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Impact of various fertigation levels and weed management practices on the soil rhizospheric microbiome of chickpea

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Abstract

A field investigation was carried out at the experimental field of the AICRP on Weed Management of the Department of Agronomy, Dr. P.D.K.V., Akola (M.S.), India, during *rabi* 2021–22, to study the impact of various fertigation levels and weed management practices on the microbial population dynamics of the rhizospheric soil of chickpea. The experiment was designed in a split-plot design with four main plot treatments of fertigation levels and five sub-plot weed management treatments, which were replicated three times. The recommended dose of fertilizer applied was 25:50:30 NPK kg/ha. Among the weed management treatments, results clearly showed that treatment, weedy check, recorded significantly higher microbial populations at all stages of observation, which was found to be on par with the treatment of farmer practices, i.e., one hoeing at 30 DAS, fb 2 HW at 20 and 40 DAS. Whereas, among weed management treatments using herbicides, pendimethalin 1 kg/ha PE *fb* topramezone 0.0136 kg/ha at 30-35 DAS recorded a higher microbial count as compared to all other herbicide treatments, which was followed by the treatment of oxyfluorfen 0.140 kg/ha PE *fb* quizalofop-ethyl 0.050 kg/ha at 20–25 DAS. However, the effect of various fertigation levels as well as the interaction of fertigation levels and weed management treatments on the microbial count was found to be non-significant.

Keywords: Chickpea, herbicide, topramezone, bacteria, fungi and actinomycetes

Introduction

The chickpea (*Cicer arietinum* L.) is an ancient crop that has recently gained popularity for its versatility in different climate zones of the country. For *rabi* chickpea, weeds are a major hindrance to healthy growth, development, and yield. Weeds compete fiercely with crops for sunlight, water, nutrients, and growing space. Chickpea is not a good weed-competitive crop, particularly in the early stages of growth when development is modest (Barker, 2017)^[3]. This makes weed competition one of the most challenging aspects of chickpea production. Weeds may cause a loss of 30–54 percent in chickpea yields (Mukherjee, 2007)^[10].

Chickpea weeds are often managed by time-consuming and costly traditional practices like manual weeding or hoeing. Modern crop farming now utilizes chemical weed control to improve upon conventional approaches. Therefore, in addition to enhancing chickpea productivity and profitability, it is urgent to identify a weed management strategy involving new-generation post-emergence herbicide molecules for effective weed control during the critical period of weed competition. Farmers often use herbicides, which are agrochemicals, for effective control of weeds. Farmers frequently overlook the long-term and short-term effects of using these herbicides. Most of these herbicides have the ability to decrease the number of delicate soil biota. Herbicides are chemicals, so they may have unexpected effects, including changing the population and activity levels of soil microbes if used without studying them, which can disrupt the delicate microbial ecological balance in the soil and indirectly reduce soil productivity. Soil bacteria, fungi, and actinomycetes populations were found to be significantly influenced after herbicide application, which corroborated the results of Jing *et al.* (2010)^[7] and Ramesh and Nadanassababady (2005)^[12]. The widespread use of herbicides in farming has the potential to upset the delicate biological balance of the

soil (Grossbard, 1976) ^[6]. Therefore, studying how herbicides affect soil microbe populations is vital for assessing soil quality and health. The present experiment was conducted to gain insight into the effects of different fertigation levels and various weed management treatments on soil microorganism populations in order to better deploy weed management treatments in *rabi* chickpea.

Materials and Methods

A field investigation was carried out at the experimental field section of the A.I.C.R.P. on Weed Management, Department of Agronomy, Dr. P.D.K.V., Akola (M.S.), India, during *rabi* 2021–22, to study the impact of various fertigation levels and weed management practices on the microbial population dynamics of the soil rhizosphere of chickpea. The experimental site was situated at 20.703494^o latitude and 77.030027° longitude. The recommended dose of fertilizer applied was 25:50:30 NPK kg/ha.

The experiment was designed in a split-plot design with four main plot fertigation levels and five sub-plot weed management treatments. The main plot treatments comprised different levels of fertigation: F_2 : 50% RDNK in 3 splits, F_3 : 75% RDNK in 3 splits and F_4 : 100% RDNK in 3 splits, and these treatments were compared with the F_1 : 100% RDF soil application (25:50:30) NPK kg/ha (N in 2 splits); however, P was applied as a basal dose in all treatment plots. Three fertigation splits (40% RDNK, 30% RDNK, and 30% RDNK) of treatments of F_2 , F_3 and F_4 were
applied at basal, 20 DAS, and 40 DAS, applied at basal, 20 DAS, and 40 DAS, respectively. Whereas, sub-plot treatments comprised five weed management treatments, *viz.*, W₁: pendimethalin 1 kg/ha PE *fb* propaquizafop + imazethapyr 0.125 kg/ha at 20- 25 DAS; W2: oxyfluorfen 0.140 kg/ha PE *fb* quizalofopethyl 0.050 kg/ha at 20-25 DAS; W_3 : pendimethalin 1 kg/ha PE *fb* topramezone 0.0136 kg/ha at 30-35 DAS; W4: farmer practices: 1 hoeing at 30 DAS *fb* 2 HW at 20 and 40 DAS; and W5: weedy check. The chickpea variety "PDKV, Kanchan" was sown on 14th November 2021 and harvested on 6th March, 2022, respectively. Pre-emergence and postemergence herbicides were applied as per the respective treatments. Observations were recorded, before the sowing stage, the next day after the spraying of the pre-emergence herbicide stage, five days after the spraying of the postemergence herbicide stage and at harvest, respectively.

Microbial population dynamics

Composite soil samples were collected from each treatment plot before sowing, after application of pre-emergence herbicide, after application of post-emergence herbicide, and at harvest to determine the number of fungi, actinomycetes, and bacteria in the soil using a serial dilution technique. The medium was prepared and sterilized by autoclaving. Starting with a 1-gram soil sample, we used the serial dilution approach to dilute it in 10 ml of sterilized water (Wollum (1982) ^[18], Dhingra and Sinclair (1995) ^[5] and Sharma $(2012))$ ^[15].

Bacterial Count

After spreading pre-prepared Nutrient Agar (NA) medium on petri plates, we collected the supernatant (1 ml) in a pipette and diluted it serially to a concentration of 10-6 .

Fungi Count

Once the supernatant (1 ml) was diluted by a factor of 10^{-5} , it was pipetted onto petri plates containing Potato Dextrose Agar (PDA). The bacterial growth in the PDA medium was inhibited by the addition of Rose Bengal.

Actinomycetes count

The supernatant (1 ml) from a serial dilution of 10^{-4} was collected and spread out in a uniform manner on petri plates of Munairs and Kenknight's medium. The poured plates (NA, PDA, and Munairs and Kenknight and incubated for a period of 72 hours at 28±1 °C. A colony counter was used to count the number of fungal, actinomycetes, and bacterial colonies expressed in CFU.

Table 1: Microbial count (bacteria) influenced by different fertigation levels and weed management treatments (CFU g⁻¹ 10⁻⁶) at periodical growth stages in chickpea during 2021-22

Table 2: Microbial count (fungi) as influenced by different fertigation levels and weed management treatments (CFU g⁻¹ soil 10⁻⁵) at periodical growth stages in chickpea during 2021-22

	2021-22			
Treatments	Before	After	After	At
	sowing		Pre-emergence Post-emergence harvest	
A. Fertigation levels				
F_1 -100% RDF (Soil 25:50:30 kg/ ha R.D.F. of NPK (N in 2 splits)	13.07	9.20	13.67	9.56
F ₂ -50% RDNK in 3 Splits	11.80	8.53	12.60	8.13
F_3 -75% RDNK in 3 Splits	13.87	11.87	14.73	11.17
F ₄ -100% RDNK in 3 Splits	15.53	13.47	18.00	13.48
$SE(m)$ ±	2.29	1.08	1.55	1.25
CD at 5%	NS	NS	NS	NS.
B. Weed management practices				
W ₁ - Pendimethalin 1 kg/ha PE fb propaquizafop + imazethapyr 0.125 kg/ha at 20- 25 DAS	11.50	6.00	8.58	3.92
W_2 - Oxyfluorfen 0.140 kg/ha PE fb quizalofop-ethyl 0.050 kg/ha at 20-25 DAS.	11.00	5.33	9.92	4.83
W_3 -Pendimethalin 1 kg/ha PE fb topramezone 0.0136 kg/ha at 30-35 DAS	13.08	8.17	11.42	5.75
W ₄ -Farmer practices-1 hoeing at 30 DAS fb 2 HW at 20 and 40 DAS	15.42	16.83	21.50	18.28
W ₅ -Weedy check	16.83	17.50	22.33	20.15
$SE(m) \pm$	1.76	0.79	1.16	1.17
CD at 5%	NS	2.28	3.33	3.38
C. Interaction (FL X WM)				
$SE(m)$ ±	3.52	1.59	2.31	2.35
CD at 5%	NS	NS	NS	NS
GM	13.57	10.77	14.75	10.59

Table 3: Microbial count (actinomycetes) as influenced by different fertigation levels and weed management treatments (CFU g^{-1} soil $\times 10^{-4}$) at periodical growth stages in chickpea during 2021-22

Results and Discussion

Soil micro-flora (fungi, bacteria, and actinomycetes) were observed at different stages, *viz.,* before sowing, after preemergence spraying, after post-emergence spraying, and at harvest, to evaluate the impacts of different fertigation levels and herbicide application regimes.

Different treatments of weed control had a considerable impact on the microbial dynamics. The findings demonstrate that there was a non-significant difference in microbial count before sowing, but the microbial count dropped precipitously when pre-emergence herbicide treatments were applied. However, after post-emergence herbicide application, population growth rate picked up might be due to the rhizosphere environment provided by the crop and weed densities as well as increased moisture availability in the soil, and microbial count decreased after harvest due to decreased moisture availability and increased temperature. The current research clearly shows that beneficial microorganism populations were temporarily suppressed but subsequently rebounded in the soil depending upon moisture availability and herbicide impact over a period of time.

1. Microbial count (bacteria) as influenced by different fertigation levels and weed management treatments (CFU g-1 10-6) at periodical growth stages in chickpea during 2021-22

The data pertaining to the microbial count (bacteria) as influenced by different fertigation levels and weed management treatments (CFU g^{-1} 10⁻⁶) at periodical growth

stages in chickpea during 2021–22 is presented in Table 1 and graphically depicted in Fig. 1.

Effect of various fertigation levels

The findings demonstrated that at any stage of crop development, the microbial count (bacteria) was not noticeably affected by the four varied fertigation levels. This result agrees with those of Thakare (2019)^[16] and Mane $(2023)^{[8]}$.

Effect of various weed management practices

The bacterial count was observed to be considerably higher at all stages in the treatment of weedy check, i.e., W_5 , which was found to be on par with the treatment W4*,* i.e.*,* farmer practices- 1 hoeing at 30 DAS *fb* 2 HW at 20 and 40 DAS. It's possible that the high bacterial count in both treatments as compared to herbicide treatments might be due to the fact that no chemical herbicides were applied here. Tyagi *et al.* $(2018)^{[17]}$ and Xian *et al.* $(2019)^{[19]}$ found similar outcomes. One possible explanation for the declining periodic soil bacterial count in herbicide application treatment might be due to the effect of pre- and post-emergence herbicides have on the metabolic activities of soil bacteria (Milosevic and Govedarica 2000 ^[9]. The use of herbicide resulted in reduction of the microbial population as compared to weedy check and weed free treatments. Comparable outcomes reported by Jing *et al.* $(2010)^{7}$, Arunkumar *et al.* $(2020)^{2}$, and Rathod *et al.* (2021)^[13].

Among the various herbicide treatments applied as PE, pendimethalin 1 kg/ha as PE applied in treatments W_1 and W³ recorded a higher bacterial count as compared to the other pre-emergence herbicide application treatment W**2**, i.e.*,* oxyfluorfen 0.140 kg/ha as PE treatment. Similar results were reported by Chauhan *et al.* (2018)^[4].

Whereas among all herbicide treatments, treatment, W_{3,} i.e., pendimethalin 1 kg/ha PE *fb* topramezone 0.0136 kg/ha at 30-35 DAS, recorded a higher bacterial count, which was followed by treatment W**2**- oxyfluorfen 0.140 kg/ha, PE *fb* quizalofop- ethyl 0.050 kg/ha at 20-25 DAS at all stages of observation. Ramesh and Nadanassababady (2005) ^[12], Anjum Ahmad $(2017)^{[1]}$, and Sah $(2022)^{[14]}$ reported similar results.

However, treatment W1, i.e., pendimethalin 1 kg/ha PE *fb* propaquizafop + imazethapyr 0.125 kg/ha at 20–25 DAS, recorded the lowest bacterial count among the weed management treatments at all stages of observation.

Interaction effect

Weed management treatments and fertigation levels were not observed to interact significantly with respect to bacterial count. All of these findings are consistent with Thakare $(2019)^{[16]}$ and Mane $(2023)^{[8]}$.

2. Microbial count (fungi) as influenced by different fertigation levels and weed management treatments (CFU g-1 soil 10-5) at periodical growth stages in chickpea during 2021-22

Data in respect of microbial count (fungi) as influenced by different fertigation levels and weed management treatments $(CFU g^{-1}$ soil 10^{-5}) at periodical growth stages in chickpea during 2021–22 is given in Table 2 and graphically illustrated in Fig. 2.

Effect of various fertigation levels

The results showed that the fungal count was not significantly influenced by different fertigation levels at any

stage of crop growth. The results of the present research agree with those of Thakare $(2019)^{[16]}$ and Mane $(2023)^{[8]}$.

Effect of various weed management practices

Various weed management treatments have substantial effects on the total number of fungal counts. As may be seen from the data, the findings show that the weedy check (W_5) treatment had the higher fungal count, which was found to be comparable with the treatment W_4 , i.e., farmer practices of 1 hoeing at 30 DAS *fb* 2 HW at 20 and 40 DAS. Tyagi *et al.* (2018)^[17] and Xian *et al.* (2019)^[19] also discovered comparable results, suggesting that the higher fungal count in both treatments may be attributable to the lack of chemical use in the treatments.

Herbicide-treated plots had significantly lower total fungal counts compared to the treatments of weedy check treatment, i.e., W_5 and treatment (W_4) farmer practices, i.e., 1 hoeing at 30 DAS *fb* 2 HW at 20 and 40 DAS. Pre- and post-emergence herbicide applications result in a periodic decrease in the microbial count due to their effects on the metabolic activities of soil microbes (Milosevic and Govedarica 2000)^[9]. Arunkumar *et al.* (2020)^[2], Jing *et al.* (2010) ^[7] and Rathod *et al.* (2021) ^[13] found similar reductions in the microbial population as compared to weedy check and weed-free treatments.

Among the various herbicide treatments as PE, pendimethalin 1 kg/ha applied in treatments W_1 and W_3 recorded a higher fungal count as compared to the other preemergence treatment, W**²** i.e. oxyfluorfen 0.140 kg/ha treatment. Given results supported by Chauhan *et al.* 2018 [4] .

Treatment W3, i.e., pendimethalin 1 kg/ha PE *fb* topramezone 0.0136 kg/ha at 30-35 DAS, recorded a higher fungal count at all stages as compared to all other herbicide treatments, which was followed by treatment W**2**, i.e., oxyfluorfen 0.140 kg/ha PE *fb* quizalofop-ethyl 0.050 kg/ha at 20-25 DAS. Whereas, treatment W_1 , i.e., pendimethalin 1 kg/ha PE *fb* propaquizafop + imazethapyr 0.125 kg/ha at 20–25 DAS, recorded the lowest fungal count among the weed management treatments at all stages. Possible causes include chemical herbicides' knock-on effect of reducing the fungal population, causing a setback in the fungal population. Similar results were reported by Raghavendra *et al.* $(2017)^{[11]}$ and Sah $(2022)^{[14]}$.

Interaction effect

An interaction effect with respect to fungal count was found to be non-significant between various fertigation levels and weed management practices. These findings are consistent with those of Thakare $(2019)^{[16]}$ and Mane $(2023)^{[8]}$.

3. Microbial count (actinomycetes) as influenced by different fertigation levels and weed management treatments (CFU g^1 soil \times 10⁻⁴) at periodical growth **stages in chickpea during 2021-22**

Data in respect of microbial count (actinomycetes) as influenced by different fertigation levels and weed management treatments (CFU g^{-1} soil \times 10⁻⁴) at periodical growth stages in chickpea during 2021-22 are given in Table 3 and graphically depicted in Fig. 3.

Effect of various fertigation levels

None of the treatments of fertigation levels significantly influenced the actinomycetes count throughout the course of the whole observation period. These findings are consistent with the results of Thakare $(2019)^{[16]}$ and Mane $(2023)^{[8]}$.

Effect of various weed management practices

Findings revealed that the total number of actinomycetes is greatly impacted by the various weed management practices. Findings show that the Weedy check (W_5) treatment recorded higher values in respect of actinomycetes counts. Those results of treatment Weedy check (W_5) found at par with the treatment (W_4) i.e., farmer practices of 1 hoeing at 30 DAS *fb* 2 HW at 20 and 40 DAS. It might be because chemical herbicides weren't applied in those treatments, i.e., in treatment W_4 and treatment W_5 . Tyagi *et* al. 2018^[17], and Xian *et al.* 2019^[19] also discovered similar results.

Among the various herbicide treatments after application of pre-emergence herbicide stage, pendimethalin 1 kg/ha, which applied in treatments W_1 and W_3 recorded higher actinomycetes count as compared to the treatment W_2 i.e. oxyfluorfen 0.140 kg/ha treatment. Given results supported by Chauhan *et al*. 2018 [4] .

Whereas, treatment W3, i.e. pendimethalin 1 kg/ha pe *fb* topramezone 0.0136 kg/ha at 30-35 DAS, recorded a higher actinomycetes count at all stages of observation as compared to all other herbicide treatments, which was followed by W**²** i.e*.* oxyfluorfen 0.140 kg/ha PE *fb* quizalofop- ethyl 0.050 kg/ha at 20-25 DAS. However, treatment W¹ i.e., pendimethalin 1 kg/ha PE *fb* propaquizafop + imazethapyr 0.125 kg/ha at 20–25 DAS, resulted in the lowest actinomycetes count. Possible causes include chemical herbicides' effect on reducing the microbial population, causing a setback in the actinomycetes count. Similar results were reported by (Raghavendra *et al*. 2017 and Sah 2022)^[11, 14].

Actinomycetes counts were considerably lower in herbicidetreated plots at all observation stages, i.e., after preemergence and post-emergence herbicide treatment and again at harvest, compared to both the treatments weedy check (W5) and farmer practices i.e., 1 hoeing at 30 DAS *fb* 2 HW at 20 and 40 DAS (W_4) . A decline in the actinomycete count might have been caused by the use of chemical herbicides. Possible causes include chemical herbicides' knock-on effect of reducing the actinomycetes population, causing a setback in the actinomycetes population (Arunkumar *et al.* 2020, Jing *et al.* 2010^[2, 7], and Rathod *et al.* 2021) $[13]$, which reported comparable

outcomes of reduction in the actinomycetes count as compared to the weedy check and weed free treatments.

Interaction effect

An interaction effect with respect to actinomycetes count was found to be non-significant between various fertigation levels and weed management practices. These findings are consistent with those of Thakare (2019) [16] and Mane (2023) [8] .

Fig 3: Microbial count (actinomycetes) as influenced by different fertigation levels and weed management treatments (CFU g^{-1} soil $\times 10^{-4}$) at periodical growth stages in chickpea during 2021-22

Conclusions

On the basis of various weed management practices, the weedy check treatment recorded a significantly higher microbial count of bacteria, fungi, and actinomycetes. However, among the various herbicide treatments, pendimethalin 1 kg/ha PE *fb* topramezone 0.0136 kg/ha at 30-35 DAS recorded a higher microbial count of bacteria, fungi, and actinomycetes at all stages as compared to other treatments.

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