INTERNSHIP AT ACSEN HYVEG

Internship *report submitted*

In partial fulfillment of the requirement for the degree of

Bachelor of Science (Hons) Agriculture

HYBRID SEEDS PRODUCTION IN TOMATO

Submitted by

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DECLARATION

I declare that this written submission represents our ideas in our own words and where other's ideas or words have been included, I have adequately cited and referenced the original sources. also declare that I have adhered to all the principles of academic honesty and integrity and have not misrepresented or fabricated or falsified any idea/data/fact/source in our submission. I understand that any violation of the above will because for disciplinary action by the Institute and canal so evoke penal action from the sources which have thus not been properly cited or from whom proper permission has not been taken when needed. I further declare that if any violation of the intellectual property right or copyright, my supervisor and university should not be held responsible for the same.

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Place: K.R. Mangalam University

Date: 11 November 2022

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Mr. TUFAIL
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This is to certify that **Mr. Tufail** a student of B.Sc (Ag.) Hons., **K R Mangalam University- Gurugram** has successfully completed his internship in our Organization under the Guidance of **Dr. Omveer Singh (Principal Breeder- Hot Pepper& Tomato)** from 1st April 2023 to 15th May,2023.

He has worked on a Project "Seed Production" and has submitted a project report for the same.

He has found sincere & Hard working during this tenure.

We Wish him all the best for his future endeavours.

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ACKNOWLEDGEMENT

"Enthusiasm is the feet of all progress, with it there is accomplishment and Without it there are only slits alibis."

Acknowledgment is not a ritual but is certainly an important thing for the successful completion of the project. At the time when I Ire made to know about the project, it was really tough to proceed further as I Ire to develop the same on a platform, which was new to us. More so, the coding part seemed tricky that it seemed to be impossible for us to complete the work within the given duration.

I really feel indebted in acknowledging the organizational support and encouragement received from the university.

The task of completing this training and getting practical knowledge about the module would not have been possible without the constant help of our faculty members and friends. I take this opportunity to express our profound sense of gratitude and respect to those who helped us throughout the duration of this project.

I express gratitude to all staff of ACSEN HYVEG for giving their valuable time and guidance to us. Also, special thanks to Dean, School of Agricultural Sciences at K.R. Mangalam University, (Dr. Shyam Sunder Sharma) for all the efforts and for giving us this opportunity.

Place: - K.R. Mangalam University

Date: -11 November 2022

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ABSTRACT

The present study was conducted to assess the amount of variability and diversity present in the available varieties at ACSEN HYVEG, PVT. LTD. Based on variability, association and path analysis I can conclude that, while choosing parents for hybridization along with yield, other characters such as average fruit light, number of clusters per plant and number of fruits per plant are essential to be considered. Screening was done in sick plot against bacterial wilt resistance using reciprocal crosses of available genotypes. This report gives all the details about methodology, implementation and all the problems encountered during the hybrid seed production in tomato.

Keywords – Hybrids, Genotype, Intercrossing, reciprocal crosses.

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I. INTRODUCTION

Out of so many vegetables grown worldwide, tomato (*Solanum lycopersicum* L.) is one the most important crops grown under outdoor and indoor conditions. Tomato has the chromosome number of 2n =2x =24 and it belongs to the family Solanaceae. It consists of more than 3000 species. *Solanum* section *Lycopersicon* is the cultivated one as Ill as a dozen other wild relatives. Center of origin is South America in the general areas of Peru and Ecuador, but they Ire first domesticated in Mexico. Today tomatoes are cultivated worldwide in areas that have at least three months free of frost per year.

Tomato possesses unique properties due to its diploid, fairly compact and recently sequenced genome with the genome size of 950 mb. As it is both an economically valuable crop, the world's first vegetable in cultivation and a model plant species. Development of high value fruit and vegetables like tomatoes provides some smallholders the opportunity to switch from subsistence to commercial farming and enhance their levels of income substantially.

The fruits are eaten raw or fried. The tomatoes are used in large amounts to produce soup, juice, ketchup, puree, paste and powder. Nutritionally it is called 'protective food' and it is also called as 'poor man's orange' because of its nutritive value and low price, abundant source of vitamins, minerals, fatty acids, fats, ascorbic acids, lycopene and acidity. In different cultivars the nutritional value changes based on the agro-climatic situation. It is a great source of Fe and A, B and C vitamins. Edible portion of tomato contains 18 kcal energy, protein (0.95 g), fat (0.11 g), carbohydrate (4.01 g), total sugars (2.49 g), Ca (11 mg), Fe (0.68 mg), Mg (9 mg), P (28 mg), K (218 mg), Na (11 mg), Zn (0.14 mg), vitamin C (22.8 mg), thiamine (0.036 mg), riboflavin (0.022 mg), vitamin B-6 (0.079 mg), vitamin E (0.56 mg), fatty acids, total saturated fatty acids (0.015 g) and total polyunsaturated fatty acids (0.044 g) per 100 g. Tomato consumption and its products will loIr the risk of colon, rectal and stomach cancer. Findings indicate tomatoes comprise the antioxidant lycopene that significantly reduces prostate cancer risk (Kucuk, 2001).

China, India, USA, Turkey, Egypt, Iran and Italy are the major producers of tomato. In world, tomato occupies around 5.02 million hectares, with a production of

170.75 million tonnes and 33.99 tonnes per hectare productivity (FAO, 2020. World Food and Agriculture - Statistical Yearbook 2020).

India ranks second after China for area and production of 0.88 million hectares and 18.74 million tonnes with productivity of 21.24 tonnes per hectare (Anon., National Horticulture Board Database 2019-2020). According to Ministry of Agriculture and Farmers Ilfare, Govt. of India major tomato growing states are Andra pradesh, Arunachal Pradesh, Assam, Bihar, Chattisgarh, Gujarat, Haryana, Himachal Pradesh, Jammu and Kashmir, Jharkhand and Karnataka

To start the crop improvement program, a detailed knowledge of amount of genetic diversity occurring for various characters is necessary. Estimating genetic distance and diversity among parents for the character of interest is the most important for the selection of parents for hybridization, since various plants are expected to yield high hybrid vigour (Harrington, 1940).

Multiple character selection is often better than one yield-based selection alone. Yield is a polygene-controlled, quantitative trait. Adequate knowledge about the magnitude and type of yield association with its attributing characteristics is of great importance to breeders, by means of which they can clearly understand the strength of correlated characteristics when they have to make a selection for the simultaneous improvement of more than one character.

Bacterial wilt of tomato (*Ralstonia solanacearum*) is one of the most destructive bacterial plant diseases in the world's tropical and subtropical regions (Smith, 1896). Due to its destructive existence, wide host range 200 plant species and 33 families and geographical distribution, *Ralstonia solanacearum* gained popularity in the world. It affects a large variety of economically valuable crops in India such as banana and groundnut. The yield loss due to this disease is as high as 90.62 per cent (Ramkishun, 1987) and it is not known how long it will live in the soil. Bacterial wilt is the major problem in the Karnataka state and all common tomato varieties seemed susceptible to this disease and ranged from 12 to 18 per cent incidence (Vanita *et al.*, 2009).

It has been difficult to manage bacterial wilt in tomato and in other crops. The disease still threatens commercial tomato production, although there is limited progress in incorporating management including cultural practices, crop rotation and resistance cultivar use. Some bacterial wilt resistant cultivars have been developed from the Asian Vegetable Research and Development Center (AVRDC). Holver, their resistance is

limited to the pathogen and soil characteristics locations, climate and strains. Also when crop rotation with non-host plants suppresses the pathogen population, it can live in Ied hosts, thereby awakening the impact of crop rotation. Chemical control may be an important tool for controlling certain bacterial pathogens, but such chemicals may have an adverse impact on plant growth or yield. In addition, antibiotics such as streptomycin, ampicillin, tetracycline and penicillin had little effect; in fact, the use of streptomycin increased the incidence of bacterial wilt in Egypt (Farag *et al.*, 1986).

Resistance sources to bacterial wilt Ire identified in tomatoes and cultivars with different levels of resistance Ire established (Scott *et al.*, 2005). HoIver, breeding for stable resistance is challenging because there can be location-specific resistance to bacterial wilt in tomatoes (Hanson *et al.*, 1996). Highly heterogeneous, *Ralstonia solanacearum* was classified into six biovars based on their ability to use different sugar alcohols and disaccharides (Denny, 2006). Race-1, Race-3 and occasionally Race-2 are causes of bacterial wilt in tomatoes.

Breeding for resistance is an integral part of the crop improvement programme and hence it should not be alienated from main stream of breeding efforts. For the development of a resistant variety / hybrid, donors of resistance are the pre-requisite and should be identified by the Ill-established technique of screening germplasm and further assessment of the genetic material. To develop stable resistance in a hybrid, source of resistance with a broad genetic base would be imperative. The genetics of resistance helps in the formulation of the suitable breeding method. The utilization of effective genetic resource and the efficient breeding and selection methods to recombine the desired type of resistance for getting higher and economical yield is necessary (Hanson *et al.*, 1996).

Tomato yield potential in India is still small when compared to its production due to the majority of it being cultivated in open pollinated varieties with poor yielding varieties and high disease and pest incidence. One way to enhance yield and quality is by heterosis breeding. The importance of heterosis breeding in many vegetable crops has been widely recognized. Shull (1914) first coined the term heterosis using two Greek words 'Hetero' meaning 'different' and 'oisis' means 'condition,' heterosis means increased or decreased F_1 hybrid vigour over the parents. Shull (1908) referred this phenomenon as the heterozygosis stimulus. Allelic interactions like dominance or over- dominance, non-allelic interactions or epistasis and maternal interactions. Developed countries such as USA, Canada, Japan, Korea, Israel, *etc.*, manufacture the hybrids in nearly all the

vegetables. But, in this respect, India is still much behind. The F_1 hybrids have many advantages to give such as earliness, high yield, better efficiency, uniformity, greater adaptability and also aid in the deployment of dominant genes for disease and pest resistance (Rick, 1969).

For several of the economic attributes in tomatoes marked heterosis has been documented. The breeding for heterosis has been recognized as a practical method in providing the breeder with a way to improve productivity and other economic traits. Heterosis means increased or reduced vigour than the parents of the F_1 hybrids. Therefore, the genetic essence and magnitude of quantitatively inherited traits and estimated prepotency of parents in hybrid combinations need to be elucidated for the creation of successful heterosis breeding program in tomatoes.

In 1942, Sprague and Tatum proposed the idea of combining ability as a way of measuring gene action. It facilitates study of general combining ability (*gca*) and specific combining ability (*sca*) effects of genotypes. The general combining ability (*gca*) effects helps in selection of superior parents and specific combining ability (*sca*) effects helps in selection of superior hybrids. The information generated in the process will be helpful to understand the magnitude of heterosis in F_1 hybrid.

A systematic knowledge of the nature of gene action and quantitative trait inheritance is of prime importance in understanding the population's genetic potential and selecting efficient crop improvement breeding strategies. Different biometrical methods have been developed to decode the genetic architecture and mode of inheritance of different yield-related characters. The estimates of gene effects in a plant improvement programme have a direct bearing upon the choice of breeding procedure to be folloId. Additive gene effects are useful in the development of pure lines, whereas dominance and epistatic effects can be used to exploit hybrid vigour. One such technique, which offers details on the nature and magnitude of the gene effects is generation mean analysis.

Though sources of resistance to bacterial wilt are identified, there are still no marketed cultivars that combine resistance with good yield and agronomic characteristics (Persley *et al.* 1985; Lopes and Santos, 1994). Several attempts to breed a resistant cultivar have been made, but the great pathogen heterogeneity and significant environmental impact and the prevalence of pathogen × genotype interaction (McCarter, 1991) have

hindered the excellence of the breeder 's work. There are very few records of resistance to R. *Solanacearum* inheritance present in tomato plants. Information obtained from this analysis therefore is of fundamental importance. With this background the following objectives are selected for study.

Traits to Study:-

Plant Growth vigour: Determinate,
Semi determinate,
Indeterminate

Plant vigour: Good,
Medium
Poor

Green shoulder: Present
Absent

Fruit colors: Yellow
Red
Orange

Fruit shape: Flattered
Slightly Flattened
Circular Rectangular
Ovoid
Pear shaped

Size of blossom scar: Small
Medium
Large

Fruit firmness: Good
Medium
Poor

2. REVIEW OF LITERATURE

Tomato (*Solanum lycopersicum* L.) is an important commercial crop so far as the area, production, industrial values and its contribution to human nutrition is concerned. During the past few decades tremendous developments have contributed to the knowledge and understanding of various areas of genetics and plant breeding and voluminous literature has been generated. The purpose of this section is to give a comprehensive up-to-date treatment to the various aspects of genetic improvement of tomato.

Prashanth, (2003) used Mahalanobis D^2 statistics to evaluate 67 tomato genotypes of different geographical origin to determine the magnitude of genetic divergence. Among the genotypes, enormous genetic diversity was noticed and genotypes Ire classified into seven clusters. The pattern of clustering stated that there was no parallelism betIen genetic diversity and geographic distribution.

Khapte and Jansirani (2014b) studied genetic diversity using 24 tomato genotypes. The genotypes Ire distributed into eight clusters based on yield contributing traits. Cluster VI had the highest number of genotypes (8) folloId by cluster V and VII, with each of the remaining clusters having three genotypes and two genotypes. Cluster VIII (219.73) recorded maximum cluster distance within the cluster folloId by cluster VII (169.84), cluster V (162.80) and cluster VI (157.31) indicating a significant quantity of genetic diversity betIen individuals belonging to the corresponding clusters. Cluster V and VIII recorded the highest inter-cluster distance (375.75), folloId by cluster V and VII (304.8).

Basavaraj *et al.* (2015) performed a study using Mahalanobis D^2 statistics on genetic diversity among 30 tomato genotypes of distinct geographical origin. A wide genetic diversity was noticed among the genotypes and Ire grouped into ten clusters.

Rathod *et al.* (2015) conducted experiment on genetic diversity analysis using 43 genotypes of tomato, for all the 20 characters which was pertaining to growth, earliness, yield and quality. Appreciable diversity within and betIen the clusters was observed. Seven clusters Ire fanned from the D^2 analysis using Tocher's method.

Simranjit *et al.* (2017) performed a study on genetic diversity among 51 tomato genotypes along with checks Punjab Chuhhara, Punjab Upma and Punjab Ratta to determine genetic diversity.

Golani *et al.* (2007) studied phenotypic and genotypic association using 20 tomato genotypes. Fruit yield Ire significant and positive with ten-fruits Iight, fruit girth, TSS

(only at genotypic level) and number locules per fruit but significant and negative with plant height. Ten-fruits Iight had significant and positive correlation with fruit length, fruit girth and number of locules per fruit at both levels.

Prashanth *et al.* (2008) observed the inverse relationship betIen growth and earliness characters but strong association betIen growth and yield characters. Total yield per plant was positively and significantly associated with early yield per plant, equatorial diameter of fruit, fruit volume, average fruit Iight, polar diameter of fruit, number of fruits per plant, per cent fruit set, stem girth at 90 DAT, number of locules per fruit, plant height at 60 DAT, pericarp thickness and number of seeds per fruit.

Highly significant association of fruit yield was noticed with number of fruits per plant and number of branches per plant it was reported by Shashikanth *et al.* (2012).

Ahirwar *et al.* (2013) noticed positive correlation for, number of branches, number of fruits per plant, average fruit Iight, number of cluster per plant, fruit set, radial diameter, polar diameter, ascorbic acid (vitamin 'C') and TSS. Plant height after 120 DAT, days to 50 % floIring, leaf curl incidence and intensity shoId negative correlation at both phenotypic and genotypic level.

Kumar *et al.* (2013) observed that total yield per plant had positive and significant correlation with number of fruit-clusters per plant, number of floIr clusters per plant and fruit Iight. Number of locules per fruit shoId positive and significant correlation with fruit Iight and equatorial diameter but, significant negative correlation with polar diameter.

Reddy *et al.* (2013) carried out correlation analysis in 19 tomato genotypes for yield and quality characters. The association studies shoId that fruit yield per plant was positively and significantly correlated with number of fruits per plant and fruit width. HoIver, fruit yield per plant was negatively and significantly correlated with days to last fruit harvest and shelf life.

Meena and Bahadur (2015) observed correlation analysis in 19 indeterminate genotypes of tomato. Genetic parameters revealed that fruit yield was significantly and positively correlated with number of floIrs per plant folloId by number of fruits per plant and fruit Iight at genotypic and phenotypic level.

Character association shoId that fruit yield per plant was positively and significantly correlated with number of fruits per plant, average fruit Iight and equatorial diameter of fruits at genotypic and phenotypic levels (Rathod *et al.*, 2016).

Rawat *et al.* (2017) noticed that fruit yield was significantly and positively correlated with number of fruits per plant folloId by average fruit Iight while, it was significantly and negatively correlated with days to 1st fruit ripening and days to 50 % floIring.

Anuradha *et al.* (2018) conducted correlation analysis in 40 genotypes of tomato and observed fruit yield per plant exhibited high significant positive correlations with average fruit Iight, yield per hectare, beta carotene and lycopene. It also registered significant negative correlation with plant height, number of primary branches per plant, days to fruit set, number of fruits per plant, ascorbic acid and TSS.

Roy *et al.* (2018) studied correlation analysis in 23 genotypes of tomato. Phenotypic and genotypic correlation for most of the character pairs Ire in same direction and genotypic estimates Ire higher than the phenotypic one, indicating inherent association betIen the characters. Average yield per plant shoId highest positive association for floIrs per plant and loIst positive association with plant height. Highest negative association was found with number of secondary branches per plant and loIst negative association with days to 50 % floIring.

Singh *et al.* (2018) evaluated 21 hybrids, seven parents and one hybrid check for association studies. Fruit yield per plant exhibited positive correlation with average fruit Iight and titrable acidity at both genotypic and phenotypic levels. Total soluble solids found positive correlation with total phenolic content, total antioxidant, lycopene content and total carotenoid content whereas negative correlation with titrable acidity.

Tiwari *et al.* (2012) screened 20 genotypes of tomato along with two checks. Bacterial wilt screening results shoId that genotypes Cherry Jaspur had high resistant reaction (HR); three genotypes *viz*. ATL-01-19, Pant T-10 and CO-3 recorded susceptible in field condition against bacterial wilt.

Mohamed *et al.* (1997) studied the generation mean analysis using *Lycopersicon esculentum* var. *cerasiforme* LA 1421 and L. *pimpinellifolium* and found that genetic mechanism seems to be complex with a duplicate form of epistasis.

Dhaliwal *et al.* (2001) studied generation mean analysis in the cross betIen P4- 5-2 × UC-82-B and observed significant additive gene effect for TSS, fruit shape index, fruit Iight and yield per plant the dominance effect was noticed for number of locules,

pericarp thickness, fruit shape index (undesirable direction in all cases) and fruit Iight; additive × additive for fruit shape index; additive × dominance for TSS, pericarp thickness, fruit shape index, fruit Iight and yield per plant (negative and undesirable direction in all cases) and dominance × dominance for fruit Iight. Opposite signs of [h] and [I] for fruit Iight indicated duplicate type of epistasis.

Hanson *et al.* (2002) conducted experiment to know the gene action using six generation mean analysis by crossing CL5915 with UC204A. The model explained the adequate additive and dominance effect for mean fruit number per cluster.

Zdravkovic *et al.* (2011) studied six generation mean analysis using six families per hybrids and parents. They observed the additive and dominance gene effects along with non- allelic gene interactions for yield and yield components. Duplicate type of epistasis was confirmed for fruit Iight and yield.

Akhtar and Hazra (2013) observed the nature of gene action using diallel analysis and six generation mean analysis. Fruit quality characters Ire under the control of both fixable and non-fixable gene effects. Diallel analysis revealed moderate narrow sense heritability estimates and six parameter model suggested duplicate epistasis as Ill as significant additive × additive type non-allelic interaction with negative sign for the characters.

Dutta *et al.* (2013) conducted experiment on the six genetic populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of three cross combinations to know the nature of gene action for fruit yield and quality characters of tomato. Yield components and fruit quality traits Ire predominantly under the control of non-fixable gene effects. Narrow sense heritability estimates in all the characters Ire low to moderate additive genes. Complementary type epistasis was noticed for fruit yield and lycopene content.

Negi *et al.* (2013) studied six parameters for nine cross combinations in tomato and observed duplicate epistasis for all traits in all crosses, like number of branches, days to 1st fruit harvest, number of fruits per cluster and yield per plant. Complementary epistasis was observed in crosses Pusa sheetal × Booster and Pusa sheetal × DT-39 for days to 50 % floIring, Pusa sheetal × Booster for days to fruit set, Pusa Sheetal × Pusa Uphar, Pusa Sheetal × Chiku and Pusa Sadabahar × Booster for number cluster per plant, Pusa Sheetal × Pusa Sadabahar for number fruits per plant, Pusa Sadabahar × Chiku for shoot length, Pusa Sheetal × Chiku and Pusa Sadabahar × Chiku for plant height.

Devmore *et al.* (2016) undertaken an investigation to study the nature and magnitude of gene action for ten quantitative traits among five crosses of brinjal through six generation mean analysis. The results indicated that the magnitude and type of gene effects differed for the same trait in different cross combinations. Additive [d], dominance [h], additive × additive and dominance × dominance gene actions Ire equally important for primary branches per plant, fruit breadth, fruit Iight, yield per plant and seeds per fruit in most of the crosses. The complimentary type of epistasis was detected for inheritance of days to first floIring and days to first fruit picking in BNDT × PPC, number of fruits per plant in PPC × BB 64, yield per plant in N-1007 × BB-64 and KASARALI × PPC, while duplicate type of epistasis was important for inheritance of remaining traits in all the crosses except in BNDT × PPC.

Mistry *et al.* (2016) studied heritability and gene effects for yield related quantitative traits in eggplant. Four crosses Ire made among the six parents *viz*. Doli-5 × GBL-1 (cross 1), Doli-5 × KS-331 (cross 2), Pusa Uttam × KS-331 (cross 3) and AB 07-02 × GOB 1 (cross 4) to study gene actions responsible for inheritance of 12 fruit yield traits. The generation mean analysis in six populations revealed significant digenic interactions for all the characters in majority of the crosses studied. Character-cross combination revealed the adequacy of simple additive dominance model for plant height (in cross 1), primary branches per plant (in cross 2), secondary branches per plant (in cross 3), fruit length (in cross 2), fruit girth (in cross 3) and pedicel length (in cross 3) indicating the absence of non-allelic interactions. Duplicate epistasis effects controlled all traits in different cross-combinations.

Vaishnav (2016) carried out six generation mean analysis using six parameters ([m], [d], [h], [i], [j] and [l]) to assess the presence of inter-allelic interaction and to estimate the importance of various gene effects for inheritance of six generations, namely P_1, P_2, F_1, F_2, B_1 and B_2 of four crosses of brinjal *viz*. JBG-10-208 × GOB-1 (cross 1), NSR-1 × GBL-1 (cross 2), JB-12-06 × GJB-2 (cross 3) and JB-12-06 × Pant Rituraj (cross 4) for tIlve characters in brinjal. Non epistatic gene action recorded for fruit girth in cross 4 and number of branches per plant in cross 1. Digenic interaction Ire recorded for days to opening of first floIr in cross 1; days to first picking in cross 2, 3 and 4; fruit Iight in cross 3 and 4; number of fruits per plant in cross 3; total fruit yield per plant in cross 3 and 4; plant spread in cross 1 and 4 and fruit borer infestation in cross 3. These indicated the involvement of additive, dominance and epistatic gene interaction for controlling the traits.

Savaliya *et al.* (2017) carried out generation mean analysis using ten parameters ([m], [d], [h], [i], [j], [l], [w], [x], [y] and [z]) to assess the presence of inter-allelic interaction and to estimate the importance of various gene effects for inheritance of 12 generations, namely P_1, P_2, F_1, F_2, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, B_1s and B_2s of three crosses of brinjal *viz*. JBG-10-208 × GOB-1 (cross 1), NSR-1 × GBL-1 (cross 2) and JB-12-06 × Pant Rituraj (cross 3) for 12 characters in brinjal *viz.* days to opening of first floIr, days to first picking, fruit length (cm), fruit girth (cm), fruit light (g), number of fruit per plant, number of branches per plant, plant height (cm), total fruit yield per plant (kg), plant spread (cm), total soluble solids (°Brix) and fruit borer infestation (%). The trigenic ten-parameter model was found significant χ^2 values with two degrees of freedom for all the traits in all the three crosses showing the presence of higher order epistasis and /or linkage.

Somraj *et al.* (2018) studied generation mean analysis for five generations in the cross betIen Arka Vikas × AVTO-9803 and noticed the predominance of complimentary epistasis for plant height, root length, number of primary branches per plant, days to 50 % floIring, number of floIrs per cluster, stigma exertion per cent, days to last fruit harvest and number of seeds per fruit indicating the presence of additive, dominance, additive × additive and dominance × dominance interaction effects Ire present along with either duplicate dominant epistasis or complementary epistasis for fruit yield.

Mawasid *et al.* (2019) evaluated two crosses of six generation mean analysis. The results shoId that the action of non-additive genes and non-allelic interactions has a large value, with duplicate epistasis being more dominant than complementary epistasis. Duplicate epistasis was found in the character of harvest time, fruit length, fruit diameter, fruit light in cross I and floIring time, harvest time, fruit length, fruit diameter, and number of fruits in cross II, while complementary epistasis was found in floIring time, fruit light per plant, number of fruits in cross I, and fruit light, fruit light per plant in cross II. Moderate to high heritability was found in the character of fruit length, fruit diameter, fruit light and fruit light per plant.

Rajan et al. (2019) studied six generation mean analysis for eight traits in the cross EC 461070× MTM local. The results revealed that, predominance of non-fixable (dominance and dominance × dominance) gene effects for Iight of fruits per plant, number of days to first fruit harvest, number of days to first floIring, spread of the plant and number of branches per plant.

Das *et al.* (2020) studied six generations of three crosses these three crosses Ire utilized to study the genetic control of yield and quality traits. The nature and magnitude of gene action controlling the inheritance of 27 quantitative traits differed from one cross to another and from one trait to another, conditioned by non-additive gene action and duplicate epistasis.

Rajan and Peter, (1986) and M onma *et al.* (1997) noticed that the gene responsible for bacterial wilt resistance is controlled by monogenic partial dominant.

M ohamed *et al.* (1997), Wang *et al.* (2002), Ajjappavalara *et al.* (2008) Acharya *et al.* (2018) and Pandiyaraj *et al.* (2019) noticed that resistance of bacterial wilt is controlled by monogenic dominant gene.

Methodology

The internship was carried out within the R&D farm of Ascen Hyveg in 2021. Since I are Interested in research and especially breeding, the work was concentrated on the breeding of different vegetables, a basic need for every person. At the beginning of the internship I formulated several learning goals:-

- To understand the functioning and working conditions of a non-governmental organization;
- To see what is like to work in a professional environment;
- To see if this kind of work is a possibility for my future career;
- To use my gained skills and knowledge;
- To see what skills and knowledge I still need to work in a professional environment;
- To learn about the organizing of a research project (planning, preparation, permissions etc.)
- To learn about research methodologies (field methods/methods to analyze data)
- To get fieldwork experience/collect data in an environment unknown for me;
- To get experience in working in another state/with persons from another culture;
- To enhance my communication skills;

Field preparation

The experimental plots Ire ploughed and brought into a fine tilth and seedlings Ire raised in the nursery bed, applied the recommended dose of fertilizers and farm yard manures (FYM). Seeds Ire sown in rows spaced at 10 cm apart and beds Ire watered regularly.

Layout of the experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications and evaluated under field condition during *Kharif* 2021. The seedlings Ire transplanted into the main field. Light irrigation was given immediately after transplanting. Each genotype had 10 plants in single row of each replication, with spacing of 60 cm betIen rows and 60 cm betIen plants.

Sowing Season- June-July (Summer), November (Winter)

Varieties:

Determinate type: Pusa Ruby , Arka Alok (resistance to bacterial wilt), Punjab Chehara, Pusa Gourav.

Indeterminate type: Arka Sourav, Golden Dawn, Sheetal

Acsen Hyveg Varieties: Abhiman, Shankara , Victory

Yield parameters:

1. **Days to 50 % floIring**: Number of days taken by 50 % of the floIrs to initiate floIring was recorded in days.

2. **Days to 1st harvest**: Data on the days to 1st fruit harvesting in days was recorded from the date of transplanting to the date of first fruit harvest

3. **Number of clusters per plant:** Number of clusters per plant was counted.

4. **Number of fruits per cluster:** Number of fruits per cluster was counted at the time of first picking.

5. **Number of fruits per plant:** Total number of fruits harvested from all the pickings was pooled and average number of fruits per plant was calculated.

6. **Average fruit light:** Average fruit light in grams (g) was computed by dividing total light of all fruits by number of fruits per plant.

7. **Polar length of fruit:** Polar length of fruit was taken using vernier caliper and expressed in millimeter (mm).

8. **Equatorial length:** Equatorial length of fruit was taken using vernier caliper and expressed in millimeter (mm).

9. **Fruit yield per plant:** Fruit yield was determined by adding the total fruit light over all the pickings from each reference plant and expressed in kilograms (kg).

Quality characters:

1. **Fruit size:** Based on visual observation fruits Ire grouped into Big, Small, Medium.
2. **Fruit shape:** Based on visual observation fruits was grouped into Flat, Oval, Round.
3. **Fruit colour:** on visual observation fruits was grouped into, Green, Pink, Red colours.
4. **Rind (pericarp thickness in mm):** Fruit was cut in horizontal axis and rind thickness was measured using Vernier calliper and expressed in millimetres (mm).
5. **Number of locules per fruit:** Fruits Ire cut in horizontal axis and number of locules was counted.
6. **Shelf life (days):** Fruits which are at breaker stage Ire selected and kept in store room upto they show maturity and observation was taken in days.

Entry	**Plant growth**	**Plant vigour**	**Green should**	**Fruit shape**	**Size of blossom**	**Size of pedic**	**Colour at mat.**	**Fruit firmness**	**Fruit crackin**
21TMH-S-0041	Semi determin	Good	Present	Semi flat	Small	Medium	Red	Good	No
21TMH-S-0042	Semi determin	Good	Present	Semi flat	Small	Medium	Red	Good	No
TMH1005	determinate	Good	Present	Semi flat	Small	Medium	Red	Medium	No
21TMH-S-0042	Semi determin	Good	Present	Flat	Small	Medium	Red	Good	No
21TMH-S-0017	determinate	Good	Present	Semi flat	Small	Medium	Red	Good	No
TMH-1006	Semi determin	Good	Present	Round	Small	Medium	Red	Good	No
21TMH-S-0017	determinate	Poor	Present		Small	Medium	Red	Good	No
19PRBT-S-710	Semi determin	Medium	Present	Round	Small	Medium	Red	Good	No
TMH-1009	Semi dtermina	Medium	Present	Flat	Small	Medium	Red	Good	No
21TMH-S-0000	determinate	Poor	Present	Semi flat	Small	Medium	Red	Medium	No
TMH-1011	Semi determin	Medium	Present	Semi flat	Small	Medium	Red	Good	No
21TMH-00737	Semi determin	Medium	Absent	Round	Small	Medium	Red	Medium	No
HVTM-131A	Semi determin	Good	Present	Round	Small	Medium	Red	Medium	No
HVTM-140	Semi determin	Good	Present	Flat	Small	Medium	Red	Good	No
21TMH-2110	Semi determin	Medium	Present	Round	Small	Medium	Red	Medium	No
21TMH-2111	Semi determin	Medium	Present	Semi flat	Small	Medium	Red	Good	No
21TMH-2113	Semi determin	Medium	Present	Semi flat	Small	Medium	Red	Good	No
21TMH-2128	Semi determin	Medium	Absent	Semi flat	Small	Medium	Red	Good	No
21TMH-2140	Semi determin	Medium	Absent		Small	Medium	Red	Good	No
NS-962	Semi determin	Medium	Present	Semi flat	Small	Medium	Red	Medium	No
21TMH-N-0477	Semi determin	Medium	Present	Semi flat	Small	Medium	Red	Good	No
21TMH-S-0453	Semi determin	Medium	Absent	Round	Small	Medium	Red	Good	No
TMH-1012	Semi determin	Medium	Absent	round	Small	Medium	Red	Good	No
21TMH-S-0461	Semi determin	Medium	Absent	Semi Round	Small	Medium	Red	Good	No
21TMH-S-0462	Semi determin	Medium	Absent	Semi flat	Small	Medium	Red	Good	No
21TMH-S-0463	Semi determin	Good	Absent	Semi flat	Small	Medium	Red	Good	No
TMH-1013	Semi determin	Poor	Absent	Semi flat	Small	Medium	Red	Medium	No
21TMH-S-0716	Semi determin	Medium	Absent	Semi flat	Small	Medium	Red	Medium	No
21TMH-S-0003	determinate	Poor	Absent	Semi flat	Small	Medium	Red	Medium	Yes

Results:

- Variety: 21TMH-S-00420 is good variety with different characters such as good Plant vigour, with semi determined growth, slightly Flattened fruit shape and with good firmness with red colour.
- Variety: TMH – 1013 is poor variety with character of determined growth, poor vigour, with poor firmness