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Evaluation of rice genotypes for their interaction with *Bacillus subtilis* for yield and yield-related traits

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Abstract
The present investigation was carried out ARS, Gangavati during *Kharif* 2021. The experiment was comprised of 20 rice genotypes with 2 replications for both separate *Bacillus subtilis* treated and untreated in RCBD design. The treated (*B. subtilis*) and untreated rice genotypes were assessed for heritability, genetic variability and genetic advance for days to 50% flowering, no of tillers per hill, plant height, no of panicles per hill, flag leaf length, panicle length, panicle weight, grain number per panicle, test weight and yield per plant. Analysis of variances for both treated and untreated rice genotypes revealed sufficient genetic variation has been present in all the traits that studied. High heritability along with high genetic advance as percent of mean was found in the traits *viz.,* plant height, panicle number, flag leaf length, panicle weight, grain number per panicle and test weight. High heritability but the moderate value of genetic advance for days to maturity, days to 50% flowering and panicle length in *B. subtilis* treated genotypes. Thus, selection based on these traits will be effective in improving grain yield in rice along with seedling treatment by *B. subtilis.* Advances in crop mainly demands the presence of wide genetic variability.

Keywords: Rice genotypes, *Bacillus subtilis*, yield and yield-related traits

Introduction
For roughly half of the world's population, rice is one of the main food crops. In the past two decades, it has been noticed that output growth has turned into stagnate. Enhancing the interactions between rice plants and the soil microbiome that occurs around, on and inside the plant is one approach to advance rice output. Today, it is thought that using microorganisms to enhance rice growth and production is an environmentally beneficial way to practise excessive agriculture without harming the environment with agrochemicals or mechanical interventions. the degree to which fitness variations are caused by natural diversity in host genotypes and the associated microorganisms. The results of both agronomic and molecular investigation reveal how microbes control rice plant development, physiological traits, and molecular signalling.

Crops need to be strengthened with salt tolerance, disease resistance, drought tolerance, heavy metal stress tolerance and better nutritional value in order to move toward a sustainable agricultural revolution. Utilizing soil microorganisms (bacteria, fungus, algae, etc.) that increase the water usage efficiency and nutrient absorption capacity is one way to achieve the aforementioned agricultural attributes. The most effective of these latent soil microorganisms are the bacteria known as plant growth-promoting rhizobacteria (PGPR). In this way, PGPR may be employed to stimulate plant growth rate and improve plant health without contaminating the environment. These rhizobacteria have a significant beneficial effect on plant development, and both direct and indirect processes contribute to this. One of the direct techniques is the creation of substances that stimulate plant growth and reduce stress (Goswami *et al*., 2016) [15]. Plant development and the decrease of abiotic and biotic stressors are positively impacted by PGPR's interaction with plant roots in both direct and indirect ways. Antibiosis, systemic resistance induction, competitive omission, and other processes increase plant growth. (Tripathi *et al*., 2012) [13].

The connection between hosts and microbial partners is complex. According to the environment, host genetic impacts on microbial populations vary greatly, making it difficult to draw conclusions about which microorganisms are hindered and which plant activities are crucial. The microbial communities are consistently impacted by host genetic variation across settings, and these effects also contribute to fitness variance across host genotypes. Because host genetics closely correspond with ecologically central bacteria, whether it is beneficial or

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harmful, there will be variance in how well hosts perform when they interact with microbes. (Brachi *et al.,* 2022) [2].

Knowledge of the type and degree of diversity in the available germplasm, the relationship between yield and other agronomic characteristics, and the degree to which environmental conditions promote the expression of these traits are typically necessary for genetic improvement of any breeding programme (Edukondalu *et al.,* 2017) [4]. The capacity of qualities to vary genetically is crucial for breeding and choosing the correct genotype. Understanding a genetic trait's response to selection depends critically on how heritable it is. Heritability can be used to gauge how easily desirable qualities will be passed on to offspring during mating (Sabesan *et al.,* 2009.) [8]. Heritability and genetic advancement have a strong relationship. The most successful conditions for breeders to rapidly pick and advance desirable traits in a population are high genetic advance and high heritability estimates (Larik *et al*., 2000) [6]. Variation in a population is also critical for genetic advancement. Different genetic variability parameters, such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance for yield ascribing traits, are of great concern to any plant breeder and for crop improvement programs.

The main component of breeding programmes for expanding the gene pool of rice is genetic diversity for agronomic qualities. Plant breeders frequently choose yield-related traits that tangentially boost yield. A trait's heritability (h2) is crucial in determining how it reacts to selection. It has been previously discovered that in order to create a well-structured breeding programme, genetic improvement of plants for quantitative traits requires accurate estimations of heritability. Any breeding program's success depends on taking into account the genetic makeup of the target character, the formation and projection of genetic variability in succeeding generations and their interactions with other traits. Since yield is a composite trait that is influenced by many other characteristics, it is crucial to establish the correlation between other characteristics and yield in addition to the genetic variability information. The settings strongly influence and are associated with yield-contributing characteristics (Chandra *et al*. 2009; Prasad *et al*. 2001) [3, 7]. In order to choose the best breeding method and advance both the quantitative and qualitative features, it is essential to assess the various forms of gene activity. To analyse the genetic component of variance for yield and its components, as well as to compute the heritability and genetic progress for 10 characteristics, various genetic investigations in treated and untreated rice genotypes were conducted.

Material and Methods
Twenty genotypes were used as experimental subjects for the current investigation and were obtained from ARS, Gangavathi. Information is provided in Table 1. In the current investigation, the experimental material was assessed using a Randomized Block Design with two replications for both treated (*B. subtilis*) and untreated conditions. On July 24, 2021, seeds were sowed in the seed bed. On August 21, 2021, seedlings were transferred to the main field with a spacing of 20 x 15 cm, and the net plot area was 8 m^2. For the evaluation of yield and yield-attributing features, specifics of the experimental design are provided in Table 2.

Bacillus subtilis strain was obtained from the Centre for DNA Fingerprinting Diagnosis (CDFD) Hyderabad. *B. subtilis*

strain was mass multiplied and treated to the rice seedlings at the time of transplanting for the yield assessment.

B. subtilis was multiplied in Luria broth as per the method adopted by Xie *et al.,* (2015) [14]. Composition of Luria broth is shown in Table 3. Pure culture of *B. subtilis* was inoculated into the Luria Broth and kept for incubation for three days and then the broth culture was mixed with lignite powder as carrier material in the ratio of 1:2 and left for microbial growth for four days in the carrier material. Then the population of *B. subtilis* in carrier material was determined by counting the colony-forming units (CFUs) following the serial dilution method (Johnson and Curl, 1972) [5]. The powder solution was made by dissolving in water. Later the seedlings were dipped in the suspension for 20 min and transplanted to the main field. Standard agronomic procedures were adopted for normal crop growth. The crop was raised by following recommended package of practices. Fertilizers were applied at the rate of 120 kg N, 40 kg P_2O_5 and 40 kg K_2O per hectare. At the time of transplanting half of the nitrogen and the entire dose of P_2O_5 and 50 percent of the K_2O were applied as basal dose. The remaining nitrogen was applied in two equal split doses, one at 30 days after transplanting and another at the panicle initiation stage, remaining 50 percent of the K_2O was applied along with the last dose of N. Intercultural operations like weeding was done at regular intervals and necessary plant protection measures were adopted during the crop growth stage for yield-related traits. Recommended packages of practices were followed during the crop growth period. Observations were recorded for ten characters viz., days to 50% flowering, plant height, no of tillers per hill, no of panicles per hill, flag leaf length, panicle length, panicle weight, grain number per panicle, test weight and yield per plant. Genotypic and phenotypic, Coefficient of variation, heritability and genetic advance were estimated for all ten characters.

Table 1: List of rice genotypes used in the study

Sl. No.	Genotypes	Sl. No.	Genotypes
1.	GNV -1108	11.	Ralhugalli
2.	IET 27870	12.	Gowri sanna
3.	IIRR-93R	13.	Madrasa sanna
4.	GNV 1905	14.	Jasmin black
5.	GNV 1109	15.	Gangavathi sona
6.	IET 25220	16.	BPT-5204
7.	IET 28695	17.	IR 64
8.	RP-BIO-226	18.	RNR 15048
9.	IET-28706	19.	GNV 10-89
10.	Asaliya	20.	MTU 1010

Table 2: Details of the experimental layout

Total number of rice genotypes	20
Plot length	4.0 m
Width of plot	2.0 m
Net plot size	8.0 m^2
Replication	2
Spacing	20 x 15 cm
No. of rows/plot	20
No. of plants/row	13
Total plant population	266 plants/plot
Date of sowing	July 24, 2021
Date of transplanting	August 21,2021
Treatment	*B. subtilis* inoculated to seedlings during transplanting
Untreated	Non-inoculated

Table 3: Luria Broth composition

Ingredients	g / Litre
Tryptone	10
Yeast extract	5
Sodium chloride	5
Final pH (at 25 °C)	7
Distilled water	1000 mL

Result and Discussion

The results of coefficient of variation, heritability and genetic advance for untreated and treated condition are presented in table 4 and table 5. In general, the magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits. The high estimates of phenotypic and genotypic coefficient of variation (> 20%) were recorded for no of tiller per hill (GCV-20.40, PCV-22.85), flag leaf length (GCV-20.47, PCV-21.74), panicle weight (GCV-24.97, PCV-27.58), grain number per panicle (GCV-30.89, PCV-32.37), test weight (GCV-21.86, PCV-22.74) and yield per plant (GCV-22.18, PCV-24.81) for untreated rice genotypes (Fig 1). The treated rice genotypes have shown high estimates of phenotypic and genotypic coefficient of variation (> 20%) for traits (Fig 3) *viz.,* tiller no per hill (GCV-20.17, PCV-23.11), panicle weight (GCV-20.03, PCV-23.06), grain number per panicle (GCV-27.82, PCV-29.37), panicle weight (GCV-20.40, PCV-22.85) and yield per plant (GCV-22.50, PCV-25.28). Differences between GCV and PCV values were implying the influence of the environment on the genotypes. High heritability with high genetic advance were recorded for traits *viz.,* plant height (h^2-74.10, GAM-31.48), tiller no per hill (h^2-79.69, GAM-37.51), panicle number per hill (h^2-70.96, GAM-34.36), flag leaf length (h^2-88.71, GAM-39.72), panicle weight (h^2-81.96, GAM-46.56), grain number (h^2-91.09, GAM-60.73), test weight (h^2-92.38, GAM-43.28) and yield per plant (h^2-79.88, GAM-40.83) for untreated rice genotypes(Fig 2). High heritability with high genetic advance were recorded for traits *viz.,* plant height (h^2-67.89.10, GAM-27.91), tiller no per hill (h^2-76.14, GAM-36.25), panicle number per hill (h^2-72.84, GAM-31.37), flag leaf length (h^2-85.59, GAM-37.33), panicle weight (h^2-75.02, GAM-35.63), grain number (h^2-89.70, GAM-54.28), test weight (h^2-89.46, GAM-38.42) and yield per plant (h^2-79.22, GAM-41.25) for *B. subtilis* treated rice genotypes (Fig 4). High heritability (h^2) with high genetic advance (GAM) shows traits controlled by additive gene action, which might be improved through simple selection methods. Bhor *et al.* (2020) [1], Sudeepthi *et al.* (2020) [12], Srivastava *et al.* (2017) [11], Sandeep *et al.* (2018) [9], Singh *et al.* (2012) [10] and Brachi *et al.* (2022) [2].

Table 4: Mean and other genetic parameters of yield and yield-related traits of untreated rice genotypes

Sl. No.	Characters	Untreated									
		Mean	Range		Variances		Coefficient of variation (%)		H (%)	GA @ 5%	GAM
			Min	Max	Genotypic	Phenotypic	GCV	PCV			
1	DFF	95.93	84.50	110.00	50.42	66.17	7.40	8.48	76.20	12.77	13.31
2	PTH	108.62	80.50	153.50	371.71	501.60	17.75	20.62	74.10	34.19	31.48
3	TN	13.39	8.80	20.50	7.46	9.36	20.40	22.85	79.69	5.02	37.51
4	PN	11.69	7.50	18.00	5.35	7.54	19.80	23.50	70.96	4.01	34.36
5	FL	25.83	14.71	36.00	27.97	31.53	20.47	21.74	88.71	10.26	39.72
6	PL	21.92	16.10	26.10	5.67	8.91	10.87	13.61	63.73	3.92	17.87
7	PW	3.25	1.92	4.95	0.66	0.81	24.97	27.58	81.96	1.52	46.56
8	GN	165.11	71.20	288.50	2601.16	2855.51	30.89	32.37	91.09	100.27	60.73
9	TW	21.52	12.35	29.10	22.12	23.95	21.86	22.74	92.38	9.31	43.28
10	YPP	28.06	15.35	42.50	38.73	48.48	22.18	24.81	79.88	11.46	40.83

Abbreviations: GCV- Genotypic coefficient of variance; PCV- Phenotypic coefficient of variance; Heritability in a broad sense; GA- Genetic advance; GAM- Genetic advance as percent of the mean; DFF- Days to 50% flowering; PTH-Plant height in centimetres; TN- Number of tillers per plant; PN- Number of panicles per plant; FL- Flag leaf length in cm; PL- Panicle length in cm; PW Panicle weight in grams; GN- Number of grains per panicle; TW- Thousand seed weight in grams; YPP- Yield per plant in gram.

Table 5: Mean and other genetic parameters of yield and yield-related traits of *Bacillus subtilis* treated rice genotypes

Sl. No.	Characters	Treated									
		Mean	Range		Variances		Coefficient of variation (%)		H (%)	GA @ 5%	GAM
			Min	Max	Genotypic	Phenotypic	GCV	PCV			
1	DFF	95.73	86.00	112.00	50.58	74.02	7.43	8.99	68.34	12.11	12.65
2	PTH	117.74	86.85	160.25	374.75	552.00	16.44	19.95	67.89	32.86	27.91
3	TN	14.85	9.50	22.50	8.97	11.78	20.17	23.11	76.14	5.38	36.25
4	PN	12.88	8.50	18.30	5.28	7.24	17.84	20.91	72.84	4.04	31.37
5	FL	27.81	16.30	38.50	29.68	34.68	19.59	21.17	85.59	10.38	37.33
6	PL	23.80	19.35	29.50	5.40	8.64	9.77	12.35	62.53	3.79	15.91
7	PW	3.73	2.50	5.50	0.57	0.74	20.03	23.06	75.02	1.33	35.63
8	GN	179.70	81.90	299.00	2499.29	2786.16	27.82	29.37	89.70	97.54	54.28
9	TW	23.44	13.95	30.80	21.37	23.88	19.72	20.85	89.46	9.01	38.42
10	YPP	31.53	16.45	45.00	50.33	63.53	22.50	25.28	79.22	13.01	41.25

Abbreviations: GCV- Genotypic coefficient of variance; PCV- Phenotypic coefficient of variance; H-heritability in broad sense; GA- Genetic advance; GAM- Genetic advance as percent of mean; DFF- Days to 50% flowering; PTH-Plant height in centimetres; TN- Number of tillers per plant; PN- Number of panicles per plant; FL- Flag leaf length in cm; PL- Panicle length in cm; PW Panicle weight in grams; GN- Number of grains per panicle; TW- Thousand seed weight in grams; YPP- Yield per plant in gram
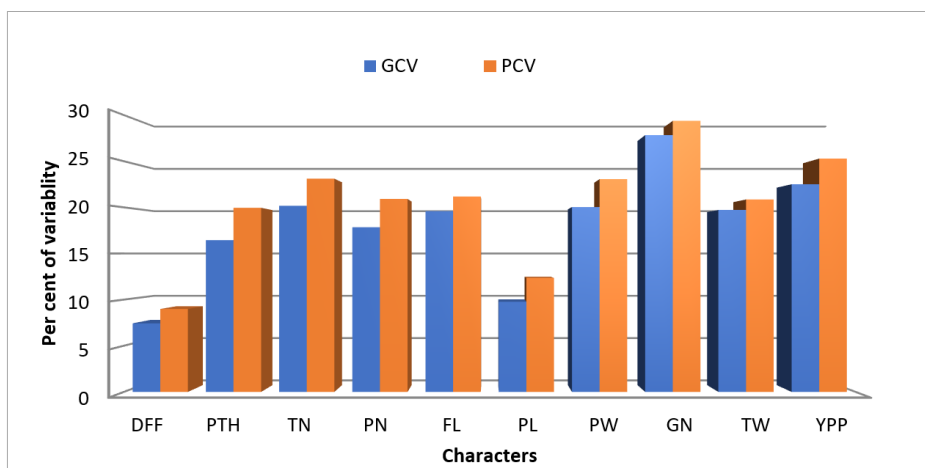
Fig 1: Genotypic (GCV) and phenotypic (PCV) coefficient of variation for different yield and yield-related traits in untreated rice genotypes
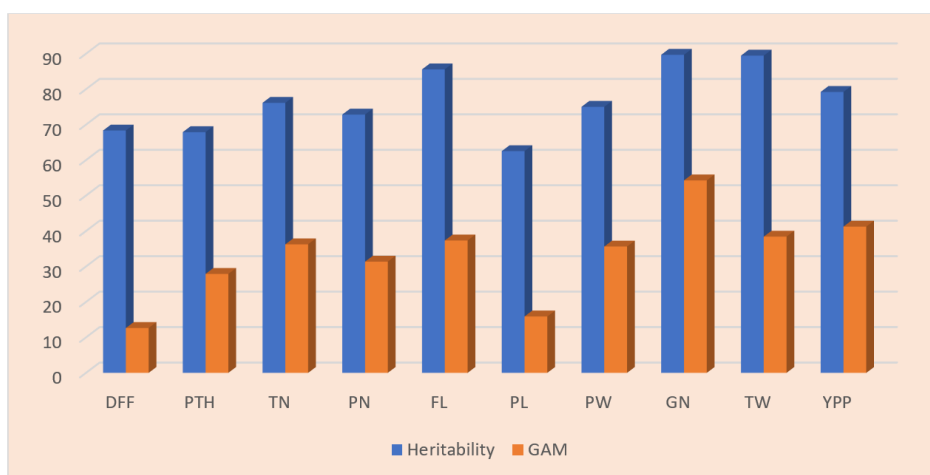

Fig 2: Heritability and Genetic Advance as percent of Mean (GAM) for different yield and yield-related traits in untreated rice genotypes
Abbreviations: DFF- Days to 50% flowering; PTH-Plant height; TN- Number of tillers per plant; PN- Number of panicles per plant; FL- Flag leaf length; PL-Panicle length; PW- Panicle weight; GN- Number of grains per panicle; TW-Thousand seed weight; YPP- Yield per plant.
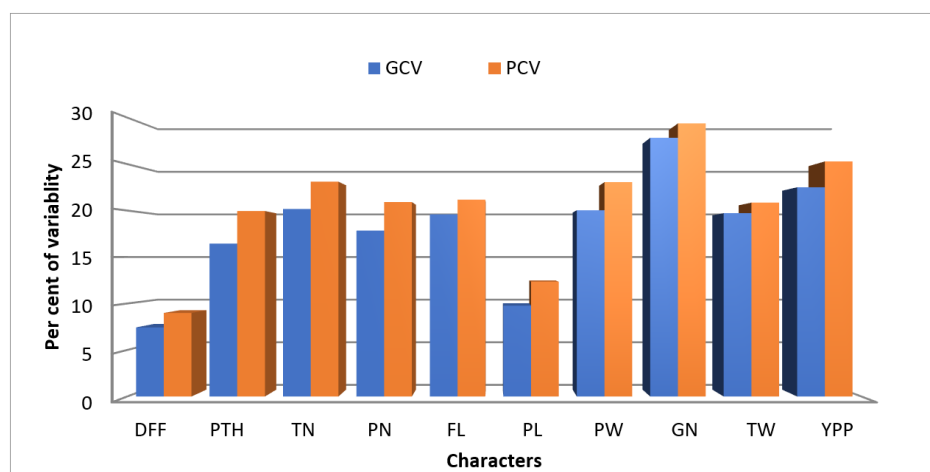

Fig 3: Genotypic (GCV) and phenotypic (PCV) coefficient of variation for different yield and yield-related traits in *Bacillus subtilis* treated rice genotypes
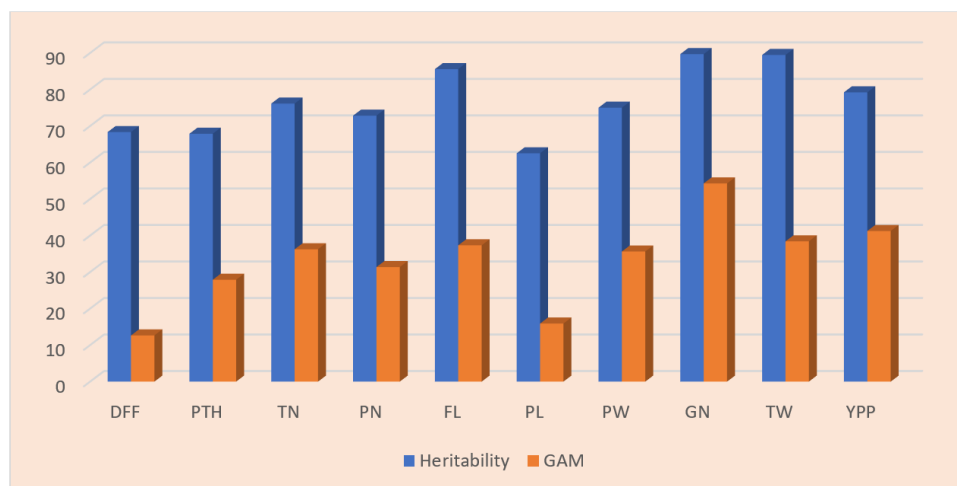
Fig 4: Heritability and Genetic Advance as percent of Mean (GAM) for different yield and yield-related traits in *Bacillus subtilis* treated rice genotypes

Abbreviations: DFF- Days to 50% flowering; PTH-Plant height; TN- Number of tillers per plant; PN- Number of panicles per plant; FL- Flag leaf length; PL-Panicle length; PW- Panicle weight; GN- Number of grains per panicle; TW-Thousand seed weight; YPP- Yield per plant.

Conclusion

The proportional amount of variance among the various qualities is really provided by the coefficient of variation. Higher magnitudes of GCV and PCV suggest more variability for the characteristic under discussion between B. subtilis treated and untreated genotypes. All of the qualities under examination had PCV values that were higher than GCV. However, differences in the magnitude of GCV and PCV detected across all traits revealed the influence of the environment on their expression in genotypes that had not been treated, and for genotypes that had, differences in the magnitude of GCV and PCV detected across all traits may be attributed to the influence of *B. subtilis* and environment. The occurrence of increased trait variability is indicated by higher GCV, PCV, heritability, and GAM. The heritability is most likely caused by additive gene effects, and selection for these characteristics may be successful. The attributes plant height, flag leaf length, panicle number, panicle weight, grain quantity per panicle, and test weight were shown to have strong heritability as well as high genetic progress as a percentage of the mean. In genotypes treated with *B. subtilis*, genetic progress for days to maturity, days to 50% blooming, and panicle length is moderate but heritability is high. In order to increase rice grain production, selection based on these traits will be used in conjunction with *B. subtilis* seedling treatment.

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