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Effect of Beneficial Micro-organisms on Yield of Quinoa (*Chenopodium quinoa* Wild) Based on Relationship among Nutrients Observed in Semi-arid Alfisols

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Abstract

An assessment was made to identify a superior combination of microbial inoculants for attaining maximum quinoa yield based on the relationships among soil nutrients with different beneficial micro-flora and yield under semi-arid alfisols under green house conditions. Five microbial cultures *viz*., *Azotobacter chroococcum*, *Bacillus megaterium, Fraturia aurantia, Pseudomonas fluorescens* and *Glomus fasciculatum* were tested in the study. Pure cultures of selected isolates were sub-cultured on specific medium and maintained in slants for further studies. Seventeen treatments were tested for identifying a superior treatment for attaining maximum soil nutrients, apart from the beneficial microflora and quinoa yield. The Analysis of Variance indicated that the treatments differed significantly in influencing the different parameters and quinoa yield. Based on Duncan's Multiple Range Test, T_{17} inoculated with *Azotobacter chroococcum + Bacillus megaterium + Pseudomonas fluorescens* was superior for attaining significantly higher soil N and P nutrients, seed calcium, magnesium and zinc, free living N fixers and phosphorus solubilizing bacteria, while T_{16} was superior for attaining significantly higher soil K, nutrients and potassium solubilizing bacteria. However, T_{15} was superior for chlamydospore count per 50 g of soil.

Keywords : Beneficial micro-organisms, Quinoa, Nutrient obserption

Among different crops, Quinoa (*Chenopodium quinoa* Wild) commonly known as golden grain, is one of the main food crops of the Andean mountains of Latin America. The crop species has been safe guarded for thousands of years by the inhabitants of Andean region and many countries have recently discovered this crop. The species is characterized by an outstanding protein quality, apart from a high content of most of the vitamins and minerals. The Food and Agricultural Organization (FAO) has considered quinoa as one of the crops that is destined to offer food security in the 21stcentury. An increased consumption of quinoa in the western world and also Asia would improve the markets in all countries which have a traditional production of quinoa. There is a necessity of about 300-1000 mm of rainfall during growing season and no rain is required during the seed maturity and harvesting stages. The quinoa crop would grow efficiently in a sandy, well drained soil with low nutrient content, moderate salinity with soil pH value of about 6.0-8.5. The seed bed should be well prepared and also properly drained in order to avoid water logging condition. The crop would respond to fertilizer Nitrogen and requires NPK @ 120:50:50 kg/ha.

As per FAO, the quinoa grain would provide all amino acids that are essential to the human life in optimum quantities and could be comparable with milk. The protein content of quinoa would range from 7.47-22.08 per cent with high concentration of lysine, isoleucine, methionine, histidine, cystine and glycine. The ash content of quinoa would be about 3.4 per

cent and contains high amount of calcium, iron, zinc, copper and manganese. The oil content is about 1.8-9.5 per cent and is rich in essential fatty acids like linoleate and linolenate. Quinoa seed is rich in thiamine (0.4 mg), folic acid (78.1 mg), vitamin C (16.4 mg), riboflavin (0.39 mg) and carotene (0.39 mg) in 100 g seed. The calorific value is about 350 cal/100 g grain, which is more than that of other cereal and legume foods. Quinoa contains natural anti oxidants like α-tocopheral (5.3 mg), γ-tocopheral (2.6 mg) in 100 g seed and phytoestrogens which prevent chronic diseases like osteoporosis, breast cancer, heart diseases and other feminine problems caused by lack of oestrogen during menopause stage (Bhargava *et al*., 2006).

The importance of beneficial soil micro-organisms in increasing crop productivity has been well documented. The microbial inoculants includes both symbiotic and asymbiotic Nitrogen fixing bacteria, phosphate solubilizing or mobilizing microorganisms, organic matter degraders *etc*. Many researchers have worked on the fundamental as well as applied aspects of various microbial inoculants in various crops. Soil bio-amendments would provide a promising alternative to reduce the harmful effects of pesticides and chemical fertilizers (Bashan, 1998). The plant growth promotion by PGPB may be either through bio-fertilization, phytostimulation or bio-control of plant pathogens (Bashan and De Bashan, 2005). The ability of microorganisms to release various metabolites affecting the plant health and growth would be considered as one of the most prominent factors in the soil fertility (Ping and Boland, 2004). In addition to the above mentioned traits, PGPB must also be rhizosphere competent to flourish and survive in the soil following inoculation (Cattelan *et al.,* 1999). It would be essential to study the effectiveness of different beneficial microorganisms to maximize the plant growth responses. Based on their adaptability and efficiency, both *in-vitro* and *in-vivo* study, we could use these micro-organisms under real agricultural situations for efficient management of soil health in order to promote plant growth, apart from crop production.

Material and Methods

A research study was conducted at University of Agricultural Sciences (UAS), Bangalore to study the effect of beneficial microorganisms on the free living nitrogen fixers, phosphorus solubilizing bacteria, potassium solubilizing bacteria and Chlamydospore count per 50 g of soil and yield of quinoa under pot culture conditions. Free living nitrogen fixer, phosphate solubilizer and potassium solubilizer were collected, purified, mass multiplied, formulated and used in the study. The procedures and techniques adopted as well as material used in the study are described in the following sections.

Microbial Culture Collection and its Maintenance

Different microbial cultures used in our study are (i) *Azotobacter chroococcum* (ii) *Bacillus megaterium* (iii) *Frateuria aurantia* (iv) *Pseudomonas fluorescens* and (v) *Glomus fasciculatum.* These cultures were obtained from Biofertilizer lab, Department of Agricultural Microbiology, UAS, Bangalore. The 24-h old pure cultures of *Azotobacter chroococcum Bacillus megaterium, Pseudomonas fluorescens* and *Fraturia aurantia* were inoculated aseptically into flasks containing Waksmann No.77 broth, Sperber's broth, King's B broth and Aleksandrow broth medium respectively with the help of inoculation loop and were incubated at 30^0C for 3 days for growth. The pure cultures were maintained in the slants for future study (Sahu and Brahmaprakash, 2018).

Azotobacter chroococcum was grown on Waksman No.77 medium, while *Bacillus megaterium* was grown on Sperber's medium. Similarly, *Pseudomonas fluorescens* was grown on king's B medium, while *Frateuria aurantia* was grown on Aleksandrow Agar medium. Pure cultures of *Azotobacter chroococcum*, *Bacillus megaterium, Fraturia aurantia* and *Pseudomonas fluorescens* isolates were subcultured on the specific medium *viz*., Waksman No.77, Pikovskaya's agar medium, Aleksandrow Agar and king's B medium respectively and were maintained in the slants for future study (Gangaraddi and Brahmaprakash, 2018).

TABLE 1
Chemical properties of the soil

Chemical properties	Parameter value	Reference
Soil pH	6.6	pH meter (Piper, 1966)
Electrical conductivity (dS m^{-1})	0.24	Conductometry (Jackson, 1973)
Organic carbon (%)	0.56	Wet oxidation method (Piper, 1966)
Available nitrogen (kg ha^{-1})	342	Alkaline permanganate method (Subbaiah and Asija, 1956)
Available phosphorus (kg ha^{-1})	38.21	Bray's method (Jackson, 1973)
Available potassium (kg ha^{-1})	234.5	Flame photometry method (Jackson, 1973)

Experimental Details

The experiment was conducted with the objective of studying the effect of selected microbial inoculants on the growth and yield of quinoa under greenhouse condition with 17 treatments and each with 3 replications. The soil was sieved with a 4 mm sieve and mixed thoroughly in order to get a homogenous mixture. The pots were filled with well homogenised pot mixture of the soil:sand: FYM in the ratio of 2:1:1 @ 10 kg/pot.

Soil Chemical Properties

The soil samples were analyzed for different parameters *viz*., soil reaction (pH), electrical conductivity (EC), organic carbon (OC), nitrogen (N), phosphorus (P) and potassium (K) by standard procedures as described in Table 1.

Estimation of soil available N was made by using alkaline potassium permanganate method (Subbaiah and Asija, 1956). The soil of 0.5 g was treated with an excess of alkaline 0.32 per cent potassium permanganate (alkaline with 25 % NaOH solution). The liberated ammonia was trapped in the boric acid and was determined by the titration against the standard 1N H_2SO_4. The available N (kg/ha) was computed using the titer value. The available phosphorous in soil (kg/ha) was measured by using Brays-1 reagent. The extracted P was measured by the ascorbic acid method. The intensity of blue colour was measured by using the Spectrophotometer at 660 nm as described by Jackson (1973). The soil K was extracted from air-dried soil samples by shaking with 0.5M ammonium acetate solution for 30 minutes. This was found to effectively displace the potentially available K ions. The K content of the filtered extract was determined by using the flame Photometer (Jackson, 1973).

Treatment Details

Seventeen treatments were considered by including a control (uninoculated) treatment. The treatments were : (i) T_1: Control (only RDF); (ii) T_2: *Azotobacter chroococcum*; (iii) T_3: *Bacillus megaterium*; (iv) T_4: *Glomus fasciculatum*; (v) T_5: *Frateuria aurantia*; (vi) T_6: *Pseudomonas fluorescens*; (vii) T_7: *Azotobacter chroococcum + Bacillus megaterium;* (viii) T_8: *Azotobacter chroococcum + Glomus fasciculatum*; (ix) T_9: *Azotobacter chroococcum + Frateuria aurantia;* (x) T_{10}: *Azotobacter chroococcum + Pseudomonas fluorescens*; (xi) T_{11}: *Bacillus megaterium + Glomus fasciculatum*; (xii) T_{12}: *Bacillus megaterium + Frateuria aurantia*; (xiii) T_{13}: *Bacillus megaterium + Pseudomonas fluorescens*; (xiv) T_{14}: *Glomus fasciculatum + Pseudomonas fluores cens*; (xv) T_{15}: *Glomus fasciculatum + Frateuria aurantia*; (xvi) T_{16}: *Frateuria aurantia + Pseudo monas fluorescens* and (xvii) T_{17}: *Azotobacter chroococcum + Bacillus megaterium + Pseudomonas fluorescens*.

Treatment Imposition / Inoculation

The microbial inoculants of *A. chroococcum*, *B. megaterium, F. aurantia and P. fluorescens* cultures were separately mixed with carrier (talc) and kept for a week for stabilization at room temperature. About 10 g of each carrier based inoculants was applied in each pot just before sowing. Before sowing of quinoa crop, the seed germination (%) test was conducted in

laboratory condition by paper towel method. About 90 per cent germination was observed for the given seeds. The different parameters assessed in this study.

Statistical Analysis

Statistical analysis of data was carried out based on Analysis of Variance using WASP 2.0 (Web Agri Stat Package) software (www.icargoa.res.in/wasp/index.php). Based on Duncan's Multiple Range Test (DMRT), the treatments were compared and tested for significant differences. The treatments were ranked for different parameters and superior treatments were identified based on the rank sums. Estimates of correlation between different parameters were derived and tested to assess the importance of different parameters for explaining the variability in data.

Results and Discussion

Effect of Microbial Inoculants on Post-Harvest Soil Nutrients

Based on Analysis of Variance, the treatments were significantly different in influencing the post-harvest soil N, P and K nutrients at $p < 0.05$ level of significance. The soil N ranged from 315.4 - 367.1 kg/ha with mean of 333.7 kg/ha (CV of 4.2%), while the soil P ranged from 30.4 - 48.2 kg/ha with mean of 39.1 kg/ha (CV of 14.9%). The soil K ranged from 146.5-215.4 kg/ha with mean of 168.1 kg/ha (CV of 13.6%).

Significantly higher soil nitrogen of 367.1 kg/ha and soil P of 48.2 kg/ha were attained by T_{17} of *Azotobacter chroococcum* + *Bacillus megaterium* + *Pseudomonas fluorescens*, while lowest soil N of 315.4 kg/ha and soil P of 30.4 kg/ha were attained by T_1. However, significantly higher soil K of 215.4 kg/ha was attained by T_{16} of *Frateuria aurantia* + *Pseudomonas fluorescens*, while lowest soil K of 146.5 kg/ha was attained by T_1. Based on DMRT criteria, T_{17} was superior compared to all other treatments for attaining significantly higher post-harvest soil N and P, while T_{16} was superior for post-harvest soil K (Table 2).

The increase (%) in soil N of a treatment over control ranged from 0.3-14.1 per cent with mean of 5.7 per cent (CV of 65.2%), while the increase in soil P of a treatment over control ranged from 3.3-36.9 per cent with mean of 21.9 per cent (CV of 51.3%). Similarly, the increase in soil K of a treatment over control ranged from 0-32.0 per cent with mean of 12.2 per cent (CV of 90.2%) (Table 2). Highest soil N and P were attained by the triple inoculant receiving treatment. This was due to the microbial inoculants that favour N fixation capacity by *Azotobacter chroococcum* and also PGPR activity. Chandra *et al*., (2010) reported about an increased dry matter production by application of microbial inoculants, which in turn significantly enhanced the nutrition with respect to N and P supply to the crop, apart from maintaining significantly higher soil N and P under all inoculated treatments. In a study by Bhattacharya (2001), the author has observed about significant response to application of biofertilizers for different crops in agriculture. Das *et al.,* (2007) observed significant effect of microbial inoculants when they applied in *Stevia rebaudiana Bert* commonly grown under the sub-tropics in India.

Effect of Microbial Inoculants on the Beneficial Microflora in Quinoa

Based on Analysis of Variance, the treatments were significantly different in influencing the beneficial microflora (No × $CFUg^{-1}$ of soil) at $p < 0.05$ level of significance. The Free living N fixers (10^3) ranged from 44.60 - 46.28 mg/100 g with mean of 45.15 mg/100 g (CV of 1.0%), while the phosphorus solubilizing bacteria (PSB) ranged from 19.31-37.21 with mean of 20.74 (CV of 16.1%). The potassium solubilizing bacteria (KSB) ranged from 14.12-31.61 with mean of 20.74 (CV of 32.0%), while the chlamydospore count per 50 g of soil ranged from 21.2-58.2 with mean of 34.6 (CV of 28.4%). Significantly higher free living N fixers of 48.31 and PSB of 37.21 were attained by T_{17} of *Azotobacter chroococcum* + *Bacillus megaterium* + *Pseudomonas fluorescens*, while significantly higher KSB of 31.61 was attained by T_{16} of *Frateuria aurantia* + *Pseudomonas fluore scens* and significantly higher chlamydospore of 28.2 was attained by T_{15} of *Glomus fasciculatum* +

TABLE 2

Effect of different treatments on post-harvest soil N, P and K nutrients and their increase over control in quinoa

Treatments	NPK content of soil (Kg/ha)			Increase (%) over control		
	N	P	K	N	P	K
T_1 = Control (only RDF)	315.40 ^{j}	30.41 ^{m}	146.46 ^{j}			
T_2 = *Azotobacter chroococcum* (Ac)	340.40 ^{b}	39.33 ^{g}	160.40 ^{ef}	7.3	22.7	8.7
T_3 = *Bacillus megaterium* (Bm)	332.60 ^{def}	45.33 ^{c}	184.32 ^{d}	5.2	32.9	20.5
T_4 = *Glomus fasciculatum* (Gm)	316.33 ^{j}	31.55 ^{l}	146.46 ^{j}	0.3	3.6	0.0
T_5 = *Frateuria aurantia* (Fa)	325.40 ^{ghi}	42.45 ^{f}	159.24 ^{f}	3.1	28.4	8.0
T_6 = *Pseudomonas fluorescens* (Pf)	334.40 ^{cde}	44.33 ^{d}	190.15 ^{c}	5.7	31.4	23.0
T_7 = *Azotobacter chroococcum* + *Bacillus megaterium*	341.60 ^{b}	32.08 ^{l}	147.60 ^{ij}	7.7	5.2	0.7
T_8 = *Azotobacter chroococcum* + *Glomus fasciculatum*	333.60 ^{cde}	43.35 ^{e}	162.22 ^{e}	5.5	29.9	9.7
T_9 = *Azotobacter chroococcum* + *Frateuria aurantia*	338.24 ^{bc}	37.26 ^{i}	184.32 ^{d}	6.8	18.4	20.5
T_{10} = *Azotobacter chroococcum* + *Pseudomonas fluorescens*	362.33 ^{a}	31.45 ^{l}	146.60 ^{j}	13.0	3.3	0.1
T_{11} = *Bacillus megaterium* + *Glomus fasciculatum*	327.20 ^{fgh}	46.33 ^{b}	162.53 ^{e}	3.6	34.4	9.9
T_{12} = *Bacillus megaterium* + *Frateuria aurantia*	326.26 ^{gh}	45.60 ^{c}	189.60 ^{c}	3.3	33.3	22.7
T_{13} = *Bacillus megaterium* + *Pseudomonas fluorescens*	330.33 ^{efg}	36.53 ^{j}	150.60 ^{gh}	4.5	16.8	2.7
T_{14} = *Glomus fasciculatum* + *Pseudomonas fluorescens*	337.33 ^{bcd}	35.33 ^{k}	150.06 ^{ghi}	6.5	14.0	2.4
T_{15} = *Glomus fasciculatum* + *Frateuria aurantia*	320.40 ^{ij}	37.33 ^{i}	210.20 ^{b}	1.6	18.6	30.3
T_{16} = *Frateuria aurantia* + *Pseudomonas fluorescens*	324.24 ^{hi}	38.56 ^{h}	215.40 ^{a}	2.7	21.2	32.0
T_{17} = *Azotobacter chroococcum* + *Bacillus megaterium* + *Pseudomonas fluorescens*	367.13 ^{a}	48.20 ^{a}	152.22 ^{g}	14.1	36.9	3.8
Minimum	315.4	30.4	146.5	0.3	3.3	0.0
Maximum	367.1	48.2	215.4	14.1	36.9	32.0
Mean	333.7	39.1	168.1	5.7	21.9	12.2
SD 14.1	5.8	22.9	3.7	11.3	11.0	
CV (%)	4.2	14.9	13.6	65.2	51.3	90.2

Frateuria aurantia. The lowest free living N fixers of 16.67, PSB of 19.31 and chlamydospore count per 50g of soil of 21.2 were attained by T_1, while lowest KSB of 14.12 was attained by T_3 of *Bacillus megaterium* (Bm) treatment. Based on DMRT criteria, T_{17} was superior for attaining significantly higher free living N fixers and PSB, while T_{16} was superior for KSB and T_{15} was superior for chlamydospore count per 50 g of soil and compared to all other treatments based on the study (Table 3).

TABLE 3

Beneficial microflora influenced by different treatments and their increase over control in quinoa

Treatments	Beneficial microflora (No × CFUg^{-1} of soil)				Increase (%) over control			
	Free living N fixers (10^3)	PSB (10^2)	KSB (-10^2)	Chlamydospore count per 50g of soil	Free living N fixers (10^3)	PSB (10^2)	KSB (-10^2)	Chlamydospore count per 50g of soil
T_1 =Control (only RDF)	16.67 ^{op}	19.31 ^{l}	15.10 ^{j}	21.20 ^{m}				
T_2	35.10 ^{j}	24.01 ^{k}	16.10 ^{i}	31.08 ^{i}	52.5	19.6	6.2	31.8
T_3	22.05 ^{l}	37.10 ^{a}	14.12 ^{j}	29.11 ^{j}	24.4	48.0	-6.9	27.2
T_4	18.21 ^{n}	36.31 ^{b}	29.81 ^{c}	53.21 ^{b}	8.5	46.8	49.3	60.2
T_5	23.61 ^{k}	35.32 ^{c}	30.81 ^{b}	37.30 ^{f}	29.4	45.3	51.0	43.2
T_6	20.11 ^{m}	27.00 ^{i}	19.20 ^{f}	31.03 ^{i}	17.1	28.5	21.4	31.7
T_7	46.01 ^{c}	37.10 ^{a}	17.30 ^{g}	32.10 ^{h}	63.8	48.0	12.7	34.0
T_8	43.21 ^{d}	30.80 ^{fg}	14.21 ^{j}	35.00 ^{g}	61.4	37.3	-6.3	39.4
T_9	38.33 ^{g}	33.10 ^{d}	16.10 ^{i}	38.30 ^{e}	56.5	41.7	6.2	44.6
T_{10}	47.61 ^{b}	29.21 ^{h}	17.20 ^{g}	29.787 ^{j}	65.0	33.9	12.2	28.8
T_{11}	39.33 ^{f}	30.61 ^{g}	17.31 ^{g}	42.10 ^{c}	57.6	36.9	12.8	49.6
T_{12}	38.32 ^{g}	31.20 ^{ef}	17.41 ^{g}	31.33 ^{hi}	56.5	38.1	13.3	32.3
T_{13}	36.21 ^{i}	31.60 ^{e}	16.61 ^{h}	25.10 ^{k}	54.0	38.9	9.1	15.5
T_{14}	41.21 ^{e}	31.20 ^{h}	19.76 ^{e}	41.07 ^{d}	59.5	38.1	23.6	48.4
T_{15}	37.21 ^{h}	26.31 ^{j}	30.71 ^{b}	58.20 ^{a}	55.2	26.6	50.8	63.6
T_{16}	38.21 ^{g}	35.41 ^{c}	31.61 ^{a}	29.23 ^{j}	56.4	45.5	52.2	27.5
T_{17}	48.31 ^{a}	37.21 ^{a}	29.26 ^{d}	23.07 ^{l}	65.5	48.1	48.4	8.1
Minimum	16.67	19.31	14.12	21.20	8.5	19.6	-6.9	8.1
Maximum	48.31	37.21	31.61	58.20	65.5	48.1	52.2	63.6
Mean	34.69	31.34	20.74	34.60	49.0	38.8	22.2	36.6
SD	10.48	5.06	6.63	9.84	18.2	8.4	21.1	14.8
CV (%)	30.2	16.1	32.0	28.4	37.2	21.7	94.8	40.3

The increase (%) in free living N fixers attained by a treatment over control ranged from 8.5-65.5 per cent with mean of 49.0 per cent (CV of 37.2%), while the increase in PSB of a treatment over control ranged from 19.6-48.1 per cent with mean of 38.8 per cent (CV of 21.7 %). Similarly, the increase in KSB of a treatment over control ranged from -6.9-52.2 per cent with mean of 22.2 per cent (CV of 94.8%), while the increase of chlamydospore count per 50 g of soil of a treatment over control ranged from 8.1-63.6 per cent with mean of 36.6 per cent (CV of 40.3%) (Table 3). Based on the analysis, the treatment T_{17} gave highest increase of free living N fixers and PSB, while T_{16} gave highest increase of KSB and T_{15} gave highest increase of chlamydospore count per 50 g of soil compared to all other treatments. T_4 gave lowest increase of 8.5 per cent of free living N fixers, while T_2 gave lowest increase of 19.6 per cent of PSB. Similarly, T_3 gave lowest increase of -6.9 per cent of KSB, while T_{17} gave lowest increase of 8.1 per cent of chlamydospore count per 50 g of soil compared to all other treatments. In a study by Gu *et al*. (2009), the authors observed similar results on the effects of different amendments on the beneficial urease, invertase, dehydrogenase and polyphenoloxidase activities in a paddy soil.

Effect of Microbial Inoculants on the Yield of Quinoa

Based on Analysis of Variance, the treatments were significantly different in influencing the quinoa grain yield (kg/ha) at $p < 0.05$ level of significance. The grain yield ranged from 1683-2350 kg/ha with mean of 1943 kg/ha (CV of 9.4%). Significantly higher grain yield of 2350 kg/ha was attained by T_{17} involving *Azotobacter chroococcum* + *Bacillus megaterium* + *Pseudomonas fluorescens*, while lowest grain yield of 1683 kg/ha was attained by T_1. The increase (%) of a treatment over control ranged from 2.0-28.4 per cent for grain yield with mean of 13.5 per cent and CV of 55.5 % (Table 4). Thus, significantly higher grain yield (kg/ha) was attained by T_{17} involving *Azotobacter chroococcum* + *Bacillus megaterium* + *Pseudomonas fluorescens* compared to other treatments. Based on DMRT criteria, T_{17} was superior compared to all other treatments for attaining significantly higher quinoa grain yield (kg/ha) (Table 4). Our results are in agreement with the results reported by Shehata *et al*., (2010) on the celeriac plant and also with the results of Erdal Elkoca *et al.,* (2008) in a study on chickpea.

Relationship Between Beneficial Microflora of Free N Fixers, PSB and KSB and Chlamydos Pore count in Quinoa

The relationships between beneficial microflora (No x CFU/g soil) *viz.,* free living N fixers, phosphorus solubilizing bacteria (PSB) and potassium solubilizing

TABLE 4

Effect of beneficial microorganisms on yield and yield increase (%) over control in quinoa

Treatments	Grain yield (kg/ha)	Increase (%) over control
T_1 = Control (only RDF)	1683 ^{q}	
T_2 = Azotobacterchroococcum	2117 ^{c}	20.5
T_3 = Bacillus megaterium	1842 ^{j}	8.6
T_4 = Glomus fasciculatum	1717 ^{op}	2.0
T_5 = Frateuriaaurantia	1883 ^{i}	10.6
T_6 = Pseudomonas fluorescens	1783 ^{m}	5.6
T_7 = Azotobacterchroococcum+Bacillusmegaterium	2050 ^{e}	17.9
T_8 = Azotobacterchroococcum+Glomusfasciculatum	2083 ^{d}	19.2
T_9 = Azotobacterchroococcum + Frateuriaaurantia	2117 ^{c}	20.5
T_{10} = Azotobacterchroococcum + Pseudomonas fluorescens	2183 ^{b}	22.9
T_{11} = Bacillus megaterium + Glomus fasciculatum	1767 ^{n}	4.7
T_{12} = Bacillus megaterium + Frateuriaaurantia	1833 ^{k}	8.2
T_{13} = Bacillus megaterium+Pseudomonas fluorescens	1933 ^{g}	12.9
T_{14} = Glomus fasciculatum+Pseudomonas fluorescens	1967 ^{f}	14.4
T_{15} = Glomus fasciculatum + Frateuriaaurantia	1817 ^{l}	7.4
T_{16} = Frateuriaaurantia + Pseudomonas fluorescens	1900 ^{h}	11.4
T_{17} = Azotobacterchroococcum + Bacillus megaterium + Pseudomonas fluorescens	2350 ^{a}	28.4
Minimum	1683	2.0
Maximum	2350	28.4
Mean	1943	13.5
SD	183	7.5
CV (%)	9.4	55.5

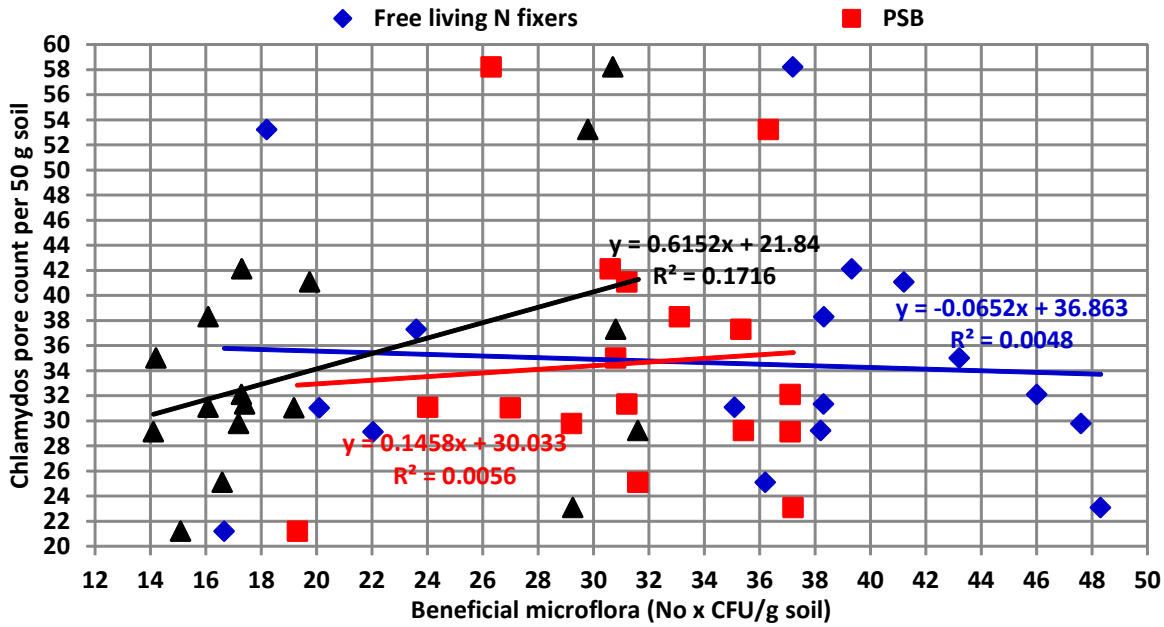

Fig. 1 : Relationship between beneficial microflora and chlamydos pore count of soil in quinoa

bacteria (KSB) with Chlamydos pore count per 50 g of soil are depicted in Fig. 1. The Chlamydos pore count per 50 g of soil was found to decrease with a rate of change of -0.065 for an unit change in free living N fixers, while it increased with a rate of change of 0.145 for an unit change in PSB and 0.615 for an unit change in KSB based on the study. The changes in chlamydos pore count per 50 g of soil occurred with a coefficient of determination values of 0.004, 0.005 and 0.171 for predicting through free living N fixers, PSB and KSB respectively. When VAM fungus was inoculated in cowpea, Thiagarajan and Ahmad (1994) have observed significant relationship between phosphatase activity and cytokinin content in cowpea. In a similar study by Nannipieri *et al.,* (2003), the authors have observed significant relationships based on the different microbial activities on the soil chemical and biological parameters.

An assessment has been made in this paper to identify a superior combination of microbial inoculants based on the soil nutrients with different beneficial micro-flora under semi-arid Alfisols. The study was conducted under glass house conditions in the University of Agricultural Sciences, Bangalore. Five microbial cultures *Viz., Azotobacter chroococcum*, *Bacillus megaterium, Fraturia aurantia, Pseudomonas fluorescens* and *Glomus fasciculatum* were tested in the study. Pure cultures of selected *Azotobacter chroococcum*, *Bacillus megaterium, Fraturia aurantia* and *Pseudomonas fluorescens* isolates were sub-cultured on specific medium and maintained in slants for further studies. Seventeen treatments were tested for identifying a superior treatment for attaining maximum soil, plant and seed nutrients, apart from the beneficial microflora and quinoa yield. The Analysis of Variance indicated that the treatments differed significantly in influencing the different parameters and quinoa yield. Based on Duncan's Multiple Range Test, T_{17} inoculated with *Azotobacter chroococcum* + *Bacillus megaterium* + *Pseudomonas fluorescens* was superior for attaining significantly higher soil N and P nutrients, free living N fixers and phosphorus solubilizing bacteria, while T_{16} was superior for attaining significantly higher soil K nutrients and potassium solubilizing bacteria. However, T_{15} was superior for chlamydospore count per 50 g of soil.

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