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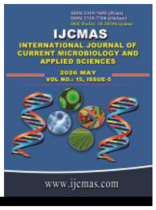

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Functional Potential of Organophosphate-Tolerant Actinobacteria and their Diversity Revealed from Cotton Field Soils

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ABSTRACT

The extensive use of organophosphate pesticides in cotton agroecosystems have caused long-term contamination of soil and there is a need to identify robust microbial communities which can survive and transform xenobiotic organic substances. The current research examined Natural diversity and functional potential of actinobacteria that were isolated in a study of pesticide-contaminated cotton soils in Beed district, India. Eight y-eight soil samples exhibited 73 actinobacterial isolates, giving a turn-over of 82.95%, and a great deal of spatial variability across sites. Screening at 500 ppm showed that there was an extensive adaptive resistance, with 19.18% of the isolates having a broad-spectrum resistance and 65.75% having a three-or-more pesticide resistance, showing prevalence of multi-pesticide resistance phenotypes. Nonetheless, when treated to high stress (1000 ppm), the tolerance decreased drastically as only 6.85% of the isolates were viable with all pesticides, which indicated close concentration-dependent toxicity as well as metabolic limitations. Phenotypic and biochemical characterization identified them to associate with actinobacterial taxa having elevated metabolic flexibility. Findings of molecular identification of the most effective isolate (PTA-52) showed that it has 99-99.6% similarity to *Nocardiopsis,* and phylogenetic analysis was observed to have a strain-level divergence, which is indicative of adaptations evolution due to big data changes pesticides. The results collectively indicate that the financially key actinobacterial community is present in cotton soils exposed to pesticides and that a small subset of the highly tolerant strains have great potential in high-load bioremediation systems.

Keywords

Organophosphate, Bioremediation, *Nocardiopsis,* Actinobacteria, Soil health

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Introduction

In the growing intensity of modernizing agriculture, the use of organophosphate pesticides has increased significantly leading to their extensive deposition in soil ecosystems and posing grave environmentally unsustainable and soil health concerns (Tanveer *et al.,* 2024). Cotton (*Gossypium hirsutum* L.), is one of the primary cash crops, and recent field-scale evaluations show that the consequences of repeated application can be residual amounts of over 400-800 ppm in agricultural soils with continuous cropping regimes (Naveen Kumar & Babalad, 2017; Kilonzi & Otieno, 2024). These pesticides, such as chlorpyrifos, dimethoate, and monocrotophos have been identified to follow robust suppression impacts on non-target soil microbiota by disrupting vital enzymatic processes, derailing membrane structure, and causing oxidative stress (Pakar *et al.,* 2024). Nevertheless, a few species of indigenous microbial communities persist, develop into special group which may either tolerate or convert these xenobiotic compounds. The *Actinobacteria* are one of the phylogenetically and functionally diverse group of soil microflora which plays pivotal role in organic matter recycling, xenobiotic degradation (Prabhaharan Renganathan *et al.,* 2025). More recent genome resolutions have shown that organophosphorus hydrolases (OPH) and methyl parathion hydrolases are among the large catabolic gene clusters carried by the actinobacteria, and the hydrolysis of the phosphoester linkages in organic phosphates, as well as numerous other esterase clusters (Lyagin & Efremenko, 2021; Hadjer *et al.,* 2024). These enzymes aid in the conversion of the pesticides, which are toxic, to less toxic intermediates like dialkyl phosphates and in this way help in the detoxification process itself (Thakur *et al.,* 2019). It is notable that transcriptomic measurements have shown that genes that govern the oxidative stress response, membrane transportation system, and secondary metabolism are upregulated in actinobacteria in response to exposure to organophosphates. Culture-specific and metagenomic studies have recently produced evidence that long term exposure to pesticides is a powerful selective force, initiating an accumulation of actinobacterial taxa with increased tolerance and degradative ability (El Baz *et al.,* 2015; Komicho & Tipayno, 2025). As an example, there were studies in intensively cultivated soils, which have reported a significant shift in the relative abundance of *Streptomyces, Nocardiopsis,* and *Micromonospora* genera in response to the repeated application of pesticides, indicating its ecological competitiveness under the stressful conditions of xenobiotic conditions (Barka *et al.,* 2015). These groups are defined by their filamentous morphology, well-developed cell wall, and capacity to secrete a large repertoire of extracellular enzymes, which all play a role in their stability and metabolic plasticity (Mohammadipanah & Dehhaghi, 2017). Moreover, it has been experimentally shown that there are actinobacterial isolates that are able to endure the presence of organophosphate at concentrations such as 1000 ppm, albeit with a relatively narrow subset of highly selected straining, suggesting that there is significant selection pressure that is highly sensitive to concentrations. Mechanisms that cause tolerance to organophosphates in actinobacteria are intricate and are composed of several physiological and genetic approaches. They are enzymatic degradation, detoxification by efflux, and modification of the membrane to make it less permeable and the induction of stress response pathways (Pashirova *et al.,* 2024). The importance of horizontal gene transfer in spreading the pesticides degrading genes among soil bacteria to cause rapid evolution of resistance populations has recently been noted by molecular research (Britti, 2026).

Moreover, adaption mutations and optimization of regulatory networks have been demonstrated to be effective in improving the efficiency and the selectivity of enzymes, and subsequent adaptation of some strains to survive high concentrations of pesticides (Yasemi, *et al.,* 2025; Srivastava *et al.,* 2026). In spite of these developments, there is a lack of sufficient understanding on how well these mechanisms works in natural agricultural soils and especially under the conditions of multi-pesticide exposures. Repeated and extended chemical stress is applied to the microbiome of the soil in semi-arid agroecosystems like the Marathwada region of India, where cotton is cultivated, and pesticides are highly utilized (Sarwade *et al.,* 2025). Nevertheless, a futility of systematic studies targeting the isolation, characterization and functional evaluation of native actinobacteria that can stand up to various organophosphate pesticides is observed (Rani *et al.,* 2022). The majority of literature examined individual compounds degradation, or used mixed microbial consortia, thus restricting our knowledge of strain specific tolerance, and its ecological importance. Furthermore, the tolerance threshold, functional potential, and phylogenetic adaptation in these environments is mostly unaddressed (Cao *et al.,* 2022). In this context, the present study aims to elucidate the diversity and functional potential of organophosphate-tolerant actinobacteria isolated from cotton-growing soils of Beed district, Maharashtra. This study plans to isolate highly adapted strains with high-levels of pesticide tolerance through the use of systematic isolation, screening of multi-pesticides at varying concentrations, characterization (phenotypic and biochemical) in detail, and molecular identification using 16S rRNA gene analysis. Special focus is given to the view of the tolerance trait distribution, concentration-dependent nature of resistance and the evolutionary niche of the high-tolerant isolates. These findings are most expected to provide valuable information on how microorganisms adapt to xenobiotic stress, as well as on effective designs in bioremediation strategies to handle the issue of soils in agriculture that have been contaminated with organophosphates.

Material and Methods

Study Area and Sample Collection

Soil samples were collected from several cotton (*Gossypium hirsutum* L.) fields in geographically different locations in Beed district, Maharashtra, India. Sampling at 10-15cm using sterile tools and composite samples were prepared to avoid spatial heterogeneity. Samples were air-dried in aseptic condition followed by sieving (2 mm) and stored at 4^0C prior to microbiological analysis.

Isolation of Actinobacteria

Actinobacteria were isolated using the serial dilution and spread plate technique on Starch Casein Agar (SCA) supplemented with antifungal agents to suppress non-target growth. Plates were incubated at 28 ± 2 °C for 7–10 days. Morphologically distinct colonies exhibiting characteristic actinomycete features were purified through repeated subculturing and maintained on SCA slants for further analysis.

Primary Screening for Organophosphate Tolerance

The screening of all the isolates was carried out using panel of the organophosphate pesticides, which included chlorpyrifos, dimethoate, profenofos, phenthoate, monocrotophos, and thiamethoxam. The screening was carried out on Minimal Salt Agar (MSA) with 500 ppm each pesticide as the sole source of carbon. Growth response was recorded after incubation at 28 ± 2 °C for 7–10 days. Isolates exhibiting consistent manner were regarded as tolerant.

Secondary Screening and Determination of Tolerance Threshold

Potent isolates from primary screening were subjected to higher pesticide stress (1000 ppm) to study their tolerance limits. Growth intensity and survival patterns were comparatively investigated to identify highly resistant strains. Tolerance profiles were determined based on multi-pesticide resistance patterns.

Phenotypic and Biochemical Characterization

Isolates were selected on the basis of optimal performance and the determined characters of the isolates were identified using standard protocols which were described by Bergey's Manual of Determinative Bacteriology in terms of culture, morphology and biochemical characteristics. Parameters such as colony pigmentation, spore morphology, Gram staining and enzymatic activities were assessed in order to determine the taxonomic identity.

Molecular Identification (16S rRNA Gene Analysis)

Genomic DNA of selected isolates was extracted using standard protocols (Desai *et al.,* 2016). The 16S rRNA gene was amplified using universal primers and sequenced. Obtained sequences were compared with NCBI GenBank database using BLAST, and phylogenetic relationships were inferred to confirm taxonomic affiliation by using MEGA 11.

Data Analysis and Functional Interpretation

Tolerance data were investigated in order to identify inter-isolate and inter-sampling tendencies of multi-organophosphate resistant. The comparison of the assessment allowed determining ecologically adapted strains with a wide spectrum of tolerance. The functional potential was derived using tolerance spectrum and ecological distribution; focusing on the ones that would be utilized in bioremediation.

Results and Discussion

Isolation and Distribution of Actinobacteria

Out of a total of 88 composite soil samples (n = 88) that were collected in six cotton-growing sites in Beed district, the overall isolation efficiency was 82.95% (Figure-1). Isolate distribution showed apparent spatial variability, which means that there were differences in the abundance and recovery efficiency of actinobacterials between sites. Nathapur gave the best isolation efficiency of 20 isolates of the total 22 samples (n = 20; 90.91%), and Amla produced 16 isolates of the total 18 samples (n = 18; 88.89%). The recovered isolates of 15 were contributed by 18 samples from Dharur (n = 15; 83.33%), which is a rather high though realistic recovery efficiency. Sawargaon produced 10 isolates out of 16 samples (n = 10; 62.50%), Khadki and Chausala produced relatively fewer isolates with 7 out of 10 samples (n = 07, 62.50%), and 5 out of 8 samples (n = 05, 62.50%), respectively.

Regarding proportional contribution to total isolate pool of n = 73, Nathapur contributed 27.40%, Amla contributed 21.92% and Dharur contributed 20.55% and Sawargaon contributed 13.70% and Khadki contributed 9.59% and Chausala contributed 6.85% of the recovered actinobacterial diversity.

Primary Screening for Organophosphate Tolerance

All 73 actinobacterial isolates displayed diverse levels of tolerance to one or more organophosphate pesticides at a starting screening concentration of 500 ppm of pesticide, indicating widespread adaptive resistance in the native microbial population. Multiplication of pesticides showed that 14 isolates (19.18%) had a complete broad-spectrum tolerance and survived the presence of all six pesticides (chlorpyrifos, dimethoate, profenofos, phenthoate, monocrotophos and thiamethoxam) thus indicating a highly robust functional group. It was also found that 48 isolates (65.75%), could survive three or more pesticides evidence of high prevalence of multi-pesticide resistance phenotype characteristics in the recovered actinobacteria.

Contrastingly, 2 isolates (2.74%) were fully sensitive and did not show growth at all in all treatments (Figure-2), therefore, indicating these were non-adapted phenotypes without adaptation mechanisms. The specific analysis of pesticides showed specific gradients of tolerance, highest frequency of tolerance was observed to phenthoate (83.56%; 61/73 isolates), monocrotophos (80.82%; 59/73 isolates), followed by profenofos (69.86%; 51/73 isolates Together, these findings reveal the prevalence of functional adapted actinobacterial populations in pesticide-contaminated cotton soils, and the nature of tolerance profiles indicates the presence of multiple and potentially overlapping detoxification processes that allow tolerance to emergent multi-organophosphate stress environments..

Secondary Screening and Determination of Tolerance Threshold

The increase in tolerance of actinobacterial isolates after exposure to high concentration of pesticides (1000 ppm) was drastic and already showing the inhibitory effect of intensified xenobiotic stress on the growth of microbes. Of all 73 isolates, only 5 isolates (6.85%), namely, PTA-10, PTA-22, PTA-50, PTA-52 and PTA-70, could show steady growth in all 6 organophosphate pesticides, thus being termed as highly tolerant isolates (Figure-3).

However, at 500 ppm concentration, 18 isolates (24.66%) showed broad-spectrum tolerance resulting in an approximate 3.6-fold decrease of multi-pesticide tolerant isolates at higher concentration. And, although the percentage of isolates (47 of 73; 64.38%) that could survive at least three pesticides at 500 ppm were relatively high, the percentage became significantly lowered at 1000 ppm, as most isolates exhibited poor growth or no growth whatsoever. The decrease in broad-spectrum resistance in 24.66 to 6.85% indicates the high concentration-dependent character of organophosphate resistance and displays the net resultant effects of metabolic loads, enzymatic suppression, and cellular damages in presence of high pesticidal stress levels. These data imply that the subset of the actinobacterial population with efficient and effective detoxification systems has the potential to grow at extreme chemical concentrations, which supports the ecological relevance and may have potential applications in bioremediation systems with high loads.

Phenotypic and Biochemical Characterization

Phenotypic and biochemical characterization of the high performing isolates identified following a tolerance screening (PTA-10, PTA-22, PTA-50, PTA-52, and PTA-70) indicated characteristic *actinobacterials.* Slow-growing, dry, powdery colonies with well-developed aerial and substrate mycelia and variable pigmentation of a white to greyish tone in all the isolates. Branched filamentous hyphae with spores in chains were observed under a microscope, and Gram staining showed that all isolates were Gram-positive. The biochemical investigation exhibited significant metabolic versatility, with all isolates demonstrating catalase activity, starch hydrolysis and most responding positively to casein hydrolysis and nitrate reduction. The use of citrate and gelatine liquefaction produced variable outcomes which implied that there is strain-specific metabolic diversity.

Their morphological and cultural characters, as well as biochemical features, are typical of the genus *Streptomyces*.

16S rRNA Gene Based Molecular Identification

Isolate PTA-52 exhibited constant growth in all the organophosphate pesticides under high stress (1000 ppm) and thus was selected to undergo molecular identification. The 16S rRNA Gene sequence comparison and a BLAST search against NCBI GenBank against the database showed that the high similarity of 99 to 99.6% with the representatives of the genus *Nocardiopsis*.

This identification was further supported by phylogenetic analysis where PTA-52 strongly clustered with the *Nocardiopsis* clade and generated a tightly corresponding lineage with *Nocardiopsis* sp. strain An26 with a high bootstrap value (100) which is a good indication of evolutionary confidence (Figure-4). Although closely related, PTA-52 occupied its own sub-branch of the relationship marked by very short, but discernible lengths of the branch, indicating strain level genetic divergence at the strain level.

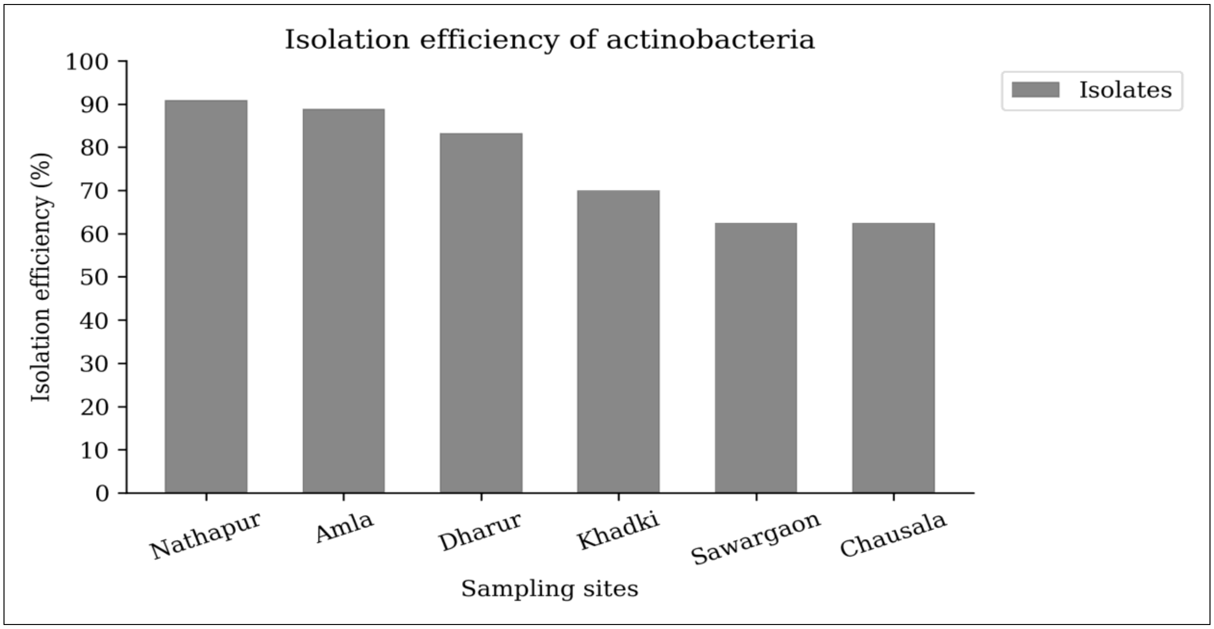
This subtle phylogenetic division is probably due to some adaptive evolutionary changes in response to long-term exposure to organophosphates, which could also have led to its superior tolerance capacity. Overall, the clustering trend validates that PTA-52 has preserved lineage traits of *Nacardiopsis,* and their segregation suggests functional differentiation, potentially relating to the route of xenobiotic degradation, which underscores their potential uses in bioremediation of contaminated environments with organophosphates. *Pseudomonas aeruginosa* was analyze as an outgroup candidate to root the tree in order to establish obvious evolution.

The present study revealed that the soils of the cotton rhizosphere, which have been long-term affected by the influence of the organophosphate, contain a well-structured and adaptively functional actinobacterial community under strong anthropogenic selection pressure. The combination of high isolation efficiency (82.95%) and strong spatial heterogeneity over sites of sampling suggests that edaphic variables, together with history of exposure to pesticides are a key determinant of actinobacterial diversity and abundance. The same patterns of enhancement have also been observed in agroecosystems with chronic pesticide contamination, where taxa of microbes with a high level of metabolic plasticity are preferentially selected (Cycoń *et al.,* 2017). The large portion of high-input agricultural sites like Nathapur and Amla also tend to support the hypothesis that the repeated use of pesticides becomes an ecological filter, facilitating the increase of xenobiotic-tolerant microbial communities (Janssens *et al.,* 2022). The initial screening outcomes from the multi-pesticide tolerance indicated that 65.75% of the isolates showed multi-pesticide tolerance, 19.18% showed full broad-spectrum tolerance at 500 ppm, and 11.87% of the isolates showed a multi-pesticide tolerance of three or more pesticides. Such a general tolerance is in line with the previous evidence that actinobacteria are able to have a wide range of enzymatic systems that can degrade, or convert, organophosphate-based compounds, such as organophosphorus hydrolases, phosphotriesterases, and esterases (Singh and Walker, 2006; Kumar *et al.,* 2018). Some genera of *Streptomyces* and *Nocardiopsis* have especially been known to have the ability to break down structurally complex pesticides via diverse metabolic pathways (Tang *et al.,* 2020).

The identified pesticide-specific tolerance gradients (greater tolerance to phenthoate and monocrotophos and a relative lower tolerance to chlorpyrifos and dimethoate) are consistent with earlier findings on the recalcitrance nature and high toxicity of chlorpyrifos that can inhibit microbial enzyme activity significantly (Yang *et al.,* 2005). High concentration (1000 ppm) of pesticides had a great reduction in tolerance with only 6.85% of the isolates maintaining the broad-spectrum tolerance.

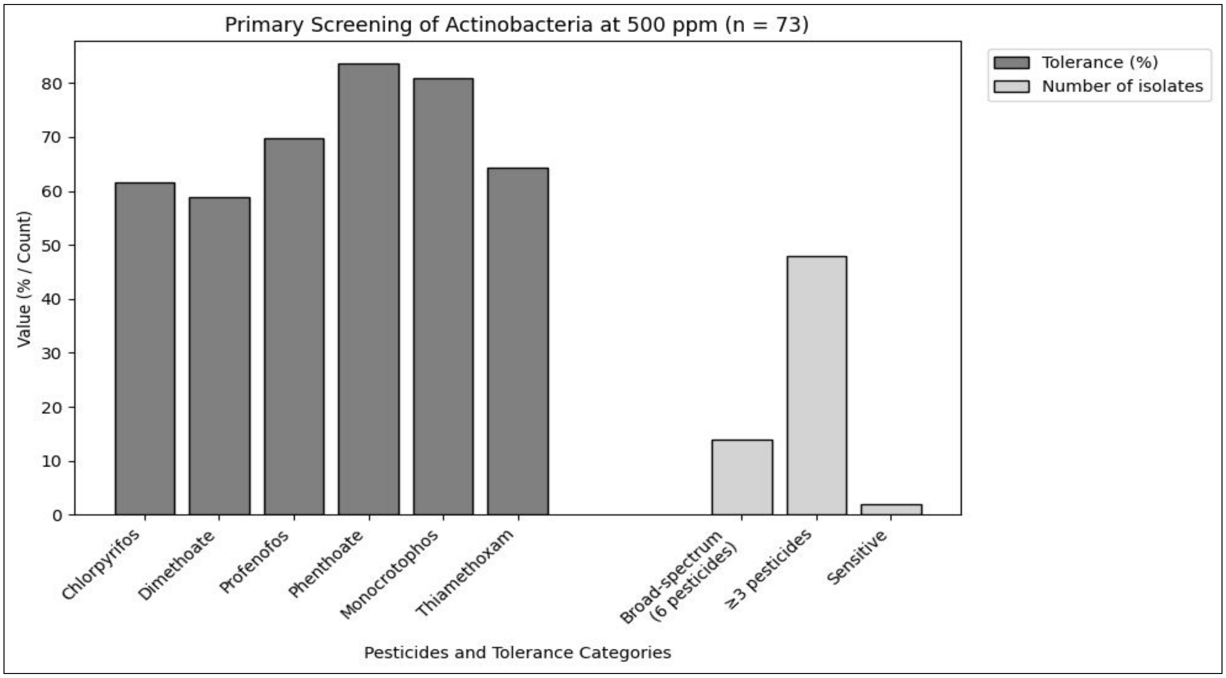
This is in decrease with 19.18% at 500 ppm and a clear indication of the concentration dependent acute of organophosphates and the limitation of the metabolite under excessive xenobiotic stress. Such results have been described in recent ecotoxicological researches, in which higher concentrations of pesticides trigger oxidative stress, membrane destabilization, and inhibition of important metabolic pathways, thus reducing the survival of microorganisms (Cycoń *et al.,* 2017). The ability to survive of a small group of highly tolerant isolates is indicative of the existence of effective detoxification schemes, perhaps by an increased expression of a specific enzyme, control of a gene or degradation via a plasmid (Singh and Walker, 2006). It is possible to refer to these isolates as elite functional groups that have a great ecological value and could be used in bioremediation strategies.

Figure.1 Isolation efficiency of Actinobacteria across sampling sites



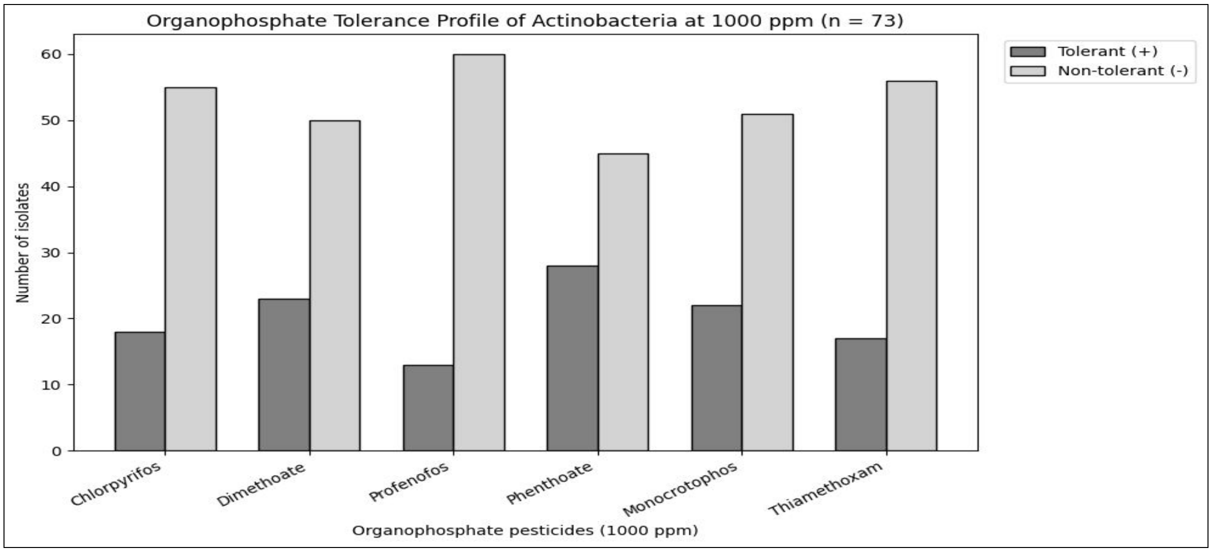
Caption: *Bar graph on isolation efficiency on them (in percent) of actinobacterial isolates taken on cotton growing soils in six sampling sites of Beed district (n = 88 samples; n = 73 isolates). Nathapur and Amla had the greatest recovery efficiencies and Sawargaon and Chausala had relatively lesser efficiencies meaning that there was site-specific variation of the actinobacterial abundance in the presence of agrochemicals.*

Figure.2 Primary screening of Actinobacterial isolates for organophosphate tolerance



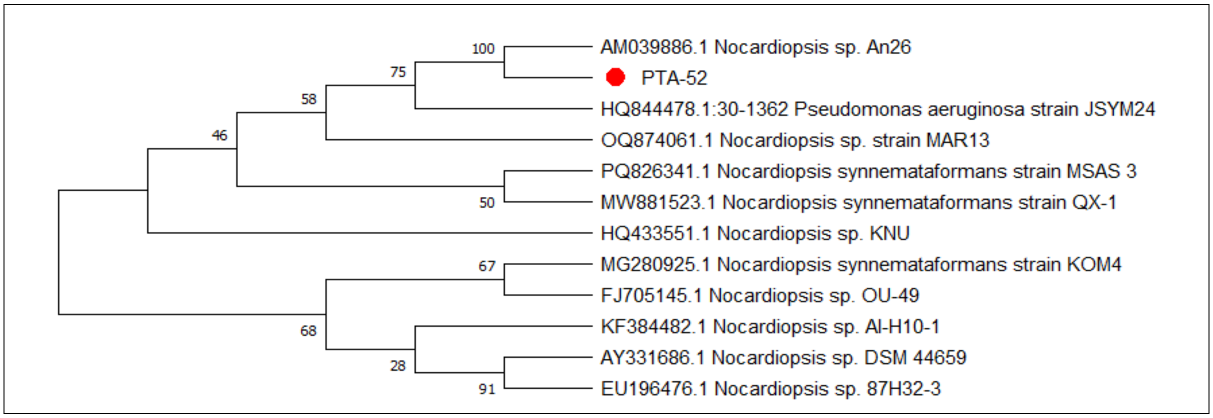
Caption: *Bar graph representing the distribution of actinobacterial isolates showing tolerance (+) and non-tolerance (–) to different organophosphate pesticides at 500 ppm concentration. The findings show that there is a high rate of multi-pesticide tolerant isolates with the highest level of tolerance to phenthoate and monocrotophos with relatively low tolerance to chlorpyrifos and dimethoate. There were 73 total isolates analyzed.*

Figure.3 Secondary screening of actinobacterial isolates under elevated organophosphate stress (1000 ppm)



Caption: *Bar graph that shows the tolerance profile of the actinobacterial isolates to organophosphate pesticide at a concentration of 1000 ppm. Loss of tolerance was significantly found in contrast to primary screening where a few of the isolates continued to grow with high pesticide stress. This shows that there is a good inhibitory action of the high concentration of organophosphates concentration on the survival of the microbes. The number of total isolates analyzed was 73.*

Figure.4 Phylogenetic analysis of isolate PTA-52



Caption: *Neighbor-joining phylogenetic tree highlighting the taxonomic position of isolate PTA-52 into the Nocardiopsis genus. Support of branches is indicated by bootstrap values.*

Table.1 Phenotypic and Biochemical Characteristics of Selected Organophosphate-Tolerant Actinobacterial Isolates

Isolate	Colony Characteristics	Key Biochemical Traits	Presumptive Identification
PTA-10	Filamentous, powdery, aerial mycelium	Catalase+, Starch+, Casein+, Nitrate+	*Streptomyces* sp.
PTA-22	Chalky, branched, aerial hyphae	Catalase+, Starch+, Casein+, Nitrate+	*Streptomyces* sp.
PTA-50	Dry, powdery, rough colonies	Catalase+, Starch+, Casein+, Nitrate+	*Streptomyces* sp.
PTA-52	Dense filamentous, raised colonies	Catalase+, Starch+, Casein+, Nitrate+	*Streptomyces* sp.
PTA-70	Powdery, filamentous colonies	Catalase+, Starch+, Casein+, Nitrate+	*Streptomyces* sp.

Phenotypic and biochemical descriptions of the chosen high-performing isolates showed typical characteristics of actinobacteria such as filamentous morphology, aerial mycelium formation, and high-level hydrolytic enzyme activity. Catalase, starch hydrolysis, casein degradation and nitrate reduction have positive responses, and this represents great metabolic versatility which is one of the main determinants of environmental adaptability and biodegradation ability. Actinobacteria have been extensively reported to exhibit such enzymatic diversity, which is said to be necessary to degrade complex xenobiotic compounds. PTA-52 also helped in the determination of the affiliation of this identified isolate to the genus. *Nocardiopsis* owing to the close sequence similarity (99-99.6%) and the high clustering of isolate. PTA-52 in the Nacardiopsis clade. The use of the *Pseudomonas aeruginosa* as a. outgroup has been the assurance of correct phylogenetic foundationalism and the clear differentiation in evolution. The emergence of a separate sub-cluster of PTA-52 with short yet significant divergence of the branches, is evidence of an amount of strain-level differentiation, likely to occur. Transformed into having a form of adaptative evolution to protracted exposure to pesticides. Recent research has underscored the idea that environmental stressors and xenobiotics are able to mobilize genetic diversification via mutation, horizontal gene transfer, and regulatory adaptation to confer improved functional capabilities (Kumar *et al.,* 2018). The branch phylogenetic position of PTA-52 is thus probably an evolutionary response to the high degree of tolerance to organophosphates. In general, the result of this paper indicates that the soils covered with pesticides in cotton serve as reservoirs of ecologically and biotechnologically relevant functionally specialized actinobacteria. The discovery of the very tolerant strains especially the PTA-52, highlights its usefulness in bioremediation of the organophosphate-contaminated soil. These findings add to the existing body of literature that highlights the importance of native microbial communities in reducing environmental pollution and can help develop microbe-based remediation approaches that are sustainable (Cycoń *et al.,* 2017).

In conclusion, the current report indicates that long-term use of organophosphates followed by exposure of cotton rhizosphere soils to organophosphates results in a structurally diversified and functionally specialized actinobacterial community that is a result of intense chemical selection pressure. The adaptive resistance to isolate actinobacteria is indicated by the high isolation efficiency (82.95%) and multi-pesticide tolerance at 500 ppm, which is nearly 100%, but the reduction in tolerance to 6.85% at 1000 ppm, highlights the limitations of microbial detoxification abilities under intense xenobiotic pressure. The occurrence of elite strains, the isolate PTA-52 of Nocardiopsis (99.6-99.4% similarity) and its distinct position in the phylogenetic space testify to the impact of adaptive evolutionary responses to enhanced. Organophosphate tolerance. All these facts locate pesticide-contaminated cotton soils as sources of extremely specialized actinobacteria that have immense potential in being used in bioremediation. The work includes important details on how microorganisms adapt, their functional resilience, and tolerance limits, thus creating a scientific base of the development of atmospherically innovative, microbe-based, solutions to solve the issues of organophosphate pollution in agricultural settings.

Author Contributions

Chavan Suresh Sudam: Investigation, formal analysis, writing—original draft.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

References

Barka, E. A., Vatsa, P., Sanchez, L., Gaveau-Vaillant, N., Jacquard, C., Klenk, H.-P., Clément, C., Ouhdouch, Y., & van Wezel, G. P. (2015). Taxonomy, Physiology, and Natural Products of Actinobacteria. *Microbiology and Molecular Biology Reviews*, *80*(1), 1–43. https://doi.org/10.1128/mmbr.00019-15

Bhatt, P., Huang, Y., Zhan, H., & Chen, S. (2019). Insight Into Microbial Applications for the Biodegradation of Pyrethroid Insecticides. *Frontiers in Microbiology*, *10*, 1778. https://doi.org/10.3389/fmicb.2019.01778

Britti, D. (2026). Molecular mimicry in the agroecosystem: A new paradigm for understanding how pesticide residues drive the emergence of antimicrobial resistance. *Environmental Toxicology and Pharmacology*, *123*, 104974. https://doi.org/10.1016/j.etap.2026.104974

Cao, Z., Yan, W., Ding, M.-Z., & Yuan, Y.-J. (2022). Construction of microbial consortia for microbial degradation of complex compounds. *Frontiers in Bioengineering and Biotechnology*, *10*. https://doi.org/10.3389/fbioe.2022.1051233

Cycoń, M., Mrozik, A., & Piotrowska-Seget, Z. (2017). Bioaugmentation as a strategy for the remediation of pesticide-polluted soil: A review. *Chemosphere*, *172*, 52–71. https://doi.org/10.1016/j.chemosphere.2016.12.129

Desai, D. A., Kukreja, G. P., Raorane, C. J., & Patil, S. B. (2016). Partial sequencing of serendipitously isolated antifungal producer, Pseudomonas tolaasii strain GD76 16s ribosomal RNA gene. *Int J Curr Microbiol App Sci*, *5*(1), 455-458.

El Baz, S., Baz, M., Barakate, M., Hassani, L., El Gharmali, A., & Imziln, B. (2015). Resistance to and Accumulation of Heavy Metals by Actinobacteria Isolated from Abandoned Mining Areas. *The Scientific World Journal*, *2015*, 1–14. https://doi.org/10.1155/2015/761834

Hadjer Rebai, Essam Nageh Sholkamy, Mohamed, Pratheesh Prakasam Thanka, Hassan, A. A., Pack, S. P., Ki, M.-R., & Allaoueddine Boudemagh. (2024). Soil Actinobacteria Exhibit Metabolic Capabilities for Degrading the Toxic and Persistent Herbicide Metribuzin. *Toxics*, *12*(10), 709–709. https://doi.org/10.3390/toxics12100709

Janssens, L., Van de Maele, M., Delnat, V., Theys, C., Mukherjee, S., De Meester, L., & Stoks, R. (2022). Evolution of pesticide tolerance and associated changes in the microbiome in the water flea Daphnia magna. *Ecotoxicology and Environmental Safety*, *240*, 113697. https://doi.org/10.1016/j.ecoenv.2022.113697

Kilonzi, J. M., & Otieno, S. (2024). Degradation kinetics and physiological studies of organophosphates degrading microorganisms for soil bioremediation. *Stress Biology*, *4*(1). https://doi.org/10.1007/s44154-023-00138-6

Komicho, J. D., & Tipayno, S. C. (2025). Organophosphate Degradation and Plant Growth-Promoting Activity of Soil Bacteria Isolated from Vegetable Farms in Benguet, Philippines. *Journal of Pure and Applied Microbiology*, *19*(3), 2184–2199. https://doi.org/10.22207/jpam.19.3.46

Kumar, S., Kaushik, G., Dar, M. A., Nimesh, S., López-Chuken, U. J., & Villarreal-Chiu, J. F. (2018). Microbial Degradation of Organophosphate Pesticides: A Review. *Pedosphere*, *28*(2), 190–208. https://doi.org/10.1016/s1002-0160(18)60017-7

Lyagin, I., & Efremenko, E. (2021). Enzymes, Reacting with Organophosphorus Compounds as Detoxifiers: Diversity and Functions. *International Journal of Molecular Sciences*, *22*(4), 1761. https://doi.org/10.3390/ijms22041761

Mohammadipanah, F., & Dehhaghi, M. (2017). Classification and Taxonomy of Actinobacteria. *Biology and Biotechnology of Actinobacteria*, 51–77. https://doi.org/10.1007/978-3-319-60339-1_4

Naveen Kumar, B. T., & Babalad, H. B. (2017). Response of Cotton (Gossypium hirsutum L.) to Different Conservation Agricultural Practices under Rainfed Situations. *International Journal of Current Microbiology and Applied Sciences*, *6*(11), 2279–2286. https://doi.org/10.20546/ijcmas.2017.611.270

Pakar, N. P., Rehman, F. U., Mehmood, S., Ali, S., Zainab, N., Munis, M. F. H., & Chaudhary, H. J. (2024). Microbial detoxification of chlorpyrifos, profenofos, monocrotophos, and dimethoate by a multifaceted rhizospheric Bacillus cereus strain PM38 and its potential for the growth promotion in cotton. *Environmental Science and Pollution Research International*, *31*(27), 39714–39734. https://doi.org/10.1007/s11356-024-33804-x

Pashirova, T., Rym Salah-Tazdaït, Djaber Tazdaït, & Masson, P. (2024). Applications of Microbial Organophosphate-Degrading Enzymes to Detoxification of Organophosphorous Compounds for Medical Countermeasures against Poisoning and Environmental Remediation. *International Journal of Molecular Sciences*, *25*(14), 7822–7822. https://doi.org/10.3390/ijms25147822

Prabhaharan Renganathan, Gaysina, L. A., Cipriano García Gutiérrez, Omar, E., & Sainz-Hernández, J. C. (2025). Harnessing Engineered Microbial

Consortia for Xenobiotic Bioremediation: Integrating Multi-Omics and AI for Next-Generation Wastewater Treatment. *Journal of Xenobiotics*, *15*(4), 133–133. https://doi.org/10.3390/jox15040133

Rani, A., Mathur, A., & Gupta, S. (2022). Isolation and screening of actinobacterial isolates from chemical pesticides usage fields of the Uttarakhand region. *Journal of Advanced Scientific Research*, *13*(06), 69–73. https://doi.org/10.55218/jasr.202213611

Sarwade, P., Gaisamudre (Sarwade), K. N., Bhise, D. S., Chandanshive, S. S., & Gaikwad, R. S. (2025). Impact of Mycorrhizae on Soil Health and Fertility in Maharashtra's Agricultural Lands: A Critical Analysis. *Plantae Scientia*, *8*(2), 20–33. https://doi.org/10.32439/ps.v8i2.20-33

Singh, B. K., & Walker, A. (2006). Microbial degradation of organophosphorus compounds. *FEMS Microbiology Reviews*, *30*(3), 428–471. https://doi.org/10.1111/j.1574-6976.2006.00018.x

Srivastava, S., Mir, R. A., Hussain, S. J., Mitra, S., Srivastava, S., Kumar, P., & Kaur, H. (2026). Microbial engineering for pesticide degradation: current insights and future directions for sustainable agriculture. *Frontiers in Microbiology*, *17*. https://doi.org/10.3389/fmicb.2026.1751932

Tang, J., Hu, Q., Lei, D., Wu, M., Zeng, C., & Zhang, Q. (2020). Characterization of deltamethrin degradation and metabolic pathway by co-culture of Acinetobacter junii LH-1-1 and Klebsiella pneumoniae BPBA052. AMB Express, 10(1). https://doi.org/10.1186/s13568-020-01043-1

Tanveer, S., Ilyas, N., Akhtar, N., Akhtar, N., Bostan, N., Hasnain, Z., Niaz, A., Zengin, G., Gafur, A., & Fitriatin, B. N. (2024). Unlocking the interaction of organophosphorus pesticide residues with ecosystem: Toxicity and bioremediation. *Environmental Research*, *249*, 118291. https://doi.org/10.1016/j.envres.2024.118291

Thakur, M., Medintz, I. L., & Walper, S. A. (2019). Enzymatic Bioremediation of Organophosphate Compounds—Progress and Remaining Challenges. *Frontiers in Bioengineering and Biotechnology*, *7*. https://doi.org/10.3389/fbioe.2019.00289

Yang, L., Zhao, Y., Zhang, B., Yang, C.-H., & Zhang, X. (2005). Isolation and characterization of a chlorpyrifos and 3,5,6-trichloro-2-pyridinol degrading bacterium. *FEMS Microbiology Letters*, *251*(1), 67–73. https://doi.org/10.1016/j.femsle.2005.07.031

Yasemi, M., Jalali, A., Asadzadeh, M., & Komijani, M. (2025). Organophosphate pesticides and their potential in the change of microbial population and frequency of antibiotic resistance genes in aquatic environments. *Chemosphere*, *376*, 144296. https://doi.org/10.1016/j.chemosphere.2025.144296

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