Research article

Evaluation of suitability and biodegradability of the organophosphate insecticides to mitigate insecticide pollution in onion farming

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ABSTRACT

Organophosphates constitute a major class of pesticides widely employed in agriculture to manage insect pests. Their toxicity is attributed to their ability to inhibit the functioning of acetylcholinesterase (AChE), an essential enzyme for normal nerve transmission. Organophosphates, especially chlorpyrifos, have been a key component of the integrated pest management (IPM) in onions, effectively controlling onion maggot *Delia antiqua*, a severe pest of onions. However, the growing concerns over the use of this insecticide on human health and the environment compelled the need for an alternative organophosphate and a potential microbial agent for bioremediation to mitigate organophosphate pesticide pollution. In the present study, chloropyrifos along with five other organophosphate insecticides, phosmet, primiphos-methyl, isofenphos, iodofenphos and tribuphos, were screened against the target protein AChE of *D. antiqua* using molecular modeling and docking techniques. The results revealed that iodofenphos showed the best interaction, while tribuphos had the lowest interaction with the AChE based on comparative binding energy values. Further, protein-protein interaction analysis conducted using the STRING database and Cytoscap software revealed that AChE is linked with a network of 10 different proteins, suggesting that the function of AChE is disrupted through interaction with insecticides, potentially leading to disruption within the network of associated proteins. Additionally, an *in silico* study was conducted to predict the binding efficiency of two

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organophosphate degrading enzymes, organophosphohydrolase (OpdA) from *Agrobacterium radiobacter* and *Trichoderma harzianum* paraoxonase 1 like (ThPON1-like) protein from *Trichoderma harzianum*, with the selected insecticides. The analysis revealed their potential to degrade the pesticides, offering a promising alternative before going for cumbersome onsite remediation.

1. Introduction

Onion (*Allium cepa* L.) is the oldest known and significantly high-value spice cum bulbous vegetable crop grown worldwide. It has layers of health benefits and is a nutrient-dense vegetable. It has become an important ingredient in the global diet and is often considered the queen of kitchen. It is ranked as the third most important vegetable in the world, and its production has emerged as the forte of developing countries [1]. However, the susceptibility of onions to a wide array of insect pests poses a significant challenge to successful onion cultivation, resulting in economic losses in terms of both quality and quantity from fields to storehouses. Onion maggot (*Delia antiqua* Meigen) is one of the most devastating pests of onion and allied *Allium* crops in the Northern temperate zones of the world [2]. An average loss of 20–100 percent has been reported in onions without any pest control measure [3,4]. The damage associated with the pest is caused when maggots feed on the plant's roots and the bulb, resulting in wounds that subsequently contribute to secondary rots in storage. Therefore, the current management approaches aim to specifically target the maggots. Common techniques for controlling maggots include the application of insecticides in the furrow while planting, seed coating treatments for onions, and adding pesticides to the irrigation water used in onion fields [5,6]. Historically, the control has been achieved by oil (1930s), mercury (1940s), and organochlorines (1950s), followed by organophosphates, neonicotinoids, and other newer insecticides (1960s to present). The most often applied insecticides are group 1B organophosphates [5,7]. Chlorpyrifos has been widely used since the beginning of the 1980s to control onion maggots as a key Integrated Pest Management (IPM) tool in onions [8]. Until recently, chlorpyrifos was commonly used as a drench treatment at planting either alone or with insecticide seed treatments. However, the Environmental Protection Agency (EPA) in early 2022 banned it for use on all crops, considering its unintended effects on non-target organisms and the environment [9]. Because of the pervasive use of these chemicals for onion maggot control, these have found their way into the groundwater and soils. Therefore, the need to discover the possible ways of minimizing their toxicological side effects has sharply increased. There is a dire need for an alternative organophosphate that farmers can use to reduce the pest population significantly and potential microorganisms producing pesticide-degrading enzymes to decontaminate soils containing residual pesticides.

The most reliable parameter for evaluating the toxicity of organophosphates is to check the activity of acetylcholinesterase (AChE) [10]. Acetylcholine is the primary excitatory neurotransmitter at synapses in the insect nervous system. AChE (EC 3.1.1.7) is a hydrolytic enzyme of the serine hydrolase superfamily responsible for terminating the transmission of impulses by catalyzing the breakdown of acetylcholine into choline and acetic acid [11,12]. Several groups of insecticides kill insect pests by interrupting the activity of AChE [13]. Organophosphates are synaptic poisons and potent inhibitors of AChE, inhibiting the activity of AChE by phosphorylating the serine hydroxyl group within the enzyme's active site [14]. As a result, acetylcholine builds up in the synapsis, keeping the acetylcholine receptors open constantly. This causes higher neuronal excitation, rapid twitching of muscles, and eventually muscle paralysis and death [15].

The accumulation of pesticide residues in different ecosystems, including agricultural soils, has resulted from the unregulated use of pesticides [16]. An innovative, potentially safer, and economically viable solution to decontaminate the soils is microbial bioremediation. Multiple pathways for pesticide degradation are reported in different microorganisms, which involve one or the other pesticide-degradative enzymes [17]. Pesticide-degrading enzymes in these microorganisms enable them to break down the toxic pesticide molecules by cleaving their specific bonds, such as P–O, P–F, P–S, and P–C bonds [18]. Organophosphate hydrolyzing enzymes are the most specific and extensively studied in terms of pesticide degradation [19].Among these are organophosphohydrolase (OpdA) from *Agrobacterium radiobacter*, zinc-containing phosphotriesterase (PTE) from *Pseudomonas diminuta*, diisopropylfluorophosphatase (DFPase) from *Loligo vulgaris*, serum paraoxonase (PON1) from *Oryctolagus cuniculus*, phosphotriesterase-like lactonase (SsoPox) from *Sulfolobus solfataricus*, and organophosphate acid anhydrolase (OPAA) from *Altermonas* sp [20].

Most biological processes involve interactions between different proteins, which provide potential targets for the drug design. The identification of many protein target sites and their interactions with other proteins, biomolecules, or chemicals has been made possible by advancements in bioinformatics. Advances in computational biology tools have resulted in an *in-silico* study of protein-protein interactions before screening the target biomolecules in vitro. Molecular docking is an essential tool for determining the mode of action of small molecules against potent protein targets for developing novel drug molecules [21]. Due to the availability of annotated protein sequences of insects, researchers have explored the most critical proteins essential for the survival of insects and their invasion of hosts as potential targets for drug design. An *in-silico* approach aids in screening biomolecules or chemicals to determine their inhibitory activity towards pests [22]. It can also be employed to predict the biodegradation potential of an organism and can, therefore, be used to gather rapid, low-cost, and timely information before beginning with onsite treatment of harmful contaminants [23]. *In-silico* bioremediation can address research gaps and rapidly forecast customized degradative enzymes to eliminate hazardous pesticides [24]. The degradation capability of microbial cultures will be better applied in bioremediation to ameliorate pesticide pollution if the interaction mechanism of OPs with enzyme proteins in microbial cultures is better understood. In recent years, a multitude of exciting studies have examined the levels of organophosphate pesticides in biological matrices like blood serum and urine [25–27], while also identifying and quantifying these pesticides in environmental mediums such as soil, sediments,

water, and air [28–30]. Developing safe, reliable, cost-effective, and environmentally friendly methods to eliminate OPs pesticides from our surroundings is imperative. Bioremediation techniques, harnessing the power of microbes or microbial-biocatalysts, are emerging as promising solutions to combat OP pesticides, offering a beacon of hope for a cleaner and healthier environment. *Trichoderma harzianum* is one of the most frequently used species in the management of plant diseases, with several studies demonstrating its potential to control onion basal rot, another significant concern for onion growers [31,32]. *Agrobacterium radiobacter* has been reported to control *Agrobacterium tumefaciens*, the causal agent of crown gall disease in plants [33,34].

In the present study, we investigated the AChE inhibitory potential of five OP insecticides; phosmet, primiphos-methyl, isofenphos, iodofenphos, and tribuphos, via docking analysis in an attempt to trace out the best alternative organophosphate to chlorpyrifos against *D. antiqua*. These insecticides have demonstrated high effectiveness against the target pest species. A study conducted has also shown that these insecticides when used as seed treatment gave adequate control of dieldrin resistant flies. Seed treatment of isofenphos and iodofenphos have been reported to exhibit low [35]. This characteristic is paramount as it ensures minimal impact on crop health and productivity. Given the established efficacy of *A. radiobacter* and *T. harzianum* in agricultural settings, we sought to explore their potential application in the bioremediation of organophosphate pollution in onion soils thereby encouraging their further application beyond the realm of disease control. Therefore, the practicable binding mechanism of the selected pesticides with organophosphohydrolase (OpdA) enzyme of *A. radiobacter* and *Trichoderma atroviride* paraoxonase 1 like (TaPON1-like) protein of *T. harzianum* which are reported to be involved in the degradation of OP pesticides were also studied using *in silico* protein modeling and molecular docking studies to screen potential microorganisms before onsite bioremediation.

Table 1
Molecular characteristics of selected organophosphate pesticides.

Name	Molecular formula	Molecular weight	Structure
Phosmet	$C_{11}H_{12}NO_4PS_2$	317.3 g/mol	
Pirimiphos-methyl	$C_{11}H_{20}N_3O_3PS$	305.34 g/mol	
Isofenphos	$C_{15}H_{24}NO_4PS$	345.4 g/mol	
Iodofenphos	$C_8H_8Cl_2IO_3PS$	413.00 g/mol	
Tribufos	$C_{12}H_{27}OPS_3$	314.5 g/mol	
Chlorpyrifos	$C_9H_{11}Cl_3NO_3PS$	350.6 g/mol	
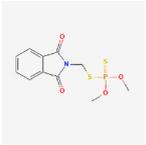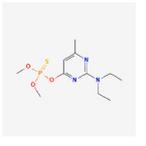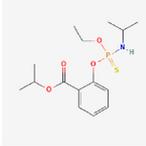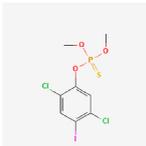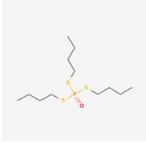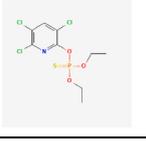
2. Materials and methods

2.1. Molecular modeling of the target proteins

The sequences of the protein targets AChE, OpdA, and ThPON1 were retrieved from the UniProt database. The selected protein targets were searched for experimentally and computationally determined structures in the Protein Data Bank, and no hits were found. Therefore, molecular modelling of the protein targets was done using SWISS-MODEL [36]. Based on homology modeling in the SWISS server, the 3D protein structure was built by comparing the experimentally validated structures available in PDB. Likewise mutation of AChE was performed using FoldX program and the final structure was obtained by SWISS-MODELLING [37]. The excellent quality of the modelled structure was ensured using the sequence identity percentage (30–50 %), the highest query coverage, and the Global mean quality Estimation (GMQE) score of about 1.

2.2. Validation of the target proteins

The quality of the modelled protein structure was validated using model building with known sequences. The reliability of these structures was further confirmed through SAVES v6.0 (Structural Analysis and Verification Server). Procheck v.3.5 program was used to evaluate the overall stereochemistry of the protein and check the quality of the modelled structure by comparing with well refined structures of similar resolution. Subsequently, PDB format file of the structure was uploaded to run the program, so as to get the Ramachandran plot to find out the residues in the allowed and disallowed regions. Further, visualization, energy minimization and loop building of the structure was done for the residues in the disallowed region using SWISS PDB VIEWER. After loop refinement, residues were checked for their feasible conformations [38].

2.3. Ligand preparation

The PubChem database (https://pubchem.ncbi.nlm.nih.gov/) was used to retrieve the structures of the ligands phosmet, primiphos-methyl, isofenphos, iodofenphos, chlorpyrifos, and tribuphos in the structure data files (SDF) format [39]. Open Babel was used to convert SDF to Protein Data Bank (PDB) files [40] (Table 1, Fig. 1).

2.4. Molecular docking

Molecular docking of ligands with the protein targets AchE, AchE mutated, OPDA, and ThPON1-Like Protein was done using the AutoDock vina module of PyRx 0.8 [41]. Target proteins were uploaded to PyRx software and converted to macromolecules using the "make macromolecule" option in the PyRx program. The PrankWeb server was used to identify the binding sites of protein targets [42]. The predicted binding sites are mentioned in Table 2. Besides, the grid configuration and docking were done using parameter files about AutoDock4 and Autogrid4. Further, visualization of the docked complexes was done using BIOVIA Discovery Studio.
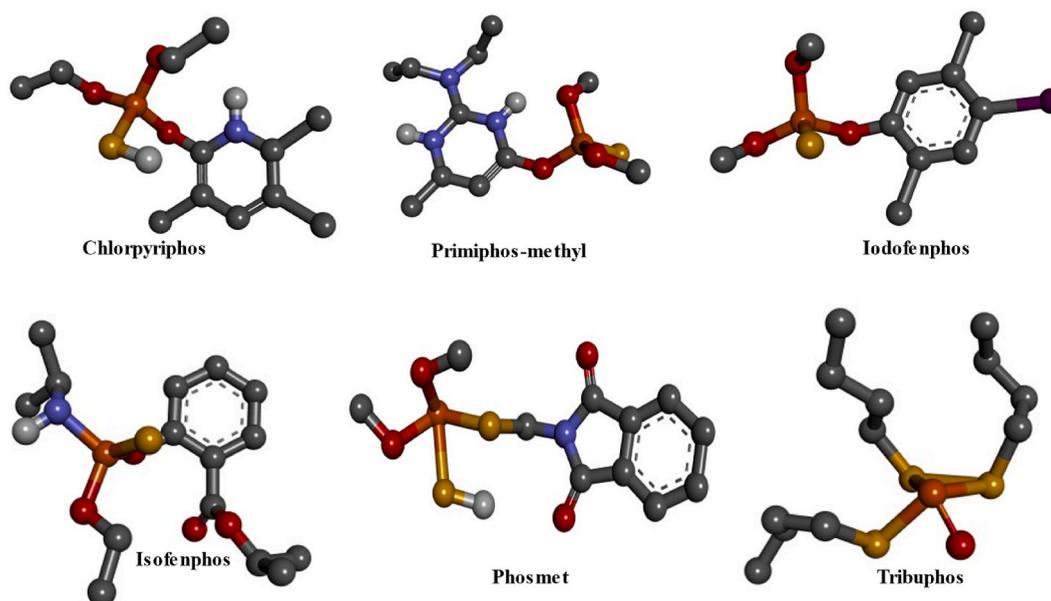
Fig. 1. Three-dimensional structure of the ligands.

Table 2
Active binding sites predicted in AChE using CASTp server.

Protein name	Sequence	Binding Sites	Location of Binding Sites
Acetylcholinesterase (AChE)	>tr|Q5DV29|Q5DV29_9MUSC Acetylcholinesterase (Fragment) OS = Delia antiqua OX = 265456 GN = ace-2 PE = 2 SV = 1TS EKAVDIGKALINDCNCNASLLSENPQAVMPCMRSVDAKTISVQ	A_17 A_18 A_19 A_22 A_29 A_33	
Phosphotriesterase (OPDA)	>tr|Q93LD7|Q93LD7_RHIRD Phosphotriesterase OS=Rhizobium radiobacter OX = 358 GN=OpdA PE = 1 SV = 1 MQTRRDALKSAAAITLLGGLAGCASMARPIGTGDLI NTVRGPIPVSEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRG LRHARSAGVQTIVDVSTFDIGRDVRLLAEVSRAADVHIVAATGLWFDPPLS MRMRSVEELTQFFLREIQHGIEDTGIRAGIIKVATTGKATPFQELVLKAAARA SLATGVPVTTHTSASQRDGEQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTG LAARGYLVGLDRMPYSAIGLEGNASALALFGTRSWQTRALLIKALIDRGYKDRIL VSHDWLFGFSSYVTNIMDVMDRINPDGMAFVPLRVIPFLREKGVPPETLAGVTV ANPARFLSPTVRAVVTRSETSRPAAPIPRQDTER	A_135 B_105 B_130 B_131 B_168 B_172 B_200 B_201 B_202 B_203 B_204 B_229 B_232 B_253 B_256 B_269 B_270 B_271 B_272 B_274 B_279 B_300 B_302 B_305 B_307 B_308 B_56 B_59	
ThPON1-like protein	>tr|A0A4D6GQM1|A0A4D6GQM1_HYPAT TAPON1-like protein OS=Hypocrea atroviridis OX = 63577 PE = 2 SV = 1 MAARASITAVLLAVLLGYAYNSYVQRALVVMGAFRQPGSTELAPGDFVVI EGTTHCEDLHHHESTGLIFTACEGFKGARLKWFPPIDHFFEPSHPELVKG NLQVIDPKTLKAQVLELEGFSGPFVTHGIDVIDDPKKPKGEAVYIFAVNHRPN PKHYGENGDAKAPQCYSVIELFHHVVGSGKARHVRTIWHPLITTPNDIFAMS PTSFLVTNDHYFRTGLPRMLEDVLSLIARTNTVHVQLQDLKPVKSDDAGVHAS VALDKLHNLNGLGHGRTEDEVFVTGCSSGVIHVGKISEGKDAEKIISVSKTIEFSS PVDNPTYFKDPYANKTFDASGVVASGPTRAVDWFSNKALEDVLDPSMVWMAS PRSGGQKGEGAAKGEEDWDLKLIFQDDGQRVRTSSASVLLAIDPKEEQGRRRA WLFVSSYQAKNAIAVKIDL	A_127 A_199 A_215 A_224 A_227 A_228 A_266 A_268 A_284 A_285 A_31 A_315 A_317 A_341 A_344 A_347 A_399 A_400 A_426 A_57 A_85 A_86	

2.5. STRING analysis

The STRING database (Search Tool for the Retrieval of Interacting Genes/Proteins) was used to investigate the interactions of different proteins in *Delia* [43]. *Delia's* genome was queried using protein sequences from AChE to discover the proteins interacting with each other. A degree-sorted network was constructed using genes and proteins that interacted with one another. The information regarding the query proteins, the protein domains it interacts with, and the number of other domains in the network that fall under a certain domain were all examined. For better understanding, it was investigated how the query protein and its interaction partners are related functionally. A minimum of 10 participants and a medium level of confidence of 0.40 were used to construct the network. Cytoscape 3.9.1 was used to import the STRING database result for further analysis.
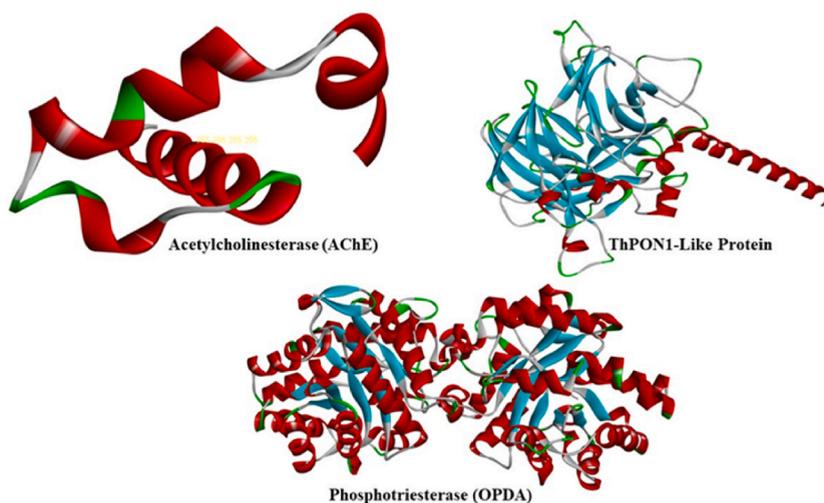
Fig. 2. Three-dimensional structure of the protein target.

Table 3

Molecular modeling of protein targets of AChE, OPDA, and ThPON1 using SWISS-MODEL.

UniProt ID	Protein target name & sequence length	Template protein PDB ID	Sequence identity %	Sequence similarity %	Coverage %	GMQE
Q5DV29	Acetylcholinesterase-45	6XYY	84.44	55	100	0.82
Q93LD7	Phosphotriesterase-384	6GBJ	87.58	57	86	0.82
A0A4D6GQM1	ThPON1-Like Protein-438	A0A6V8QS53	84.70	57	100	0.94

3. Results

3.1. Molecular modelling of target proteins of D. antiqua

The AChE, OPDA, and ThPON1-like protein target proteins used SWISS-MODEL software. The 3D structure and modeling details of the target proteins are mentioned in Fig. 2 and Table 2. (Fig. 2 and Table 3).
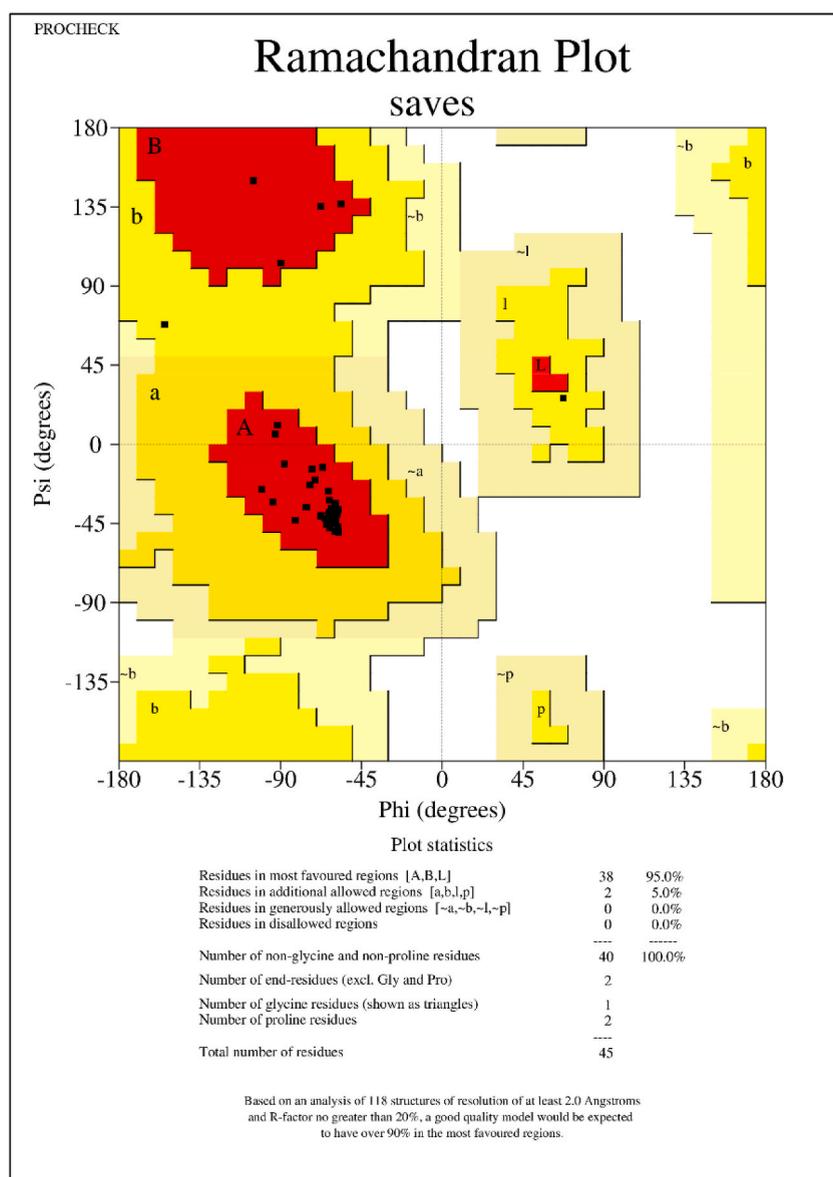
Fig. 3. Ramachandran plot for the protein target AChE.
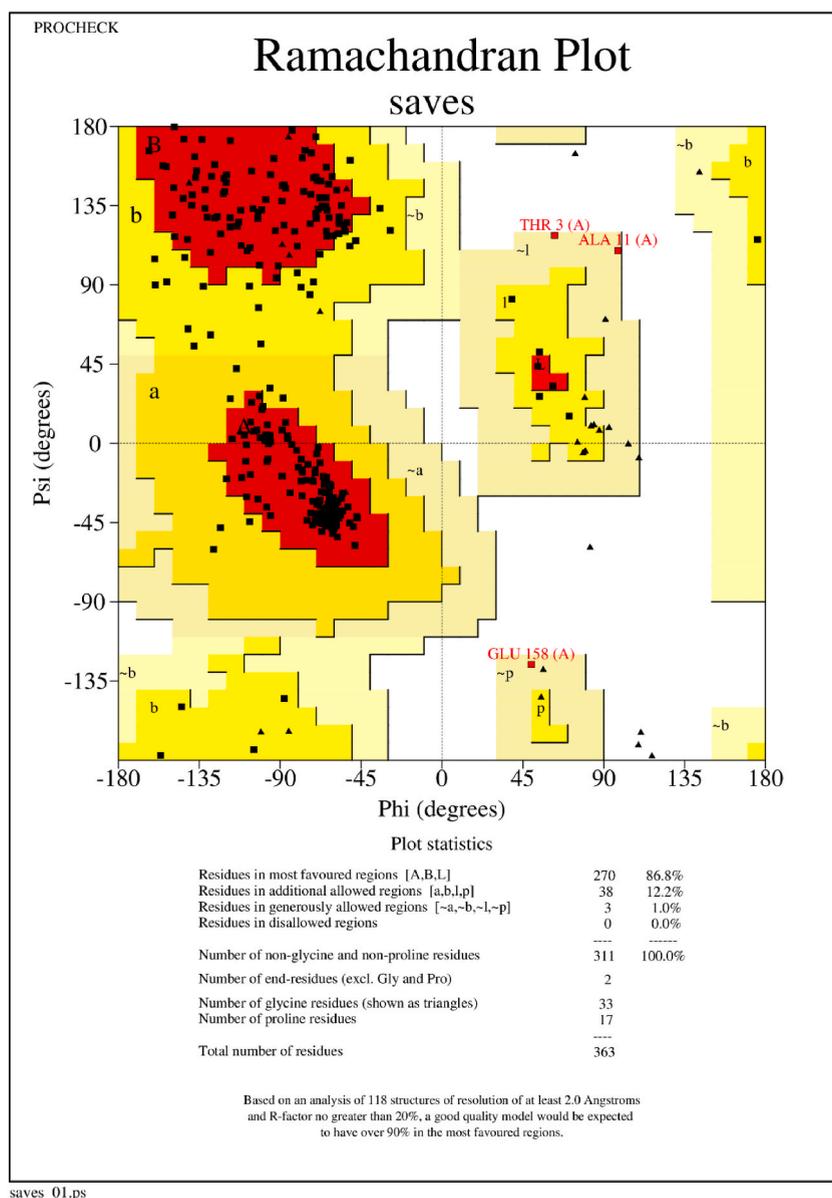
Fig. 4. Ramachandran plot for the protein target OPDA.

SAVES server validated AChE, OpdA, and ThPON1 target proteins via Ramachandran plot. It revealed that AChE had 92.5 percent of the residues that were found in the most favoured region and 7.5 percent in the additional allowed region, OpdA had 89.90 percent of the residues in the most favoured region, 9.5 % in the additionally allowed region, and likewise ThPON1 had 90.7 percent of the residues in the most favoured region, 8 percent in the additionally allowed region (Figs. 3–5).

3.2. Molecular docking of the selected ligands with the protein target (AChE) of D. antiqua

Molecular docking tools were employed to evaluate the binding energy of the modelled target proteins AChE, OpdA, and ThPON1 with different organophosphates. The binding affinity of iodofenphos, isofenphos, phosmet, pirimiphos-methyl, tribufos, and chlorpyrifos with the target protein AChE was −4, −3.9, −3.8, −3.9, −2.9 and 1.2 kcal/mol respectively. Likewise, binding affinity of mutated AChE with phosmet, primiphos-methyl, iodofenphos, isofenphos, chlorpyriphos and tribufos was −4.2, −3.8, −3.7, −4.0, 2.2 and −3.2 kcal/mol respectively. Similarly, the binding energy of iodofenphos, isofenphos, phosmet, pirimiphos-methyl, tribufos, and chlorpyrifos with the target protein OPDA was −5.2, −6.6, −6, −6.3, −4.9 and −5.8 kcal/mol respectively. Similarly, the binding affinity of iodofenphos, isofenphos, phosmet, primiphos-methyl, tribufos, and chlorpyrifos with the target protein ThPON1 was −6.4, −7.1, −7.1, −7, −5.9 and −6.8 kcal/mol respectively (Figs. 6–11).
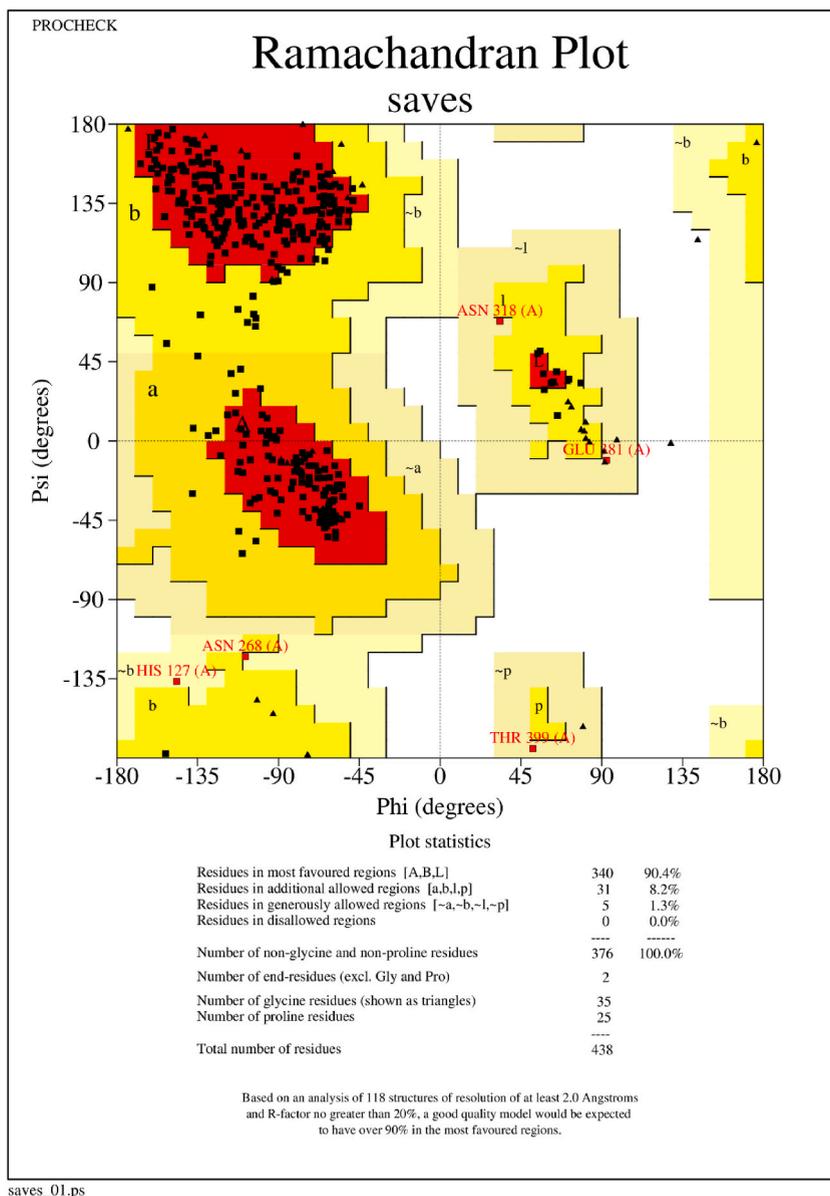
Fig. 5. Ramachandran plot for the protein target ThPON1.

3.3. Analysis of protein-protein interaction of AChE

STRING analysis was performed to understand how AChE-related genes interact with other proteins and their conserved domains. The majority of the proteins that interacted with each query protein, as determined by our data, were grouped in the network and shared comparable conserved domains. Based on the insect's genome, the interaction partners were extracted using the protein sequence of the AChE-related genes as the input.

Interactions of AChE protein with other proteins are suggested, including a large family of proteins with a wide range of functions. It was found that the AChE protein was making a network with other 10 proteins *viz*, Choline acetyltransferase (ChAT), Muscarinic acetylcholine receptor (mAChR) 60 C, CG2201 Isoform B, CG2818 Isoform A, Acetylcholine receptor subunit beta-like 1, Vesicular acetylcholine transporter VAChT, Carboxylic ester hydrolase, Chorion protein S38, Beta-amyloid protein precursor, and protein Arginine N-methyltransferase capsuleen. The functions of these proteins are mentioned in Table 4 (Fig. 12a and b).

4. Discussion

In recent years, molecular docking technique has emerged as an indispensable tool to predict the preferred orientation and
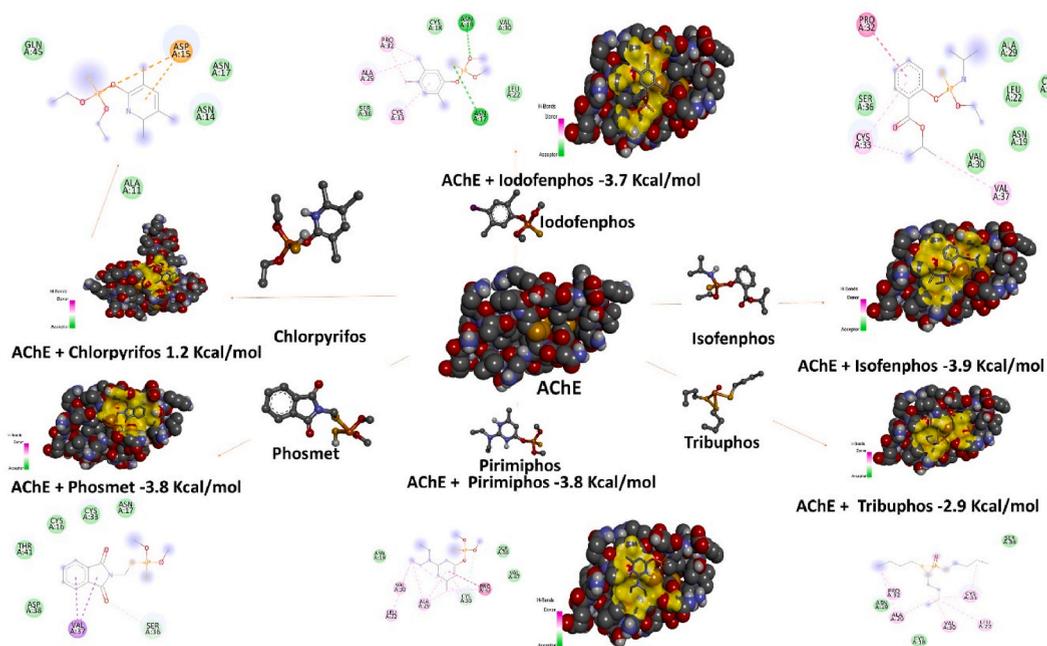
Fig. 6. 3D and 2D interactions of ligands with the Ache of *D. antiqua.*
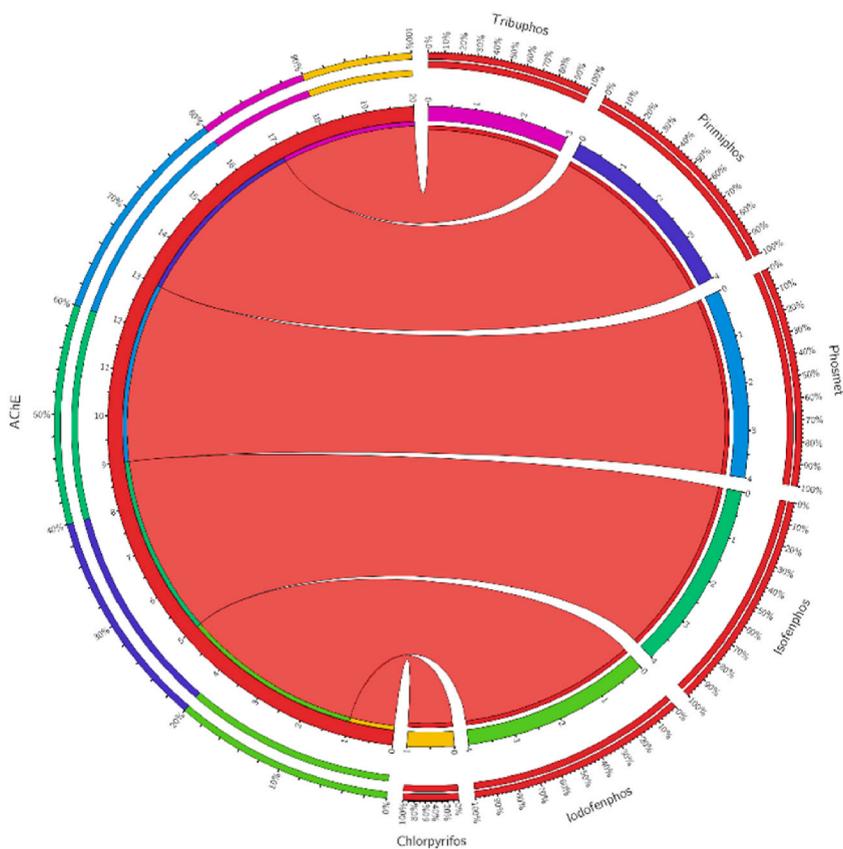
Fig. 7. Circos Plot showing the binding affinity of insecticides with the target protein AChE.
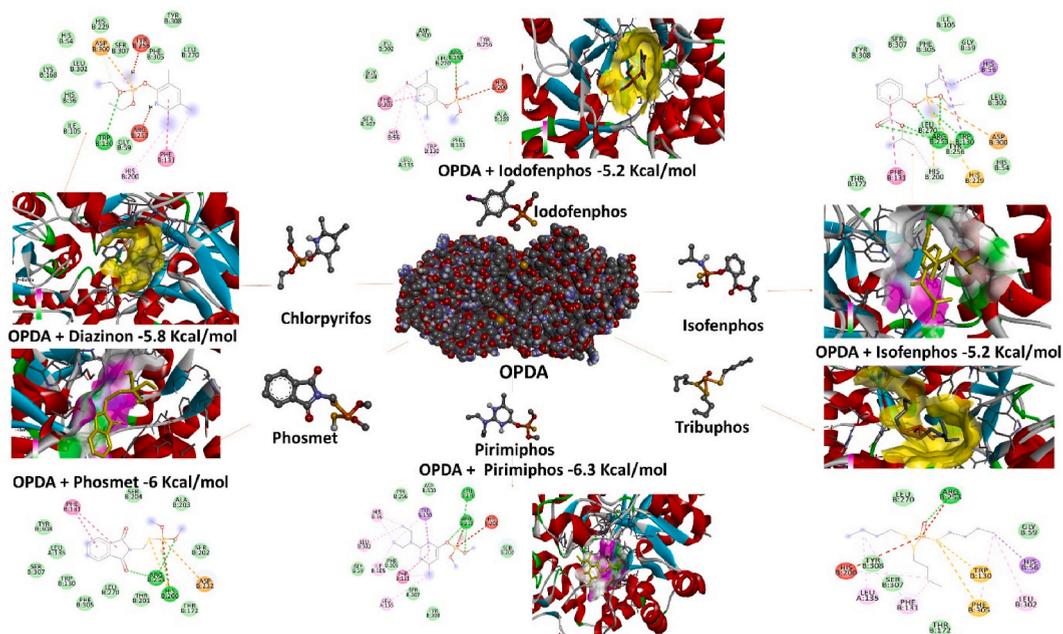
Fig. 8. 3D and 2D interactions of insecticides with the target protein OpdA.
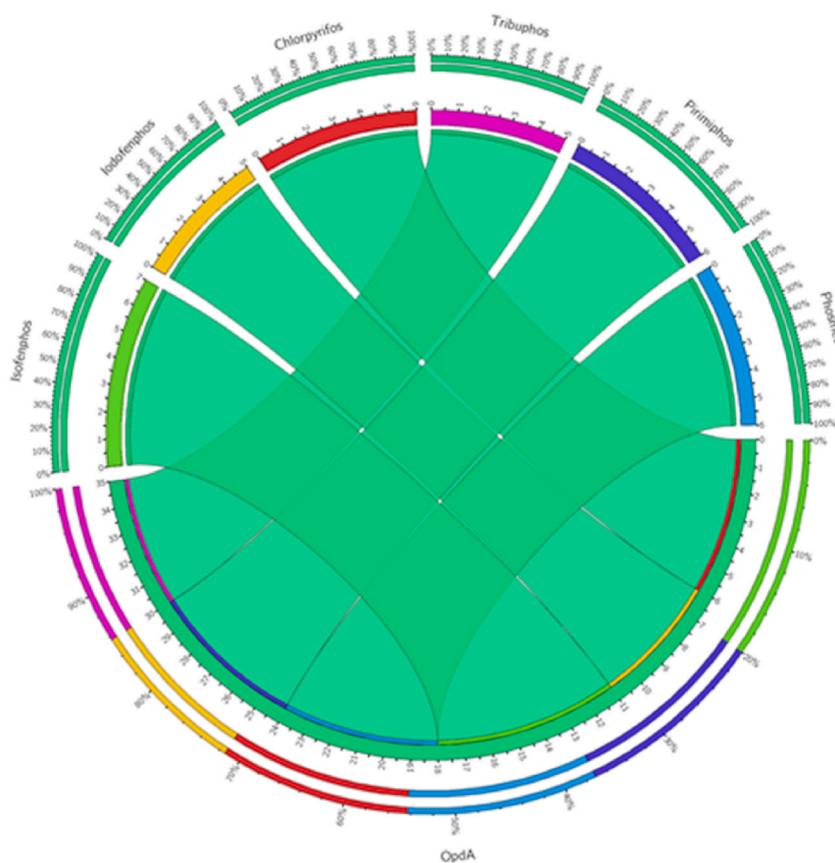
Fig. 9. Circos Plot showing the binding affinity insecticides with the target protein OpdA.
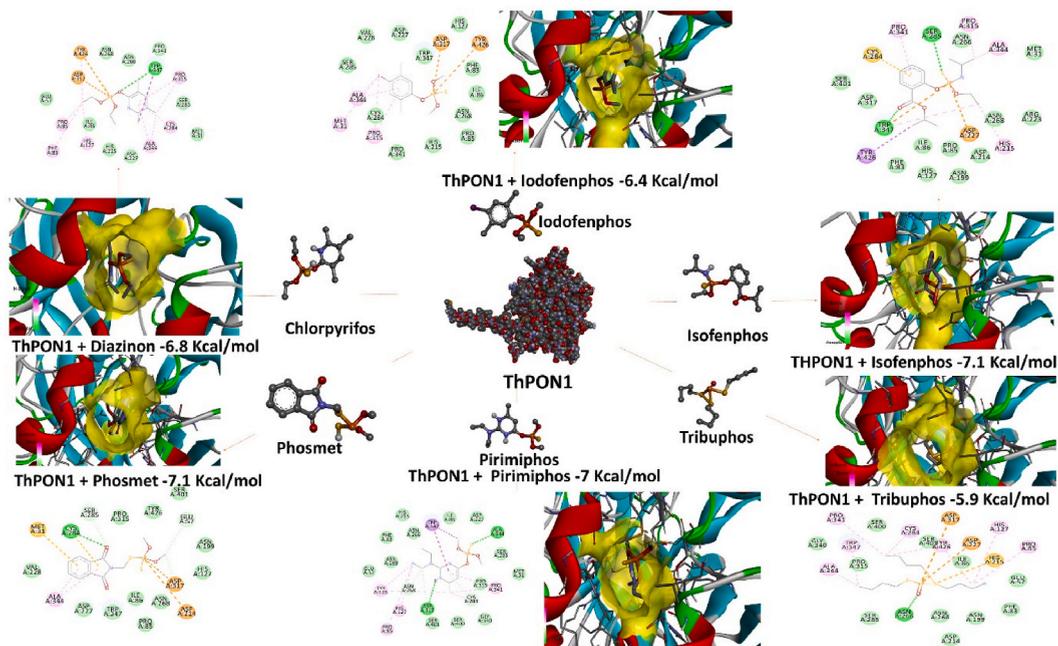
Fig. 10. 3D and 2D interactions of insecticides with the target protein ThPON1.
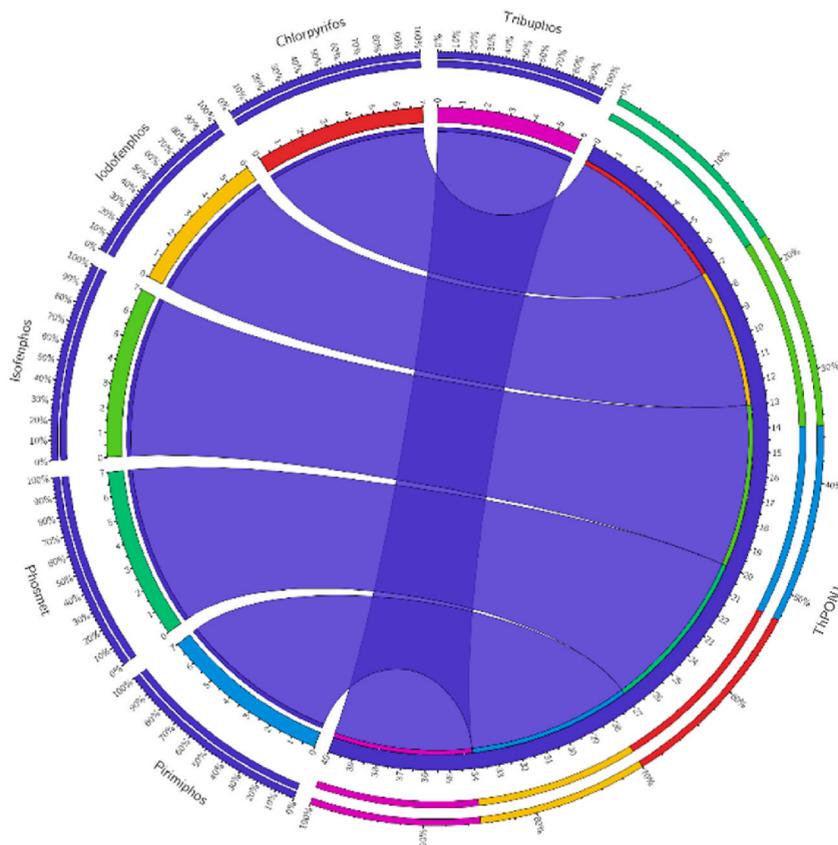
Fig. 11. Circos Plot showing the binding affinity insecticides with the target protein ThPON1.

Table 4
Protein-protein interaction analysis of the protein target AChE of *D. antiqua*.

Name of the protein	Functions	References
Acetylcholine esterase	It belongs to the type-B carboxylesterase/lipase family that Catalyzes the hydrolysis of the neurotransmitter acetylcholine into choline and acetate, thus resetting the neurotransmission mechanism at the neuromuscular junctions.	[44].
Choline acetyltransferase	It catalyzes synthesis of the neurotransmitter acetylcholine (ACh) using the substrates acetyl-CoA and choline	[45]
Muscarinic acetylcholine receptor 60 C	It mediates various cellular responses, including inhibition of adenylate cyclase, increased phosphoinositide breakdown, and modulation of K+ channels via action of G-proteins.	[46].
CG2201 isoform B	Choline and ethanolamine kinase are involved in the CDP-choline pathway and phosphatidylethanolamine biosynthetic process. It is predicted to be active in the cytoplasm.	[47].
Vesicular Ache transporter	Vesicular acetylcholine transporters (VAChT) are essential enzymes for synthesizing and transporting acetylcholine (ACh).	[48].
Acetylcholine receptors	Acetylcholine receptors in insects are neuron-specific oligomeric proteins essential for the central transmission of sensory information.	[49]
Amyloid precursor protein	The Amyloid Precursor Protein family regulates multiple types of neuronal motility.	[50].
Chorion protein S38	It is the structural constituent of chorion. It is involved in the biological process, like egg development.	[51].
CG2818 isoform A	Phosphoric diester hydrolase activity	[51].
Arginine methyltransferase	Protein arginine methyltransferase in insect cells has been implicated in signal transduction, transcriptional control, and protein trafficking.	[52].
Beta-amyloid protein	Belongs to APP family and plays a role in the regulation of neddylation pathway.	[53].
Carboxylic ester hydrolase	Carboxylesterases (EC 3.1.1.1) distribute broadly in insects and play an important role in their metabolism, with various functions.	[54].

interaction of small molecules (ligands) to larger molecules proteins or nucleic acids to form a stable complex, aiding in drug discovery, virtual screening of compound libraries, and understanding molecular recognition processes. This technique identifies compounds that bind firmly to the active site of the target molecule with minimal binding energy (ΔG), which marks them as potential candidates for further evaluation [55]. This methodology has been used to screen insecticides for their ability to bind and form complexes with the target site. Singh et al. [56] used molecular docking studies to find out the affinity of 2,3-dimethyl maleic anhydride against the AChE of *Sitophilus oryzae*, and *Periplaneta americana* and acetylcholinesterase may be inhibited by OP and carbamate esters [44]. Likewise, Reyes-Espinosa et al. [37] conducted an *in silico* analysis on the interaction between complex-ligands of nine acetylcholinesterase (AChE) structures of Lepidopteran organisms and 43 organophosphorus (OPs) pesticides with previous resistance reports. They employed computational tools like homology modelling and molecular docking to predict potential resistance by structural modifications in Lepidoptera insects, revealing insights into mutations affecting enzyme phosphorylation. Furthermore, Renault et al. [57] studied the silverleaf whitefly *Bemisia tabaci*, a significant invasive herbivorous insect pest. By employing *in silico techniques*, they detected sequence polymorphisms in the ace1 gene of naturally occurring *B. tabaci* variants from 30 populations in Egypt and Pakistan. They identified novel mutations influencing insecticide resistance, elucidating the impact of mutation-induced changes in form 1 acetylcholinesterase (AChE1) structure on carbamate and organophosphate insecticides' interactions. Similarly, in the present study, we employed molecular docking to assess the binding affinity of five organophosphate insecticides with AChE. Our findings revealed varying degrees of interaction between the insecticides and AChE, with iodofenphos demonstrating the highest binding affinity and tribufos the lowest. The differences observed in binding affinities among the tested compounds may be attributed to their structural variations, chemical bonds, and molecular size. Furthermore, our analysis uncovered potential interactions between AChE and 10 other associated proteins, which might also be blocked during the interaction with the insecticides, leading to paralysis and death of *D. antiqua*.

In several other studies, this approach has been utilised for screening microbial proteins and enzymes that have the capability to bind and form stable complexes with hazardous contaminants [24,58]. Molecular docking of chlorpyrifos with the microbial enzymes organophosphorus hydrolase (OPH) and methyl parathion hydrolase (MPH) revealed that chlorpyriphos had the best binding affinity with OPH. Hence, it is essential for chlorpyriphos degradations [59]. Likewise, molecular docking of pyridyl pyrazolo carboxylate derivatives and Ryanodine receptors (RyRs) of *Plutella xylostella* showed that RyRs may be a potential target of this series compounds and explained the difference in insecticidal activities [60]. Prior to in vitro or on site testing, docking studies can predict the binding energies of the complexes and help in the identification of a potential molecule. Similarly, Bhatt et al. [61] reported that the allethrin binding interactions with esterase and its bioremediation potential using an isolated bacterial strain CW7, identified as *Pseudomonas nitroreducens*. OpdA and ThPON1 docking results revealed that isofenphos showed the best interaction with a binding affinity of −6.6 and −7.1, respectively. Isofenphos, therefore, may be effective in controlling onion maggot. Our results revealed that while iodofenphos displayed the strongest interaction with AChE, indicating its high toxicity, isofenphos exhibited the greatest potential for bioremediation by OpdA and ThPON1 enzymes. Therefore, considering both factors, we suggest that isofenphos may be the most suitable option for controlling onion maggot infestation while minimizing environmental impact. Our findings hold practical significance for pesticide management and environmental protection. The present study offers insights into the comparative efficacy of various organophosphate compounds against *D. antiqua*, an important agricultural pest. By elucidating the potential interaction mechanisms involved in pesticide degradation, we contribute to developing more effective strategies for safely removing and detoxifying these chemicals from the environment. This knowledge can inform the design of enzyme-based remediation processes, ultimately leading to more sustainable and eco-friendly solutions for pesticide pollution mitigation. This information can aid in selecting the most suitable pesticides for pest control measures, helping to optimize agricultural practices and minimize the
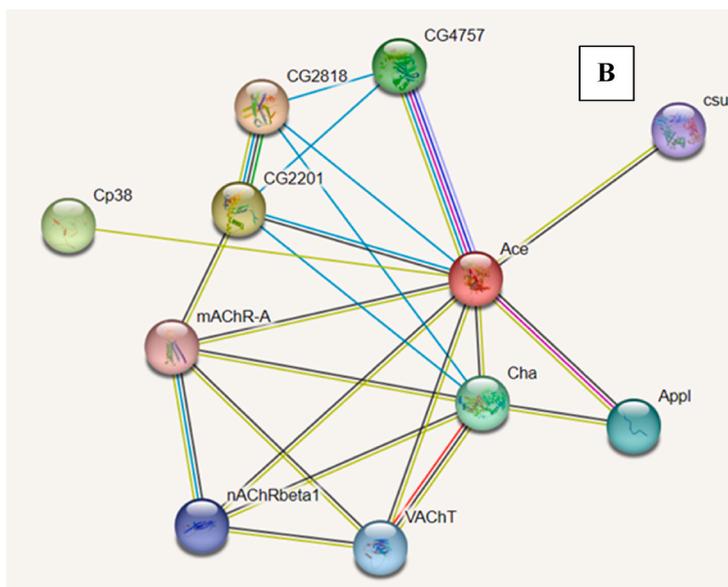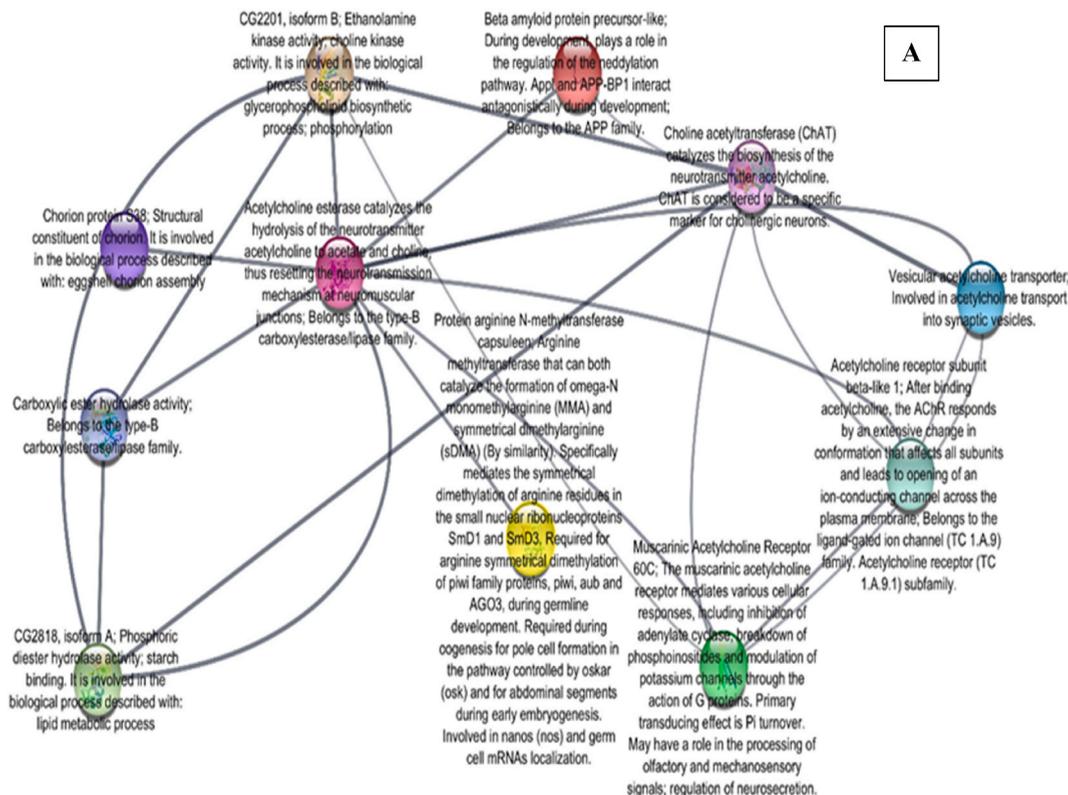
Fig. 12a. Fig. 12 a & b Protein-protein interaction analysis of AChE in *D. antiqua*.

environmental impact associated with pesticide use. It is also important to acknowledge the limitations of our study. Computational docking studies, while informative, are predictive and may not fully capture the complexity of enzyme-substrate interactions *in vivo*. Additionally, our study focused on a specific set of enzymes and may not represent the entire spectrum of degradation pathways for organophosphates. Future research could expand the scope by considering other enzymes and environmental factors that influence pesticide degradation.

5. Conclusion

In this computational docking study, we aimed to predict the insecticidal performance of organophosphate insecticides and investigate the degradation processes of these chemicals under the influence of enzymatic activities of OpdA and ThPON1. We explored the binding affinities and structural interactions between the insecticides and these enzymes by employing computational docking techniques. This dual approach enhances our understanding of the potential risks and benefits of these chemicals in agricultural and environmental contexts, contributing to more informed decision-making in pesticide management and pest control strategies.

Ethics approval

The present study does not involve human or animal experiments.

Consent to publish

All the authors consented to the publication of this study.

Consent to participate

All the authors have consented to participate in this submission.

Code availability

Not applicable.

Availability of data and material

All the data of the present study is included in the manuscript file.

CRediT authorship contribution statement

Nusrat Fatimah: Writing – original draft, Methodology, Formal analysis, Conceptualization. **Suhail Ashraf:** Methodology, Investigation, Formal analysis. **Krishna Nayana R U:** Software, Methodology, Conceptualization. **P.B. Anju:** Visualization, Validation, Software. **Mansoor Showkat:** Methodology, Investigation, Formal analysis, Conceptualization. **Kahkashan Perveen:** Formal analysis, Data curation, Conceptualization. **Najat A. Bukhari:** Writing – original draft, Supervision, Methodology, Conceptualization. **R.Z. Sayyed:** Writing – original draft, Supervision, Formal analysis, Conceptualization. **Andrea Mastinu:** Writing – review & editing, Supervision, Funding acquisition, Data curation.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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