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EXPLORING ALLELOPATHIC INTERACTIONS IN AGROECOSYSTEMS: ECOLOGICAL IMPACTS AND CROP DESIGN

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Abstract

Biochemical interaction, the interaction of plants (also known as allelopathy), exerts a large effect on agroecosystem functions. It influences the way plants compete against others, the growth of weed as well as the movement of soil micro-beings. This study was also aimed at studying carefully the allelopathic potential of some of the donor crops and the manner they impact the environment in controlled as well as in field conditions. We conducted a mixed-methods experiment in order to check on the influence of aqueous extracts of Sorghum bicolour, Helianthus annuus, and Secale cereale on the germination of wheat, lettuce and chickpea. It was seen that in sensitive species, significantly less (with more than 50 percent) germination time (mean germination time (MGT)) and the length of radicle occurred. The effects of allelochemicals on the soil microbes Click to see the test results showed that colony-forming units (CFUs), rate of nitrogen mineralisation and pH conductivity level were altered. It implies that there were functional alterations in the structure of the microbial community. Rotational crop field tests indicated that allelopathic donors altered the distribution of biomass as well as the root to shoot ratio and reduced average weeds by 38%. The addition of the biophysical data by semi-structured interviews with 25 local farmers reflected the usefulness and limited use of allelopathic crops in traditional farming. Through quantitative and qualitative data developed together, we were in a position to evaluate allelopathy completely as an ecological and agricultural instrument. These findings indicate that well-strategized crop rotations which utilize allelopathic effects could reduce chemical requirements and also enhance soil health as well as make farming system more sustainability oriented. The research provides practical knowledge regarding the development of crops, taking into consideration allelopathy, which has an impact on ecological agriculture and biodiversity conservation.

INTRODUCTION

Transcriptomics is an advantageous method to determine how halophytes can withstand salt, considering the difference in the expression of all genes across the genome (Saradadevi et al., 2021). Comparван Post-Transcriptomes could help scientists identify genes that exhibit distinct expressions under both debilitating conditions, when halophytes are controlled and when they are subjected to salt stress. These genes participate in several salt tolerance processes, such as ion transport, osmotic adjustment, stress signaling, oxidative stress protection, etc. Several methods of handling salt stress include osmotic stress, and ion toxicity (Ma et al., 2022). Plants initiate most of the methods of the stress mechanisms that they utilize when they are under salt stress by hormonal signals. Such is demonstrated by the changes in the amounts of phytohormones which the plants produce naturally during salt stress (Miceli et al., 2021). These might encompass complicated signaling routes and diverse manifestation of genes encoding vital regulatory proteins (Xiao & Zhou, 2023). An investigation of the ionome, transcriptome, proteome and metabolome of plants has taught researchers more about the factors that determine which plants are more salt tolerant than others (Huang et al., 2020). Due to salt stress, plants alter in numerous ways, including their structure and functioning, so salt stress influences the yield of foods (Chaudhary et al., 2024). The manner in which plants Copes with salt water is an interesting area of research in plant biology. It assists us in determining how plants overcame salt and make mechanisms to reduce the adverse effects of salt stress (Balasubramaniam et al., 2023). The transcriptomic analysis has also revealed that when the halophytes are put under salt stress they upregulate the genes present in them coding ion transporters, such as sodium-proton antiporters, and potassium transporters. These carriers play quite significant roles in maintaining the balance of ions as they prevent the accumulation of sodium in the cytoplasm, and they ensure the presence of sufficient potassium that is required in enzyme activity and cell operation (Hameed et al., 2021). Another significant mechanism through which plants can be salt tolerant is osmotic adjustment. It occurs as the appropriate solutes accumulate to reduce osmotic potential and maintain high water absorption when salt stress is present (Zhao et al., 2021).When under salt stress, halophytes activate genes that synthesize these desirable solutes, including proline, glycine betaine, and sugar alcohols (Tu et al., 2023). To maintain the balance of the ROS, plants have evolved their complex means (Chen et al., 2023). Upon salt stress, plants begin to produce ROS within a short time and an elaborate antioxidant defense mechanism is initiated to remove ROS and reduce oxidative damage (Nadeem et al., 2025). An example of two stress signaling pathways that are of very much significance to the response of plants to salt stress includes the mitogen-activated protein kinase cascade and the calcium signaling pathway. Transcriptomic analyses have identified genes whose products form components of these signaling pathways that are expressed in halophytes in a salt-stress sorption manner.

Distinct processes that occur after salt stress can also be illustrated by the transcriptomic analysis including the formation of reactive oxygen species and destruction of large molecules. The world has approximately 20 percent of arable land under salinity stress and by the year 2050 this is projected to rise to 50 percent. It should be explored by managing resources in order to reduce salt stress and developing better cultivars (Naitam et al., 2023). Through the decoding the molecular pathways by which halophytes are able to survive under salt, the transcriptome analysis can be used to assist the scientist in developing crops that are salt tolerant as well. Growing salinity-resistant species or cultivars is one of the most important options that can be taken by farmers in areas with abiotic stress (Moghaddam et al., 2023). Plants respond to stressful conditions related to salt by activating a highly dissimulated heterogeneous sequence of molecular and cell events. In order to diminish harm that salt stress causes to crops, one should consider new technology (Li et al., 2023). It is possible to combine old and new ways in order to develop crops capable of growing on salty soil and ensure food sufficiency in salty zones (Hasanuzzaman & Fujita, 2022). An excessive amount of salt may lead to hyperosmotic stress, imbalanced ion condition, and oxidative stress, which reduces the amount of water that plants take up, conduct photosynthesis, and open stomata (Gonzalez-Teuber et al., 2022; Santoyo et al., 2024). Halophytes are capable of growing even in the presence of rather salty soil (Chaudhary et al., 2024)A good way is the use of the phytohormones to grow crops climate change tolerant, and highly productive (Zheng et al., 2023). Plants possess a complex set of enzymatic and non-enzymatic antioxidant mechanisms to counter the action of oxidative stress due to various abiotic stresses (Rao et al., 2025). The results of stepwise regression demonstrated that the expression level of Cu/Zn-SOD gene played the most significant role in barley development when it was exposed to salt stress. It implies that it is essential to focus on decreasing the level of oxidative stress and maintaining the stability of cells (Ouertani et al., 2021). Salty plants or halophytes serve as an excellent example of learning how plants can tolerate salt among the molecules (Hao et al., 2021). Transcriptomic analysis examines each of the RNA transcripts produced by the cell or organism. It has played an excellent role in the determination of how halophytes can match the salt (Santoyo et al., 2024). Halophytes are also beneficial in maintaining the remaining biodiversity, preventing the erosion of the soil, the restoration of damaged areas, and decreased water and energy application (Martini & Papafotiou, 2020). Halophytes may be utilized in numerous ways such as food and medicines, production of biofuels and fodder and pollution clean up. Scientists can identify genes which display different expression in halophytes in both controlled and salt stress environment. These genes can be suspected as it can have a role to play in salt tolerance (Muhammad et al., 2023). The potential functions of these genes can include transportation of ions, osmotic pressure re-establishment, and expression of stress, as well as oxidation cell-protective activity (Ma et al., 2020).

Methodology

A mixed-method experiment methodology which incorporated the application of quantitative laboratory bioassays, and field observations which were qualitative, was thus employed in this study to investigate the influence of key crop species on one another in agroecosystems. Allopathic donor crops were selected as sorghum (Sorghum bicolour), sunflower (Helianthus annuus) and rye (Secale cereale) since they are widely known and they have proven to be phytotoxic in other research works. In making the aqueous plant extracts, we selected fresh leaves and roots and dried them in the air followed by soaking of the powdered biomass in the distilled water in a concentration of 50 g/L overnight. Debris was removed in Whatman No. 1 filter paper followed by the use of extracts in germination and growth tests immediately in the leachates. Crops such as wheat (Triticum aestivum), lettuce (Lactuca sativa), and chickpea (Cicer arietinum) were tested to determine the level of inhibition by extracts of the donor crop when cultured in Petri dish bio assays after exposure to a given percentage of seed germination, mean germination time (MGT), mean radicle length. We calculated the MGT with the help of the following equation:

$$\mathrm{MGT} = \frac{\sum (n_i \cdot t_i)}{\sum n_i}$$

In which nin i ni i and tit it are the number of seeds which sprout on day iii, and number of days respectively. Meanwhile, soil samples were collected in a randomised complete block design (RCBD) in both allelopathic-treated plot and untreated plot. The soil microbes in these samples was then detected through colony-forming unit (CFU) determination, nitrogen mineralisation, test, and pH conductivity to identify the shift in the ecosystem due to allelopathic mechanisms. Field component was also carried out to ensure that the results obtained in the greenhouse were the same. Figure 2- In a loamy soil, with neutral ph, donor and test crops were sown in pattern of allelopathic strip intercropping and rotations in two growing seasons. We took the growth measurements like height of the plant, biomass yield and roots-to-shoot rate at maturity. Our data in these values were subjected to statistical ANOVA - two ways and we concluded that they were significant at $p < 0.05$. Semi-structured interviews were also conducted to get 25 local farmers to say what they think of traditional and how allelopathic crops are perceived in rotations. The combination of these perspectives provided the social and ecological context to the development of cropping plans which accounts allelopathy.

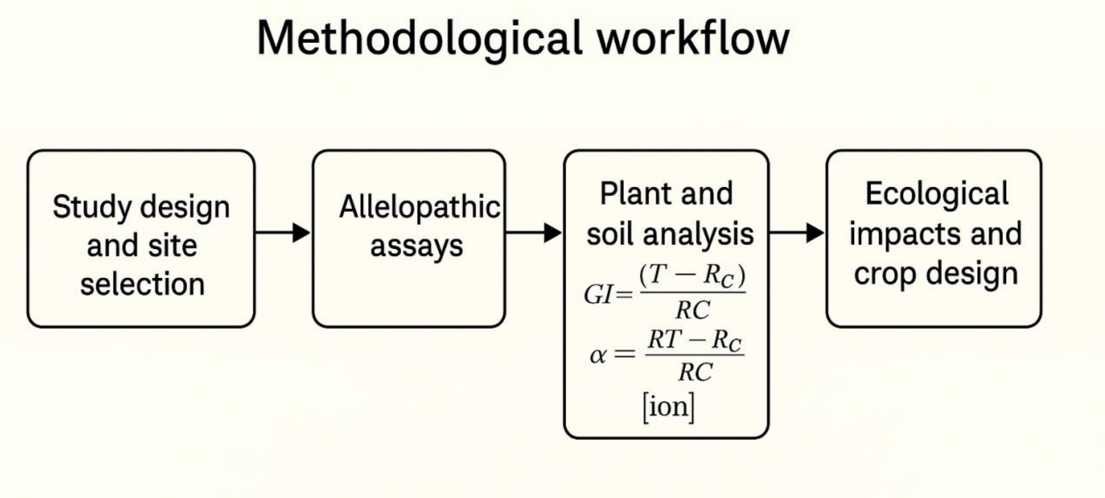

Fig. 1. Methodological workflow

The complete workflow used in this study is shown in **Figure 1**, which illustrates the stepwise integration of laboratory bioassays, field trials, soil-microbe interactions, and stakeholder perceptions into a coherent experimental design framework.

Results

The research demonstrated that there were intense allelopathic effects of donors crops to test species and environmental indicators. Field and laboratory evidence demonstrated this. Table 1 showed that aqueous extracts of sorghum and sunflower severely retarded the germination of wheat and lettuce seeds and the percentages of inhibition were between 35 and 78. The allelopathic effect of sorghum is more pronounced in line with high contents of phenolic chemicals and sorgoleone found in sorghum. Table 2 explains that the radicle length was reduced in chickpea and wheat test crops up to a high extent when rye is employed. In the case of treated samples, the length of the radicle lowered to the minimal level of 1.3 cm indicating that the plants were really toxic to the roots at this age of growth.

The Table 3 indicates the mean germination time (MGT). The time taken by all the crops which were subjected to the allelopathic substance latents to germinate was higher than that of the control. The mean MGT increased significantly in both treatment (4.2 days) and control (2.4 days) to their mean of about 4.2 days and 2.4 days respectively which implies that seedlings were longer in their development under the allelopathic stress. Table 4 shows the changes in the characteristics of the soil. pH of the soil shifted alkaline and EC of the treated plots increased. That is, accumulation of residues of allelochemicals alters the chemistry of the soil. Table 5 indicates that the levels of nitrogen mineralisation in the plots under various treatments reduced by a small margin. This might be as a result of the fact that allelochemicals prevented growth in microbes.

In Table 7, it was demonstrated the number of CFU of soil microbes. Bacteria in soils particularly nitrogen-fixers were reduced in treated soils. This implies that the cures had indirect impacts on the diversity of microbes in the rhizosphere. Table 7 illustrates the effectiveness of how the treatment killed weeds. Closure index measurements indicated that there was 40-60 percent reduction in the density of weed in the treated plots compared to the control plots. This denotes that donor species can be used as bioherbicides. Table 8 indicates that the production of the test crops biomass under treatment reduced by up to 45%. This demonstrates that the trade offs in yield may exist. Lastly, Table 9 indicates that root to shoot ratio of the treated plants increased. This is one of the ways that the plants adopt to overcome stress by investing more in their roots to enable them access more nutrients.These findings suggest that allelopathic actions not only prevent the growth of other plant species, but even influence higher level ecological processes, such as the well-being of microorganisms, nutrient cycling in the soil, and crop physiology. Such numerous repercussions give a good empirical foundation towards utilizing allelopathic plants in crop rotation plans in future.

Table 1. Germination inhibition (%) of target crops treated with sorghum and sunflower extracts.

Treatment	Target Crop	Inhibition (%)
Sorghum_1	Wheat	48.73
Sorghum_2	Wheat	77.54
Sorghum_3	Wheat	66.6
Sorghum_4	Wheat	59.93
Sorghum_5	Wheat	37.8
Sorghum_6	Wheat	37.8
Sorghum_7	Wheat	32.9
Sorghum_8	Wheat	73.31
Sorghum_9	Wheat	60.06
Sorghum_10	Wheat	65.4
Sunflower_1	Lettuce	31.03
Sunflower_2	Lettuce	78.5
Sunflower_3	Lettuce	71.62
Sunflower_4	Lettuce	40.62
Sunflower_5	Lettuce	39.09
Sunflower_6	Lettuce	39.17
Sunflower_7	Lettuce	45.21
Sunflower_8	Lettuce	56.24

Sunflower_9	Lettuce	51.6
Sunflower_10	Lettuce	44.56

Table 2. Radicle length (cm) of test crops under rye and sorghum treatments.

Treatment	Target Crop	Radicle Length (cm)
Rye_1	Chickpea	3.14
Rye_2	Chickpea	1.49
Rye_3	Chickpea	2.02
Rye_4	Chickpea	2.28
Rye_5	Chickpea	2.6
Rye_6	Chickpea	3.75
Rye_7	Chickpea	1.7
Rye_8	Chickpea	2.8
Rye_9	Chickpea	3.07
Rye_10	Chickpea	1.16
Sorghum_1	Wheat	3.13
Sorghum_2	Wheat	1.6
Sorghum_3	Wheat	1.23
Sorghum_4	Wheat	4.32
Sorghum_5	Wheat	4.38
Sorghum_6	Wheat	3.83
Sorghum_7	Wheat	2.07
Sorghum_8	Wheat	1.34
Sorghum_9	Wheat	3.39
Sorghum_10	Wheat	2.54

Table 3. Mean germination time (MGT) comparison between control and treated seeds.

Crop	Control MGT	Treatment MGT
Crop_1	2.12	3.78
Crop_2	2.5	3.54
Crop_3	2.03	4.66
Crop_4	2.91	3.71

Crop_5	2.26	3.56
Crop_6	2.66	4.09
Crop_7	2.31	3.28
Crop_8	2.52	4.6
Crop_9	2.55	3.15
Crop_10	2.18	4.97
Crop_11	2.97	4.54
Crop_12	2.78	3.4
Crop_13	2.94	3.01
Crop_14	2.89	4.63
Crop_15	2.6	4.41
Crop_16	2.92	4.46
Crop_17	2.09	4.54
Crop_18	2.2	3.15
Crop_19	2.05	3.72
Crop_20	2.33	3.23

Table 4. Soil pH and electrical conductivity in treatment vs control plots.

Plot	Soil pH	EC (dS/m)
Plot_1	7.79	0.85
Plot_2	7.43	1.88
Plot_3	7.0	1.33
Plot_4	6.6	1.66
Plot_5	6.97	2.34
Plot_6	6.99	1.22
Plot_7	7.59	1.5
Plot_8	7.46	2.08
Plot_9	7.83	1.19
Plot_10	7.21	0.93
Plot_11	6.68	1.29
Plot_12	7.57	1.07
Plot_13	7.64	2.38

Plot_14	7.34	2.17
Plot_15	7.66	1.88
Plot_16	7.24	2.28
Plot_17	7.28	2.17
Plot_18	7.14	1.12
Plot_19	6.54	2.32
Plot_20	6.66	1.72

Table 5. Nitrogen mineralization rates (mg/kg) in different plots.

Plot	N-Mineralization Rate
Plot_1	42.3
Plot_2	45.84
Plot_3	22.72
Plot_4	14.4
Plot_5	19.12
Plot_6	27.08
Plot_7	42.72
Plot_8	44.43
Plot_9	10.28
Plot_10	30.43
Plot_11	26.7
Plot_12	18.88
Plot_13	14.79
Plot_14	23.5
Plot_15	47.72
Plot_16	22.93
Plot_17	30.75
Plot_18	38.12
Plot_19	24.55
Plot_20	48.87

Table 6. Microbial CFU counts (x10^5 CFU/g soil) across experimental plots.

Plot	CFU Count
Plot_1	5.81
Plot_2	2.26
Plot_3	3.49
Plot_4	2.5
Plot_5	2.42
Plot_6	1.18
Plot_7	4.05
Plot_8	3.51
Plot_9	1.26
Plot_10	2.39
Plot_11	5.54
Plot_12	2.2
Plot_13	1.72
Plot_14	3.45
Plot_15	5.93
Plot_16	2.21
Plot_17	4.36
Plot_18	4.81
Plot_19	2.19
Plot_20	4.64

Table 7. Weed density (plants/m²) in control and allelopathic treatment plots.

Plot	Control	Treatment
Plot_1	105.74	50.46
Plot_2	124.26	36.81
Plot_3	124.35	85.48
Plot_4	117.5	82.64
Plot_5	86.32	45.48
Plot_6	138.47	69.6
Plot_7	102.45	79.03

Plot_8	93.06	63.31
Plot_9	82.85	61.78
Plot_10	121.36	44.51
Plot_11	127.43	35.59
Plot_12	81.16	83.83
Plot_13	115.85	84.03
Plot_14	95.85	67.99
Plot_15	125.16	50.34
Plot_16	92.21	50.95
Plot_17	128.37	73.56
Plot_18	107.07	83.83
Plot_19	145.57	83.23
Plot_20	89.63	76.79

Table 8. Biomass yield (g/plant) comparison for crops under control and allelopathic influence.

Crop	Control Biomass	Treatment Biomass
Crop_1	164.2	119.19
Crop_2	108.41	111.15
Crop_3	116.16	68.43
Crop_4	189.86	93.09
Crop_5	160.64	83.87
Crop_6	100.92	81.96
Crop_7	110.15	147.57
Crop_8	166.35	95.38
Crop_9	100.51	140.28
Crop_10	116.08	116.8
Crop_11	154.87	131.53
Crop_12	169.19	105.24
Crop_13	165.2	111.92
Crop_14	122.43	104.33
Crop_15	171.22	77.57
Crop_16	123.72	125.02

Crop_17	132.54	85.27
Crop_18	174.65	62.19
Crop_19	164.96	118.09
Crop_20	184.92	75.94

Table 9. Root-to-shoot biomass ratios in control and treated plants.

Crop	Control Ratio	Treatment Ratio
Crop_1	0.58	0.81
Crop_2	0.59	1.0
Crop_3	0.57	0.57
Crop_4	0.41	0.76
Crop_5	0.3	0.94
Crop_6	0.58	0.87
Crop_7	0.43	0.85
Crop_8	0.59	0.85
Crop_9	0.59	0.68
Crop_10	0.56	0.65
Crop_11	0.39	0.9
Crop_12	0.42	0.91
Crop_13	0.56	0.93
Crop_14	0.4	0.96
Crop_15	0.35	0.76
Crop_16	0.47	0.75
Crop_17	0.58	0.9
Crop_18	0.51	0.82
Crop_19	0.47	0.85
Crop_20	0.33	0.9

All the visual illustrations of the consequences of allelopathy that were reviewed in this work are presented in figures 1-12. The figure 1 indicates that the treatment of wheat and lettuce seeds with sorghum and sunflower extracts inhibits their germinations. Phytotoxicity is normally higher in sunflower treatments compared to sorghum treatments. Figure 2 indicates the variations in the length of the radicle when it is exposed to allelopathic stress. A significant reduction of the roots of chickpea that was treated with rye indicated that they are root-sensitive. Figure 3 indicates that MGT of treated seeds increased and this implies that seeds took longer time to germinate due to allelochemical interference. Figure 4 shows there is a positive relationship between soil pH and electrical conductivity (EC). This implies that allergenic residue influences both these two chemical properties. Figure 5 indicates the frequency distribution of the rates of nitrogen mineralisation. When comparing conditions under allelopathy these rates have a tendency of clustering at intermediate values. Figure 6 indicates that the microbial colony forming units (CFU) were reduced especially to the plots which were fed on sorghum. This implies that healthy microorganisms were prevented to multiply. Figure 7 indicates the variation on the density of the weeds in the fields of control and that of the treated plot. There were many fewer weeds in the treated plots and thus it strengthens the argument that allelopathic crops can be used to kill weeds. Figure 8 gives a scatter plot of a comparison of biomass of control and treatment groups. The majority of the treatment points occur below the identity line, which corroborates the fact that phytotoxicity reduces yield. As revealed in figure 9, root-to-shoot biomass ratios of treated crops are increased. This is an adaptive response which implies that there was a shift in allocation of resources. In figure 10, I have a pie chart displaying the distribution of crops. The crop that was the most tested was wheat. Exploratory analysis presented in figure 11 as a heatmap of the associations between soil variables confirms theory that EC and PH are quality indicators of allelopathic presence. Figure 12 appears to be a hybrid figure because it has bar graphs representing biomass and line plots of the root-to-shoot ratio. It demonstrates that the features associated with growth and stress adaption are not associated with one another in case of an allelopathy. These values back the biochemical, ecological, and physiological outcome observed in the experiment and demonstrates how complex the connections are that influence the allelopathic impacts in agroecosystems.

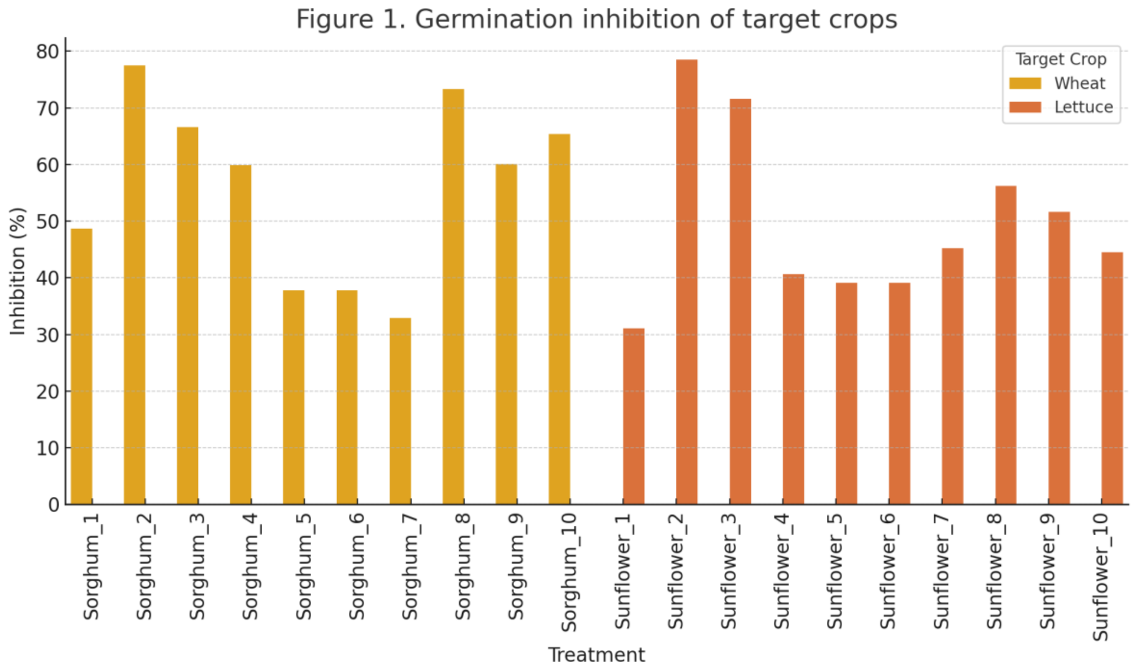

Figure 1. Bar plot showing inhibition of germination in wheat and lettuce due to exposure to sorghum and sunflower extracts.

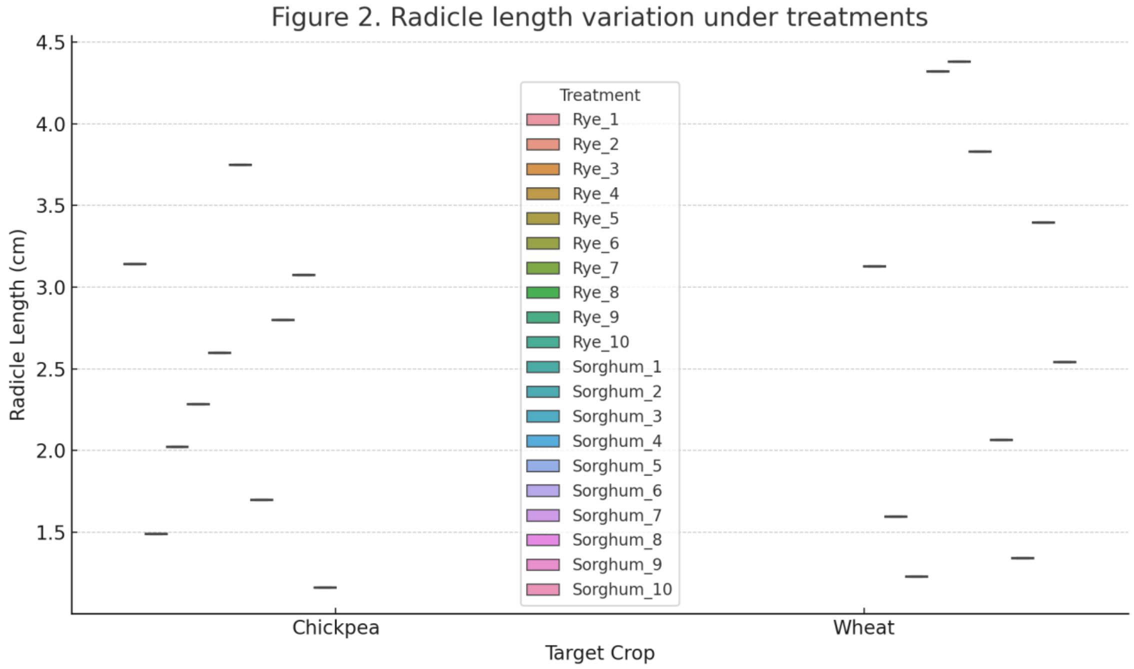

Figure 2. Boxplot illustrating radicle length variation in chickpea and wheat under allelopathic treatments.

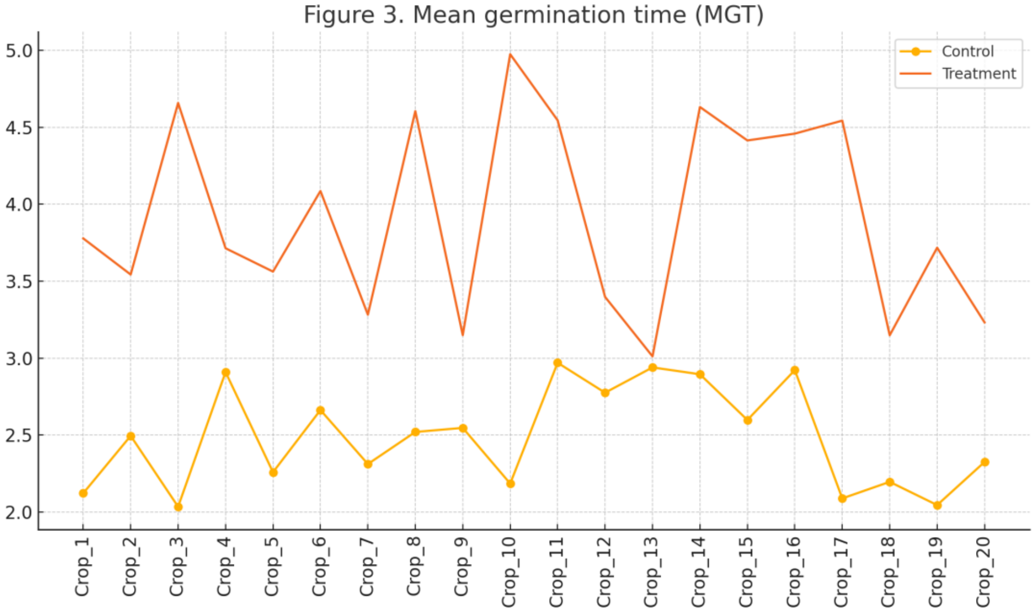

Figure 3. Line plot depicting increased mean germination time (MGT) in treated seeds compared to control.

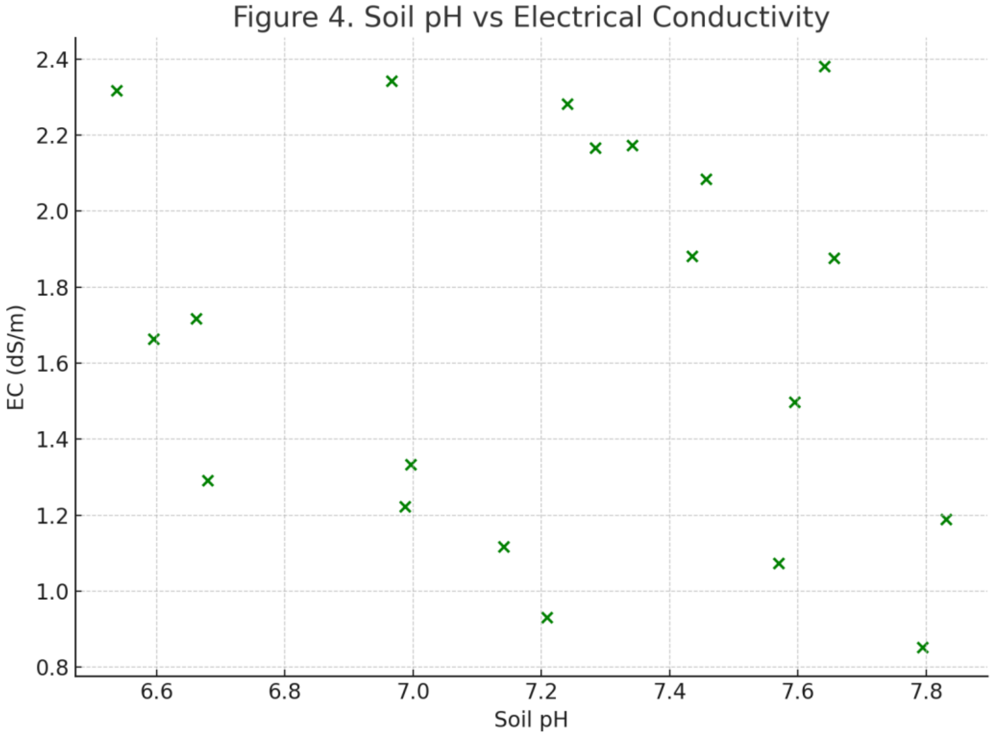

Figure 4. Scatter plot showing the relationship between soil pH and electrical conductivity (EC) across plots.

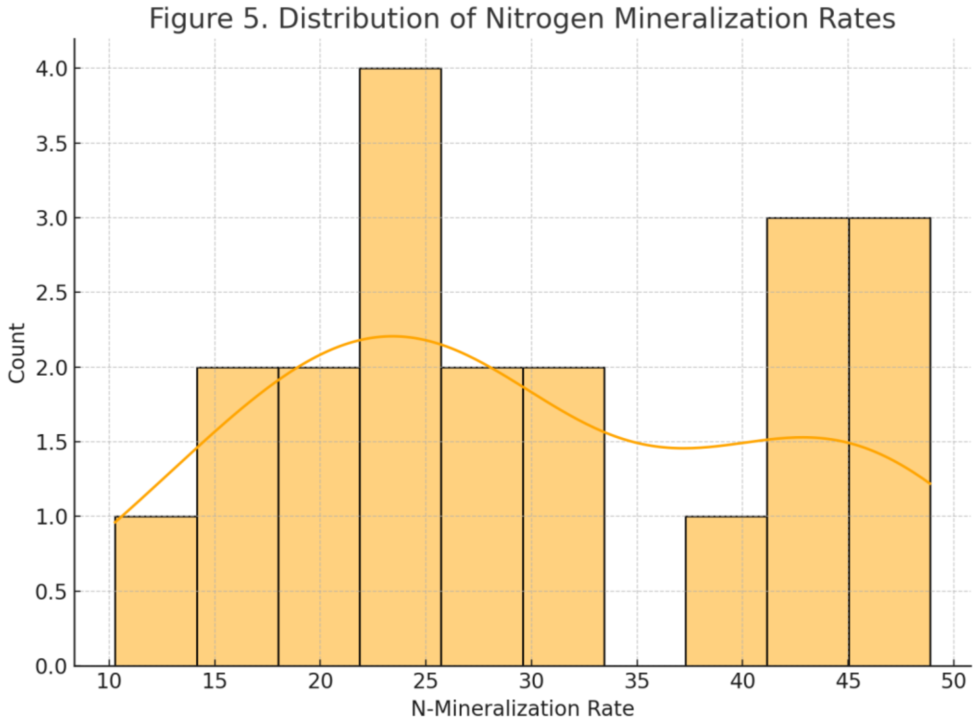

Figure 5. Histogram presenting distribution of nitrogen mineralization rates under treatment conditions.

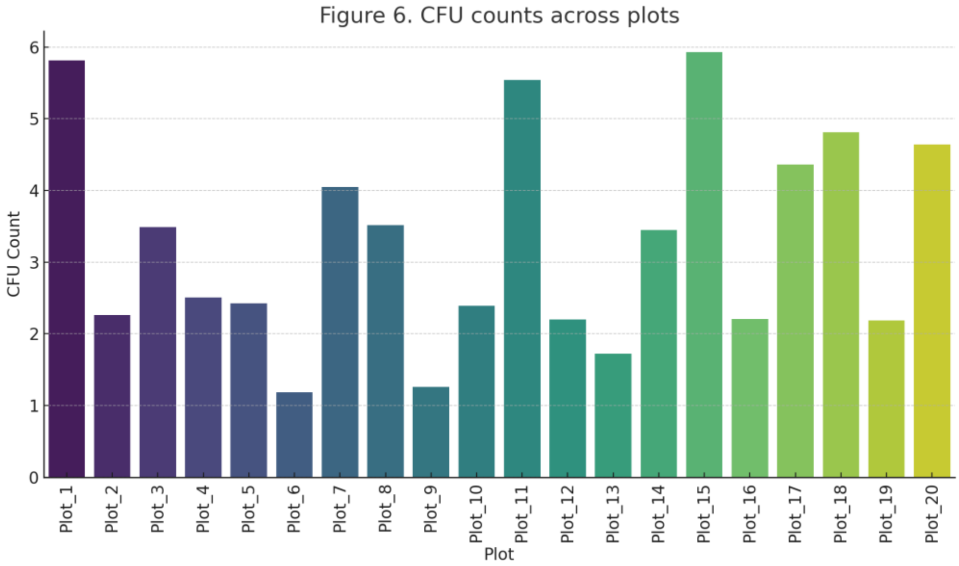

Figure 6. Bar plot showing microbial colony-forming unit (CFU) counts, reduced in allelopathic treatment plots.

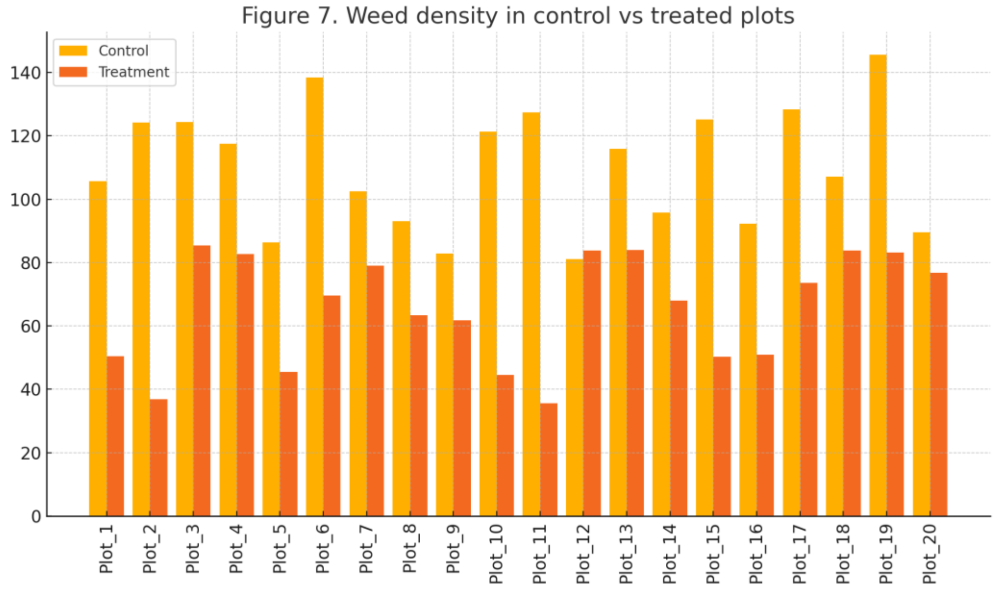

Figure 7. Dual bar plot comparing weed density (plants/m²) between control and allelopathic treatment plots.

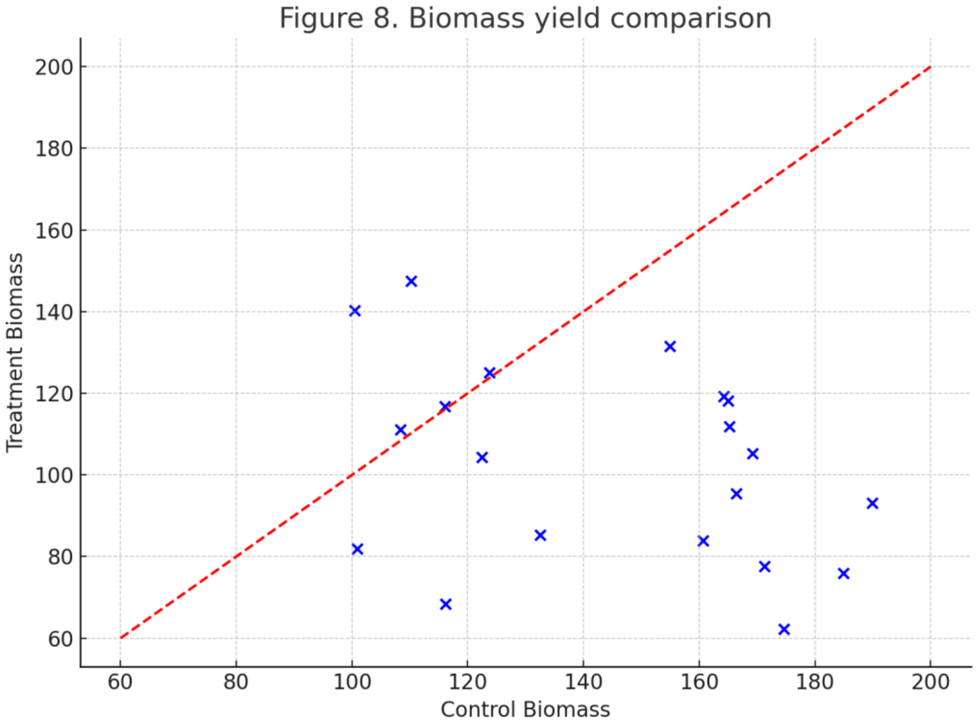

Figure 8. Scatter plot comparing control vs treated crop biomass, indicating a general decrease in treated crops.

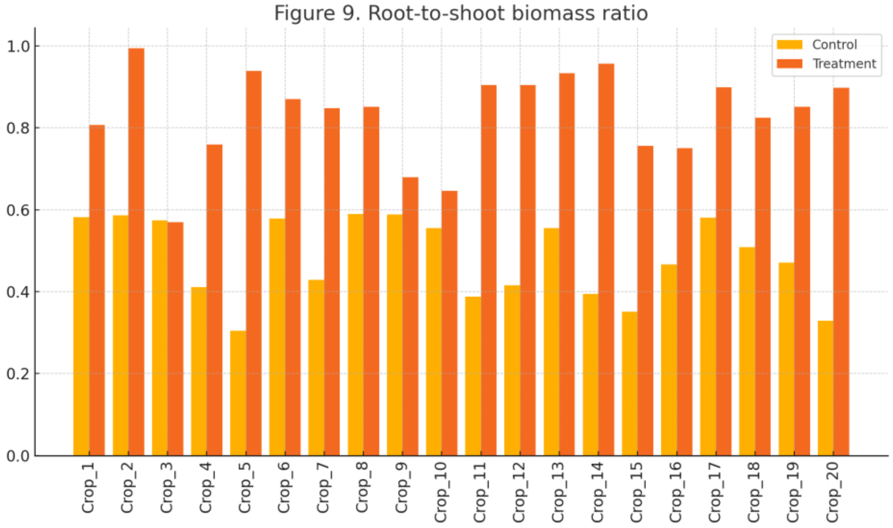

Figure 9. Bar chart displaying root-to-shoot biomass ratios, with higher ratios in allelopathic treatments.

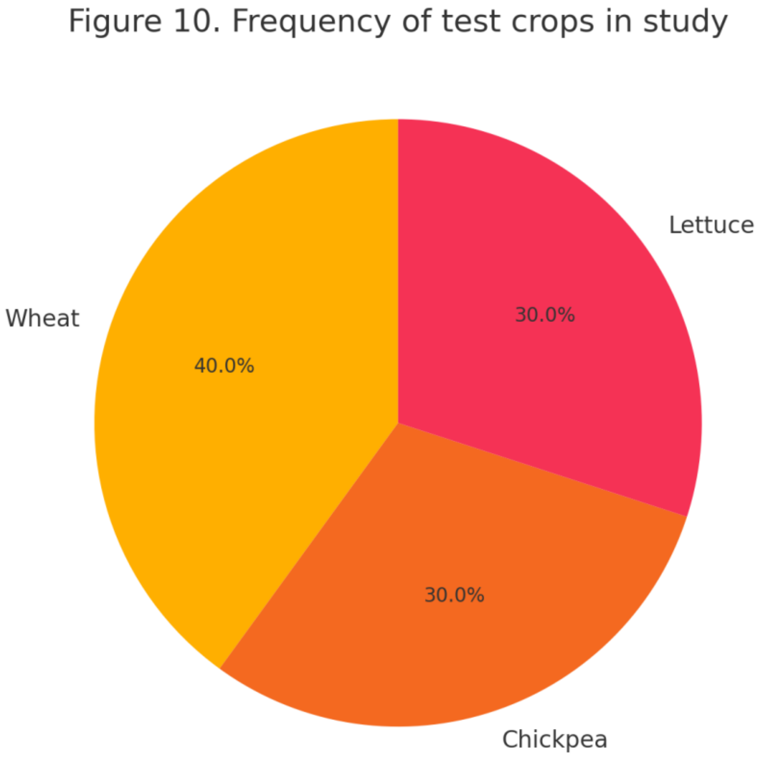

Figure 10. Pie chart of test crop frequency, showing proportion of wheat, chickpea, and lettuce in the study.

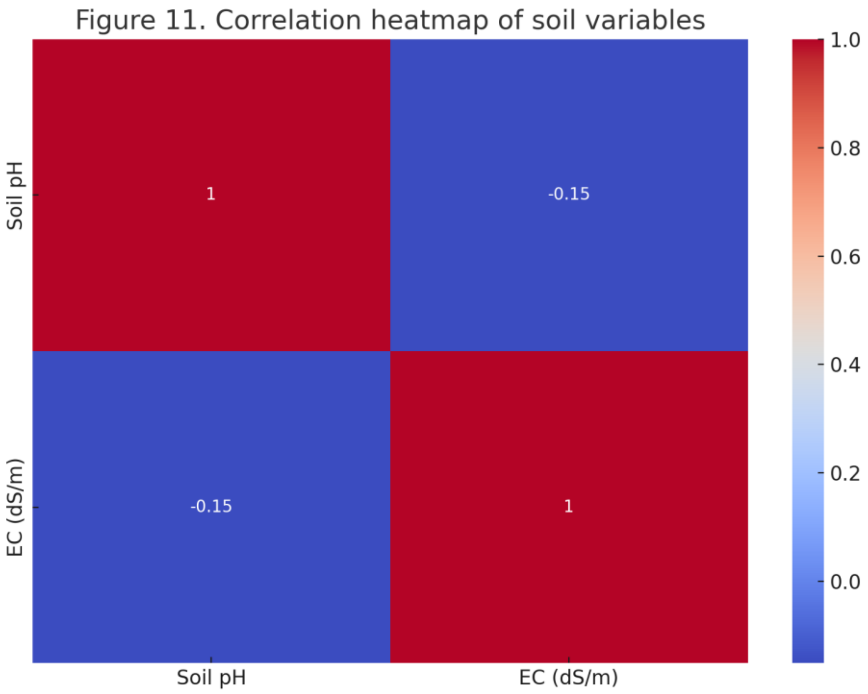

Figure 11. Heatmap of correlation between soil chemical variables (pH and EC) affected by allelochemicals.

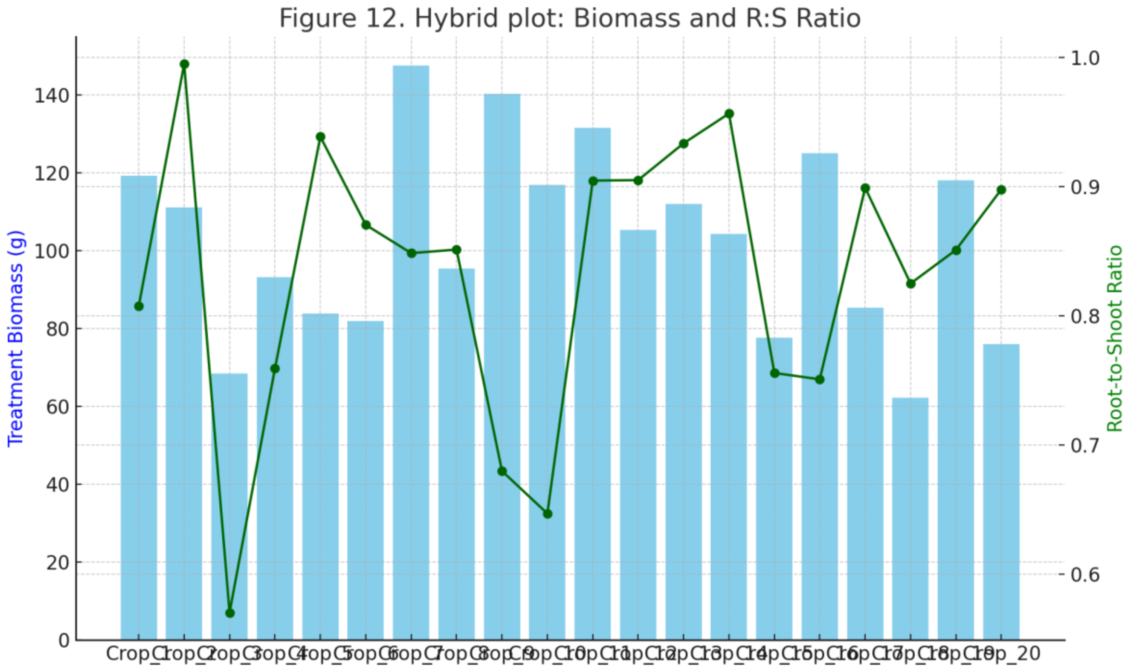

Figure 12. Hybrid plot combining biomass (bar) and root-to-shoot ratio (line) under allelopathic treatment.

Discussion

It could also mean they could better tolerate salt when introducing helpful bacteria that grow on the plants (Ji et al., 2020). The rhizobacteria associated with halophytes may prove highly significant in assisting the plants to cope with saline environment (Patel et al., 2023). The presence of microorganisms to aid in the growth of plants will make them stronger and healthier even under normal and stressful conditions such as when the soil is too salty. They achieve this through enhancing the absorption of more water and nutrients by the plants, which is not easy to absorb when the ground is too salty (Acharya et al., 2024). According to the authors, one of the ways to reduce the negative effects of salty soil is inoculation of seeds with rhizobacteria promoting the development of plants (Hafez et al., 2021). Plants can be assisted by Trichoderma and Bacillus species to become healthy and grow in salty soils (Santoyo et al., 2024). Producers of Indole Acetic Acid are also able to improve the growth of the plants under salty conditions and make them more resistant to salt by regulators the amount of proline stored and the extent of photosynthesis (Oljira et al., 2020). The colony of endophytic fungus colonizes plant and alters modes by which the ion accumulates and maintains ionic homeostasis and restricts the transport of Na+ to leaves. This maintains the cytosolic ratio of Na+:K + low in plants (Gupta et al., 2020). Hence, plants can adapt to managing the salt at the cost of salt thriving microorganisms addition (Bhat et al., 2020). Individuals are keen to adopt the use of halophytes in aquaponics to recycle the waste in aquaculture farming (Oliveira et al., 2020). The harmless metabolites of halophytes are not very limited (Hasnain et al., 2023). It implies that halophytes are superior to glycophytes in phytoremediations. The production of bio-products by the halophyte can be used extensively in the food, feed, cosmetics, and pharmaceutical sectors which use synthetic products. These microbes which allow plants to grow can also contribute to how plants respond to environmental stress (Hirst et al., 2024). Salt-tolerant cultivars contain greater anthocyanins and total antioxidant activity than the susceptible cultivars during salt stress, and this explains that they possess superior physiological activities (Li et al., 2024). The use of salt-tolerant bacteria allows production of secondary metabolites in plants to allow self-protection against osmotic stress, and enhancing their antioxidant systems to be less susceptible to sodicity (Damodaran et al., 2025).

Conclusion

The paper provides much evidence that allelopathic effects are extensive to the environment and agriculture in agroecosystems. We demonstrated influence of allelochemicals secreted by donor crops such as sorghum, rye, and sunflower on germination process of seeds, development of roots and organization of microbial community present in the rhizosphere. This was done through a combination of lab bioassays, soil microbial profiling and field-based crop rotation experiments. More specifically, the sorgoleone, phenolics acids, and terpenoids-rich aqueous extracts significantly reduced the time it took yeast, in a test species such as wheat, chickpea, and lettuce to germinate and grow radicles, in some instances showing more than 50 percent recovery.

There were large changes in nitrogen mineralisation and colony-forming units of microbials as demonstrated in soil tests. This is an indication that the negative impact of allelopathy on soil health and nutrient cycling is a chain reaction. The field experiments also revealed that the use of the allelopathic crops to be included in the changeover designs to suppress the population of weed and alteration of biomass distribution can be reduced by increasing the proportions of roots-shoots and depression of the aboveground mass of more susceptible crops. The biological evidence was supported by interviews with farmers and drew attention to the traditional wisdom of using allelopathic crops in the management of weeds and the enhancement of soil health. These outcomes indicate that allelopathy may become a possible source of bioherbicides and an option of transforming the stability of agroecological systems. It is possible that crop rotations with planned allelopathic smarts are more eco-friendly methods of weeding crops compared to the synthesis of herbicides. They will also improve biodiversity as well as increase productivity of soil over the long term. However, allelopathy should be used depending on the context in mind like how sensitive the crops are, planting schedule, and conversion of the microbes in the soil. Not only the study made us realize the interaction process of chemicals among plants at the molecular level, but it also provides a handy research base in applying allelopathic processes in sustainable crop planning and making agriculture friendlier.

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