per ha.	17150.00	

Earning

Particulars	**Rates (Rs/kg)**	**Income (Rs.)**
Hybrid seed production 1886 kg/ha	50	94300
Male seed production 319 kg/ha	15	4785
Total Income		99085

Profit (Rs.) : 99085- 17150 = 81935 or
Seed cost of hybrid seed = 9.09 or Rs 9.00/kg
Profit /kg of seed = Rs 43.44 or 43.00

Looking Ahead

The future of hybrid programme in pigeonpea seems very bright with lot of attention given on diversification of parental materials. The crux of the programme can be gauged from the fact that in Gujarat alone there are 55 R and 53 A well established lines that have been characterized, documented and grouped according to different core characters like maturity, seed colour, seed weight and growth habit. Some of them have been registered with the NBPGR, New Delhi as sui-generis materials. Still another half century materials of A and R lines are in the final stage of characterization. Other centers in the country are also developing materials as per their regional requirements. All these materials are stable for male sterility and fertility restoration over locations. The B and R lines are being studied for yield component characters for better complementation in hybrids. The performance of new test hybrids contributed by various test centres of the country in the ISOPOM project as well as national policies are really encouraging and is surely going to impact pigeonpea production in the country both in early and medium maturity group.

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Effect of mulches and antitranspirants on biometric components and seed yield of castor (*Ricinus Communis* L.) under rainfed conditions

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Abstract

A field experiment was conducted during kharif seasons of 2000 to 2004 under rainfed conditions to find out the suitable mulches and antitranspirants on seed yield of castor. In pooled data mulches showed non-significant results but crop residue mulch @ 5 t ha^{-1} resulted the improvement in seed yield of 17.68 per cent higher when compared to soil mulch. Among the different antitranspirants, kaolin spray @ 5% recorded significantly higher castor seed yield of 1308 kg ha^{-1} and it was 26.0 % higher than absolute control.

Key words: Mulches, antitranspirant, rainfed, castor

Introduction

Castor (*Ricinus comnumis* L.) is an important cash crop of this region. In Gujarat productivity of rainfed and irrigated castor is 1290 and 2810 kgha^{-1}, respectively. In rainfed areas, castor generally faces late season drought resulting in low yield. Various workers have reported the favourable effect of mulches (Ravi and Christopher 1996, Solaippan and Dasan 1998 and Das and Gautam 2003) and prevention of moisture loss through the plant body (Ravi and Christopher 1996, Kaushik and Lal 1997 and Das and Gautam 2003).

One of such residues may be the use of mulches and antitranspirants for reducing the soil moisture loss through evaporation and prevention of water losses through plant body by transpiration. There is no any information available, hence the present investigation was undertaken to determine the extent of the effect of mulches and antitranspirants on yield of rain fed castor.

Materials and methods

A field experiment was conducted during kharif season of 2000 to 2004 at the AICRP for dryland Agriculture, Regional Research Station, S. D. Agricultural University, Sardarkrushinagar. The soil of the experimental plot was loamy sand in texture, well drained having low in organic carbon (0.30%), available phosphorus (42 kg ha^{-1}) and potash (195 kg ha^{-1}) with pH 8.2. Ten treatment combinations consist of two mulches (Soil mulch and crop residue mulch @ 5 t ha-1) and five antitranspirants (5% kaolin, 0.1 % PMA, 0.75% Cetyle alcohol, water spray 500 lit ha-1 and absolute control) were evaluated in FRBD design with four replications. Soil mulch was carried by interculturing at 30 and 60 DAS and castor shell mulch (5 t ha^{-1}) was spread uniformly in between the crop leaving no soil exposed at 45 DAS. Different treatments of antitranspirants were imposed at 45, 75 and 105 days after sowing. Castor GCH-4 was sown on 18th July, 6th Aug., 1st Aug., 16th July and 2nd Aug. during 2000, 2001, 2002, 2003 and 2004, respectively, with inter row spacing of 90 cm and intra row spacing of 60 cm. Uniform fertilizers were applied @ 30 kg N and 30 kg P205 ha^{-1} as basal and @ 30 kg N as top dressing at 45 DAS under sufficient soil moisture condition. The rainfall received during 2000, 2001, 2002, 2003 and 2004 were 400.2, 571.1. 201.9, 766.3 and 380.3 mm), respectively. Yield attributes were recorded from five randomly selected plants in each treatment. Soil moisture at harvest was taken from 0-30 cm soil depth. Yield data were also recorded treatment wise and used for statistical analysis.

Table 1. Yield attributes and yield of castor as influenced by mulches and antitranspirants

Treatments	Seed yield (Kg ha^{-1})						Length of Primary spike	No. of Capsules/ main spike	No. of effective branches/plant	Moisture % at Harvest (0-30cm)
	2000	2001	2002	2003	2004	Pooled				
Mulches										
M_1 : Soil mulch	667	1144	371	1463	1500	1029	50.6	56.9	3.75	1.91
M_2 : CRM	722	1177	425	1975	1754	1211	66.9	64.7	3.90	2.18
S.Em±	16.4	23.6	6.4	44.0	61.2	65.0				
CD at 5%	47.6	NS	18.4	127.9	177.7	NS				
Antitranspirant										
A_1: Kaolin @ 5%	764	1427	519	1993	1836	1308	61.8	69.0	4.88	2.23
A_2:P.M.A.@ 0.1%	608	1085	353	1606	1381	1007	53.0	55.9	4.03	2.10
A_3:Cetyl Alcohol @ 0.75%	716	1187	367	1712	1726	1141	58.4	58.7	4.04	2.15
A_4: Water spray	698	1074	380	1699	1676	1106	60.1	60.0	3.60	1.91
A_5:Absolute control	688	1029	371	1585	1515	1038	59.8	60.6	3.58	1.85
S.Em±	25.9	37.3	10.0	69.7	96.8	33.7				
C.D. at 5%	75.2	108.4	29.1	202.2	281.0	101.0				
CV%	10.55	9.10	7.14	11.47	16.84	14.47				
Interaction										
CD at 5%	NS	NS	NS	NS	NS	NS				

Results and discussion

Effect of mulches

The yield was directly influenced by the development of some parameters known as the yield attributing characters. These include length of primary spike, number of branches per plant and number of capsules per main spike. All these characters were better developed in the treatment consisting of crop residue mulch (Table 1). All yield attributes improved due to crop residue mulch created a physical barrier and cut off the solar radiation falling on the soil surface. This reduced the energy supply to the evaporating soil surface and thus reduced the evaporation loss and soil temperature. Soil moisture at harvest (2.18 %) was also higher in crop residue mulch plot due to more moisture conserve in this treatment.

Individual yield data were found significant during all the years except during 2001 and it was higher in crop residue mulch treatment as compared to soil mulch. Whereas five years pooled data showed that mulches was found non-significant results but crop residue mulches @ 5 t ha^{-1} led to improvement on seed yield of 17.68 % higher than soil mulch. Similar results were also obtained by Solaiappan and Dasan (2) and Ravi and Christopher (1) in cotton and Rana *et. al* (5) in sugarcane.

Effect of antitranspirants

The growth and yield attributes of castor measured in terms of number of branches per plant, length of main spike and number capsules per main spike (Table 1) were recorded significantly higher values in kaolin spray of 5 % while absolute control recorded lower values. Favorable effect of kaolin spray on plant growth might be attributed to reduction transpirational loss of water due to reflection of part of solar radiation incident on leaf surface, thus making the soil moisture available over a longer period. Soil moisture at harvest (2.23%) was also higher in kaolin 5 % treatment. The beneficial effect of kaolin spray is in conformity with the findings of Das and Gautam (3) and Thakuria *et. al.* (6).

Individual, year wise yield data as well as pooled were found significant and gave significantly highest seed yield of castor (1308 kg ha^{-1}) in kaolin 5 %, which was 29.9, 14.6, 18.3 and 26.0 per cent higher than PMA, Cetyle alcohol, water spray and absolute control, respectively. Significantly lower yield was recorded in PMA 0.1 % treatment might be due to toxic effect on plant growth. These findings are corroborated those of Kaushik and Lal (4) and Das and Gautam (3).

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Efficacy of botanicals against *Uroleucon compositae* (Theobald) infesting flowering crop Gaillardia in field

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Abstract

Investigations on management of *Uroleucon compositae* (Theobald) infesting ornamental crop Gaillardia puchella Foug. through botanicals were carried out at B.A. College of Agriculture, Anand Agricultural University, Anand during the year 2003-04. Among the evaluated botanicals, neem seed kernel extract @ 3 %, neem leaf extract and arduso leaf extract @ 10 % were found effective against this pest. Maximum flowers harvested from the treatment of neem seed kernel extract followed by neem leaf extract and arduso leaf extract. The avoidable losses due to the incidence of U. compositae ranged from 2.84 to 15.08 percent in different treatments.

Key words : Botanicals, gaillardia, bioefficacy

Introduction

Gaillardia is one of the most popular flowers in our country and commonly known as 'blanket flower'. The plant has got attractive flower colours with long duration of flowering. Gaillardia grown for its profuse flowers and the same are used for making garlands in religious ceremony and for making flowerbeds and herbaceous flower border. As a cut flower, it is very useful for the lasting qualities. The gorgeously coloured flowers are best arranged in copper bowls, simple plain or colored vases (1). Floriculture in Gujarat occupies 4300 to 4500 ha of land and producing 14650 MT of flowers worth Rs. 25 crores. Of which flowers of a Rs. 4 crores were exported during the year 2000-01.In Gujarat, mainly this crop is cultivated in Vadodara, Surat, Ahmedabad, Kheda and Anand districts(2).This crop was found to be severely and regularly attacked by aphid Uroleucon compositae (Theobald) (3) in Gujarat. Therefore, the present investigation was carried out to find out the effective botanicals against this pest.

Materials and methods

With a view to find out the effective and economical botanicals various plant extracts were evaluated against U. compositae infesting Gaillardia crop. The experiment was carried out in Randomized Block Design. The gross and net plot size was 3.0 x 1.2 m and 2.4 x 0.6 m, respectively. Each treatment was replicated thrice. Observations on number of aphids per 15 cm per twig of plant present on each of the tagged plant was recorded before and after 1, 3, 7 and 14 days of spray application. The data on mean number of aphids per plants thus obtained were statistically analyzed. The picking-wise flowers were weighed from each treatment separately and the total weight of flowers in tonnes per hectare (tonnes/ha) was calculated for each treatment. On the basis of gaillardia flower yield harvested from various treatments under study, the avoidable losses due to aphid infestation was calculated by applying formula of Poul (4).

Results and discussion

The leaf extracts, Arni (*Clerodendrum multiflorum F.* -ALE), Latana (*Lutana cumera L.* - LLE), Mint (*Menthu piperata L.* -MLE), Ardoso (*Ailanthus excelsa Roxb.*-ADLE), Naffatia (*Ipomoea fistulosa* Mart. - NFLE), Karen (*Nerium indicum* Mill. - KLE), Ratanjyot (*Jatropha gossypifolia L.*-(RLE), Neem (*Azadirachta indica A. Juss.*- NLE) were tested @ 10 % and seed extract of Neem (*Azadirachta indica A. Juss.*- NSKE) @ 3 % were evaluated for their efficacy against U. compositae on gaillardia crop.The data obtained on

number of aphids/plant are given in Table 1. Data (Table 1) showed that the plots treated with NSKE exhibited least (30.75) population of aphids and it was at par with NLE (40.46) and ADLE (43.72) after one day of application. The KLE, ALE, MLE and LLE treated plots noted aphid numbers between 51 and 55. After 3 days of application, significantly lowest (21.40%) aphid numbers noted in the plots treated with NSKE than all the plant extracts except NLE (29.53). Remaining treatments (ADLE, RLE, NFLE, MLE, KLE, LLE and ALE) were statistically at par with each other. The data on numbers of aphids recorded after 7 days of application revealed that NSKE (36.95) was found significantly superior over rest of the treatments except NLS (39.70), ADLE (46.15), NFLE (50.05) and LLE (50.34). After 14 days of application, significantly lowest (49.34) aphid population was found in NKSE than ALE. The remaining plant materials were found equally effective against U. compositae on gaillardia crop (Table 1). Pooled over period results clearly indicated that the superiority of NSKE treatment was noted in preventing the build up of aphid population. Among the botanicals tested against U. compositae, NSKE treated plots registered significantly least (36.22) number of aphids per plant except the treatment of NLE (42.01). The ADLE was found equally effective as NLE. The plots treated with NFLE, LLE, MLE, KLE and RLE exhibited more or less equal numbers (46.70 to 55.45) of aphids.

Increased in yield over control varied from 3.25 to 17.76 % due to application of various plant extracts (Table 2). Maximum yield was increased in the plots treated with NSKE (17.76 %) followed by NLE (14.42 %), ADLE (12.29 %) and NFLE (10.29 %). Enhancement of yield due to effect of plant products was poor (3.25 to 8.35 %) in plots treated with ALE, RLE, KLE, MLE and LLE. So far avoidable losses (Table 2) in yield of gaillardia flowers were concerned, it varied from 2.84 to 12.33 % in different treatments. Considering maximum (25.39 tonnes/ha) yield of NSKE taken as base, the avoidable loss was lowest (2.84 %) in the treatment of NLE followed by ADLE (4.65 %) and NFLE (6.35 %) as against 15.08 % in control plots.

The effectiveness of neem seed kernel extract against *U. compositae* was proved by Manjunatha *et al.*, (3) on gaillardia and Mallapura *et al.* (5) on safflower, respectively. These references are in corroborative with the present conclusion drawn from field studies indicating the effectiveness of neem seed kernel extract, neem leaf extract and arduso leaf extract against U. compositae infesting gaillardia crop. The application of arni, ratanjyot, Karen and mint leaf extracts evaluated @ 10 % were found less effective in protecting the gaillardia crop against *U. compositae*.

Table 1. Bio-efficacy of botanicals against *U. compositae* infesting gaillardia in field conditions.

Botanicals	Conc. (%)	Aphids/plant day after spray					Pooled
		Before	1	3	7	14	
KLE	10	8.64* (74.15)	7.44 (54.85)	6.78 (45.46)	7.27 (52.32)	8.01 (63.66)	7.39 (54.11)
NFLE	10	8.36 (69.38)	6.90 (47.11)	6.59 (42.93)	7.11 (50.05)	7.98 (63.18)	7.23 (51.77)
MLE	10	8.15 (65.92)	7.30 (52.79)	6.64 (43.59)	7.31 (52.93)	7.67 (58.33)	7.26 (52.20)
ADLE	10	7.84 (60.97)	6.65 (43.72)	6.40 (40.46)	6.83 (46.15)	7.29 (52.64)	6.87 (46.70)
LLE	10	8.70 (75.19)	7.21 (51.48)	6.79 (45.60)	7.13 (50.34)	7.62 (57.56)	7.23 (51.77)
ALE	10	8.19 (66.58)	7.43 (54.70)	7.33 (53.23)	7.80 (60.34)	8.32 (68.72)	7.79 (60.18)
RLE	10	8.04 (64.14)	6.94 (47.66)	6.44 (40.97)	7.64 (57.87)	8.13 (65.60)	7.48 (55.45)
NSKE	3	8.21 (66.90)	5.59 (30.75)	4.68 (21.40)	6.12 (36.95)	7.06 (49.34)	6.06 (36.22)
NLE	10	8.35 (69.22)	6.40 (40.46)	5.48 (29.53)	6.34 (39.70)	7.28 (52.50)	6.52 (42.01)
Control	-	7.95 (63.15)	9.26 (85.25)	8.59 (73.29)	9.71 (93.78)	10.68 (113.56)	9.30 (85.99)
S.Em. ±	-	0.32	0.43	0.52	0.38	0.42	0.241
C.D.0.05	-	NS	1.29	1.53	1.14	1.24	0.69
C.V. %	-	6.70	12.54	13.48	9.09	9.04	16.12

Table 2. Effect of various botanical materials on gaillardia flower yield and avoidable losses due to *U. compositae*

Botanicals control (%)	Conc. (%)	Yield of flowers (tonnes/ha)		
		Yield of flowers (tonnes/ha)	Increased in yield over	Avoidable loss (%)
NSKE	3	25.39	17.76	-
NLE	10	24.67	14.42	2.84
ADLE	10	24.21	12.29	4.65
NFLE	10	23.78	10.29	6.35
LLE	10	23.36	8.35	8.00
MLE	10	23.21	7.65	8.59
KLE	10	22.86	6.02	9.97
RLE	10	22.67	5.15	10.71
ALE	10	22.26	3.25	12.33
Control	-	21.56	-	15.08
S.Em. ±		0.67		
C.D.0.05		2.00		
C.V. %		8.71		

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Inventory and species composition of grasshopper fauna in different ecosystems of north Gujarat

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Abstract

In the present investigation field surveys were conducted during 2002-04 in agro, forest and grassland ecosystems of north Gujarat to enlist the grasshopper fauna of the region and its taxonomic composition. The study revealed the existence of fifty one grasshopper species belonging to three major families viz., Acrididae, Pyrgomorphidae and Tettigoniidae in the study area. Out of 51 species recorded (49 were identified), members of Acrididae represented maximum (36), followed by Tettigoniidae (12) and Pyrgomorphidae (3). The members of the family Acrididae were distributed among ten sub-families of which Oedipodinae was the dominant group represented by 13 species followed by Acridinae (7). The Tettigoniidae was represented by five sub-families and Pyrgomorphidae comprised of three species.The species and its group differed greatly in different ecosystems. Agroecosystem and forest ecosystem recorded highest number of 26 species, whereas, grassland ecosystem contained 25 species. Acridinae and Oedipodinae were important representatives of agro and forest ecosystem, where as Eyprepocneminae and Oedipodinae formed the major group in forest ecosystem.

Key words : Agroforest and grassland ecosystem, grasshoppers, acrididae, pyrgomorphidae,tettigoniidae

Introduction

The impact of Agriculture on natural resources and thereby on environment is quite significant in recent years. System of intensive plant and animal production in developed countries has led to the loss of many plant and animal species, which is an important global environmental concern with wide ramifications for agriculture. As a large proportion of plant, animal and insect species are facing the threat of extinction, conservation efforts are needed to protect such obscure plant and insect species, the extinction of which may lead to ultimate unsustainability of our agricultural production system. Insects the most evolved invertebrates on earth represented 6.44 per cent in India of which 30.34 per cent belong to endemic species (1). Gujarat has a rich biodiversity owing to its geographic and climatic variations and many endangered species and species on the verge of extinction are found to reside in Gujarat. Grasshoppers have been always of great interest to man and ecologist because of its direct competition with man and his domesticated animals for food and fodder. They are perhaps the most conspicuous of all insect pests and are abundant insects of agriculture field, dry grassland desert etc. and their high diversity, functional importance, sensitivity to disturbance and ease of sampling make them potentially useful bioindicators for land management. Accoding to Roonwal (2) and Parihar (3) many of the grasshopper species are continuously adjusting to changing man made natural ecological situations and several species like Hieroglyphus nigrorepletus have undergone evolutionary adoption to fit in the areas of some uncertain habitat like Rajasthan desert. Jhala and Sisodiya (4) reported heavy damage caused by rice grasshopper, Hieroglyphus nigrorepletus to cereals in Gujarat. Muralidharan *et al.*, (5) reported the crop losses due to this insect to the tune of 500-9000 kg/ha in fodder sorghum in north Gujarat. Published information is lacking regarding the diversity of grasshopper fauna of this region. Hence, present study on grasshoppers has been taken up with an objective to prepare an inventory of grasshopper fauna and its taxonomic composition in different ecosystems of north Gujarat. The study will also help to assess the biodiversity of grasshopper fauna of the region.

Material and methods

Roving survey was undertaken during 2002 to 2004 for collecting grasshopper species to ascertain biodiversity in three different ecosystems viz. agro, forest nad grassland (51 sites (Fig. 1), 42 agricultural fields, 6 forest lands and 3 grasslands). Sampling was done by catch per unit time method which involoved intensive searching entire ground level vegetation and hand picking from the vegetation after locating them during morning hours between 9 a.m. to 11 a.m as described by Sanjayan *et al.*,, (6). Preliminary identification of the collected specimens were carried out using pertinent literature and later confirmed with experts from G.S. Gill Research Institute, Gurunanak College, Vellacherry, Chennai and Department of Entomology, University of Agricultural Sciences, Dharwad (Karnataka). The unidentified, morphologically similar species were separated out and referred to as Recognizable Taxonomic Units (RTU) as per Gadagkar *et al.* (8).

Results and discussion

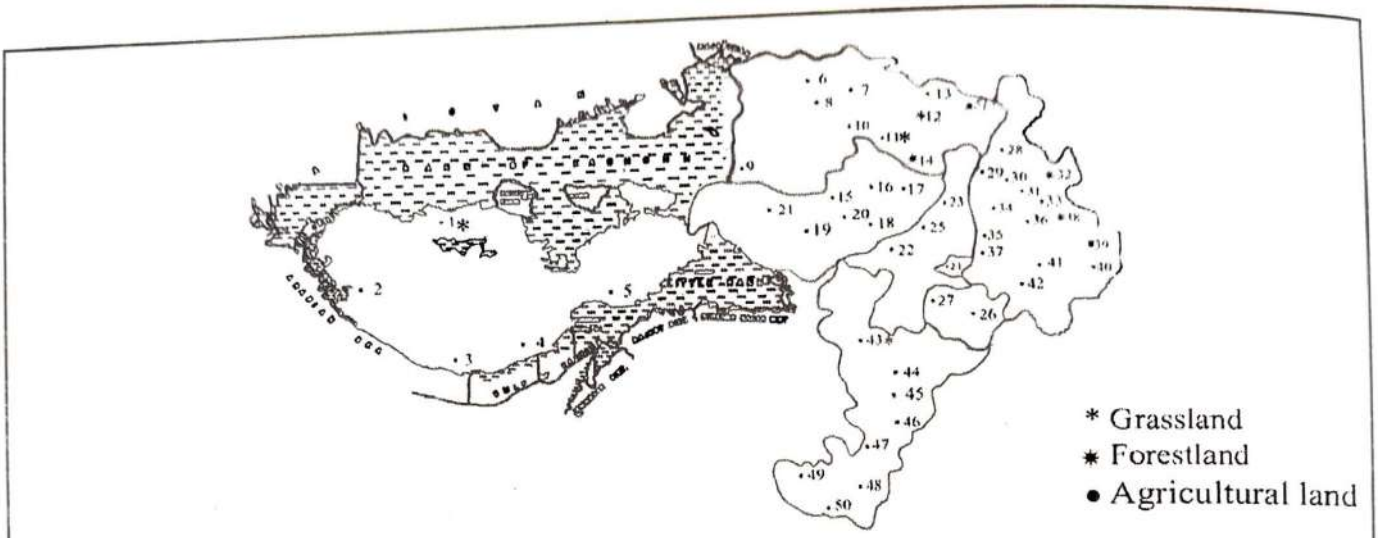
The study have resulted in recording a total of 51 species of grasshoppers belonging to three families viz. Acrididae, Pyrgomorphidae and Tettigoniidae, which is given in table 1 along with the taxonomic position. The results indicated that among the different groups, Acrididae was represented by maximum number of species (36), followed by Tettigoniidae (12) and Pyrgomorphidae (3). The members of Acrididae was distributed among ten subfamilies (Fig.2) in which Oedipodinae represented maximum number of 13 species followed by Acridinae (7), Eyprepocneminae (4), Gomphocerinae and Hemiacridinae (3 each) and Oxyinae (2). The remaining subfamilies viz., Calliptaminae, Catantopinae, Cyrtacanthacridinae and Truxalinae were represented by only one species each. The family Tettigoniidae represented by five subfamilies, two RTUs and one species, whose taxonomic

Table 1. List of grasshopper species collected from different ecosystems of north Gujarat.

Sr. No.	Name of species	Sub-family	Agro ecosystem	Forest ecosystem	Grassland ecosystem
[I]	**Super family : Acridoidea**				
	(a) Family Acrididae				
1.	*Acrida exaltata* (Walker)	Acridinae	+	-	+
2.	*Acrida lugubris* (Burr)	Acridinae	+	-	+
3.	*Phlaeoba infumata* (Brann)	Acridinae	+	-	-
4.	*Phlaeoba panteli* (Bolivar)	Acridinae	+	-	+
5.	*Phlaeoba cinctalis*	Acridinae	+	+	+
6.	*Gelastorhinus semipictus* (Walker)	Acridinae	+	+	+
7.	*Ceracris nigricornis* (Walker)	Acridinae	-	-	+
8.	*Acorypha glaucopsis* (Walker)	Calliptaminae	-	+	-
9.	*Diabolocatantops pinguis* (Dirsh & Uvarov)	Catantopinae	+	+	-
10.	*Cyrtacanthacris tatarica tatarica* (Linnaeus)	Cyrtacanthacridnae	+	-	-
11.	*Heteracris pulchra* (I. Bolivar	Eyprepocneminae	+	+	+
12.	*Heteracris elegans* (Walker)	Eyprepocneminae	-	+	-
13.	*Heteracris robusta* (Serville)	Eyprepocneminae	-	+	-
14.	*Tylotropidius varicornis* (Walker)	Eyprepocneminae	-	+	-
15.	*Aulacobothrus luteipes* (Walker)	Gomphocerinae	-	+	-
16.	*Aulacobothrus sp.*	Gomphocerinae	-	+	-
17.	*Aulacobothrus sp.*	Gomphocerinae	-	+	-
18.	*Hieroglyphus nigrorepletus* (I.Bolivar)	Hemiacridinae	+	+	+

19.	*Parahieroglyphus bilineatus* (I.Bolivar)	Hemiacridinae	-	+	-
20.	*Spathosternum prasiniferum* (Walker)	Hemiacridinae	+	-	+
21.	*Acrotylus humbertianus* (Saussure)	Oedipodinae	+	-	-
22.	*Aiolopus thalassinus tamulus* (Fabricius)	Oedipodinae	+	+	-
23.	*Aiolopus thalassinus* (Fabricius)	Oedipodinae	+	-	-
24.	*Oedaleus abruptus*	Oedipodinae	-	+	-
25.	*Oedaleus sp.*	Oedipodinae	-	-	+
26.	*Acrotylus sp.*	Oedipodinae	-	-	+
27.	*Acrotylus sp.*	Oedipodinae	-	-	+
28.	*Spingonotus savignyi* (Saussure)	Oedipodinae	-	-	+
29.	*Quiroguesia blanchardiana* (Saussure)	Oedipodinae	-	+	+
30.	*Trilophidia annulata* (Thunberg)	Oedipodinae	+	-	-
31.	*Dnopherula sp.* (Karny)	Oedipodinae	-	-	+
32.	*Locusta migratoria* (Linnaeus)	Oedipodinae	+	-	+
33.	*Acorypha insignis* (Thunberg)	Oedipodinae	-	+	+
34.	*Oxya fuscovittata* (Marschall)	Oxyinae	+	-	-
35.	*Oxya hyla hyla* (Serville)	Oxyinae	+	-	+
36.	*Truxalis indica* (I.Bolivar)	Truxalinae	-	-	+
	(b) Family : Pyrgomorphidae				
37.	*Atractomorpha crenulata*		+	-	+
38.	*Chrotogonus oxypterus*		+	-	+
39.	*Poekilocerus pictus*		+	+	+
[II]	**Super family : Tettigonioidea**				
	(a) Family : Tettigoniidae				
40.	*Conocephalus maculata* (Le Guillou)	Conocephalinae	+	+	+
41.	*Euconocephalus incertus* (Walker)	Conocephalinae	+	-	-
42.	*Mecopoda elongata* (Linnaeus)	Mecopodinae	-	+	-
43.	*Mecopoda sp.*	Mecopodinae	-	+	-
44.	*Elimaea* (Orthelimaea) *securigera* (Brunner)	Phaneropterinae	+	+	-
45.	*Trigonocorypha unicolor* (Stall)	Phaneropterinae	+	+	-
46.	*Sathrophyllia fuliginosa* (Stall)	Pseudophyllinae	-	+	-
47.	*Sathrophyllia rugosa* (Stall)	Pseudophyllinae	-	+	-
48.	*Hexacentrus annulicermis*	Listrocelidinae	-	-	+
49.	Recognizable Taxonomic Unit (RTU-1)		-	+	-
50.	Recognizable Taxonomic Unit (RTU-2)		-	-	+
51.	Schizodactylus monstrosus		+	-	-
		Total	26	26	25

+ Presence - Absence



* 1.Dhordo
2.Naliya
3.Mandvi
4.Mundra
5.Anjar
6.Sardarkrushinagar
7.Palanpur
8.Khadosan
9.Suigam
10.Jagana
* 11.Mervada
* 12.Danta
13.Ratanpur
*14.Amba ghata
15.Patan
16.Sidhpur
17.Chandravati
18.Modera
19.Dathakarodi
20.Sonal
21.Radhanpur
22.Nardipur
23.Vijapur
24.Itadara
25.Jagudan
26.Dehgam
27.Vavol
28.Khedbrahama
29.Daroi
30.Vadali
31.Choriwad
* 32.Vijayanagar
33.Bhiloda
34.Idar
35.Himmatnagar
36.Navanagar kampa
37.Monanva
*38.Vireshwar
*39.Shyamalaji
40.Hadiol
41.Modasa
42.Shinol
* 43.Charodi
44.Arnej
45.Lothal
46.Haripura
47.Raika
48.Khadol
49.Dhandhuka
50.Rojka
*51.Ambaji

Fig. 1 Map showing fields visited during 2002-2004 for survey of grasshopper fauna

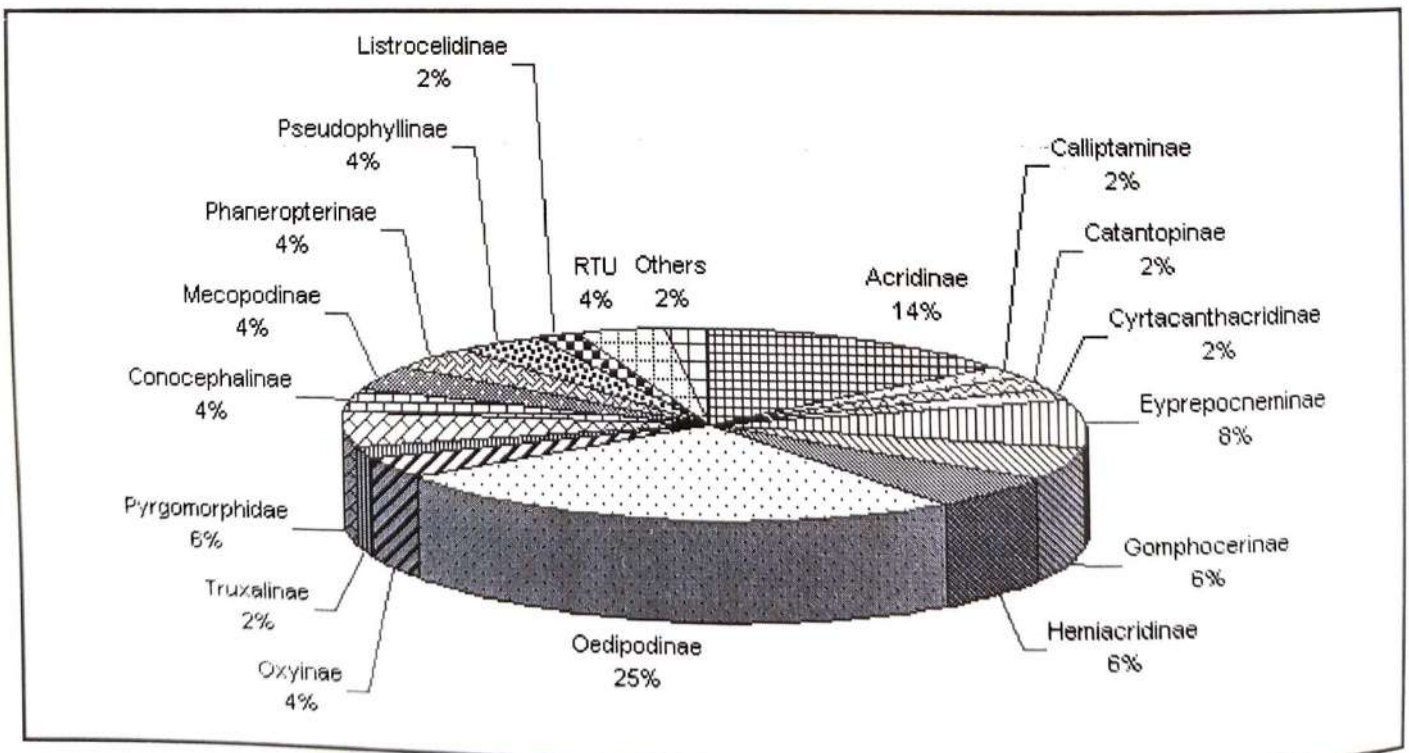


Fig. 2 Composition of different subfamilies in the study area of north Gujarat

position is not clear. Among the subfamilies, Conocephalinae, Mecopodinae, Phaneropterinae and Pseudophyllinae were represented by two species each (4 %) and Listrocelidinae was represented by only one species. The family Pyrgomorphidae was represented by three species. The further classification up to subfamily level was not available. The species composition in different ecosystems are given in table 1 and fig. 2 to 5. The total number of species encountered during the survey was maximum in agroecosystem and forest ecosystem (26 each) followed by grassland ecosystem (25). There was a great variation among the taxonomic groups present in different habitats. The family Acrididae was represented maximum in grassland (19 species) followed by agroecosystem and forest ecosystem representing 18 and 17 species respectively. The maximum number of species representing Tettigoniidae was observed in forest ecosystem (8) followed by agroecosystem (5), whereas, the grassland ecosystem contained the least number of tettigoniid species (3). The representation of Pyrgomorphidae was maximum in agroecosystem and grassland ecosystem (3 species each), whereas forest ecosystem contained only one species. Among the subfamilies, Acridinae (24 %) and Oedipodinae (21 %) were the richest taxonomic group, representing six and five species respectively in agroecosystem (Fig.3), which also contained all the three species of Pyrgomorphidae. Among Acrididae, the subfamilies, Calliptaminae, Gomphocerinae and Truxalinae and from Tettigoniidae, four subfamilies viz., Mecopodinae, Pseudophyllinae and Listrocelidinae were not observed in agroecosystem. The major group of grasshoppers in forest ecosystem belonged to Eyprepocneminae and Oedipodinae representing four species each followed by Gomphocerinae and Hemacridinae containing three and two species respectively (Fig.4). The Acridinae represented 2 species and Calliptaminae and Catantopinae represented only one species each, whereas no representation of subfamilies viz., Cyrtacanthacridinae, Oxyinae and Truxalinae were observed in forest ecosystem. Among the subfamilies of Tettigoniidae, forest ecosystem supported two species each of Mecopodinae, Phaneropterinae and Pseudophyllinae, whereas, members of subfamily Listrocelidinae was not encountered in this area. Pyrgomorphidae was represented by only one species in forest ecosystem. The subfamily, Oedipodinae dominated in grassland ecosystem contributing 32 per cent, represented by 8 species followed by Acridinae 24 per cent represented by 6 species (Fig.5). The representation of Pyrgomorphidae was 12 per cent with three species. Hemiacridinae was represented by two species where as Eyprepocneminae, Oxyinae and Truxalinae represented by only one species each, however species belong to four subfamilies viz., Calliptaminae, Catantopinae, Cyrtacanthacridinae and Gomphocerinae did not colonize in grassland ecosystem. The representation of Tettigoniidae was also poor (12 %) in grassland ecosystem as only one species each of the subfamilies Conocephalinae and Listrocelidinae could observe during survey. Thus, it

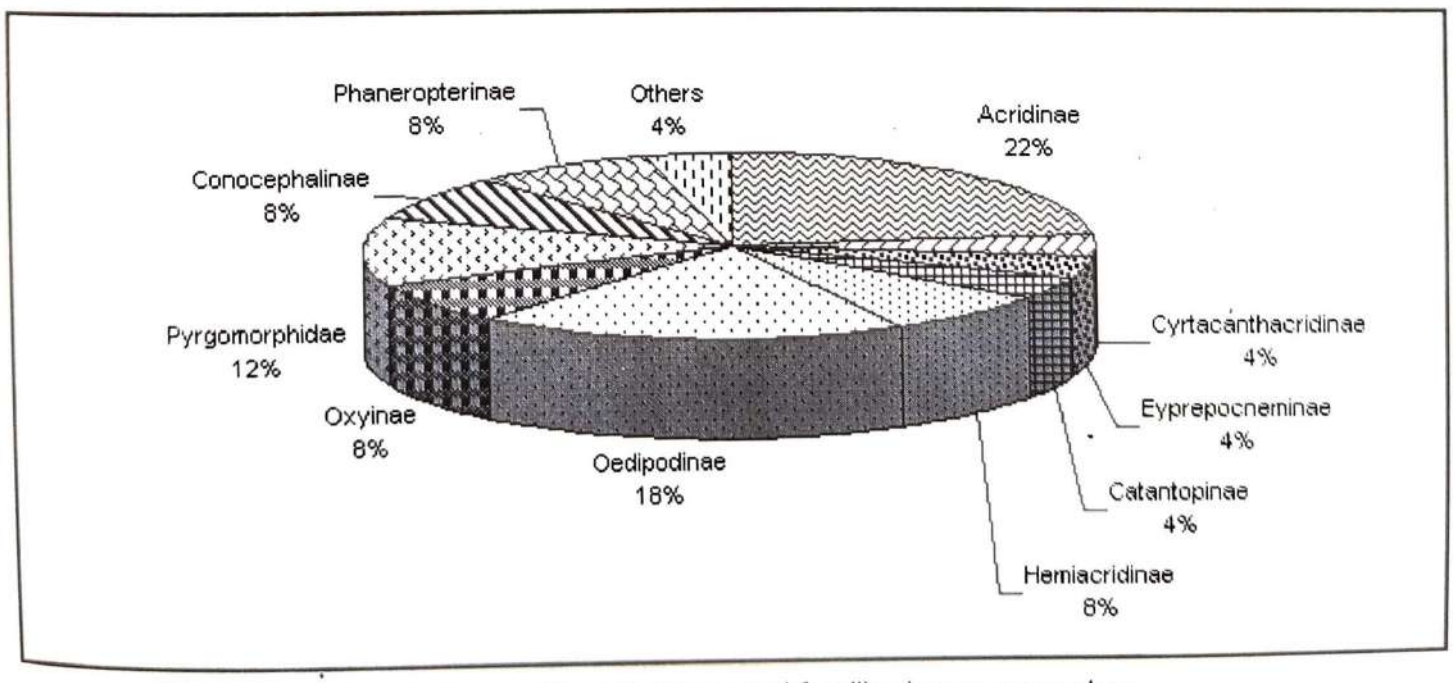


Fig. 3 Composition of different subfamilies in agroecosystem

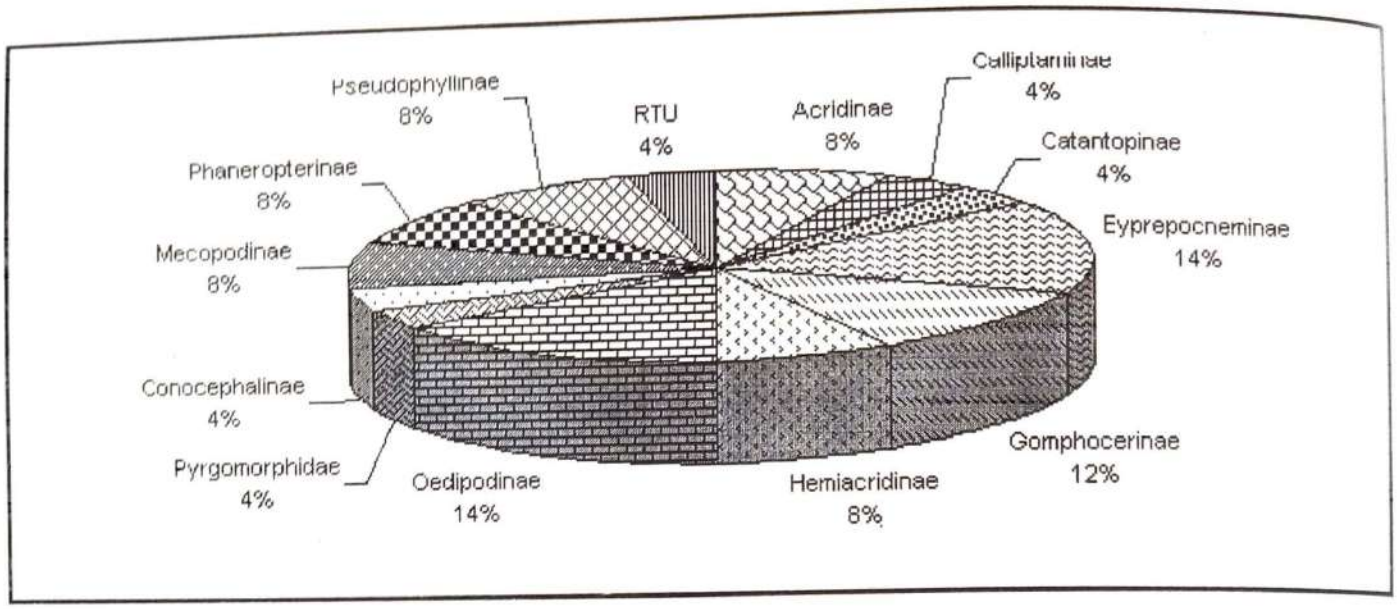


Fig. 4 Composition of subfamilies in forest ecosystem

can be inferred that the species composition differed greatly according to habitats and Acridids was the most predominant grasshopper in the region followed by Tettigoniids. Among acridids, the members of Oedipodinae and Acridinae dominated in the study area. Acridinae and Oedipodinae were the important representative of agro and grassland ecosystems, where as Eyprepocneminae and Oedipodinae formed the major group in forest ecosystem.

No published information is available in the form of inventory to support the present status of grasshopper species of Gujarat, hence, the list of identified grasshoppers mentioned here form the first report from the Gujarat except for H. nigrorepletus and P. pictus which was earlier reported by Bhatia and Ahluvalia (9) and Parihar (10). Many research workers have reported varying number of grasshopper species belonging to different subfamilies from various corners of India. Mahto and Bhanotar (11) reported 19 subfamilies of acridids, representing 52 species and 32 genera from Delhi region. Parihar (12) revised the list of grasshopper fauna of Rajasthan state, reporting 45 species representing nine subfamilies indicating dominance of Oedipodinae (representing 12 species) in the desert region of

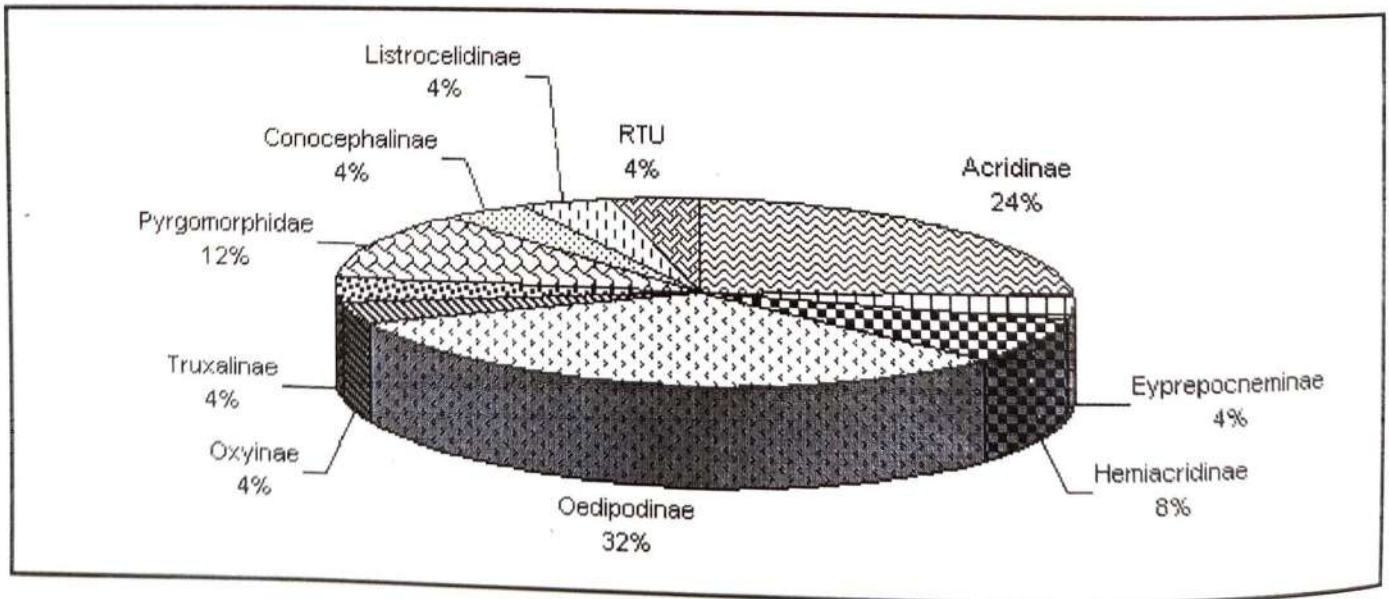


Fig. 5 Composition of different subfamilies in grassland ecosystem

Rajasthan, adjoining to north Gujarat. Vastrad *et al.*, (13) reported 50 species belonging to 42 genera, two families and 12 subfamilies of acridids from Dharwad, Karnataka. More recently Muralirangan *et al.*, (14) reported 39 species of Acrididae, six species of Pyrgomorphidae and 26 species of Tettigoniidae belonging to six subfamilies from different habitats of Tamilnadu. Hence, it is very clear that the existence of species vary greatly in different geographical region and ecosystem.

Acknowledgements

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Influence of Imidacloprid as seed treatment on natural enemies of insect pests infesting Bt. Cotton

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Abstract

A field experiment was conducted at Anand in Gujarat State, India, during 2005-06 and 2006-07 to study the influence of Imidaclorpid as seed treatment (10 g./ kg seed) on arthropod natural enemies and their prey (hosts) in Bt. cotton. Non-Bt. cotton viz. G. Cot. H.8 and G. Cot. H.10 were used as local check for comparison. Results revealed that significantly minimum population of aphids, leaf hoppers and whitefly was found in the treatment of Bt. cotton grown with Imidaclorpid treated seeds. Similarly, Bt. cotton without seed treatment was also found to be promising treatment by exhibiting less number of sucking pests as compared to the local non-Bt. cultivars. Incidence of Earias spp. on buds and green bolls was also reduced significantly in plots of Bt. cotton with Imidaclorpid treatment over the plots with Bt. cotton without imidaclorpid treatment. However, both the Bt. treatments under study were at par and exhibited more or less same level of locules damaged by spotted bollworm and pink bollworm. On the other hand, non-Bt. cultivars registered significantly higher incidence of bollworms. Results also revealed that Bt. cotton raised either with or without seed treatment of imidaclorpid enhanced the population of major natural enemies such as *Chrysoperla carnea* (Stephens), *Cheilomenes sexmaculata* (Fab.), *Geocoris ochropterus* (F.) and *Paederus fuscipes* (Curtis). However, parasitism rate due to *Rogas aligarhensis* (Quadri) on larvae of Earias and *Trichogramma chilonis* (Ishii) on bollworm eggs was found to be low in Bt. cotton as compared to non-Bt. varieties tested. Reduction in pest population and enhancement of natural enemies in Bt. cotton with imidaclorpid seed treatment resulted in increase in seed cotton yield. Amongst the two non-Bt. cultivars evaluated, G.Cot.H.10 performed better by registering low incidence of insect pests and producing higher yield over G.Cot.H.8.

Key words: Imidacloprid, seed treatment, insect, cotton.

Introduction

In recent era, the approach of seed treatment in various field crops has been routinely adopted as it reduces the adverse effects on beneficial fauna and also lowers the pesticidal load in the environment beside protecting the crop from pest infestation. With the invention of neonicotinoids - a novel group of modern insecticides heralded a new chapter in insect pest management programme. Imidaclorpid and thiamethoxam of this group used as seed treatments have shown spectacular results especially in cotton crop and solved the problem of early sucking pests. Simultaneously, the development of transgenic Bt cotton provided relief from bollworms. Various workers in India and abroad have evaluated separately the performance of Bt cotton and the effect of insecticidal treatment against insect pests, but very scanty information is available on their combined effect in Bt cotton. Present study on influence of imidaclorpid as a seed treatment on natural enemies of the insect pests attacking Bt cotton was planned with this intension. The results obtained are presented here in.

Materials and methods

A field experiment was carried out at Agronomy farm, B. A. College of Agriculture, Anand Agricultural University, Anand, (Gujarat State) during two consecutive Kharif seasons of 2005-06 and 2006-07, to study the influence of insecticidal seed treatment on natural enemies as well as insect pests attacking Bt cotton. For the purpose, a field of 800 sq. m. area

was divided into four equal blocks of 200 sq. m. each. Each block was considered as one treatment. There were four treatments. Treatment T_1 consisted of Bt cotton treated with imidaclorpid (Gaucho) 70 WS @ 10 g./kg seeds while treatment T_2 consisted of Bt cotton without any seed treatment. Two non-Bt cotton cultivars viz. G.Cot. Hybrid-8 and G.Cot. Hybrid-10 without any seed treatment were selected as treatments T_3 and T_4, respectively as local check for comparison. Both Bt and non-Bt cultivars were sown during the first week of July at a spacing of 120 X 60 cm. The crop was raised following all the routine agronomical practices except plant protection.

To assess the impact of insecticidal seed treatment on natural enemies and subsequently their effect on cotton pests, the observations on various parameters were recorded. For the purpose, each block under respective treatment was further divided into five equal sub-plots. Five plants were randomly selected from each sub-plot and tagged for recording the observations at fortnightly interval throughout the crop period. The observations were recorded during the peak activity of natural enemies as well as insect pests.

Population of sucking pests viz. Aphid, *Aphis gossypii* Glov., leafhopper, *Amrasca bigutulla bigutulla Ishida* and whitefly, *Bemesia tabaci* (Gen.) were assessed from three (top, middle and bottom) leaves of the tagged plants. Based on the data recorded, mean population of each individual sucking pests/ 15 leaves was worked out and the data thus obtained were analysed after square root transformation. Mean population of the sucking pests in various treatments under study is presented in Table 1.

The incidence of spotted bollworm, *Earias* spp. was assessed by counting total and damaged buds as well as green bolls on five tagged plants from each sub-plot. Fully opened cotton bolls harvested from five tagged plants from each sub-plot were critically observed for the locule damage by *Earias* and pink bollworm, *Pectinophora gossypiella* Saunders. Based on these observations, per cent incidence of respective bollworm species was worked out and the data obtained were analysed after Arc sin transformation. The data on per cent incidence of cotton bollworms in different treatments are given in Table.2.

To determine the impact of cotton seed treatment on natural enemies, their numbers present on five tagged plants from each sub-plot were recorded. In case of *C. carnea* and *coccinellid*, *C. sexmaculata*, the

Table 1. Effect of insecticidal seed treatment in Bt. cotton on sucking pests of cotton.

Sr. No.	Treatments	Av. No. of sucking pests / 15 leaves								
		Aphid			Leaf hopper			Whitefly		
		05-06	06-07	Pooled	05-06	06-07	Pooled	05-06	06-07	Pooled
T_1	Bt. cotton with seed treatment	3.31* (9.96)	4.45* (18.80)	3.88* (4.05)	2.06* (3.24)	2.17* (3.71)	2.12* (3.49)	1.77* (2.13)	2.01* (3.04)	1.89* (2.57)
T_2	Bt cotton without seed treatment	4.63 (20.44)	5.63 (30.70)	5.13 (25.32)	2.36 (4.57)	2.98 (7.88)	2.67 (6.13)	1.93 (2.72)	2.32 (4.38)	2.12 (3.49)
T_3	Non-Bt cotton G.cot.Hy-8	6.27 (38.31)	7.52 (55.56)	6.90 (46.61)	2.91 (7.47)	3.55 (11.60)	3.23 (9.43)	2.28 (4.20)	2.65 (6.02)	2.46 (5.05)
T_4	Non-Bt cotton G.cot.Hy-10	5.74 (31.95)	7.32 (52.58)	6.53 (41.64)	2.66 (6.08)	3.34 (10.16)	3.00 (8.00)	1.98 (2.93)	2.50 (5.25)	2.24 (4.02)
	S.Em ±	0.09	0.05	0.07	0.04	0.03	0.04	0.03	0.03	0.03
	C.D. at 5%	0.26	0.17	0.21	0.14	0.09	0.11	0.10	0.11	0.10
	C.V.(%)	9.29	4.73	6.92	9.71	5.40	7.50	9.12	7.84	8.42

* $\sqrt{X+1}$ transformed values. Figures in parenthesis are retransformed values

Table 2. Effect of insecticidal seed treatment in Bt cotton on bollworm incidence.

Treatments	Damage (%) by *E. vittella* on									Damage (%) by P. *gossypiella* on locules		
	Buds			Green bolls			Locules					
	05-06	06-07	Pooled	05-06	06-07	Pooled	05-06	06-07	Pooled	05-06	06-07	Pooled
T_1 Bt cotton with seed treatment	3.75* (0.43)	6.05* (1.11)	4.90* (0.73)	3.67* (0.41)	7.63* (1.76)	5.65* (0.97)	5.19* (0.82)	5.22* (0.83)	5.20* (0.82)	5.11* (0.79)	5.28* (0.85)	5.20* (0.82)
T_2 Bt cotton without seed treatment	4.76 (0.69)	8.44 (2.15)	6.60 (1.32)	4.58 (0.64)	10.69 (3.44)	7.64 (1.77)	6.11 (1.13)	6.23 (1.18)	6.17 (1.16)	6.19 (1.16)	6.27 (1.16)	6.23 (1.18)
T_3 Non-Bt cotton G.cot. Hy-8	15.34 (7.00)	15.83 (7.44)	15.59 (7.22)	20.92 (12.75)	18.03 (9.58)	19.47 (11.11)	19.91 (11.60)	20.51 (12.28)	20.21 (11.93)	28.93 (23.40)	27.81 (21.77)	27.83 (21.79)
T_4 Non-Bt cotton G.cot. Hy-10	13.99 (5.84)	14.25 (6.06)	14.12 (5.95)	19.67 (11.33)	16.06 (7.65)	17.86 (9.41)	19.12 (10.73)	18.95 (10.55)	19.03 (10.63)	27.84 (21.81)	27.10 (20.75)	28.01 (22.05)
S.Em ±	0.15	0.27	0.21	0.26	0.54	0.42	0.32	0.36	0.27	0.38	0.64	0.43
C.D. at 5%	0.45	0.82	0.63	0.81	1.65	1.23	0.97	1.07	0.77	1.13	1.91	1.26
C.V.(%)	8.45	13.05	11.39	11.72	22.37	18.23	5.71	6.26	6.00	4.93	8.58	6.96

* Arc sin transformed values. Figures in parenthesis are retransformed values

Table 3. Effect of insecticidal seed treatment in Bt cotton on natural enemies.

Treatments	Mean no. of bioagents/ 25plants																	
	C. carnea			*C.sexmaculata*			*Geocoris sp.*			*Staphylinids*			*R. aligarhensis*			Parasitism (%) due to *T. chilonis*		
	05-06	06-07	Pooled	05-06	06-07	Pooled	05-06	06-07	Pooled	05-06	06-07	Pooled	05-06	06-07	Pooled	05-06	06-07	Pooled
T_1 Bt cotton with seed treatment	66.67	76.67	71.67	58.67	65.83	62.25	22.00	27.83	24.92	5.83	8.00	6.92	2.17	2.17	2.17	14.53	15.39	14.96
T_2 Bt cotton without seed treatment	59.50	73.17	66.34	53.33	60.00	56.67	18.67	24.33	21.50	5.50	6.50	6.00	1.17	1.50	1.34	14.13	14.46	14.30
T_3 Non-Bt cotton G.cot.Hy-8	46.17	49.17	47.67	38.83	43.00	40.92	8.67	9.00	8.84	3.50	4.33	3.92	3.00	2.50	2.75	19.59	20.56	20.08
T_4 Non-Bt cotton G.cot.Hy-10	52.33	53.50	52.92	44.83	46.67	45.75	13.17	11.17	12.17	5.00	5.00	5.00	3.33	3.50	3.42	23.01	22.95	22.98

number of eggs, larvae, pupae and adults present on plants were recorded, whereas nymphs and adults of *G. ochropterous*, adults of Staphylinid, *P. fuscipes* and mummies of *R. aligarhensis* were counted. The collective numbers in each case are mentioned in Table 3. Eggs of *Earias* spp. collected from respective treatments were brought in the laboratory and observed for parasitism by *Trichogramma* and the per cent parasitism was worked out. The data on mean population of various biocontrol agents and the rate of parasitism are mentioned in Table 3.

Seed cotton yield harvested from tagged plants was recorded treatment wise during each picking and based on this data yield in kg/ha was calculated. The data on yield of seed cotton in various treatments are presented in Table 4.

Results and discussion

Results (Table 1) revealed that the population of sucking pests differed significantly in all the treatments. Significantly least population of *A. gossypii* (4.05/ 15 leaves), *A. biguttula biguttula* (3.49/15 leaves) and *B. tabaci* (2.57/ 15 leaves) was found in Bt cotton (sown with seeds treated with imidaclorpid @ 10g/ kg.). Similarly, Bt. cotton without seed treatment was also found promising by exhibiting less number of sucking pests as compared to the local non-Bt cultivars evaluated as check. Reduction in sucking pest population in cotton crop following imidaclorpid seed treatment recorded in the present study is in agreement with earlier reports of Scarpellini and Nakamura (1), Satpute *et al.*, (2), Thirasack (3) and Rathod *et al.*, (4). Both the non-Bt cultivars registered significantly higher population of sucking pests as compared to that in Bt cultivars. G.Cot.H.8 exhibited significantly higher population of the sucking pests amongst the non-Bt cultivars tested. More or less similar trend was noticed in case of damage caused by *Earias* spp. on buds and green bolls.

Among the various treatments, significantly minimum incidence of *Earias* spp. on buds (0.73 %) and green bolls (0.97%) was recorded in Bt cotton with seed treatment followed by Bt cotton without seed treatment, which registered 1.32 and 1.77% incidence on buds and green bolls, respectively (Table 2). On the other hand, non-Bt. cultivars exhibited significantly higher damage of *Earias* spp. on buds (5.95%) and green bolls (9.41%). As far as locule damage was concerned, both the treatments of Bt cotton (T_1 and T_2) were at par and exhibited more or less similar level of incidence. However, relatively low incidence of both the borers was recorded from Bt cotton with seed treatment. Suppression of spotted and pink bollworms in Bt cotton due to imidaclorpid seed treatment can be attributed to its prolonged residual action. Thirasack (3) also opined the effectiveness of imidaclorpid due to its longest residual effect.

Population of various natural enemies recorded in different treatments under study shows remarkable variation in their numbers (Table 3). Bt. cotton with and without seed treatment of imidaclorpid registered relatively greater number of C. carnea, C. sexmaculata, G. ochropterous and P. fusipes adults over non-Bt cultivars. These results corroborate with the earlier observations of Katole and Patil (5), Vadodaria *et al.*, (6) and Satpute *et al.*, (7) who recorded higher population of ladybird beetles and Chrysoperla in

Table 4. Yield of seed cotton in different treatments under study.

Treatments	Yield (kg/ha)		
	05-06	06-07	Pooled
T_1 - Bt cotton with seed treatment	2486	2544	2515
T_2 - Bt cotton without seed treatment	2311	2386	2349
T_3 - Non-Bt cotton G.cot.Hy-8	1622	1683	1653
T_4 - Non-Bt cotton G.cot.Hy-10	1856	1903	1879
S.Em ±	97.28	88.76	75.25
C.D. at 5%	273.78	249.79	211.79
C.V.(%)	23.51	20.84	22.18

cotton crop with imidaclorpid treated seeds. According to Satpute *et al.*, (7), seed treatment was not only safe to *C. sexmaculata* and *C. carnea* on cotton but also attracted the females for oviposition. Vadodaria *et al.*, (6) also recorded higher population of these predators in thiomethoxam treated cotton plots as compared to that in imidaclorpid treated cotton plots. According to them, imidaclorpid seed treatment enhanced the growth of cotton plants which encouraged the natural enemy population. The seed treatment with neonicotinoid chemical such as imidaclorpid or thiomethoxam enhanced the crop growth which may be attributed to attract the more number of predators for shelter and seeking their preys. however, in contrast to above, lower rate of parasitism due to *R. aligarhensis* on *Earias* spp. and T. chilonis on bollworm eggs was exhibited in both the treatments of Bt cotton than in non-Bt cotton and was minimum in Bt cotton without seed treatment. The lower rate of parasitism in Bt. cotton can be attributed to the poor availability of eggs and larval stages of the hosts for further multiplication of parasitoids.

Data on seed cotton yield harvested from different treatments (Table 4) revealed that both the treatments T_1 and T_2 produced significantly higher seed cotton yield (2311 to 2544 kg/ha) over non-Bt. cotton cultivars T_3 and T_4 (1622 to 1903 kg/ha). Though, there was no significant difference in yield increase due to seed treatment in Bt cotton over Bt. cotton without seed treatment, the former treatment produced nearly 7 % higher yield than the latter. Increase in seed cotton yield following the seed treatment with imidaclorpid reported in the present study is in agreement with the earlier reports of Mote *et al.*, (8), Dandale *et al.*, (9), Vadodaria *et al.*, (6) and Rathod *et al.*, (4). There was no significant difference in the seed cotton yield harvested from both the non-Bt cotton cultivars during both the years of experimentation, however, pooled results show significantly higher yield (1879 kg/ha) in G.Cot.H.10 over G.Cot.H.8 (1653 kg/ha).

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Effect of conventional and microwave heating on the quality characteristics of vegetable oils

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Abstract

Refined groundnut, raw groundnut, refined mustard and raw mustard oils were heated by two heating methods viz., conventional heating and microwave heating. The oils were heated at a temperature 200 ± 1°C for up to 15 hours in batches of three hours in conventional heating and oils were heated at a high power setting for up to 150 minutes in batches of 30 minutes in microwave heating. The experiment was conducted in a factorial completely randomized design with three independent variables; source of oil, types of refining and heating methods, with three replications. The dependent variables were peroxide value, acid value, colour value, viscosity and sensory score of the oil. The oil samples were analysed for fatty acid profile before and after 15 hours of conventional heating and 150 minutes of microwave heating. Fatty acid analysis showed that heating constantly altered the structure and composition of oil. Severe damage occurred to PUFA at high temperature heating. For all the four oil samples, heating by microwaves resulted in lower destruction of PUFA than conventional heating.

Key words: Groundnut, mustard, fatty acid

Introduction

Vegetable oils are water insoluble substances of plant origin, which consist predominantly of glycerol esters of fatty acids or triglycerides. Fatty acids are major constituents of cell membranes. They are broadly divided into two major groups, *viz.*, saturated and unsaturated fatty acids. Oils and fats that have been heated to very high temperature for long period of time may under go chemical and physical changes. Continuous heating of fat and oil for over eight hours results in thermal oxidation. The oxidation of oils and fats gives rise to rancidity or off flavour. Heating of fat or oil results in formation of compounds with anti-nutritional properties. These compounds formed may be enzyme inhibitors, vitamin destroyers, lipid oxidation products, gastro intestinal irritants or potential mutagens. Heating of fat or oil also results in decrease in moisture, iodine value and refractive index.

In India, the rural poor and urban high income groups on an average consume < 10 g (3-20 g) and 30-50 g/ day/person fat, respectively. Since, chronic energy deficiency is a major nutritional problem in low-income groups, increasing visible fat consumption may redeem this condition. In view of the higher prevalence of obesity, cardiovascular disease (CVD) and diabetes in urban rich, they may be advised to decrease fat intake according to the level of physical activity. While careful microwave heating of vegetable oils can provide nutritional and economic advantages and a domestic microwave oven would serve as a simple and quick means of preparing a variety of culinary items including food products rich in fats, the oxidative stability of microwave heated foods are under question. Microwave heated products are subjected to molecular friction and excitation and can result in formation of free radicals and thereby increase hydroperoxide formation, which indirectly could lead to increase in development of rancidity during storage and loss of natural antioxidants in oils during microwave irradiation. Since, most of the nutritionally important fatty acids in oils or fats are highly unsaturated, it has become necessary to elucidate the effect of such irradiation on the structural stability of there acids also.

Looking into the above, it is proposed to carry out an investigation on the effect of conventional and microwave heating on the quality characteristics and fatty acid profile of vegetable oils.

Materials and methods

The present investigation was taken up with a view to assess the effect of conventional and microwave heating on the quality characteristics of vegetable oils.

The experimental materials consisted of two vegetables oils *viz.*, (i) Refined and raw groundnut oil and (ii) Refined and raw mustard oil. These two vegetable oils were obtained directly from oil mill in sealed tin containers.

In order to obtain uniform heat transfer in oil and constant surface area to volume ratio during the entire experiment, preliminary trials were conducted to find the normally encountered ratio in household frying. The ratio ranged from 0.420 to 0.446 cm^2/ml. So all the samples in the present study were heated in uniform glass beakers of 500 ml capacity. The volume of sample was fixed at 140 ml to obtain a constant surface area to volume ratio of 0.434 cm^2/ml.

One hundred forty ml of samples of each oil in 500 ml glass beaker was heated in a constant temperature hot air oven at 200° ± 1°C. Samples for analysis were drawn at 3 hours intervals. The heating was continued upto 15 hours.

One hundred forty ml of samples of each oil in 500 ml glass beaker was subjected to microwave heating in a household microwave oven (Model MG-608 AP, LG Electronics, New Delhi) at 900 W power setting (2450 MHz). Samples were drawn for analysis at 30 min. intervals. The heating was continued upto 150 min.

To assess the structural changes in the oils before and after heating, samples were taken for fatty acid analysis by gas chromatography technique. The experiment was conducted on GC model Auto system XL GC (PERKIN ELMER, USA).

Four samples of the fresh oil before heating, four samples of the oils after conventional heating for 15 hours and four samples of the oils after microwave heating for 2 ½ hours were analysed for fatty acid profile.

The experiment was carried out under the Factorial Completely Randomized Design (F-CRD) repeating each treatment combination three times. The data obtained for each characteristic were subjected to statistical analysis as per the procedure discussed by Snedecor and Cochran (1)

Results and Discussion

The experiment was attempted to know the effect of conventional heating and microwave heating on the quality characteristics of vegetable oils and to elucidate the structural changes due to heating on fatty acids present in the oil samples; for assessing these objectives all the quality parameters of the experimental samples were measured.

Peroxide Value

The data on change in peroxide value of conventionally and microwave heated vegetable oils used in this study are given in Table 1 and 2, respectively.

Table 1. Mean peroxide value (meq O_2/kg) of raw and refined groundnut and mustard oils upon conventional heating at 200 ± 1°C

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	5.79	7.67	6.18	7.87
3	8.50	11.98	11.41	15.16
6	14.12	19.04	18.24	25.09
9	23.07	27.66	26.93	39.26
12	27.70	36.10	31.83	43.83
15	30.85	41.75	35.84	46.75

Table 2. Mean peroxide value (meq O_2/kg) of raw and refined groundnut and mustard oils upon microwave heating at high power setting

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	5.79	7.67	6.17	7.87
30	7.75	11.27	11.98	14.63
60	13.13	18.67	17.72	24.97
90	22.12	27.23	25.75	38.24
120	25.96	33.23	31.02	42.35
150	29.28	38.93	35.04	46.03

The initial peroxide value of raw groundnut and mustard oils were 7.67 and 7.87 meq O_2/kg, respectively and that of refined groundnut and mustard oils were 5.7 and 6.18 meq O_2/kg, respectively. Peroxide value of

raw groundnut oil (7.67 meq O_2/kg) was lower than that of raw mustard oil (7.87 meq O_2/kg) at the beginning of heating. However, the peroxide value of refined groundnut and mustard oils were not significantly different.

Upon 15 hours of conventional heating, the peroxide value of all oils increased. The peroxide value of raw groundnut and mustard oils were 41.75 and 46.75 meq O_2/kg, respectively and that of refined groundnut and mustard oils were 30.85 and 35.85 meq O_2/kg, respectively. Peroxide value of raw groundnut oil (41.75 meq O_2/kg) was lower than that of mustard oil (46.75 meq O_2/kg) after 15 hours of conventional heating. As such the peroxide value of refined groundnut oil (30.85 meq O_2/kg) was lower than that of mustard oil (35.84 meq O_2/kg) after 15 hours of conventional heating.

Upon 150 minutes of microwave heating the peroxide value of all oils increased. The peroxide value of raw groundnut and mustard oils were 38.93 and 46.03 meq O_2/kg, respectively and that of refined groundnut and mustard oils were 29.28 and 35.04 meq O_2/kg, respectively. Peroxide value of raw groundnut oil (38.93 meq O_2/kg) was lower than that of raw mustard oil (46.03 meq O_2/kg) after 150 minutes of microwave heating. As such the peroxide value of refined groundnut oil (29.28 meq O_2/kg) was lower than that of refined mustard oil (38.93 meq O_2/kg) after 150 minutes of microwave heating.

It can be observed that highest increase in peroxide value was observed for raw mustard oil at any point of time of heating. The lowest value was observed for refined groundnut oil, followed by refined mustard, raw groundnut and lastly raw mustard oil.

It was also observed (Table 4.1.1 and 4.1.2) that for all the four oils samples heating at 200 ± 1°C for 15 hours by conventional heat caused higher peroxide value in the oils than microwave heating at high power level for 150 minutes.

Analysis of variance of data showed significant ($P < 0.05$) influence of time of heating, source of oil (Groundnut or Mustard), types of refining (Refined or raw) and method of heating (Conventional or microwave) on the peroxide value of oils. The interaction effects time x source of oil, time x type of refining, source of oil x heating methods and time x source of oil x type of refining were also significant ($P < 0.05$).

The correlation coefficients for peroxide value with other quality characteristics of the oils are given in the Table 4.7. It can be seen from the correlation analysis that peroxide value showed significant ($P < 0.01$) positive correlation with acid value, colour value and viscosity of the oil and significant ($P < 0.01$) negative correlation with sensory score of oil.

Increase in the peroxide value of oils on heating was also reported by Kotwal *et al.* (2), Parvatham *et al.* (3) reported increase in the peroxide value of vegetable oils after six hours of heating.

Acid Value

Free fatty acids are normally present in oils due to the hydrolysis of triglycerides by bacterial or enzymatic action and chemical treatment. Light, heat and moisture accelerate the process. This value is the function of the degree of purity, age, oxidation and hydrolysis of oil. The free fatty acid content of oil increases with age.

The data on change in acid value of conventionally and microwave heated vegetable oils used in this study are given in Table 3 and 4, respectively.

The initial acid value of raw groundnut and mustard oils were 0.70 and 0.77 per cent, respectively and that of refined groundnut and mustard oils were 0.49 and 0.56 per cent, respectively. Acid value of raw groundnut oil (0.70 %) was lower than that of mustard oil (0.77 %) at the beginning of heating. As such, the acid value of refined groundnut oil (0.49 %) was lower than that of mustard oil (0.56 %).

Upon 15 hours of conventional heating, the acid value of all oils increased. The acid value of raw groundnut and raw mustard oils were 1.83 and 1.90 per cent, respectively and that of refined groundnut and mustard oils were 1.42 and 1.34 per cent, respectively. Acid values of raw groundnut and raw mustard oils were not significantly different. However, the peroxide value of refined groundnut oil (1.42 %) was higher than that of mustard oil (1.34 %).

Table 3. Mean acid value of raw and refined groundnut and mustard oils upon conventional heating at 200 ± 1°C

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	0.49	0.70	0.56	0.77
3	0.92	1.27	0.85	1.19
6	0.99	1.55	0.99	1.19
9	1.21	1.62	1.13	1.41
12	1.35	1.76	1.20	1.61
15	1.42	1.83	1.34	1.90

Table 4. Mean acid value of raw and refined groundnut and mustard oils upon microwave heating at high power setting

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	0.49	0.70	0.56	0.77
30	0.86	0.91	0.85	1.27
60	0.92	1.20	0.92	1.05
90	1.07	1.41	1.06	1.19
120	1.21	1.55	1.13	1.26
150	1.28	1.62	1.28	1.62

Upon 150 minutes of microwave heating, the acid value of all oils increased. The acid value of raw groundnut and mustard oils were the same (1.62) and that of refined groundnut and mustard oils were also same (1.28 %).

It can be observed that highest increase in acid value was observed for raw mustard oil at any point of time of heating. The lowest value was observed for refined mustard oil, followed by refined groundnut, raw mustard and lastly raw groundnut oil.

It was observed (Table 4.2.1, 4.2.2) that for all the four oils samples, heating at 200° ± 1°C for 15 hours by conventional heat caused higher acid value in the oils than microwave heating at high power level for 150 minutes.

Analysis of variance of data showed significant ($P < 0.05$) influenced of time of heating, types of refining (Refined or raw) and method of heating (conventional or microwave) on the acid value of oils. The interaction effects time x source of oil and type of refining x heating methods were also significant ($P < 0.05$).

The correlation coefficients for acid value with other quality characteristics of the oils are given in Table 4.7. It can be seen from the correlation analysis that acid value showed significant ($P < 0.01$) positive correlation with viscosity and colour value of the oil and significant ($P < 0.01$) negative correlation with sensory score of oil.

Farag *et al.* (4) reported that acid values of heated oils increased with both microwave and conventional heating. Chu and Hsu (5) also reported that oil frying of shallots by microwave heating showed better oil quality, with lower acid value than after frying by gas heating.

Viscosity

The data on change in viscosity of conventionally and microwave heated vegetable oils used in this study are given in Table 5 and 6, respectively.

The initial viscosity of raw groundnut and mustard oils were 17.66 and 20.45 Cp, respectively and that of refined groundnut and mustard oils were 16.49 and 18.45 Cp, respectively. Viscosity of raw groundnut oil (17.66 Cp) was lower than that of raw mustard oil (20.45 Cp) at the beginning of heating. As such, the viscosity of refined groundnut oil (16.49 Cp) was lower than that of refined mustard oil (18.45 Cp).

Table 5. Mean viscosity (Cp) of raw and refined groundnut and mustard oils upon conventional heating at 200 ± 1°C

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	16.49	17.66	18.45	20.45
3	17.68	18.82	20.22	20.72
6	18.40	19.16	21.35	21.96
9	20.00	21.86	23.30	24.08
12	21.46	23.02	23.02	24.37
15	25.01	27.33	27.75	30.36

Table 6. Mean viscosity (Cp) of raw and refined groundnut and mustard oils upon microwave heating at high power setting

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	16.49	17.66	18.45	20.45
30	17.47	18.48	20.72	20.56
60	18.37	18.86	21.15	21.90
90	19.48	20.94	22.65	25.06
120	21.30	22.88	22.93	25.06
150	24.98	26.91	27.28	30.32

Upon heating for 15 hours in conventional heating, the viscosity of all oils increased. The viscosity of raw groundnut and raw mustard oils were 27.33 and 30.36 Cp, respectively and that of refined groundnut and refined mustard oils were 25.01 and 27.75 Cp, respectively. Viscosity of raw groundnut oil (27.33 Cp) was lower than that of raw mustard oil (30.36 Cp) after 15 hours of conventional heating. The acid value of refined groundnut oil (25.01 Cp) was lower than that of refined mustard oil (27.75 Cp) after 15 hours of conventional heating.

Upon 150 minutes of microwave heating, the viscosity of all oils increased. The viscosity of raw groundnut and mustard oils were 26.91 and 30.32 Cp, respectively and that of refined groundnut and mustard oils were 24.98 and 30.32 Cp, respectively. Viscosity of raw groundnut oil (26.91 Cp) was lower than that of raw mustard oil (30.32 Cp) after 15 hours of conventional heating. Similarly, the viscosity of refined groundnut oil (24.98 Cp) was lower than that of refined mustard oil (30.32 Cp) after 150 minutes of microwave heating.

It can be observed that highest increase in viscosity was observed for raw mustard oil at any point of time of heating. The lowest value was observed for refined groundnut oil, followed by raw groundnut, refined mustard and lastly raw mustard oil.

It was also observed (Table 5 & 6) that for all the four oil samples, heating at 200 ± 1°C for 15 hours by conventional heat caused higher viscosity in the oils than microwave hating at high power level for 150 minutes.

Analysis of variance of data showed significant ($P < 0.05$) influence of time of heating, source of oil (Groundnut or Mustard) and types of refining (Refined or raw) on viscosity of oils. The interaction effects time x source of oil, time x type of refining, time x methods of heating, time x 'source of oil x type of refining, time x source of oil x methods of heating, time x type of refining x methods of heating and time x source of oil x type of refining x methods of heating were also significant ($P < 0.05$).

The correlation coefficients for viscosity with other quality characteristics of the oils are given in the Table 11. It can be seen from the correlation analysis that viscosity showed significant ($P < 0.01$) positive correlation with colour of the oil and significant ($P<0.01$) negative correlation with sensory score of oil. Subbulaxmi *et al.* (6) upon reheating and storage of palmolein oil found that the viscosity increased with frying. Zhang *et al.* (7) reported that oxidative stability of soybean oil treated by microwaves was not significantly different from conventionally heated oil.

Colour Value

The colour of cooking oil or frying media has an important bearing as consumer preference of the medium as well as acceptability of the fried product. The natural colour of most vegetable oils is due to the fat soluble plant pigments of the food extracted in the oil like carotenoids. Due to their consumer appeal, these natural pigments in oils are not completely removed during refining. Upon heating, the natural pigments get destroyed and the oil turns dark. The development of dark colour is measured as colour value spectrophotometrically as a quality deterioration parameter.

The data on change in colour value of conventionally and microwave heated vegetable oils used in this study are given in Table 7 and 8, respectively.

Table 7. Mean colour value of raw and refined groundnut and mustard oils upon conventional heating at 200 ± 1°C

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	0.14	0.15	0.13	0.21
3	0.16	0.17	0.21	0.35
6	0.18	0.20	0.24	0.41
9	0.21	0.23	0.29	0.47
12	0.24	0.27	0.35	0.54
15	0.28	0.32	0.39	0.58

Table 8. Mean colour value of raw and refined groundnut and mustard oils upon microwave heating at high power setting

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	0.14	0.15	0.13	0.21
30	0.15	0.16	0.20	0.34
60	0.17	0.19	0.22	0.40
90	0.19	0.21	0.27	0.44
120	0.22	0.25	0.34	0.52
150	0.25	0.30	0.38	0.56

The initial colour value of raw groundnut and mustard oils were 0.15 and 0.21, respectively and that of refined groundnut and refined mustard oils were 0.14 and 0.13, respectively. Colour value of raw groundnut oil (0.15) was lower than the raw mustard oil (0.21) at the beginning of heating.

Upon 15 hours of conventional heating, the colour value of all oils increased. The colour value of raw groundnut and raw mustard oils were 0.32 and 0.58, respectively and that of refined groundnut and mustard oils were 0.28 and 0.38, respectively. Colour value of raw groundnut oil (0.32) was lower than that of raw mustard oil (0.58) after 15 hours of conventional heating. The colour value of refined groundnut oil (0.28) was lower than that of mustard oil (0.32) after 15 hours of conventional heating.

Upon 50 minutes of microwave heating, the colour value of all oils increased. The colour value of raw groundnut and mustard oils were 0.30 and 0.56, respectively and that of refined groundnut and mustard oils were 0.25 and 0.38, respectively. Colour value of raw groundnut oil (0.30) was lower than that of raw mustard oil (0.56) after 150 minutes of microwave heating. As such the colour value of refined groundnut oil (0.25) was lower than that of mustard oil (0.38) after 150 minutes of microwave heating.

It can be observed that highest increase in colour value was observed for raw mustard oil at any point of time of heating. The lowest value was observed for refined groundnut oil, followed by raw groundnut, refined mustard and lastly raw mustard oil.

It was also observed (Table 7 & 8) that for all the four oil samples, heating at 200 ± 1°C for 15 hours by conventional heat caused higher colour value in the oil than microwave heating at high power setting for 150 minutes.

Analysis of variance of data showed significant ($P < 0.05$) influence of time of heating, source of oil (Groundnut or Mustard), type of refining (Refined or raw) and methods of heating (Conventional or microwave) on the colour value of oils. The interaction effects time x source of oil, time x type of refining, time x methods of heating, source of oil x methods of heating and time x source of oil x type of refining were also significant ($P < 0.05$).

The correlation coefficients for colour value with other quality characteristics of the oils are given in the Table 4.7. It can be seen from the correlation analysis that colour value showed significant ($P < 0.01$) negative correlation with sensory score of oil.

Yegammai and Gowri (8) reported that colour of the oils after fifth heating was dark. Kotwal *et al.* (2) also reported increase in oil colour due to increased heating time.

Sensory Score

Composite scoring test designed for ranking and comparing samples of similar products is used in this investigation.

The data on change in sensory score of conventionally and microwave heated vegetable oils used in this study are given in Table 9 and 10, respectively.

Table 9. Mean sensory score of raw and refined groundnut and mustard oils upon conventional heating at 200 ± 1°C

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	92.00	86.33	87.00	79.66
3	90.66	82.66	80.86	73.00
6	85.66	74.00	65.66	62.33
9	82.00	70.00	62.00	57.33
12	76.33	65.33	56.66	47.66
15	72.00	61.00	51.00	42.33

The initial sensory score of raw groundnut and mustard oils were 86.33 and 79.66, respectively and that of refined groundnut and mustard oils were 92.00 and 87.00, respectively and that of refined groundnut and

mustard oils were 92.00 and 87.00, respectively. Sensory score of raw groundnut oil (86.33) was higher than that of raw mustard oil (79.66) at the beginning of heating. As such the sensory score of refined groundnut oil (92) was higher than that of refined mustard oil (87).

Table 10. Mean sensory score of raw and refined groundnut and mustard oils upon microwave heating at high power setting

Heating time (hours)	Groundnut oil		Mustard oil	
	Refined	Raw	Refined	Raw
0	92.00	86.33	87.00	79.66
30	91.66	84.66	82.33	73.66
60	85.33	75.00	67.33	64.33
90	82.33	72.33	62.66	56.33
120	76.66	65.66	57.00	50.00
150	73.66	62.33	52.66	44.33

Upon heating for 15 hours in conventional heating the sensory score of all oils decreased. The sensory score of raw groundnut and raw mustard oils were 61.00 and 42.33, respectively and that of refined groundnut and mustard oils were 72.00 and 51.00, respectively. Sensory score of raw groundnut oil (61) was higher than that of raw mustard oil (42.33) after 15 hours of conventional heating. As such the sensory score of refined groundnut oil (72) was higher than that of refined mustard oil (51).

Upon heating for 150 minutes in microwave heating, the sensory score of all oils decreased. The sensory score of raw groundnut and mustard oils were 86.33 and 79.66, respectively ands that of refined groundnut and mustard oils were 92.00 and 87.00, respectively. Sensory score of raw groundnut oil (86.33) was higher than that of mustard oil (79.66). The sensory score of refined groundnut oil (92) was higher than that of refined mustard oil (87) after 150 minutes of microwave heating.

It can be observed that highest decrease in sensory score was observed for raw mustard oil at any point of time of heating. The highest value was observed for refined groundnut, followed by raw groundnut, refined mustard and lastly raw mustard oil.

It was also observed (Table 9 &10) that for all the four oils samples, heating at 200 ± 1°C for 15 hours by conventional heat caused lower sensory score in the oil than microwave heating at high power level for 150 minutes.

Analysis of variance of data showed significant ($P < 0.05$) influence of time of heating, source of oil (Groundnut and mustard), type of refining (Refined or raw) and methods of heating (Conventional or microwave) on the sensory score of oils. The interaction effects time x source of oil, time x type of refining and time x source of oil x type of refining were also significant ($P < 0.05$).

Olutosin (9) reported that sensory score showed a progressive deterioration on a seven pint scale from bland to very rancid.

Fatty Acid Profile

The fatty acid profile of four samples of refined groundnut, refined mustard, raw groundnut and raw mustard oils before heating, four samples of these oils after 15 hours of conventional heating and four samples of these oils after 150 minutes of microwave heating were analysed by gas chromatography. In the chromatogram different peaks were obtained. The peaks of the component fatty acids of each sample were identified on the basis of retention time and then quantified according to their peak areas. The data so obtained are presented in Table 11 and 12, respectively for conventional and microwave heated vegetable oils. The data on fatty acid profile shows that fresh refined groundnut oil contained saturated fatty acid *viz.*, palmictic acid ($C_{16:0}$) and stearic acid ($C_{18:0}$) of 11.62 and 1.99 per cent, respectively making the total saturated fatty acids at 13.61 per cent. It contained monounsaturated (MUFA *i.e.*, Oleic acid $C_{18:1}$) fatty acid at 58.34 per cent and polyunsaturated fatty acid (PUFA *i.e.*, linoleic acid $C_{18:2}$) at 28.04 per cent making up for the total unsaturated fatty acid content of 86.38 per cent. Refined mustard oil contains saturated fatty acid *viz.*, palmictic acid ($C_{16:0}$) and stearic acid ($C_{18:0}$) and 4.32 and 1.10 per cent, respectively making up for the total saturated fatty acid content of 5.43 per cent. It contained monounsaturated fatty acid *viz.*, oleic acid ($C_{18:1}$) and ecosenoic acid ($C_{20:1}$) of 13.09 and 0.65 per cent, respectively making up for the total monounsaturated fatty acid 13.74 per cent and also contained erucic acid ($C_{22:1}$) of 39.10 per cent. It also contained polyunsaturated fatty acid *viz.*, linoleic acid

Table 11. Correlation coefficients for different quality characteristics of raw and refined groundnut and mustard oils

Characteristics	Peroxide value	Acidvalue	Viscosity	Colour	Sensory score
Peroxide value	1.000				
Acid value	0.860	1.000			
Viscosity	0.904	0.748	1.000		
Colour	0.830	0.613	0.824	1.000	
Sensory score	-0.693	-0.572	-0.686	-0.723	1.000

Legend : All estimates are significant at 1 per cent level.

Table 12. Fatty acid profile of refined groundnut, refined mustard, raw groundnut and raw mustard oils before and after microwave heating at high power setting for 150 minutes

Fatty acids	Retention time	Refined groundnut oil		Raw groundnut oil		Refined mustard oil		Raw mustard oil	
		Before heating	After heating	Before heating	After heating	Before heating	After heating	Before heating	After heating
$C_{16:0}$ Palmictic	1.95	11.62	12.53	11.88	13.00	4.32	4.18	2.13	2.51
$C_{18:0}$ Stearic	2.73	1.99	3.10	1.97	3.12	1.10	1.36	1.05	1.23
$C_{18:1}$ Oleic	3.04	57.34	62.21	52.05	56.51	13.09	14.16	11.96	12.87
$C_{18:2}$ Linoleic	3.52	28.04	18.79	33.02	16.57	19.97	15.25	15.66	14.03
$C_{18:3}$ Linolenic	4.34	-	-	1.05	1.03	21.73	14.27	18.71	14.93
$C_{20:1}$ Eicosenoic	6.09	-	-	-	-	0.653	-	1.87	3.82
$C_{22:1}$ Erucic	8.12	-	-	-	-	39.10	47.83	48.57	49.68

Table 13. Fatty acid profile of refined groundnut, refined mustard, raw groundnut and raw mustard oils before and after conventional heating at 200 ± 1°C for 15 hours

Fatty acids	Retention time	Refined groundnut oil		Raw groundnut oil		Refined mustard oil		Raw mustard oil	
		Before heating	After heating	Before heating	After heating	Before heating	After heating	Before heating	After heating
$C_{16:0}$ Palmictic	1.95	11.62	13.64	11.88	15.52	4.32	6.18	2.13	2.48
$C_{18:0}$ Stearic	2.73	1.99	2.10	1.97	2.83	1.10	1.41	1.05	1.27
$C_{18:1}$ Oleic	3.04	58.34	55.17	52.05	60.23	13.09	16.25	11.96	13.39
$C_{18:2}$ Linoleic	3.52	28.04	18.34	33.02	15.34	19.97	9.83	15.66	11.52
$C_{18:3}$ Linolenic	4.34	-	-	1.05	1.03	21.73	10.03	18.71	14.17
$C_{20:1}$ Eicosenoic	6.09	-	-	-	-	0.653	0.627	1.87	0.80
$C_{22:1}$ Erucic	8.12	-	-	-	-	39.10	52.33	48.57	55.14

Table 14 Total saturated fatty acids, monounsaturated fatty acids, polyunsaturated fatty acids, total unsaturated fatty acids and erucic acid content of different oils before and after heating

Oils	Total saturated fatty acid (%)	MUFA (%)	PUFA (%)	Total unsaturated fatty acid (%)	Erucic acid (%)
Fresh refined groundnut oil	13.61	58.34	28.04	86.38	-
Refined groundnut oil CH	15.74	55.17	18.34	73.51	-
Refined groundnut oil MH	15.63	62.21	18.79	81.00	-
Fresh refined mustard oil	5.42	13.74	41.74	55.44	39.10
Refined mustard oil CH	7.59	16.87	19.86	36.73	53.22
Refined mustard oil MH	5.54	14.16	29.52	43.68	47.83
Raw groundnut oil fresh	13.85	52.05	34.07	86.12	-
Raw groundnut oil CH	18.35	60.23	16.57	76.80	-
Raw groundnut oil MH	16.12	56.51	17.60	74.11	-
Raw mustard oil fresh	3.18	13.83	34.37	48.20	48.57
Raw mustard oil CH	3.75	14.19	25.69	39.88	55.14
Raw mustard MH	3.74	16.79	28.96	45.65	49.68

CH = Conventional heating; MH= Microwave heating

($C_{18:2}$) and linolenic acid ($C_{18:3}$) of 19.97 and 21.73 per cent, respectively making up for the total polyunsaturated fatty acid content of 41.70 per cent and total unsaturated fatty acid content of 55.44 per cent.

The per cent total saturated fatty acid content of fresh refined groundnut oil (13.61 %) was higher than that of refined mustard oil (5.42 %), as such the total unsaturated fatty acid content of refined groundnut oil (86.38 %) was higher than that of refined mustard oil (55.44 %).

Fresh raw groundnut oil contained saturated fatty acid *viz.*, palmictic acid ($C_{16:0}$) and stearic acid ($C_{18:0}$) of 11.88 and 1.97 per cent, respectively making up for the total saturated fatty acid content of 13.85 per cent. It contained monounsaturated fatty acid (MUFA *i.e.*, Oleic acid $C_{18:1}$) of 52.05 per cent and polyunsaturated fatty acid *viz.*, linoleic acid ($C_{18:2}$) and linolenic acid ($C_{18:3}$) of 33.02 and 1.05 per cent, respectively making up for the total polyunsaturated fatty acid content of 34.07 per cent and total unsaturated fatty acid content of 86.12 per cent. Raw mustard oil contained saturated fatty acid *viz.*, palmictic acid ($C_{16:0}$) and stearic acid ($C_{18:0}$) of 2.13 and 1.05 per cent, respectively making up for the total saturated fatty acid content of 3.18 per cent. It contained monounsaturated fatty acid *viz.*, oleic acid ($C_{18:1}$) and eicosenoic acid ($C_{20:1}$) of 11.96 and 1.87 per cent, respectively making up for the total monounsaturated fatty acid content of 13.83 per cent and also contained erucic acid ($C_{22:1}$) of 48.57 per cent. It also contained polyunsaturated fatty acid *viz.*, linoleic acid ($C_{18:2}$) and linolenic acid ($C_{18:3}$) of 15.66 and 18.71 per cent, respectively making up for the total polyunsaturated fatty acid content of 34.37 per cent and total unsaturated fatty acid content of 48.20 per cent.

The total saturated fatty acid content of raw groundnut oil (13.85) was higher than that of refined mustard oil (5.18 %). The total monounsaturated fatty acid content of raw groundnut oil (52.05 %) was higher than that of raw mustard oil (13.83 %). The total polyunsaturated fatty acid content of raw groundnut oil (34.07 %) was slightly lower than that of raw mustard oil (34.37 %). The total unsaturated fatty acid content of raw groundnut oil (85.07) was higher than that of raw mustard oil (48.20 %).

From the data obtained on gas chromatography, it can be found that heating constantly altered the structure and composition of refined groundnut, refined mustard, raw groundnut and raw mustard oils. The total saturated fatty acid content appears to increase from 13.61 to 15.74, 5.42 to 7.59, 13.85 to 18.35 and

3.18 to 3.75 per cent, respectively for refined groundnut, refined mustard, raw groundnut and raw mustard oils used for conventional heating at 200 ± 1°C for 15 hours. Total monounsaturated fatty acid content of raw groundnut, raw mustard and refined mustard oil increased from 52.05 to 60.23, 13.83 to 14.19 and 13.74 to 16.87 per cent, respectively, where as they decreased from 58.34 to 55.17 per cent in refined groundnut oil used for conventional heating at 200 ± 1°C for 15 hours. The total polyunsaturated fatty acid content of refined groundnut, raw mustard, raw groundnut and refined mustard oils decreased from 28.04 to 18.34, 34.37 to 25.69, 34.07 to 16.75 and 41.74 to 19.86 per cent, respectively for conventional heating at 200 ± 1°C for 15 hours. The total unsaturated fatty acid content of refined groundnut, refined mustard, raw groundnut and raw mustard oils decreased from 86.38 to 73.51, 55.44 to 36.73, 86.12 to 76.80 and 48.20 to 39.88 per cent, respectively when used for conventional heating at 200 ± 1°C for 15 hours.

Erucic acid increase was from 48.57 to 55.14 and 39.10 to 53.22 per cent, respectively in raw mustard and refined mustard oil used for conventional heating at 200 ± 1°C for 15 hours.

Upon microwave heating at high power setting the total saturated fatty acid content according to retention time of components and area of peak appears to increase from 13.61 to 15.63, 5.42 to 5.54, 13.85 to 16.12 and 3.18 to 3.74 per cent, respectively in refined groundnut, refined mustard, raw groundnut and raw mustard oils. The total monounsaturated fatty acid content of refined groundnut, refined mustard, raw groundnut and raw mustard oils increased from 58.34 to 62.21, 13.74 to 14.16, 52.05 to 56.51 and 13.83 to 16.79 per cent, respectively used for microwave heating at high power setting.

The total polyunsaturated fatty acid content of refined groundnut, refined mustard, raw groundnut and raw mustard oils decreased from 28.04 to 18.79, 41.74 to 29.52, 34.07 to 17.60 and 34.37 to 28.96 per cent, respectively when used for microwave heating at high power setting.

The total unsaturated fatty acid content decrease was from 86.38 to 81.00, 55.44 to 43.68, 86.12 to 74.11 and 48.20 to 45.65 per cent, respectively for refined groundnut, refined mustard, raw groundnut and raw mustard oils used for microwave heating at high power setting.

Erucic acid increase was 48.57 to 49.78 and 39.10 to 47.83 per cent, respectively in raw mustard and refined mustard oils used for microwave heating.

The data obtained presented in Table 14 of the total saturated fatty acids, monounsaturated fatty acids, polyunsaturated fatty acids, total unsaturated fatty acids and erucic acid content of different oils before and after heating.

Saturated fatty acid level in the oil increasing and unsaturated fatty acid level decreasing on heating of oil was reported by Kalyoubi (10). Increase in level of palmictic acid ($C_{16:0}$), stearic acid ($C_{18:0}$) and oleic acid ($C_{18:1}$) and decrease in level of linoleic acid ($C_{18:2}$) on heating of oil was also reported by Narasimhamurthy and Raina (11).

Houhoula *et al.* (12) also reported increase in level of palmictic acid and decrease in linoleic acid in heated oils. The apparent increase in saturated fatty acid upon heating may be due to products of polymerization and subsequent break down of unsaturated fatty acid. Unsaturated fatty acids on one hand give health and nutritional benefits and some of these are essential fatty acids. Their unstable structure significantly reduces their storage stability.

From the fatty acid profile of oil samples, it can be generalized that upon intermittent heating of oils there is significant reduction in the level of polyunsaturated fatty acids, which are nutritionally important, for all samples of oils. It can also be concluded that heating oils for 15 hours of conventional heating at 200 ± 1°C leads to higher destruction of PUFA than microwave heating for 150 minutes at high power setting. For all samples of oils, content of saturated fatty acids tended to increase and the content of monounsaturated fatty acid tended to increase slightly. The higher values for these fatty acids needs to be looked into taking into consideration the destructive reduction of PUFA. The total unsaturated fatty acids decrease drastically on conventional heating of the oils, but less drastically on microwave heating.

Erucic acid is a non-nutritive fatty acid and tends to increase in a pattern similar to that of saturated fatty acids.

From the results obtained and as discussed herein, it can be generalized that with increasing time of heating, the quality of the oil including sensory score

of the oil decreased. However, microwave heating deteriorate the quality of oil slower as compared to conventional heating in terms of quality characteristics including sensory score.

The results revealed that conventional heating and microwave heating significantly reduced the acceptability and stability of all the oils as all the characteristics *viz.*, peroxide value, acid value, viscosity and colour value increased and sensory score decreased with time of heating. The reduction in quality of oils was less in microwave heating in comparison to conventional heating. According to fatty acid profile, microwave heating resulted in lower decrease in PUFA content in oils as compared to conventional heating.

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Resource use efficiency and returns to scale in production of castor in Gujarat

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Abstract

A study was undertaken to evaluate the level of efficiency in castor cultivation using the Cobb Douglas regression model. Three district viz. Mahesana, Banaskantha and Sabarkantha were selected on the basis of cultivated area of castor in there districts. Data were obtained from cost of production survey programme relating to the season 2005-06. The result of study revealed that the production elasticity for human labour, seed and manure were positive and significant showing significant roll of these inputs in the castor production. Return to scale was observed 1.14, 1.48, 0.98 and 1.06 for small, medium. large and overall farmers indicating increasing marginal productivity for small, medium and overall farmers where as decreasing marginal productivity for large farmers. It indicates small and medium farmers should invest more in castor cultivation, where as large farmers should not invest more in castor cultivation for maximization of profit. In small farmers all the inputs except cattle labour and seed were under utilized. Use of fertilizers and irrigation were at optimum level. where as remaining inputs were under utilized by medium farmers. Overall the use of all inputs like plant protection, seed, manure and human labour were not efficient. It is recommended to strengthen the extension system towards resource management so that yield gap can be reduced and farm income can be increased.

Keywords : Castor, resourses use efficieny, returns, labour, fertilizer

Introduction

Castor cultivation creates a special attraction in Gujarat since the last three decades. Its production play a very important role not only in sustaining many agro based industries but also in earning foreign exchange. Its cover 2.90 lakh hectares cropped area (1). And 5.41 lakh tones production with producing 1864 kg/ha in the state. The castor production of the state has about 61.54 per cent contributes in national castor production. Such a significant role leads scientists to increase the resource use efficiency. Resource use efficiency of farmers in developing country like india is subject to many restraints surplus bullock and human labour, inadequate and unavailability of inputs like chemical fertilizers, pesticides, high yielding & good availability of hybrid varieties seeds, irrigation, funds and lack of efficient managerial ability (2). In such conditions, one of the objectives of a production unit is to co-ordinate and utilize scare and surplus resources in such a manner that they collectively yield maximum net profit. The main objective of this analysis is to arrive at some judgment about the efficiency of the prevalent factor proportions and to suggest changes in those proportions in the optimal direction.

This can be studied by estimating resource productivity, return to scale and finally resource use efficiency. With a view to know the existing resource use efficiency a study was organized with the following objectives:

1. To access resource productivity, return to scale 7and resource use efficiency in different sized farm in selected districts of the state.
2. To determine optimum resource use in castor cultivation by different farm size.

Methodology

The study for the year 2005-06 was centered in three major castor producing districts i.e., Mehsana, Banaskantha and Sabarkantha of North Gujarat which occupy about 60 per cent both area and production of castor in the state. As per the area under cultivation of castor in each district, totally ten villages selected

Table 1. Estimates of Cobb-Douglas Production Function of Castor Production by different size groups in Gujarat (2005-06)

	Small		Medium		Large		Average	
No. of Farmers	50		50		50		150	
GEOMETRIC MEAN								
Area under crop	0.3904		2.348		1.76		2.195	
Human labour	1183.86		1262.70		1663.79		1354.88	
Cattle labour	247.06		431.82		486.74		378.08	
Seed cost	179.47		197.69		2662.00		210.28	
Manure cost	32.48		32.73		31.01		32.07	
Fertilizer cost	816.58		612.07		1077.20		813.58	
Irrigation cost	1513.56		1619.20		1695.90		1607.68	
Plant protection	1.2331		1.38		1.64		1.14	
Tractor cost	267.86		230.25		67.33		160.69	
Income	8976.35		10556.01		13415.29		10831.78	
PRODUCTION ELASTICITIES								
Area under crop	0.2743**	(0.1293)	0.3011	(0.3302)	0.1219	(0.1606)	0.2971*	(0.0930)
Human labour	0.4961	(0.1442)	0.6879**	(0.2566)	0.1846	(0.2534)	0.5235*	(0.0728)
Cattle labour	-0.0046	(0.0139)	0.1698	(0.1227)	0.0545	(0.1032)	0.0143	(0.0160)
Seed cost	-0.2003	(0.1395)	0.1318	(0.1559)	0.3460**	(0.1517)	0.1476***	(0.0790)
Manure	0.0172**	(0.0069)	0.0107	(0.0084)	0.0325*	(0.0089)	0.0217*	(0.0045)
Fertilizer	0.1922	(0.1442)	0.0101	(0.0178)	0.1584	(0.1268)	0.0155	(0.0199)
Irrigation	0.2552*	(0.0711)	0.1155	(0.1672)	0.0041	(0.0210)	0.0252	(0.0193)
Plant protection	0.0075	(0.0110)	0.0068	(0.0130)	0.0145	(0.0118)	0.0091	(0.0060)
Tractor cost	0.1029	(0.0661)	0.0422	(0.1293)	0.0140	(0.0152)	0.0072	(0.0103)
Constant a	1.3553		1.6892		2.0154		2.1069	
R^2	0.9276		0.9283		0.8741		0.8555	
RETURN TO SCALE	1.1405		1.4759		0.9305		1.0612	

Figures in paraenthesis indicate standard errors
* Significant at 1 % level, ** Significant at 5 % level,*** Significant at 1 % level

proportionately i.e., four villages from Mehsana (Balisana,Chansama,Unjha and Ladol) three from Banaskantha (Chhandisar, Kuskal and Laxmipura) three farm Sabarkantha (Khedbrahma, Parabda and Dungri). From each of these selected villages 15 farmers were selected i.e. 5 farmers from each size of holding groups (i.e. small-below 2 hectares, medium-2 to 4 hectares and large- above 4 hectares). Thus, in all 150 farmers were selected for the study through three stages sampling method.

Data were collected from selected farmers in the prescribed format. These data were analyzed to work out the input use efficiency and returns to scale of castor growers. Functional analysis was used to estimate the quantitative relationship between the gross income and input variables (3). The specification of the function is as follow.

$Y = aX_1^{b1} X_2^{b2} X_3^{b3} X_4^{b4} X_5^{b5} X_6^{b6} X_7^{b7} X_8^{b8} X_9^{b9} Ut$

where,

Y = Income in Rs.
X_1 = Land used in hectare
X_2 = Human labour cost
X_3 = Cattle labour cost
X_4 = Seed cost
X_5 = Manure cost
X_6 = Fertilizer cost
X_7 = Irrigation cost
X_8 = Plant protection cost
X_9 = Tractor cost
U = Random error
a = Constant
b1,b2 ..... b9 = Production elasticities.

Separate functions were fitted for each size group and over all farmers.

The resource use efficiency could be judged based on the Marginal value Productivity which indicates the increase in gross returns from the use of additional unit of a given inputs while, keeping the other inputs constant. The Marginal Value Product (MVP) of i^{th} input factor was measured by using the following formula (4).

$$\text{MVP of} = b_i$$

$$\text{MVP of } X_i = b_i \frac{\overline{y}}{\overline{x_1}}$$

Where,

$\overline{Y}$ = Geometric mean of income
$\overline{x_i}$ = Geometric mean of input variable
b_i = Regression coefficient of respective input vriable

Resource use efficiency was assessed by computing the ratio of Marginal Value Product (MVP) and Factor Cost (FC). Unity of MVP to FC ratio indicates the optimum resource use efficiency of a particular input. The degree of deviation, if any indicates the degree of resource use inefficiency (5).

Return to scale was estimated by the sum of the production elasticities (here εbi) for each group of farmers.

ε bi > 1 = Return increase at increasing rate
$0 < \varepsilon$ bi < 1 = Return increase at decreasing rate
ε bi < 0 = Return decreasing

Results and discussion

Resource productivity

Resource productivity of a particular inputs means the charge in production due to additional investment of one rupee for particular input.

Resource productivity of inputs indicated by production elasticity and their respective standard errors computed adopting Cobb-Douglas production function is presented in Table 1 for small, medium and large farmers.

Small Farmers

The data revealed that the coefficient of multiple determination (R^2) was nearly 0.93 indicating that the explanatory variable included in the function such as area under crop, human labour, cattle labour, seed, manure, fertilizer, irrigation, plant protection and transport cost together explained the variation in gross value of output to the extent of nearly 93 per cent. Among the different inputs studied human labour, manure, irrigation and area under crop turned out to be significant and positive with production elasticties of 0.4961, 0.0172, 0.2552 and 0.2743, respectively. Though, elasticity for fertilizer was 0.1922 but it was non-significant. This indicate that 1 per cent increase of human labour would increase the gross value of output by 0.4961 per cent, when other variables kept constant. Similarly, the gross value of output would increase by 0.0172, 0.2552 and 0.2743 per cent by increasing the per cent use of manure, irrigation and area each respectively.

Medium Farmers

The input variables included in the production function as shown in table together explained nearly 93 per cent variation in output, Only human labour was found affecting significantly to the output. It means, human labour would increase the gross valie of output by

0.6879 per cent by increasing 1 per cent of its level. Though, cattle, labour, seed and irrigation has markable positive elasticity however were non significant.

Large Farmers

It is also visualized from the result that 87 per cent of variation in gross output was explained by explanatory variables. The production elasticity for seed and manure were positive and significant. It was 0.3460 and 0.0325, respectively.

Overall Farmers

The cobb-Douglass Production function of 150 selected castor growers explained nearly 86 per cent variation by human labour, cattle labour, seed, manure, fertilizer, plant protection measure, tractor use and area under castor crop. The production elasticities respectively 0.5235, 0.1476, 0.0217, and0.2971 for human labour, seed, manure and area under crop were positive and significant. It means for production of castor human labour, seed, manure and area under crop has significant role. The production elasticities for fertilizer and irrigation were positive but non- significant. It may be due to costliness of these inputs.

Return to scale

Return to scale is concerned with the proportion in which factors of production are combined to gether and how output is related to this combinations. If the increase in the factors of production and output is in the same ratio (Σ bi = 1), the return to scale are constant, if in smaller ratio (Σ bi < 1), return to scale are decreasing and if in larger ratio (Σ bi > 1), return to scale are increasing.

Return to scale (Σ bi) indicated by sum of the production elastic- ties were 1.14, 1.48, 0.93 and 1.06 for small, medium, large and overall farmers, respectively. It revealed that in case of large farmer return to scale was less than unity, whereas, in all other cases, it was greater than unity. It indicates increasing returns to scale except large farmers. The small and medium farmers were working in the first zone of production i. e., increasing marginal productivity, whereas, large farmers were working in the second zone of production i.e., decreasing marginal productivity.

Resource Use Efficiency

Equality of MVP to factor cost ratio indicates the optimum resource use efficiency of particular input. Deviation, if any,, indicate the resource use inefficiency (6). The MVP to FC ratios of different input variables for small, medium and large farms are presented in Table 2.

Small Farmers

The data in Table –2 revealed that the MVP to FC ratio of all the inputs except cattle labour and seed were greater than unity, indicating under utilization of these resource. The MVP to FC ratios of cattle labour and seed were negative indicating over use due to small scale of cultivating unit. MVP to FC ratio with regard to human labour, manure cost, fertilizer cost, irrigation cost, plant protection and tractor use were 3.76, 4.75, 2.11, 1.51, 54.60 and 3.45 respectively. Obviously, the expenditure on these resource has to be increased, but it has to be curtailed in case of cattle, labour and seed for increasing the income to small farmers.

Medium Farmers

It is observed from the Table-2 that the MVP to FC ratio with respect to fertilizer and irrigation was near to equality , which shows the use of fertilizer and

Table 2. Marginal Value Product to Factor Cost Ratio in Castor of Selected Farmers in Gujarat (Year 2005-06).

Inputs	Small Farmers	Medium Farmers	Large Farmers	Average Farmers
Human labour	3.76	5.75	1.49	4.18
Cattle labour	-0.17	4.15	1.50	0.41
Seed cost	-10.02	7.03	17.72	7.60
Mannure	4.75	3.45	14.00	7.33
Fertilizer	2.11	0.17	1.97	0.21
Irrigation	1.51	0.75	0.03	0.17
Plant protection	54.60	52.01	18.61	86.46
Tractor use	3.45	1.93	2.79	0.49

irrigation was near to optimum level. Where as, in case of other input it was positive and far away from equality , which indicates the under use of these resources. Hence, higher gross returns can be achieved by investing much on these inputs till they reached the optimum economic level (when ratio is equal to one) in cultivation of castor.

Large Farmers

It is interesting to observe that seed, manure and plant protection measures were under utilized by large farmers as reflected by high and positive MVP to FC ratio (17.72, 14.00, and 18.61) respectively. Hence, the expenditure on seed, manures and plant protection measures should be increased to increase the income. While, the MVP to FC ratio for irrigation (0.03), human labour (1.49), cattle labour (1.50) and fertilizers (1.97) were near to equality, which show input level near the optimum. However, it required minor adjustment, to have optimum utilization of these resource.

Ovreall Farmers

Overall picture of inputs used by the selected castor farmers revealed from the table-3 that inputs use were satisfactory in case of tractor use (0.49), cattle labour (0.41), fertilizer (0.21), irrigation (0.17), whereas, it required more expenditure on plant protection, seed, manure and human labour.

Thus, the MVP to FC ratios by and large indicated resource use inefficiency on castor farm. This warrants the reorganization of inputs so as to increase and stabilize castor production in the Gujarat state.

CONCLUSION

Resource use efficiency of selected castor cultivators were inefficient. The Cobb-Douglas production function for selected inputs level explained about 86 per cent variation. The production elasticities for human labour (0.5235), seed (0.1476), manure (0.0217) and area (0.2971) were positive and significant. It means that these inputs have significant role in production of castor.

Returns to scale was observed 1.14, 1.48, 0.93 and 1.06 for small, medium, large and overall farmers respectively. It indicated the increasing marginal productivity for small, medium and overall farmers where as, decreasing marginal productivity for large farmers.

In case of small farmers MVP to FC ratios of all the inputs except, cattle labour and seed were greater than unity indicating under utilization of these resource.

The MVP to FC ratio of cattle labour and seed was negative indicating over use of these resources. In case of medium farmers, it was observed that the MVP to FC ratios with respect to fertilizer and irrigation was near to equality which shows the use of fertilizer and irrigation was near to optimum level. Whereas, in case of rest of the inputs, it was positive and far away from equality, which indicates the under use of these resource. The large farmers under utilized seed, manure and plant protection measures whereas irrigation, human labour, cattle labour and fertilizer levels were used nearly optimum by them. Overall picture of inputs used by selected farmers revealed that input use was satisfactory in case of tractor use, cattle labour, fertilizer and irrigation whereas, it was felt necessary to have more utilization input like plant protection, seeds, manure and human labour in case of castor production.

In, general, it was found in the study that certain resource like seeds, manures, human labour and plant protection input are being under utilized by the farmers. Effort may be done in explaining to the farmers regarding importance of such inputs in castor cultivation.

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Personal, socio–economic, psychological and communication characteristic of the carrot grower of Patan district of Gujarat State

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Abstract

The study was conducted to know the personal, socio- economic, psychological and communication characteristics of carrot growers of Patan district in Gujarat. The Patan district is having highest area and production under carrot cultivation. One taluka from the district and ten villages from Patan taluka were selected purposively. Total 100 respondents were selected randomly. Majority of the carrot growers were middle aged (45.00 %), educated up to secondary level (35.00 %), belonged to joint family (51.00 %) with large size of family (52.00 %). Most of them had large land holding (57.00 %) with social participation. The occupation of majority farmers was farming + business (69.00 with earning medium income (49.00 %). With regard to different psychological characteristics *viz.,* scientific orientation (63.00 %), risk orientation (51.00 %) and economic motivation (59.00 %) majority were found in medium category. For different communicational characteristics *viz.,* extension contact (57.00 %) and sources of information (58.00 %) majority of them were also found in medium category.

Key words: Socio- economic, psychological, communication, carrot growers

Introduction

Carrot (*Dacus Carrota* L.) is a popular root vegetable grown in India and abroad. It is locally known as *Gajar*. The carrot is rich in various vitamins especially carotene and amino acid which are badly needed by human body. carrot is very popular among many vegetables. It is rich in carotene, a precursor of vitamin A as well as iron, thiamine, riboflavin, ascorbic acid and niacin. All over the Patan district carrot is cultivated in about 1850 hectares and production is about 29550 metric tones in D.D.A (1).

Successful vegetable cultivation requires particular knowledge, skill and accuracy. The technical knowledge regarding the cultivation of vegetable technology must reach the vegetable growers for adoption on their fields. Many efforts have been made from government, State Agricultural Universities (SAUs), Non Government Organizations (NGOs) and other institutions for efficient transfer of innovated technology from research station to the doors of the farmers. Even through, there is a wide gap between the potential yield.and average yield. Hence It is important to understand the personal, socio-Economic, psychological and communications characteristic of the, farmers in order to determine and understand towards adoption of recommended carrot cultivation technology. Keeping this in mind a study was conducted on the Personal, Socio-Economic, Communication and Physiological Characteristic of carrot grower in Patan district of Gujarat.

Methodology

Among all the taluka of Patan district, Patan taluka is the most advanced in agriculture and animal husbandry. The occupies taluka highest area under carrot cultivation among other taluka of the district. Ten villages from this taluka were selected purposively. Using proportionate random sampling technique ten carrot grower were selected from each village. A structure interview scheduled was developed for data collection.

Results and discussion

The data for characteristics of the farmers were analyzed and presented in Table 1.

Table 1 Characteristics of carrot growing farmers of Patan Taluka

S.N.	Characteristic	Category	Number	Percentage
1)	Age(Years)	Young (up to 35)Years	20	20.00
		Middle(36 to 50) Years	45	45.00
		Old (Above 50Years)	35	35.00
2)	Education	Illiterate	8	08.00
		Primary School	27	27.00
		Secondary School	35	35.00
		High secondary	17	17.00
		Collage Education	13	13.00
3)	Family type	Nuclear Family	49	49.00
		Joint Family	51	51.00
(4)	Family Size	Small (up to 5 members)	38	38.00
		Large(Above 5 members)	62	62.00
(5)	Social participator	No membership.	36	36.00
		Membership in one organization	40	40.00
		Membership more than one organization	12	12.00
		Office bearer.	12	12.00
(6)	Land Holding	Marginal (up to 1.00ha)	4	4.00
		Small(1.01 to 2.00ha)	18	18.00
		Medium(2.01 to 4.0 ha)	21	21.00
		Large(more then 4.00 ha)	57	57.00
(7)	Annual income	Low (Below RS.50,000)	12	12.00
		Medium (Rs.50,000 to Rs.1.00,000)	49	49.00
		High (Above Rs. 1.00,000)	39	39.00
(8)	Occupation	Farming only	23	23.00
		Farming + Service	5	5.00
		Farming+ Business	69	69.00
		Farming+ Business+ Service	3	3.00
(9)	Scientific Orientation	Low (up to 20 Score)	29	29.00
		Medium(21 to 25 Score)	63	63.00
		High (Above 25 Score)	8	8.00
(10)	Risk orientation	Low (up to 18 Score)	28	28.00
		Medium (19 to 23 scores)	51	51.00
		High (Above 23 Scores)	21	21.00
(11)	Economic Motivation	Low (up to 18 score)	33	33.00
		Medium (19 to 24 scores)	59	59.00
		High(Above 24 scores)	8	8.00
(12)	Extension Contact	Low (up to 4 score)	23	23.00
		Medium (5 to 11 scores)	57	57.00
		High(Above 11 scores)	20	20.00
(13)	Source of Information	Low (up to 19 score)	24	24.00
		Medium (20 to 25 scores)	58	58.00
		High(Above 25 scores)	18	18.00

Age
Majority of the respondents (45.00 %) were found in the middle age group followed by old age group (35.00 %) and young age group (20.00 %). The similar findings have been reported by Trivedi (2).

Education
Majority of the respondents (35.00 %) were found educated up to secondary level, about 27.00 per cent were found primary level, about 17.00 per cent respondents were found educated up to higher secondary level, 13.00 per cent respondents and 8.00 per cent respondents were above college level and illiterate respectively. Similar findings have been reported by Dongardive (3).

Family Type
Majority of the respondents (51.00 %) were the member of joint family, while 49.00 per cent respondents were belonged to nuclear family. The resuls are in conformity with the results reported by Dongardive (3), Nanda (4).

Family size
Majority of the respondents (62 .00 %) were found with large size of family whereas, only 38.00 per cent of them were found with small size of family. This finding has been supported by findings of Dongardive (3).

Social Participation
Majority of the respondents (40.00 %) were member in one organization followed by 36.00 per cent respondents who were not associated with any social organization. 12.00 per cent of the respondents were member in more than one organization. Remaining 12.00 per cent respondents were found holding position in various social organizations. The findings are in agreement with the findings of Desai (5).

Land Holding
Majority of respondents were having large size of land holding (57.00 %) followed by 21.00 per cent, 18.00 per cent and 4.00 per cent of them who had medium, small and marginal size of land holding, respectively. The findings are in line with the findings of Desai (5), Danger (6).

Annual Income
Majority of the respondents (49.00 %) had medium annual income (Rs. 50,001 to Rs. 1,00,000) on the other hand 39.00 per cent farmers had more than Rs.1,00,000/- annual income and 12.00 per cent respondents had annual income up to Rs.50,000/-. These findings are in conformity with the findings of Pandya (7).

Occupation
Majority of (69.00 %) the carrot growers had farming + business as their main occupation, while 23.00 per cent of them had only farming as their occupation and 5.00 per cent of carrot growers had farming + service as their occupation. Remaining 3.00 per cent of them had farming + service + business as their occupation. This findings are in conformity with the findings of Trivedi (2).

Scientific Orientation
A great majority (69.00 %) of carrot growers had medium level of scientific orientation followed by 29.00 with low scientific orientation and 8.00 per cent high level of scientific orientation. The findings are supported by Pandya (7).

Risk orientation
A little more than half respondents (51.00 %) were having medium risk orientation, while 28.00 per cent of respondents had low risk orientation. Remaining 21.00 per cent of the respondents were found to have high risk orientation. The present findings are in conformity to. Trivedi (2)

Economic Motivation
Majority of carrot growers (59.00 %) had medium level of economic motivations followed by 33.00 who had low level and 8.00 with high level of economic motivation. This is supported by Dongardive (3).

Extension Contact
Majority of respondents (57.00 %) had medium level of extension contact followed by 23.00 with low level and 20.00 per cent with high level of extension contact. This finding is supported by Jadav (8).

Mass medium Exposure
Majority of (58.00 %) the carrot growers had medium level of utilization of information sources, while, 24.00 and 18.00 per cent of them had low and high level of information sources respectively.

From the above findings, it can be concluded that majority of the carrot grower were middle age group, educated up to secondary school level, belonged to joint family and with large size of family, having medium social participation. Most of them were found cultivating large land holding with medium annual

income. The occupation of the majority respondents being farming plus business with regard to different psychology characteristic viz., scientific orientation, risk orientation and economic motivation, majority were found in medium category. Majority had medium extension contact and medium mass media exposure.

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Bovine growth hormone receptor gene polymorphism

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Abstract

The PCR-RFLP was carried out to find polymorphism in exon 10 of growth hormone receptor gene. Primer sequences used for the amplification of growth hormone receptor gene were 5' GCG TAG CTA CTC AAC TCA TCA AAC TGC CCA TAC 3' as a forward primer and 5' AGC CAA CCC TGT GCC ATT CAA 3' as a reverse primer. The amplified DNA fragments were digested with *Hae*II restriction enzymes. The growth hormone receptor locus1 (GHR1) was found to be monomorphic with *Mae*II restriction enzymes.

Introduction

Growth hormone receptor is a member of a super family of receptors with one membrane-spanning domain. This super family includes the receptors of prolactin, haematopoetin, erythropoetin, granulocyte colony stimulating factor, interferon, and many interleukins. It is a transmembrane protein found in the variety of tissues (1).

Growth hormone receptor is required to regulate the action of growth hormone. In bovines, this gene (bGHR) is also expressed in the mammary glands (2). The cDNA of the bovine GHR gene has been sequenced (2) and it is localized on chromosome 20 (3). Mutation in GHR gene has been associated with Laron type dwarfism in humans (4) and sex-linked dwarfism in chickens (5). However, in the bovine growth hormone receptor gene, only few genetic polymorphisms have been reported (1,6,7,8).

Considering the importance of growth hormone receptor genes, the present study was undertaken to find out polymorphism at exon 10 cf growth hormone receptor (bGHR) locus by using PCR-RFLP technique.

Material and methods

Experimental materials for the present study comprised of blood samples from 45 Gir, 30 Kankrej and 33 Holstein cows, randomly selected from the herds, respectively maintained at Cattle Breeding Farm, Junagadh; Livestock Research Station, Sardarkrushinagar and Holstein Unit, Anand. The collected blood samples were brought to the laboratory on ice. PCR amplification was carried out according to Ge *et al.* (9). Primer sequence was F: 5' GCG TAG CTA CTC AAC TCA TCA AAC TGC CCA TAC 3' and R: 5' AGC CAA CCC TGT GCC ATT CAA 3'. Oligo primers specific to bovine growth hormone receptor loci custom synthesized at Sigma and utilized in the present study. Oligos supplied in freeze-dried powder form were reconstituted in 0.3X TE buffer to the volume (in µl) equivalent to the mass (µg) of primer and further diluted in MiliQ water to give a final concentration of 10 pmoles / µl.

Results and discussion

PCR product obtained by GHR1 primers was digested with *Mae*II and electrophoresed on 2.5% Agarose gel. Only two bands were obtained, approximately 260 and 300bp in size in Kankrej and Gir (Plate 1).

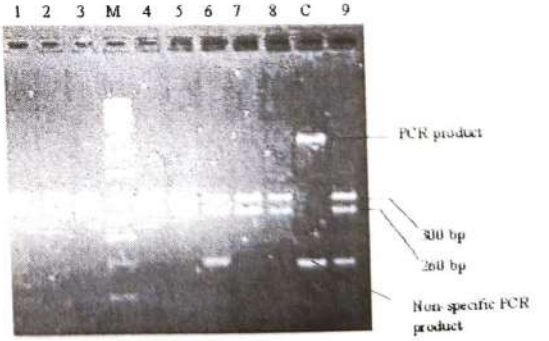

Plate 1. Mae II digestion of PCR product of GHR 1 locus in Gir and Kankrej cows

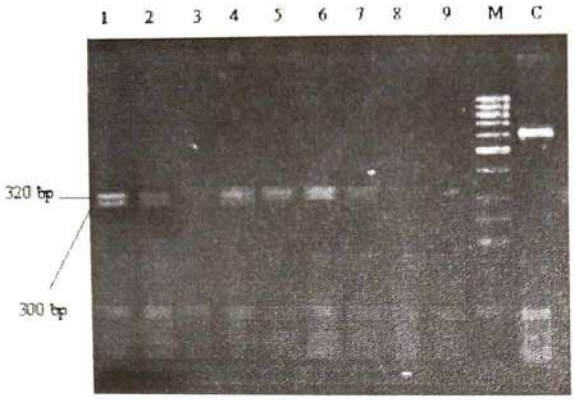

Plate 2. *Mae* II digestion of PCR product of GHR 1 locus in Holstein cows

Lane 1 to 9	:	Digested PCR products
Lane 10	:	50 to 1031 bp size maker
Lane 11	:	Undigested PCR product

However, in Holstein cows, the bands were approximately of 300 and 320 bp in size (Plate 2). Thus, GHR1 locus was found to be monomorphic for *Mae*II restriction enzyme with RR genotypes and R alleles only.

On the contrary, Ge *et al.* (9) had reported GHR1 locus as polymorphic for *Mae*II restriction enzyme in Angus calves. Similarly, Moisio *et al.*, (7) and Ge *et al.*, (9) had reported variants of growth hormone receptor gene by sequencing the PCR product and denaturing gradient gel electrophoresis (DGGE) analyses, respectively in Finnished Ayrshire and Angus cattle breeds. Aggrey *et al.*, (10) had also reported restriction fragment length polymorphisms (RFLPs) in the 5' flanking region of the bovine growth hormone receptor gene using *AluI*, *AccI*, and *StuI* restriction enzymes in Holstein bulls.

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Short communication

Combining ability in chickpea

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India is the primer chickpea growing country. The average yield of chickpea in India is very low as compared to some advanced countries. The breeding procedures what so ever applied so far have met with little success. This may be partly attributed to the inadequate information on genetic nature of various quantitative characters, because yield is a dependent character and the resultant effect of a number of quantitative characters. In hybridization programme, selection of right type of parents is a crucial step for a breeder combining ability analysis is a powerful tool to discriminate good as well as poor combiner and selecting out appropriate parental material and at the same time provide information about nature of gene action involved in the inheritance of various traits.

The materials comprise of 36 hybrids resulting from 3 lines and 12 testes. All the 36 F_1s and parents were grown in a randomized block design with three replication in *rabi* 2001. Standard tow to row and plant to plant distances were maintained. Observations on five randomly selected plants form each row were recorded for days to 50 per cent flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per pod, 100-sweed weight, seed yield per plant, harvest index per cent and protein content per cent. Analysis of variance and the estimates of combining ability effects were made by the method given by Kempthorne (1).

Analysis of variance showed that mean squares due to lines was significant for branches per plant, pods per plant and harvest index. Mean squares due to testers was non-significant in all the characters whereas mean squares due to line x tester interaction was fond significant (Table-1) in all the characters except for harvest index and protein content. The 6^2 gca/6^2 sca ratios indicated preponderance of non-additive gene action in the inheritance of all the traits except harvest index. Preponderance of non-additive variance it the expression of different traits in gram have been also reported by Singh and Mehtra (2), Sarode (3) and Girase and Deshmukh (4).

For day to 50 per cent flowering, GCP-106, GCP-9601 and GCP-9626 exhibited significant negative gca effects in desired direction. For days to maturity, GG-1 and GCP-9514 were found to be late maturing by showing higher gca for late maturity, GCP-9601 and GCP-9707 exhibited higher gca effects for plant height. In case of branches per plant, GG-1, GG-2, GCP-105, GCP-9629 and GCP-9630 were found good general combiners, GG-2, GCP-105, GCP-9709, GCP-9629 and GCP-9707 were good general combiners for pods per plant. In case of seeds per pod, GG-2 and GCP-9630 showed higher gca effects. For seed yield and 100-seed weight, GG-2, GCP-9630 and GCP-9626 were found to be good general combines. For harvest index, GG-2, GCP-105 and GCP-9630 showed high gca effects in desired direction. In case of protein content, only GG-2 found to be good general combiner (Table-2).

The parents showing higher mean performance were not good general combiners for yield related characters. For yield per plant, Dahod Yellow showed higher mean performance although GCP-9707 expressed highest gca effects. Similar trend was observed in case of yield attributing characters. High mean performance of such parents may be mainly due to the preponderance of non-additive gene effects. Therefore, the high mean performance of parents could not be transferred into hybrids uniformity in such cases.

The sca effects represent dominance and epistatic action and it can be related with heterosis. In self pollinated crops, however, the additive x additive type of interaction components is fixable in later generations. Of the present crosses GG-2 x GCP-9630 and GG-2 x GCP-9626 had high sca effects. The crosses were having both of their parents as good x good, average x good general combiners for yield. Such crosses can be exploited by straight breeding methods. The crosses GG-2 x GCP-105, GG-2 x GCP-9707 and GG-2 x GCP-9626 also showed high sca effects. However, only one of their parents was good general combiner for yield. Such effects may be

Table 1. Analysis of variance for combining ability

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pod	100-seed weight (g)	Seed yield per plant (g)	Harvest index (%)	Protein content (%)
Among lines	2	147.25	106.15	45.76	3.65*	2577.44*	0.17	156.58	94.88	375.39**	6.51
Among testers	11	67.63	144.07	66.50	0.62	480.38	0.075	62.18	25.98	69.61	1.86
Line x Tester	22	36.70**	75.34**	34.82*	0.92**	463.44**	0.086**	165.44**	16.72**	42.44	3.19
Error	70	5.86	11.87	17.58	0.26	29.12	0.048	6.69	6.06	37.55	1.94
σ^2gca		3.14	2.21	0.94	0.05	47.35	0.0017	2.491	1.942	8.002	0.044
σ^2sca		10.28	21.16	5.74	0.22	144.77	0.01	52.92	3.55	1.63	0.41

*** Exceed 5% level of significance**

**** Exceed 1% level of significance**

expected to produce some good segregants only if the epistatic effects in the cross act in the same direction so as to maximize the desirable plant characteristics.

On the basis of the estimates of sca effects the lines and testers can be divided into three groups. The first group included GG-2, GCP-9630, Dahod Yellwo and GCP-9626 showed high sca for yield and many of the yield contributing characters. The second group included GG-1, GCP-105, GCP-9707 and GCP-9626 had high specific complementation. The third group did not show such specific trend. Additive and non-additive components of genetic variance are important for most of the characters

The exploitation of both type of gene actions would be imperative recombination breeding by adopting biparental mating in F2 and diallel selective mating system used as recurrent selection as well as hybrid breeding method can be followed for the improvement of the characters studied.

Combining ability analysis involving 3 lines and12 testers was made in gram for yield and yield attributing characters. Combining ability analysis revealed that both gca and sca variances were important for inheritance of various traits. However, sca variances were higher than gca variances for all the characters, which indicated the preponderance of non-additive gene action in the expression of various traits. The estimates of gca effects indicated that GG-2, GCP-9707 and GCP-9632 were good general combiners for seed yield per plant and some of the yield components. The best specific crosses were the combinations of good x good, average x good and good x average combiners.

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Table 2. Estimates of general combining ability effects of lines and testers for different characters

Source of variation	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Pods per plant	Seeds per pod	100-seed weight (g)	Seed yield per plant (g)	Harvest index (%)	Protein content (%)
Lines										
GG-1	-1.67**	1.17**	0.84	-0.21**	-1.98**	-0.01	-1.74**	-0.40	-0.25	-0.43**
Dahod yellow	-0.58*	0.81*	-1.28**	-0.16**	-7.30**	-0.06 *	-0.57	-1.39**	-3.10**	0.02
GG-2	2.25**	-1.97**	0.44	0.37**	9.28	0.08**	2.31**	1.78**	3.35**	0.42*
SE (Gj) ±	0.28	0.39	0.48	0.06	0.62	0.03	0.30	0.28	0.70	0.16
Testers										
GCP-105	4.56**	-0.03	-3.75**	0.32*	12.94**	0.09	-2.49**	0.83	3.97*	0.09
GCP-106	-4.11**	-5.36**	-2.73*	-0.31*	-0.10	-0.09	2.33**	-0.34	-4.76**	-0.26
GCP-9504	-1.00	-4.25**	0.59	0.07	-0.90	-0.06	2.37**	-0.69	-2.06	0.09
GCP-9514	3.89	6.31**	1.93	0.07	-7.76**	-0.04	2.94**	-0.13	-2.67	0.16
GCP-9516	1.44*	4.31**	1.34	-0.31*	-14.30**	-0.09	-2.75**	-2.27**	-2.63	-0.33
GCP-9601	-3.11**	-0.69	3.92**	-0.22	-4.77**	-0.02	-1.52*	-1.24	1.50	0.09
GCP-9605	-1.22	1.53	1.79	-0.24	-5.32**	0.03	-1.26	-0.93	-0.35	0.29
GCP-9626	-3.11**	-1.03	-3.65**	-0.28*	1.74	-0.04	3.95**	-1.80**	-3.07	-0.96*
GCP-9629	-0.67	3.86**	0.78	0.34*	5.28**	-0.11	0.44	0.78	0.67	0.64
GCP-9630	2.11**	2.08*	-3.75**	0.34*	1.48	0.20**	1.99**	2.13**	3.89*	0.87
GCP-9707	1.00	0.19	2.58*	-0.02	5.12**	0.07	-3.66**	3.81**	-0.61	0.16
GCP-9709	0.22	-6.92**	0.94	0.23	6.61**	0.05	-2.34**	-0.17	0.78	-0.54
SE (Gj) ±	0.65	0.92	1.12	0.14	1.45	0.06	0.69	0.66	1.64	0.37

* Significant at 5% ** Significant at 1%

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Short communication

Effect of sex expression on seed yield of jatropha (*Jatropha curcas*)

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Jatropha curcas popularly known as Ratanjyot or Nepalo in Gujarati offers large potential to be grown as Agro-forestry crop. *Jatropha*, native to America is a small evergreen monoecious tree belonging to family Euphorbiaceae (chromosome no. 2n = 22) and closely related to castor. It thrives well on any type of soil and climate of hardy to dry weather conditions. *Jatropha* has variety of uses as medicinal, ornamental, fence and biofuel species. The oil percent in seed varies from 30-35 per cent depending upon availability of soil moisture and other environmental factors (1). The *Jatropha* oil can be used as bio-diesel, for making soaps, in cosmetics, in varnish industry and as an illuminant in villages. Since this plant can be grown on any type of soils, the face of arid wasteland can be changed if it is cultivated on commercial basis. Thus, there is a need not only to grow this crop on a large scale but also for its improvement so as to make it economically attractive and feasible to the growers.

Opening of Male –female flower is important for seed yield stability of jatropha. The present paper, therefore, is an attempt to provide some information on the causes of unstable low seed yield of Jatropha under North Gujarat conditions.

Experiment was carried out in the Jatropha plantation available at All India Co-ordinated Research Network Project on Under Utilized Crops, Center for Crop Improvement, S.D. Agricultural University, Sardarkrushinagar. Ten plants were selected randomly in each genotype of Advance Varietal trial to study number of male and female flower developed on the bunch in July-August 2007 and July-August 2008. In this investigation, ten well-developed inflorescence from each of ten plants were selected at random for recording observations on number of male and female flowers per bunch, number of capsules per bunch, number of bunches per plant and seed yield per plant.

Table1. Male-Female flower ratio and effect on seed yield per plant during *kharif* 2007 and *kharif* 2008.

Sr. No.	Genotype	*Kharif* 2007				*Kharif* 2008			
		Male Female flower Ratio	Av. No. of bunches/ plant	Av. No. of capsules/ bunch	Seed yield / plant(gm)	Male Female flower Ratio	Av. No. of bunches/ plant	Av. No. of capsules/ bunch	Seed yield / plant(gm)
1	Chatrapati	16:1	15.67	3.13	38.2	23:1	14.50	1.85	17.15
2	Urlikanchan	18:1	14.00	3.13	20.8	27:1	11.12	1.18	14.35
3	S K N Big	21:1	19.93	4.00	32.06	29:1	13.60	1.19	16.55
4	Hansraj	19:1	5.93	2.20	31.03	28:1	8.15	1.35	15.60
5	SKNJ-2	24:1	13.80	2.83	7.27	33:1	12.10	1.71	9.62
6	ISJ-1	20:1	14.40	3.67	29.05	26:1	11.16	1.35	14.56
7	PhuleJ-1	17:1	11.20	3.33	30.58	24:1	9.17	1.41	15.25
8	Hisar J-1	18:1	10.73	3.13	16.37	30:1	9.18	1.65	14.50
	Mean	19:1	13.21	3.18	25.67	28:1	11.12	1.46	14.70
	CD (0.05)		2.47	0.73	3.60		4.16	0.24	4.35
	CV (%)		18.46	22.70	13.85		19.42	12.05	14.32

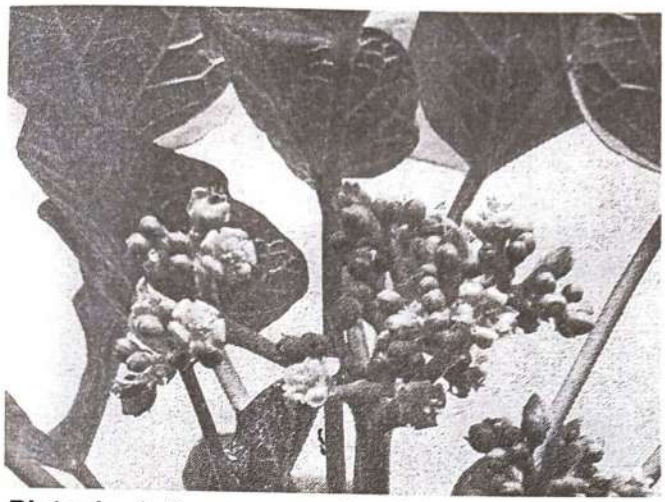

Plate 1. Inflorescence showing more number of male flower than female flower on bunch of Jatropha.

In *Jatropha*, flowering was started during first week of July and remained continue up to second week of January with its peak period during August to September. Duration of flowering observed was similar to the findings of Solomon and Ezradanam (2). Seed yield was found unstable during both the years (Table 1). The male: female flower ratio ranged from 16:1 to 24:1 and 23:1 to 33:1 during *kharif* 2007 and *kharif* 2008, respectively. These results were in accordance with the findings of Reddi and Reddi (3) in *J. gossipifolia* (11:1) and Ravindrababu *et al.*, (4) in *J. curcas* (15:1 to 19.1). Average number of bunches per plant were 13.21 and 11.12 during *kharif* 2007 and *kharif* 2008, respectively. Average number of capsules per plant were 3.18 and 1.46 in *kharif* 2007and 2008, respectively. The seed yield per plant in *kharif* 2007 was 25.67 gm/plant and in *kharif* 2008, the same was 14.70 gm/plant.

The onset of flowering was recorded in first week of July to second week of January with its peak period during August to September. The male: female flower ratio ranged from 16:1 to 33:1. Therefore, it can be seen that seed yield is unstable due to high male – female flower ratio. The opening of male and female flower depends on atmospheric temperature, soil fertility, availability of soil moisture and age of plant. Hence, it is advised that the efforts should be made to reduce male-female sex ratio through effective and appropriate breeding programme.

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Short communication

Screening of mustard genotypes for salt tolerance under laboratory condition

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Among the oilseed crops, mustard [*Brassica juncea* (L.) Czern & Coss] is an important *rabi* oilseed crops which is widely grown in this Northern belt of the country. About 7.1 lakh hectare land is salt affected in Gujarat. Information on salinity tolerance is scanty in mustard. Reports available so far generally pertain to salinity tolerance for germination (1, 2, 3) which are not the reliable index of absolute salinity tolerance in crop production. The salt tolerance in mustard varies from variety to variety (4, 5). An investigation was therefore, undertaken on various mustard genotypes to find out the effect of salinity on germination and seedling growth and to identify genotypes which have better tolerance for the said situation under controlled condition.

An experiment was conducted for one year at the Main Castor-Mustard Research Station, GAU, S. K. Nagar under laboratory conditions in petridishes adopting CRD with Twenty mustard genotypes viz., Pusabahar, RH-30, Jagannath, Pusa Agrani, Varuna, Narendra Rai, Kranti, Bio-902, T-9, RLM-619, RTM-314, T-27, Vaibhav, Pusabold, CS-52, JM-1, GM-1, GM-2, SKM-9803 and SKM-9812 at three concentrations of salinity viz., 4 ds/m, 6.0 ds/m, 8.0 ds/m and control (distilled water), each treatment repeated three times. The salt solutions of different levels (ECe ds/m) were prepared by mixing different salts keeping the SAR constant i.e.10. The experiment was under taken in Petri dish keeping the germinating paper in dish. The size of germinating paper was 10 cm. Before placing the germinating paper in dish, the paper was dipped in distilled water for 1 hour to remove toxic chemicals present in the paper. The paper was dried and two germinating paper circles of 10 cm diameter were placed at the bottom of glass Petri dishes and duly moistened with thin film of measured quantity of salt solution of desired salinity. The measured quantity of Hogland nutrient solution was also poured on germinating paper to supply required nutrients for growth of the plant in each dish. Hundred seeds of uniform size were treated with 0.02 % $HgCl_2$ solution to avoid fungus growth were evenly placed on the germinating paper in each Petri dish. The dishes were kept in growth chamber keeping required temperature and humidity. The measured quantity of distilled water was recorded daily up to 5 days after sowing. After 10 days, observations on the root, shoot length and dry weight of seedling were recorded. The Seedling Vigour Index was calculated by the following formula as suggested by Abdul-Baxi and Anderson (6).

Seedling Vigour Index = Germination % x Mean dry weight of seedling

In general, germination percentage declined in all the genotypes with increase in salinity (Table-1). However, few genotypes viz., T-9, Narendra Rai, Jagannath, RH-30, Pusabahar and Bio-902, Pusa Agrani, Kranti, RTM-314, SKM-9803 and SKM-9812 recorded sufficiently higher (97.7-99.0) germination than the other genotypes tested at 6.0 ds/m but at higher level of salinity (8.0 ds/m). RTM-314 recorded significantly the maximum germination per cent which was on par with T-9, Narendra Rai, Jagannath, RH-30, Pusabahar and Bio-902. At lower salinity level (4.0 ds/m), Pusa Agrani has the maximum germination per cent which was on par with Pusabahar, RH-30, Jagannath, Narenda Rai, Kranti, Bio-902, T-9, RTM-314, Pusa bold, SKM-9803 and SKM-9812. The low germination (%) was observed in GM-1 at all salinity levels. (1 and 7) observed similar effects of salinity on germination of Indian mustard and Safflower seeds.

There is a gradual decrease in shoot length over salinity levels from 4.0 ds/m to 8.0 ds/m. At salinity level of 4.0 ds/m, RH-30 recorded the maximum shoot length which was on par with Pusabahar and Varuna followed

Table 1. Salinity effect on germination percentage

Genotypes	Salinity (ds/m)				
	0	4	6	8	Mean
Pusabahar	100.0	98.7	98.0	97.7	98.9
RH-30	99.0	99.0	97.7	97.7	98.1
Jagannath	99.0	99.0	98.0	97.7	98.5
Pusa Agrani	99.7	99.3	99.0	98.0	99.0
Varuna	99.0	97.0	95.7	95.7	96.8
Narendra Rai	99.7	98.3	98.0	98.0	98.5
Kranti	98.0	98.3	97.7	97.0	97.8
Bio-902	99.7	99.0	97.7	97.7	98.5
T-9	99.0	98.7	98.0	98.0	98.9
RLM-619	99.3	95.7	95.0	95.0	97.2
RTM-314	99.7	99.0	98.7	99.0	99.1
T-27	99.7	96.0	96.0	96.0	98.3
Vaibhav	97.0	96.0	95.3	95.0	95.8
Pusa bold	98.0	98.0	95.7	95.3	96.5
CS-52	95.0	96.0	94.7	93.7	94.8
JM-1	98.7	94.7	94.0	95.7	96.0
GM-1	78.7	78.7	73.0	72.7	75.8
GM-2	96.3	96.0	95.7	90.7	94.7
SKM-9803	99.3	99.0	97.7	94.0	97.5
SKM-9812	98.0	98.0	97.7	92.0	96.8
Mean	97.5	96.9	96.2	94.8	
CD at 5 %					
Variety (V)					1.45
Salinity (S)					0.65
Variety x Salinity					2.89
CV %					1.88

by Pusa Agrani and T-9. At the salinity level of 6.0 ds/m, Pusabahar gave significantly the highest shoot length followed by Varuna and Vaibhav. The mustard genotype Vaibhav, RH-30 and T-9 were on par with respect to shoot length. The genotype, Pusabahar has the maximum shoot length which was on par with Varuna and Bio-902 genotypes followed by RLM-619 and RH-30.

The control treatment (0 ds/m) recorded the highest root length in all the genotypes. There is a gradual decrease in root length with increase in the levels of salinity. At the salinity level of 4.0 ds/m, Pusabahar recorded significantly the maximum root length which was on par with Varuna and T-27. Vaibhavnand SKM-9803 were next in root length. Jagannath has the maximum root length followed by RLM-619, Pusa Agrani, Varuna and SKM-9812, at 6.0 ds/m salinity level. The mustard genotypes, Jagannath recorded significantly the maximum root length. Varuna, Pusabahar, RH-30 were second highest in root length followed by RH-30 and Bio-902 which were on par. Dhawan *et al.*,(7) observed decrease in shoot and root length with the increase in salinity levels in mustard crop. Similar results were also observed in the present case in respect of root length of mustard.

Table 2. Effect of salinity on shoot length and root length

Salinity dSm^{-1} / Genotypes	Shoot length (cm)					Root length (cm)				
	0	4	6	8	Mean	0	4	6	8	Mean
Pusabahar	6.63	8.65	7.98	5.72	7.25	12.08	9.85	6.36	4.40	8.17
RH-30	5.75	.948	6.19	4.88	6.44	11.49	8.04	5.54	4.06	7.28
Jagannath	6.00	6.61	5.56	4.30	5.62	9.15	8.48	8.40	5.47	7.87
Pusa Agrani	5.40	7.53	5.83	4.31	5.77	10.35	6.88	8.71	3.28	6.80
Varuna	6.16	8.83	7.10	5.58	6.92	11.23	9.53	6.68	4.77	8.05
Narendra Rai	6.01	7.35	4.73	3.73	5.45	10.26	6.80	4.48	1.55	5.77
Kranti	5.66	6.80	5.32	4.03	5.45	8.99	6.54	3.98	2.62	5.53
Bio-902	5.72	7.49	5.47	5.23	5.98	10.38	8.16	4.32	3.51	6.59
T-9	6.23	8.09	6.19	4.49	6.25	7.42	4.47	1.52	1.34	3.69
RLM-619	5.20	7.48	5.59	4.98	5.81	10.70	6.45	7.12	3.18	7.37
RTM-314	6.59	6.77	5.49	4.75	5.89	9.56	7.69	5.59	3.06	6.48
T-27	6.92	6.42	5.80	4.11	5.81	9.86	9.55	5.22	2.35	6.75
Vaibhav	4.97	6.87	6.61	3.61	5.51	9.67	8.96	6.32	1.65	6.65
Pusa bold	5.70	6.96	5.38	3.75	5.45	10.74	8.67	5.06	2.85	6.83
CS-52	5.15	6.06	5.31	4.44	5.24	12.38	7.99	5.43	3.27	7.27
JM-1	5.19	5.51	5.38	2.18	4.57	10.88	8.00	6.25	1.17	6.57
GM-1	4.65	5.66	4.87	2.30	4.37	12.46	6.61	4.79	0.93	6.20
GM-2	5.79	6.88	5.68	4.14	5.62	12.55	7.42	5.09	2.90	6.99
SKM-9803	5.30	7.07	5.40	4.01	5.45	14.41	8.81	5.65	2.90	7.94
SKM-9812	6.08	7.02	6.05	3.71	5.72	10.77	8.58	6.74	2.57	7.17
Mean	5.76	7.15	5.80	4.21		10.77	7.97	5.56	2.89	
CD at 5 %										
Variety (V)					0.55					0.75
Salinity (S)					0.25					0.33
Variety x Salinity					1.10					1.49
CV %					12.05					11.72

The mean dry weight/seedling (Table-3) was recorded for all the genotypes. It was observed that as salinity levels increased, dry weight of seedling significantly decreased in all genotypes screened. At the salinity levels of 4.0 ds/m, Bio-902 recorded significantly the highest dry weight of seedling, which was followed by Narendra Rai, SKM-9803 and Pusa bold. At the salinity level of 6.0 ds/m, the mustard genotype GM-2 significantly recorded the highest value of dry weight of seedling which was at par with Bio-902. At the salinity level of 8.0 ds/m, GM-2 significantly gave the highest value, which was followed by Bio-902 and SKM-9803.

Seedling Vigour Index decreased significantly in all genotypes with increased in salinity (Table-3). Among the screened genotypes, Bio-902 showed significantly higher Seedling Vigour Index whereas GM-1, T-9 and Kranti exhibited lower Seedling Vigour Index.

The interaction effect of the treatment vis-à-vis genotypes presented in the Table-1, Table-2 and Table-3 clearly showed a favourable response in respect of all the parameters studied. It is concluded that Bio-902, Narendra Rai, Jagannath, Pusa Agrani, Varuna, Pusabahar and Pusabold were found to be tolerante genotypes.

Table 3. Effect of salinity on Dry weight (mg) of seedling and Seedling Vigour Index

Salinity dSm^{-1} / Genotypes	Dry weight (mg)					Seedling Vigour Index				
	0	4	6	8	Mean	0	4	6	8	Mean
Pusabahar	3.75	3.96	3.93	3.81	3.86	374.7	388.0	390.4	372.8	381.5
RH-30	3.02	3.72	3.55	3.29	3.39	296.0	368.0	347.1	320.9	333.0
Jagannath	3.66	3.97	4.29	3.81	3.93	362.4	394.7	420.1	372.0	387.3
Pusa Agrani	3.11	3.84	4.09	3.74	3.70	309.6	381.2	405.1	370.5	366.6
Varuna	3.58	3.95	4.10	3.91	3.88	354.4	382.8	392.6	373.7	375.9
Narendra Rai	3.87	4.79	4.76	3.61	4.26	386.0	470.6	466.6	353.7	419.3
Kranti	2.54	3.03	2.71	2.28	2.64	249.2	297.8	264.8	221.0	258.2
Bio-902	4.13	5.25	4.86	4.45	4.67	412.0	519.4	475.0	434.7	460.3
T-9	2.18	2.86	2.45	2.74	2.56	216.1	282.1	243.7	270.6	253.4
RLM-619	2.88	3.71	3.80	3.30	3.42	286.4	363.2	319.0	202.3	292.8
RTM-314	2.03	2.56	2.47	2.27	2.33	253.0	244.3	225.0	233.2	238.9
T-27	2.34	2.89	2.85	2.57	2.66	282.9	280.1	249.3	319.9	283.1
Vaibhav	3.30	3.89	3.87	3.64	3.67	319.9	373.5	369.4	345.5	352.1
Pusa bold	3.56	4.41	4.35	3.98	4.08	345.8	432.0	416.4	380.0	393.6
CS-52	3.06	3.96	3.83	3.56	3.60	290.4	380.2	362.6	333.6	341.8
JM-1	3.56	4.33	4.35	3.98	4.06	351.6	409.3	426.0	368.7	389.0
GM-1	3.07	3.96	3.76	3.56	3.59	241.5	311.6	274.8	259.5	271.5
GM-2	3.00	4.05	4.92	4.89	4.22	289.3	388.6	470.3	442.5	397.6
SKM-9803	3.87	4.39	4.18	4.38	4.20	384.0	434.4	407.8	411.9	409.6
SKM-9812	3.66	4.27	4.50	4.15	4.15	358.4	418.7	442.2	392.7	403.0
Mean	3.21	3.89	3.88	3.60		318.2	376.0	368.4	339.0	
CD at 5 %										
Variety (V)					0.15					15.6
Salinity (S)					0.03					7.00
Variety x Salinity					0.11					31.2
CV %					5.23					5.56

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Short communication

Effectiveness of carbosulfan (Marshal 25 EC) against Cumin aphids

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Field efficacy of some insecticidal treatments viz., carbosulfan 25 EC @ 625, 1250 and 2500 ml/ha and thiomithoxam 25 WG @ 100 gm/ha and imidacloprid 17.8 SL @ 100 ml/ha was evaluated against cumin aphids during 2001-02 and 2002-03 at Sardarkrushinagar. Application of carbosulfan 25 EC @ 2500 ml/ha was found most effective in reducing aphid infestation and increasing grain yield followed by carbosulfan 25 EC @ 1250 ml/ha .Other insecticidal treatments were also proved effective over control. Moreover, no symptoms of phytotoxicity were observed in any of the treatments. It was also found that the residue of carbosulfan was below detectable level (i.e. < 0.1 ppm) in cumin seeds.

Cumin *Cuminum cyminum* L. is one of the important seed spices of north Gujarat. The crop is attacked by few insect pests. The coriander aphid, *Hydaphis corianderi* Das and mealy plume aphid, *Hyalopterus pruni* Geoffroy were reported to damage in cumin crop (1).The population of aphids reached at a peak level during the month of January in Gujarat (2).In congenial climatic conditions the crop is infested severely by aphids resulting in heavy reduction in grain yield. The conventional systemic insecticide methyl-o-demeton when applied through high volume sprayer was found less effective than CDA for the control of aphids in cumin crop this might be due to narrow leaf canopy of cumin (3).

Field experiments were laid out during rabi season of 2001-02 and 2002-03 in RBD with 5m x 2.4m plot size to study the effectiveness of carbosulfan and some newer insecticides against aphids in cumin crop. The cumin cultivar Gujarat cumin -2 was sown in lines at a spacing of 30 cm and one spray of each treatment viz., carbosulfan (Marshal 25 EC) @ 625, 1250 and 2500 ml/ha and thiomethoxam (Actara 25 WG) @ 100 gm/ha and imidacloprid (Confidor 17.8 SL) @ 100 ml/ha was applied when the aphid infestation observed in the field. The number of umbels infested by aphids and total number of umbels were recorded from ten randomly selected and tagged plants from each plot before and 1,3,7 and 10 days after spraying. Phytotoxicity symptoms if any were recorded in each treatment after spraying. The seed yield was recorded at harvest. The residue analysis was done for cumin seed sample obtained from the treatment of carbosulfan in the laboratory of Jai Research Foundation, Vapi.

The pooled results of two seasons (Table 1) reveled that the treatment of carbosulfan (Marshal 25 EC) @ 2500 ml/ha was the most effective treatment as it recorded significantly the higher reduction in aphid infestation at 1,3,7 and 10 days after the treatment than other treatments followed by carbosulfan 25 EC @ 1250 ml/ha. The treatment, carbosulfan @ 2500 ml/ha recorded the highest reduction of 82.0 % in aphid infestation at 3 days after spraying and 57.45% reduction at 10 DAS and proved superior. The treatments thiomethoxam and imidacloprid recorded less than 40 per cent reduction and found less effective. Maximum seed yield (474.0 kg/ha) was in the treatment carbosulfan 25 EC @ 2500 ml/ha followed by carbosulfan 25 EC @ 1250 ml/ha (389.0 kg/ha). Both these treatments were also recorded the higher net gain of Rs 12405 and Rs 9345 per ha, respectively than the other treatments and proved economical for the control of aphids in cumin crop. Moreover ocular observations did not reveled symptoms of phytotoxicity in any of the treatments. It was also found that the residue of carbosulfan was below detectable level (i.e.< 0.1 ppm) in the sample of cumin seeds taken one month after the spray.

Table 1. Effect of different treatments on aphid infestation in cumin with economics

Sr. No.	Treatments	Infestation (%) Pre treatment	Reduction in aphid infestation days after spraying (%)				Cumin yield (Kg/ha)	Increase in yield over control (Kg/ha)	Cost of treatment (Rs/ha)	Realization over control (Rs/ha)	Net gain (Rs/ha)
1.	Carbosulfan 25 EC @ 1250ml/ha	61.71 (51.77)*	22.83 (28.54)	35.52 (36.58)	24.11 (29.41)	19.33 (29.08)	372.5	210.0	465.0	9450.0	8985.0
2.	Carbosulfan 25 EC @ 2500ml/ha	64.00 (53.13)	37.19 (37.58)	71.95 (58.02)	53.69 (47.12)	45.52 (42.43)	389.0	226.5	847.5	10192.5	9345.0
3.	Carbosulfan 25 EC @ 625ml/ha	61.65 (51.74)	39.43 (38.90)	82.00 (64.90)	65.29 (53.90)	57.45 (49.28)	474.0	311.5	1612.5	14017.5	12405.0
4.	Thiamethoxam 25WG @ 100gm/ha	64.37 (53.35)	16.92 (24.29)	32.44 (34.72)	26.77 (30.94)	15.27 (23.00)	328.0	165.5	682.5	7447.5	6764.5
5.	Imidacloprid 17.8 SL @ 100ml/ha	62.63 (52.32)	25.00 (30.00)	38.62 (38.42)	21.97 (27.97)	15.04 (22.82)	369.0	206.5	402.5	9292.5	8890.0
6.	Control	63.78 (53.00)	-	-	-	-	162.5	-	-	-	-
	C.D. at 0.05	NS	1.14	3.06	2.04	2.16	70.36				

*Figures in parentheses are arc sin transformed values

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Short communication

Relative susceptibility of different varieties/genotypes of okra against fruit and shoot borer, *Earias vittella* (Fabricius) on okra

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The *Earias vitella* (Fabricius), shoot and fruit borer is one of the most important pest among the various insect pests of okra crop grown in different parts of India and causes 67% damage to fruits(1) and 50% loss to fruit yield (2). To minimize this tremendous loss by the pest several insecticides are often used but using them for the purpose they also impair the valuable environment by leaving undesired residues consequently destruction of natural enemies and other non target species, hazardous to human health, resistance to insecticides and resurgence of the pest to combat pest on vegetables the bio pesticides offers great importance. However the bio pesticides are not as effective as conventional insecticides when used alone. Under this circumstance, identification of tolerant variety is very useful. Even though, it is difficult to obtain total resistance against the pests, identification of less susceptible variety can also solve the problem to greater extent.

To study the relative susceptibility of different recommended and promising okra varieties/genotypes against fruit and shoot borer, *E. vittella*, a field experiment was conducted at College Farm, College of Agriculture, Junagadh Agricultural University, Junagadh during *Kharif* 2003 in plots having size of 5 x 1.2 m(Gross) keeping 60 x 30 cm row to row and plant to plant spacing. Twenty varieties/ genotypes were tested for this purpose. Twenty treatments were replicated three times in randomized block design. All agronomic practices and crop husbandry were adopted as per scientific recommendations. Ten plants of each genotype/variety were selected randomly and were examined thoroughly and observations on number of infested and healthy shoots as well as infested fruits were recorded at each picking. The data thus, obtained were converted to per cent fruit damaged and subjected to statistical analysis for assessing the relative susceptibility of genotypes/varieties under study.

Shoot infestation

The data on mean per cent shoots infestation revealed that the infestation of *E. vittella* ranged from 7.70 to 18.65 per cent in different varieties/genotypes (Table 1)

Among different 20 varieties/genotypes of okra, the genotype JO (2000-S)-4 was least susceptible with recording 7.70 per cent damage to shoots. However, it was par with JO (2000-S)-12, JOL-1, Pusa Sawani, JOL-01-5, JOL-01-4, AOL-95-32, JOL-3, JOL-01-1, Punjab-7 and JOL-02-10 which recorded 8.29, 8.29, 9.81, 10.32, 10.73, 11.06, 12.03, 12.03, 12.17 and 13.19 per cent damage to shoots, respectively. On the basis of per cent shoots infestation the variety HRB-55 was most susceptible with 18.65 per cent shoots infestation. However, it was at par with the Arka Abhay, Gujarat Okra-1, Gujarat Okra-2, JOL-02-2, No: 210602, Arka Anamika, Pabhani Kranti and JOL-2 which showed 17.74, 17.74, 17.63, 17.63, 16.66, 15.41, 14.40 and 14.26 per cent infestation to shoots, respectively.

Fruit infestation

The data on mean per cent fruit infestation revealed that the mean per cent infestation to fruits (on number basis) due to *E. vittella*, of all the picking was ranged from 39.37 to 65.71 per cent on different 20 varieties/ genotypes (Table 1). It was evident from the data (Table 1) on mean per cent fruits infestation, the genotype JO (2000-S)-4 was least susceptible to *E. vittella* than the other varieties/genotypes and which showed 39.37 per cent infestation to fruits. However,

Table 1 Incidence of *E. vittella* in different okra varieties/genotypes under unprotected condition during *kharif*, 2003.

Sr. No.	Okra varieties/genotypes	Mean Per cent fruit infestation	Mean Per cent shoot infestation
1	JO(2000-S)-4	38.86*(39.37)	2.78**(7.70)
2	JO(2000-S)-12	39.78(40.93)	2.88 (8.29)
3	JOL-1	40.89(42.85)	2.88 (8.29)
4	JOL-2	48.56(56.19)	3.78 (14.26)
5	JOL-3	46.38(52.40)	3.47(12.03)
6	NO: 210602	49.48(57.78)	4.08 (16.66)
7	JOL-01-1	47.55(54.45)	3.47(12.03)
8	JOL-01-4	45.15(50.27)	3.28 (10.73)
9	JOL-01-5	45.66(51.14)	3.21(10.32)
10	JOL-02-2	50.61(59.73)	4.20 (17.63)
11	JOL-02-10	47.12(53.69)	3.33 (11.06)
12	AOL-95-32	47.73(54.75)	3.63 (13.19)
13	Gujarat Okra-1	52.18(62.39)	4.21(17.74)
14	Arka Anamika	48.79(56.60)	3.93 (15.41)
15	Pusa sawani	43.10(46.68)	3.13 (9.81)
16	Parbhani Kranti	48.67(56.39)	3.80 (14.40)
17	Punjab-7	46.88(53.27)	3.49 (12.17)
18	HRB-55	54.16(65.71)	4.32 (18.65)
19	Arka Abhay	50.48(59.50)	4.21(17.74)
20	Gujarat Okra-2	50.34(59.26)	4.20 (17.63)
	S. Em. ±	2.49	0.33
	C.D. at 5 %	7.13	0.93
	C.V. %	9.15	15.60

*Angular transformed values ** Square root transformed values

Figures in parenthesis indicates the retransformed values

it was par with JO (2000-S)-12, JOL-1, Pusa Sawani, JOL-01-4 and JOL-01-5 as they registered 40.93, 42.85, 46.68, 50.27 and 51.14 per cent infestation to fruits, respectively. The mean per cent infestation to fruits was maximum (65.71 per cent) in variety HRB-55 and therefore, which was rated as most susceptible to *E. vittella*. However, it was at par with Gujarat Okra-1, JOL-02-2, Arka Abhay, Gujarat Okra-2, No: 210602, Arka Anamika, Pabhani Kranti, JOL-2, AOL-95-32, JOL-01-1 and JOL-02-10 as they were recorded 62.39, 59.73, 59.50, 59.26, 57.78, 56.60, 56.39, 56.19, 54.75, 54.45 and 53.69 per cent fruits infestation, respectively. The genotype JOL-3 (52.40 per cent fruits infestation) and variety Punjab-7 (53.27 per cent fruit infestation) were moderately susceptible.

The above findings are more or less in close agreement with the results reported by Gupta and Yadav (3), Mote (4), Madav and Dumbre (5), Dhandhapani (6), Ratanpara (7), Sharma and Dhankar (1989), Sardana and Dutta (9), Vyas and Patel (10), Kumbhar *et al.*,(11), Kadivar (12) and Srinivas and Sureetha (13).

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Short communication

Correlates of annual net income from crop + dairy farming system

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In our situation having an advantage of better natural resource and endowments. maximization of returns form land can be best ensured by integrating of crop and dairy enterprises. Net returns of a farm is influenced by several components of the system.

To find out the relationship of these subtomponents with farm returns, the present study was conducted in six district of South Gujarat viz.Bharuch, Narmada, Surat, Valsad, Navsari and Dangs. These districts are located mainly in three pans of South Gujarat. viz.upper, middle and lower parts. Bharuch and Narmada districts are in the upper part of South Gujarat.Surat district is in the middle part and Valsad, Navsari and Dangs districts are located in the lower part of South Gujarat.

These districts have tribal people in all talukas. The highly tribal populated talukas were selected from these districts. Three villages from each taluk as were purposively selected on the basis of concentration of tribal population. From each village 10 respondents were randomly selected. Thus, total 180 respondents were selected for the study.

To get a comprehensive idea of the inter - correlation between annual net income from crop +dairy farming system. 23 independent variables of Bharuch, Narmada, Surat, Valsad, Navsari and Dangs district's farmers were studied. These variables were grouped in to four categoies

Socio-economic variables

It was found that annual net income from Crop + dairy farming system was positively and significantly carrelated with operational land holding, herd size and gross income from mixed farming by marginal, small, medium and pooled sampled farmers.Education of only medium and pooled sampled farmers was positively and significently corrleated with annual net income. Age and family size of all marginal, small, medium and pooled sampled farmers was not found correlated with annual net income. The present findings confirm with the findings of singh (1) and Islam *et. al.* (2).

Socio-phychological variables

It was found that annual net income from crop + dairy farming system was positively and significantly correlated with attitude towards dairy farming and management orientation by marginal, small, medium and pooled sampled farmers.

Extension contact of only medium and pooled sampled farmers was positively and significantly correlated with annual net income. Extension participation of all marginal, small, medium and pooled sampled farmers was not found correlated with annual net income. The findings get the support from the findings of singh (1) and Islam (2).

Crop enterprise variables

All six variables, namely, use of bullock labour, manual labour, FYM use, expenditure in crop enterprise, gross income in crop enterprise and net income in crop enterprise showed a positive and significant correlation with annual net income from crop + dairy farming system. This finding was in line with the findings of Singh (1).

Dairy Enterprise variables

All seven variables, namely, manual labour, milk yield, milk consumption, marketed milk, expenditure in livestock enterprise, gross income in live stock enterprise and net income in livestock enterprise were positively and significantly correlated with annual net income from crop+dairy farming system. This finding is supported by the finding of Singh (1) and Ly and Draw (3).

Out of 23 independent variable only 18 variables namely, operational land holding, herd size, gross income from mixed farming, attitude towards dairy farming, management orientation, use of bullock labour, manual labour (crop), FYM use, Expenditure (crop), Gross income (crop), Net income (crop),

Table 1. Relationship of annual net income of marginal, small, medium and pooled sample of farmers from mixed farming with independent variables.

Sr. No.	Independent Variable	Zero order correlation (r)			
		Marginal (N=60)	Small (N=60)	Medium (N=60)	Pooled (N=180)
Socio-economic variables					
1.	Age	0.16600	0.03495	-0.07105	-0.17448
2.	Education	0.20905	-0.16143	0.56338**	0.35041**
3.	Family size	-0.05083	-0.08968	-0.05844	0.0 I289
4.	Operational land holding	0.72455**	0.41672**	0.84029**	0.43704**
5.	Herd size	0.88479**	0.83836**	0.70122**	0.35418**
6.	Gross income from mixed fanning.	0.99199**	0.98002**	0.94971**	0.97339**
Socia-psychological variables					
7.	Extension part icipation	-0.35749	0.03692**	0.00144**	0.03957**
8.	Extension contact	-0.3011	0.17046**	0.46787**	0.45181**
9.	Attitude towards dairy farming	0.82612**	0.77600**	0.68242**	0.79333**
10.	Management Orientation	0.97207**	0.95552**	0.85805**	0.93815**
Crop enterprise related variables					
11.	Use of bullock labour	0.93235**	0.90889**	0.83684**	0.76782**
12.	Manual labour	0.90032**	0.94426**	0.80575**	0.89692**
13.	FYM use	0.94801**	0.93137**	0.84674**	0.89672**
14.	Expenditure (crop)	0.96538**	0.91558**	0.79804**	0.89709**
15.	Gross income (crop)	0.98418**	0.96568**	0.95116**	0.96801**
16.	Net income (crop)	0.98389**	0.97265**	0.96763**	0.97873**
Livestock enterprise related variables					
17.	Manual labour	0.87358**	0.84598**	0.79089**	0.84166**
18.	Milk yield	0.96581**	0.9451 0**	0.87526**	0.93632**
19.	Milk consumption	0.80408**	0.95454**	0.86496**	0.88470**
20.	Marketed milk	0.96590**	0.94259**	0.87590**	0.93551**
21.	Expenditure (livestock)	0.94727**	0.91483**	0.77575**	0.88197**
22.	Gross income (livestock)	0.98645**	0.97906**	0.92140**	0.96414**
23.	Net income (livestock)	0.96905**	0.94618**	0.93235**	0.95601**

** Significant at 0.01 level of probability

Manual labour (livestock). Milk yield, Milk consumption, Marketed milk, Expenditure (livestock), Gross income (livestock) and Net income (livestock) were positively and significantly correlated with annual crop+dairy farming system for marginal, small, medium and pooled sample. Education and extension contact variables showed a positive and significant correlation with annual net income from crop + dairy farming system for medium and pooed sample only.

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