



Impact of moisture regimes on yield and soil microbial population in pea (*Pisum sativum*)

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ABSTRACT

Method of application of irrigation to the crop plays one of the most crucial roles in plant growth, development and overall production of the crop. To study the effect of different types of irrigation methods on the yield of the pea (*Pisum sativum* L. var. PB-89) crop, a field experiment was conducted at the research farm of the Punjab Agricultural University, in the winter of 2016–17 and 2017–18. Five treatments, viz. drip irrigation on crop grown on level field (T1), drip irrigation on crop grown on ridges (T2), flood irrigation (T3) and furrow irrigation (T4) all at 100% ET level and rainfed irrigation (T5) were compared. Each method of irrigation application had a unique soil moisture pattern during the crop growing period. Soil microbial properties were also studied for different treatments and although there was non-significant difference in microbial population among treatments, there was significant difference of biological activity of the microbes with respect to different irrigation treatments, as reflected by the recorded dehydrogenase activity of the soil. Population of microbes was maximum at flowering stage. Yield of the crop varied significantly with the method of irrigation used. Maximum yield was obtained under drip irrigation treatment.

Keywords: Dehydrogenase activity, Irrigation, Microbial population, Moisture, Pea, Yield

India is one of the largest pulse producing countries with 17.56 million tonnes (MT) of pulses covering an area of 26.43 million hectares (mha) (Singhal *et al.* 2018). The per capita availability of total pulses in the country is about 15.2 kg annually. In India, pea (*Pisum sativum* L.) production of 4.81 MT was recorded in 2016 covering an area of 0.497 mha with the yield of fresh green peas as 9686.1 kg/ha (FAOSTAT 2018). Due to changing climatic conditions and lack of proper water management, availability of water is becoming scanty. To overcome this problem, water-saving agriculture is the possible solution. Use of water and supplements, specifically at the crop root level through drip irrigation positively influences the yield and saves water (Phene and Howell 1984) and because of such favourable circumstances, drip system is being broadly utilized in the world. Maisiri *et al.* (2005) pointed out saving of up to 50% water using drip irrigation as compared to surface irrigation. Research has also shown that in some irrigated situations, grain yield can be improved while reducing the amount of water applied to the crop (Yang *et al.* 2000, 2001).

In case of legume crops, apart from appropriate moisture for plant growth, the soil microbial population, especially rhizobia plays an important role in production. Alagawadi *et al.* (1988) reported the association of *Rhizobium* and phosphate-solubilizing bacteria on the yield and nutrient uptake of chickpea. Schnurer *et al.* (1986) reported increased nematode population and fungal respiration as a response to rapid oxygen consumption due to changes in soil moisture content. Biçer *et al.* (2004) found better growth and biological yield of chickpea cultivars under irrigated conditions compared to rainfed conditions.

Inoculation of *Rhizobium* increases nodulation and nitrogenase activity. Inoculation helps in increasing dry matter content, grain yield, improving nutrient uptake efficiency and saving fertilizer doses (Elkoca *et al.* 2008). The present experiment was aimed to study the impact of various irrigation treatments on soil moisture pattern and soil microbial behaviour and their influence on the yield of pea crop.

MATERIALS AND METHODS

The study was carried out at the research farm of the Punjab Agricultural University (PAU), Ludhiana, Punjab, India. Ludhiana is located at 30°54' N latitude and 75°48' E longitude at the height of 247 m amsl. Soil texture is sandy loam and the soil is low in nitrogen and organic carbon.

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The experiment was conducted in the winter of the year 2016–17 and 2017–18. Pea crop variety PB-89 was sown with row to row spacing of 30 cm in 3 replications under randomized block design. Seeds of pea crop were treated with bacterial culture (*Rhizobium leguminosarum*) to ensure nodule formation and quick growth. A heavy pre-sowing irrigation (10 cm depth of irrigation water) was applied to the field to ensure sufficient moisture content in the soil profile at the time of sowing. There were five treatments: four irrigation treatments along with one treatment under rainfed condition (T5). Four irrigation treatments were drip irrigation on crop grown on level field (T1) and on ridges (T2), flood irrigation (T3) and furrow irrigation (T4). Irrigation was applied at 100% ET under all irrigation treatments.

Drip irrigation was applied every 3rd day. Flood irrigation and furrow irrigation were applied when total crop evapotranspiration was 5 cm and 3 cm, respectively. The daily evapotranspiration values for the crop season were calculated using the FAO Penman-Monteith equation (Allen *et al.* 1998) based upon daily meteorological data. The efficiency of the irrigation system was taken as 90%, 60% and 70% for drip, flood and furrow irrigation, respectively.

For soil moisture analysis, soil samples were collected from eight distinct places from each replication of the different treatments at 10 cm depth to cover variation within a treatment. Samples were taken from the following places: for T1 treatment between rows with irrigation dripline (RWDL) and between rows without irrigation dripline (RWDL), for treatment T2 and T4 on ridge and from furrow and for treatment T3 and T5 one sample each was taken.

Moisture content of collected soil samples was determined by using gravimetric method at 3 days interval throughout the crop season and also just before and few hours after every irrigation.

The viable counts of bacteria, P solubilizer bacteria, *Rhizobium* and fungi were recorded on nutrient agar (NA), potato dextrose agar (PDA), yeast extract mannitol (YEM) broth and *Pseudomonas* agar mediums, respectively, at initial, flowering and harvesting stages of the crop using pour plate method. After incubation (28±2°C for 2–4 days), colonies developed and the viable count of soil microbes were enumerated by the given formula.

$$\text{Colony forming unit (Cfu) per ml of sample} = \frac{\text{Number of colonies} \times \text{Dilution factor}}{\text{Quantity of sample}}$$

Colony forming unit (Cfu) per g sample was converted in log value using the formula.

$$\text{Log}(a \times b^n) = \text{log } a + n \text{ log } b$$

where, a is the mean number of bacterial colonies and bⁿ is the dilution factor.

Dehydrogenase activity of soil was tested at flowering stage of the crop by the method of Tabatabai (1982). Dehydrogenase activity was calculated as µg of TPF/g of soil/hour.

$$\text{Dehydrogenase activity} = \frac{C}{\text{Weight of sample}} \times 24 = \frac{D}{\mu\text{TPF/g soil/h}}$$

where, Weight of soil taken is 1 g, C is the amount of Formazan (µg) produced read from the standard curve.

Yield analysis was done for all the treatments at the time of harvesting for the crop. Crop from the 2×2 m² area within the plot was harvested and grain yield was converted into kg per hectare (kg/ha) for each plot.

The data collected from the field experiment was subjected to the statistical analysis using analysis of variance (ANOVA) technique at 5% level of significance.

RESULTS AND DISCUSSION

Moisture content of soil: The variations of soil moisture in all the five treatments throughout the crop duration are presented in Fig 1a and 1b for the year 2016–17 and 2017–18, respectively. The soil moisture varied with each treatment. There was an initial spike in moisture content immediately after sowing because of application of moisture enhancing irrigation to ensure seed germination in treatments T2 and T4, where there was moisture loss during formation of ridges. Total depth of water applied apart from pre sowing irrigation for the year 2016–17 was 15.7 cm, 16.8 cm, 15.0 cm and 18.8 cm for T1, T2, T3 and T4 respectively. While for the year 2017–18, it was 13.4 cm, 14.4 cm, 15.0 cm and 14.6 cm for T1, T2, T3 and T4 respectively.

Under drip irrigation on plain area (T1), moisture content ranged between 8–10% on weight to weight (w/w) basis, which is close to field capacity, throughout the crop growth season due to frequent application of small amount of irrigation. Large spikes in curves reflect the incident of rainfall which increased moisture content up to 14–15% on w/w basis.

Moisture content curves under drip irrigation on ridges (T2) almost followed the same trend and range as that observed under T1. Initially ridges contain more moisture at the start of irrigation but on repeated irrigations the moisture moves down to the furrows and furrow moisture becomes equal or even more than that on the ridge. In furrow irrigation treatment (T4) moisture content spiked up to 15–16% in furrows where water was applied (or due to rain) whereas on the ridges the spike was 2–3% less. Between irrigations, moisture content decreased steadily by about 7–9%. In flood irrigation treatment (T3), application of irrigation increased the moisture content by about 8–10% on w/w basis and frequency of irrigation was the least.

In case of rainfed conditions, the moisture content keeps on decreasing and soil tends to dry up unless some rainfall event occurs. In the second year (2017–18), overall higher moisture content was observed than in the first year (2016–17) due to regular rains in the crop growing season.

Although there was difference in moisture pattern distribution under different irrigation methods, there was no significant difference in amount of water applied under drip, flood and furrow irrigation. This may be due to overall low water requirement of pea crop.

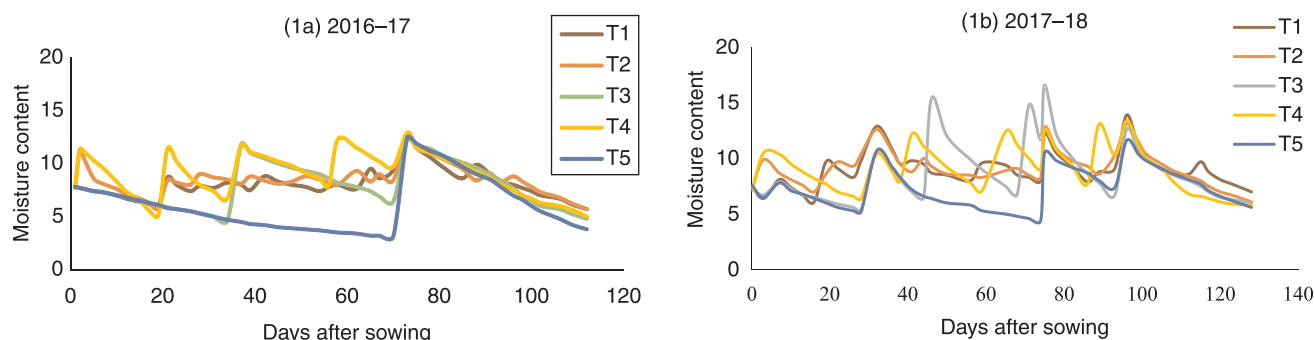


Fig 1 Moisture content of soil under different treatments in pea crop for the year (a) 2016–17 and (b) 2017–18.

Soil biological factors: Counts of bacteria, phosphorus solubilizing (*Pseudomonas*) bacteria, *Rhizobium* and fungi of the soil under different irrigation treatments were taken at initial, flowering and harvesting stages of the crop. At initial stage, the population density (log Cf/g of soil) of bacteria, P solubilizing bacteria, *Rhizobium* and fungi were recorded as 7.84, 6.80, 4.90, 4.15 log Cf/g of soil, respectively, for the year 2016–17 and 8.02, 7.02, 5.05, 4.30 log Cf/g of soil, respectively, for the year 2017–18. Higher values were recorded in second year (2017–18) as compared to the first year (2016–17) for all the soil biological factors examined under study, which may be due to improvement caused by the first year pea crop. Population count increased from initial stage to flowering stage and then decreased at harvesting stage. The minimum values occurred at harvesting stage. This variation trend through different stages was similar for all the microbes.

The soil water content regime availability is prominent

factor in determining soil microbial population (Drenovsky *et al.* 2004, Steenwerth *et al.* 2005, Singhal *et al.* 2018). Viable population density of bacteria, P solubilizing bacteria, *Rhizobium* and fungi for all treatments at flowering and harvesting stages are presented in Table 1 for both the years. For bacteria, there was no significant difference recorded among irrigation treatments in both the years except at harvesting stage in the year 2017–18. Maximum and minimum values were recorded under drip irrigation and rainfed treatment, respectively. P solubilizing bacteria was seen non-significant at harvesting stage in both the seasons but significant difference was recorded at flowering stage. Count was found significantly more in drip irrigation (T1 and T2) and furrow (T4) irrigation treatments and minimum values were recorded in rainfed (T5) treatment.

Rhizobium population is an important indicator of nodule formation and nitrogen fixation ability of legume plants. Significant difference in rhizobium population was

Table 1 Variation of viable population density of bacteria, phosphorus solubilizing (*Pseudomonas*) bacteria, *Rhizobium* and fungi under different irrigation treatments (log Cf/g of soil)

Microorganism	Stage	Year	T1 RWDL	T1 RWoDL	T2 Ridge	T2 Furrow	T3	T4 Ridge	T4 Furrow	T5	CD (P=0.05)
Bacteria	Flowering	2016–17	8.26	8.14	8.27	8.3	8.32	8.23	8.18	8.21	NS
		2017–18	8.69	8.58	8.6	8.5	8.61	8.64	8.44	8.45	NS
	Harvesting	2016–17	7.18	7.05	7.1	6.97	6.98	7.02	6.83	6.8	NS
		2017–18	7.33	7.31	7.29	7.42	7.36	7.53	7.53	7.17	0.12
P solubilizing (<i>Pseudomonas</i>) bacteria	Flowering	2016–17	7.35	7.23	7.36	7.22	7.17	7.27	7.25	7.23	NS
		2017–18	7.42	7.17	7.33	7.38	7.32	7.44	7.48	7.28	0.16
	Harvesting	2016–17	6.82	6.77	6.84	6.66	6.67	6.66	6.77	6.6	NS
		2017–18	7.24	7.21	7.23	7.19	7.13	7.19	7.15	7.11	NS
<i>Rhizobium</i>	Flowering	2016–17	5.4	5.38	5.48	5.33	5.28	5.35	5.2	5.2	0.15
		2017–18	5.61	5.58	5.61	5.5	5.56	5.59	5.3	5.48	NS
	Harvesting	2016–17	5.1	5.05	5.26	5.13	5.18	5.18	5	5.1	0.14
		2017–18	5.2	5.1	5.28	5.15	5.2	5.21	5.1	5.15	NS
Fungi	Flowering	2016–17	4.33	4.31	4.33	4.25	4.2	4.36	4.35	4.1	0.11
		2017–18	4.83	4.55	4.86	4.68	4.6	4.86	4.6	4.55	0.13
	Harvesting	2016–17	4.15	4.1	4.24	4.1	4.05	4.1	4.05	4	NS
		2017–18	4.23	4.18	4.21	4.18	4.1	4.2	4.1	4.05	NS

recorded in the first year 2016–17 at both flowering and harvesting stage whereas non-significant difference in the second year 2017–18. In 2016–17, significantly low values were recorded under rainfed treatment and in the soil sample from the furrow of the furrow irrigation treatment.

There was significant difference in fungi count at flowering stage and non-significant at harvesting stage in both the years. At flowering stage, significantly higher values were observed under drip T1 RWDL and on ridges in T4, whereas significantly low values were observed in T1 RWoDL, T3, in furrows T4 and rainfed treatment.

On the basis of two year data, soil bacteria were found as dominant group followed by P solubilizing (*Pseudomonas*) bacteria and *Rhizobium*. Comparatively higher values in the year 2017–18 are attributed to the enhancement of the soil biological and fertility status due to the legume crop grown in the year 2016–17 on the same field and similar environmental conditions (Singhal *et al.* 2018, 2021). With respect to inter-relation of microbial activity and soil moisture content, higher values may be attributed to better soil moisture regime whereas low values may be attributed to either dry or over wet soil condition.

Dehydrogenase activity values of soil are presented in Table 2 for the crop which vary significantly among irrigation treatments. Maximum and minimum values were observed under drip irrigation from dripline samples and rainfed condition respectively. Dehydrogenase activity was significantly lower in T5, T3 and samples from furrows of T4 treatment.

The differences observed may be attributed to better soil moisture regime under drip irrigation and in ridges of furrow irrigation as compared to relatively dry soil condition under rainfed (T5), wet soil condition in furrows of T4 and fluctuating soil moisture regime under T3 treatment. These results are at par with Singhal *et al.* (2018) as dehydrogenase activity is correlated with the soil moisture condition and also dehydrogenase activity varies significantly among irrigation treatments in spite of generally non-significant difference in microbial population among treatments.

Yield: Yield of the crop was recorded in kg/ha for each plot and the average for each treatment was calculated.

Table 2 Dehydrogenase activity of soil (μ TPF/g soil/h)

Treatment	Dehydrogenase activity (μ TPF/g soil/h)	
	2016–17	2017–18
T1 RWDL	14.20	15.14
T1 RWoDL	13.16	14.65
T2 RIDGE	14.16	15.40
T2 FURROW	12.60	13.53
T3	11.68	12.64
T4 RIDGE	12.04	13.48
T4 FURROW	11.40	12.04
T5	10.01	11.72
CD (P=0.05)	0.88	1.16

Maximum yields were recorded under T1 drip irrigation treatment. Numerous earlier findings including Kulathunga *et al.* (2008), Serraj *et al.* (1999), Manoj *et al.* (2014) and Singhal *et al.* (2018, 2021) also documented that sufficient moisture content in soil led to higher yields but constrained moisture regime or water stressed conditions tended to decrease the grain yield. Overall better yield was recorded in 2017–18 for all treatments which may be attributed to higher microbial activity and adequate soil moisture regime due to regular rains.

Although there was non-significant difference in microbial population among treatments, there was significant difference of biological activity of the microbes with respect to different irrigation treatments, as reflected by the recorded dehydrogenase activity of the soil. There was a high degree of positive correlation $R^2=0.9694$ and $R^2=0.8038$ between dehydrogenase activity of soil (μ TPF/g soil/h) and crop yield (kg/ha) for years 2016–17 and 2017–18, respectively, as shown in Fig 2. Therefore, it may be concluded that microbial activity is influenced by the varying moisture regime of different irrigation treatments and higher dehydrogenase activity has a positive impact on yield.

In case of the present study on peas sown in winter, the soil conditions and temperature might be favourable for propagation of microbial population in the soil and hence no significant difference was recorded under different irrigation treatments in many cases except in case of P solubilizing bacteria and fungi at flowering stage. However, enhanced crop yield under drip irrigation may be attributed to better soil moisture distribution throughout the crop growing season and its impact on increasing the dehydrogenase activity in the soil. These results are in slight variance with that for summer moong reported by Singh (2016) where a significant correlation was established between enhancement of microbial population under drip irrigation and its effect on increase in crop yield. The difference in findings may be due to lower microbial activity in the harsh summer when moong crop is taken and the positive impact on yield of increased microbial population reported under drip irrigation system due to relatively constant soil moisture regime.

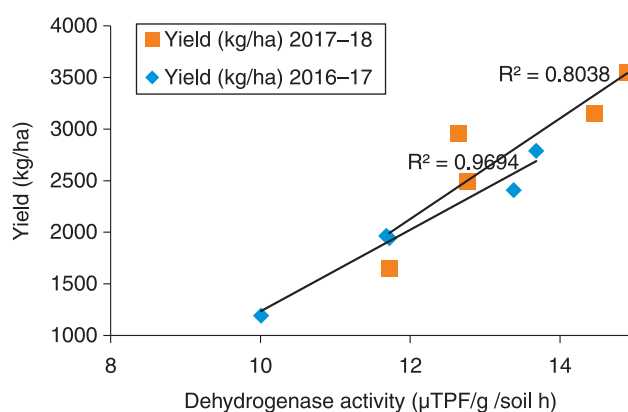


Fig 2 Correlation between Dehydrogenase activity (μ TPF/g soil/h) and crop yield (kg/ha).

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