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Molecular Docking Analysis of *Embelia ribes* for Selected Constituents as *Spodoptera frugiperda* (Fall Armyworm) Beta Glycosidase and Caspase-1 Inhibitors

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ABSTRACT

Insect pest control is one of the major issues facing the agriculture sector because of the need for new agrochemicals and biocontrol agents that are environmentally friendly, economically affordable, and safe for human health. *Spodoptera frugiperda* (fall armyworm) is one of the insect pests that causes huge damage to various crops around the globe due to its generalist nature. In the present study, three selected *Embelia ribes* Burm F (Myrsinaceae) constituents, which include embelin, 5-O-methylembelin, and vilangin; one semi-synthetic compound (potassium embelate); three synthetic compounds, namely coenzyme Q_{10} , dopaquinone, and idebenone; and two reference compounds (azadirachtin and amitraz) were assessed on the docking behavior of *S. frugiperda* (beta glycosidase and caspase-1. The docking studies showed that coenzyme Q_{10} exhibited the highest binding energies (-130.61 and -434.56 kcal. mol⁻¹) for the target enzymes *S. frugiperda* (beta glycosidase and caspase-1, respectively). Thus, the present investigation provides new knowledge in understanding *Embelia ribes* Burm F (Myrsinaceae) constituents as possible inhibitors against *S. frugiperda* (beta glycosidase and caspase-1) enzyme activities. Furthermore, the present work can help to develop new insecticides and pesticides against *S. frugiperda* and other related insect pests.

INTRODUCTION

The long-term usage of synthetic fertilizers and pesticides contaminates soil and surface water, and they are also reported to cause ill effects in animals (fish) and humans (Patel & Gajar 2001). Moreover, the use of synthetic pesticides leads to environmental issues like bioaccumulation and biomagnification, which cause huge losses to our biological wealth and resources. Similarly, overuse of chemical fertilizers (like nitrogenous, phosphoric, and potassium) has negatively affected the soil texture and altered the pH value of the soil, causing an imbalance in nutrient absorption for crops, fruits, plants, and vegetables (Dhar 2020). The increasing awareness about the ill effects

Vasantha-Srinivasan Prabhakaran: https://orcid.org/0000-0003-3415-3315 Radhakrishnan Narayanaswamy: https://orcid.org/0000-0001-5259-761X of synthetic fertilizers and pesticides has forced us to look for alternative ways (organic farming) and technologies (like traditional hydroponics and aquaponics). Moreover, there is a huge rise in demand for the use of plant-based (botanical) pesticides, especially for crop protection (Nas 2004). Now, worldwide agricultural scientists are investigating and developing botanical pesticides (using indigenous plant materials) to protect against insect infestations (Pavunraj et al. 2011). Moreover, the use of indigenously available plants or herbs in the control and management of pests is a traditional, adopted, and practiced agricultural technology in many countries, including India (Roy et al. 2005). The advantage of using botanical pesticides is that they are nonselective toxins or poisons that are active against a wide range of agricultural pests (Pavunraj et al. 2011). Several phytochemicals have been reported to be potent alternatives to chemical pesticides (Leatemia & Isman 2004). The mechanism of action of phytochemicals has been reported by

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many researchers. For instance, the antifeedant (Raja et al. 2005), larvicidal (Kabaru & Gichia 2001), ovicidal (Pavunraj et al. 2006), repellent (Paredes-Sanchez et al. 2021), etc. are the few reported mechanisms of action employed by the phytochemicals for the control and management of pests. In the present study, we focus on Spodoptera frugiperda (Fall Armyworm), which is one of the major pests and has the following crops like cotton, maize, millet, rice, sorghum, soybean, and sugarcane (Deshmukh et al. 2021).

Embelia ribes Burm. f., a dense shrub of the family Myrsinaceae, has been reported to possess numerous medicinal uses. E. ribes has been known to possess phytoconstituents, namely, christembine, daucosterol, 5-O-methylembelin, embelinol, embeliaribyl ester, embelin, embolic acid, rapanone, sitosterol, and vilangin, etc. (Mhaskar et al. 2011). Brassica juncea and E. ribes have been reported to safeguard the seeds from several fungal diseases and pests. In addition, treatment with these plant extracts also stimulates disease resistance after the germination of the seeds (Dhar 2020). Moreover, embelin (a bioactive constituent of *E. ribes*) has been reported to be effective against stored grain pests (Dhar 2020). Thus, the background mentioned above prompts us to carry out the present work on three selected constituents of *E. ribes*, namely, embelin, 5-O-methylembelin, and vilangin; one semi-synthetic compound (potassium embelate); three synthetic compounds, namely coenzyme Q10, dopaquinone, and idebenone; and two reference compounds (azadirachtin and amitraz), which were assessed on the docking behavior of S. frugiperda (beta glycosidase and caspase-1) by using the PatchDock method.

MATERIALS AND METHODS

Ligand Preparation

Chemical structures of three ligands (constituents of *E. ribes*) namely 1) embelin (CID no: 3218); 2) 5-O-methylembelin (CID no:171489); 3) vilangin (CID no:417182); one semi-synthetic compound 4) potassium embelate (CID no: 23677950); three synthetic compounds namely, 5) coenzyme Q10 (CID no: 5281915); 6) dopaquinone (CID no: 439316); 7) idebenone (CID no: 3686); two reference compounds namely, 8) azadirachtin (CID no: 5281303); and 9) amitraz (CID no: 36324) were downloaded from PubMed database. These selected ligands were prepared according to the earlier report (Mohan et al. 2022). These prepared structures were used for further study (PatchDock).

Identification and Preparation of Target Protein

The three-dimensional (3D) structure of the Spodoptera

frugiperda beta glycosidase (PDB ID: 5CG0 with a resolution of 2.09 Å) and caspase-1 (PDB ID: 1M72 with a resolution of 2.30 Å) were obtained from Protein Data Bank (PDB). A chain of both proteins was processed individually by removing other chains, ligands, and crystallographically observed water (H₂O) molecules (i.e., water without hydrogen bonds) by using UCSF Chimera software.

Molecular Docking Study

A docking study was performed for the selected (three E. ribes constituents; one semi-synthetic; three synthetic, and two reference compounds) ligands using the PatchDock online server. Finally, the binding site analysis was carried out for the best-docked pose using the PyMOL software (Mohan et al. 2022).

RESULTS AND DISCUSSION

Spodoptera frugiperda has gained much attention worldwide due to its outbursts in Africa (since 2016) and Asia (since mid-year 2018). In 2018, S. frugiperda has been reported for the first time in India, and that too in South India (Shivamogga and Davanagere districts of Karnataka State) on the maize crop (Deshmukh et al. 2021). S. frugiperda has been reported to cause primarily huge damage to maize crops, followed by other host crops like millets, vegetables, and sorghum (Day et al. 2018).

In general, beta glycosidases have been involved in hydrolyzing glycosides to release carbohydrates (Marana et al. 2000). Spodoptera frugiperda beta glycosidase (Sf β gly) is a secreted digestive enzyme present in midgut epithelial cells. Spodoptera frugiperda beta glycosidase (Sfβgly) has been previously reported in relation to its i) catalysis, ii) substrate recognition, and iii) thermal stability (Otsuka et al. 2020). Thus, in the present study, Spodoptera frugiperda beta glycosidase (Sf β gly) was selected as one of the target enzymes.

Caspases have been involved in the carrying out of the apoptosis process, and the apoptotic pathway is highly conserved in the metazoans. Thus, caspases serve as a fascinating target for medical treatment. Spodoptera frugiperda caspase-1 (Sf-caspase 1) is the chief effector caspase of S. frugiperda (Forsyth et al. 2004). Therefore, in the present study, Spodoptera frugiperda caspase-1 (Sfcaspase 1) was selected as the second target enzyme.

Table 1 shows the chemical nature and botanical source of nine selected ligands. Out of nine ligands, seven ligands belong to the quinone (55.6%). Similarly, alpha amino acid (11.1%), tertiary amino compound (11.1%), and triterpenoid (11.1%) are three other classes of selected ligands.



| S.No. | Ligand name | Nature of chemical class | Source | |
|-------|--------------------------|----------------------------|---|--|
| 1. | Coenzyme Q ₁₀ | Quinone | Arachis hypogaea, Brassica oleracea, Brassica rapa, Citrus clementina, Daucus carota, Glycine max, Malus domestica, Petroselinum crispum, Pisum sativum, Solanum lycopersicum and Solanum tuberosum | |
| 2. | Dopaquinone | Alpha amino acid | Present in the human skin and feces | |
| 3. | Embelin | Quinone | Embelia ribes, Ardisia humilis, Connarus ritchiei, Embelia barbeyana, Embelia kilimandscharica, Embelia robusta, Embelia tsjersium-cottam, Myrsine africana, Myrsine capitellata, Myrsine semiserrata and Rapanea umbellate | |
| 4. | Idebenone | Quinone | Synthetic one | |
| 5. | 5-O-Methylembelin | Quinone | Embelia ribes | |
| 6. | Potassium embelate | Quinone | Synthetic one | |
| 7. | Vilangin | Quinone | Embelia ribes | |
| 8. | Azadirachtin | Triterpenoid | Azadirachta indica | |
| 9. | Amitraz | Tertiary amino compound | Synthetic one | |

Table 1: Nature of chemical class and source of nine selected ligands.

Table 2: The interaction energy analysis of nine selected ligands with the Spodoptera frugiperda beta glycosidase using the PatchDock method

| S.No. | Ligand names | -ACE [*] (-kcal.mol ⁻¹) | Interaction of amino acid residue | Bond distance (Å) |
|----------|-------------------------|--|--------------------------------------|--------------------------|
| 1. | Coenzyme Q 10 | 130.61 | Arg189 Asn249 Glu271 | 2.9 2.8 2.8 |
| 2. | Dopaquinone | +271.02 | Gln39 Ser247 Asn249 Tyr331 | 3.5 2.9 2.9 3.3 |
| | | | Trp452 | 3.1 |
| 3. | Embelin | +40.45 | His142 Glu187 Glu451 Trp452 | 3.6 2.5 2.9 3.2 |
| 4. | Idebenone | 34.07 | Gln39 His142 Arg267 Glu271 | 2.1 2.6 3.0 3.5 |
| 5. | 5-O-Methylembelin | +52.22 | Glu187 Glu399 | 1.6, 2.3 and 2.5 2.4 |
| 6. | Potassium embelate | +22.46 | His142 Glu187 | 3.3 1.8 and 3.3 |
| 7. | Vilangin | 83.22 | No interactions | - |
| 8. 9. | Azadirachtin Amitraz | +5.95 +53.98 | Arg189 No interactions | 3.2 and 3.4 |
| | | | | |

Note: ACE*- Atomic contact energy

The docking studies revealed that coenzyme Q_{10} exhibited the highest (ACE) atomic contact energy (-130.61 kcal.mol⁻¹) with the *Spodoptera frugiperda* beta glycosidase enzyme. In contrast, idebenone showed the lowest binding energy (-34.07 kcal.mol⁻¹) with the target enzyme *Spodoptera frugiperda* beta glycosidase (Table 2).

In the present study, six ligands namely, dopaquinone (+271.02 kcal.mol⁻¹); amitraz (+53.98 kcal.mol⁻¹);

5-*O*-Methylembelin (+52.22 kcal.mol⁻¹); embelin (+40.45 kcal.mol⁻¹); potassium embelate (+22.46 kcal.mol⁻¹) and azadirachtin (+5.95 kcal.mol⁻¹) have shown poor (ACE) atomic contact energy values (Table 2).

Three ligands such as embelin, 5-O-Methylembelin, and potassium embelate were shown to interact with the Glu 187 amino acid residue of the *Spodoptera frugiperda* beta glycosidase enzyme (as shown in Table 2). Similarly,

Tamaki et al. (2016) reported that the mutation in Glu 187 amino acid position results in the worst effect on *Spodoptera frugiperda* beta glycosidase hydrolytic activity. In the present study, three ligands such as embelin, idebenone, and potassium embelate (Fig. 1) are shown to interact with the His 142 amino acid residue of the *Spodoptera frugiperda* beta glycosidase enzyme. Similarly, Tamaki et al. (2016) reported that the His 142 amino acid residue is present in the glycone binding site of the *Spodoptera frugiperda* beta glycosidase enzyme.

The docking studies showed that azadirachtin exhibited the highest (ACE) atomic contact energy (-504.85 kcal.

mol⁻¹) with the *Spodoptera frugiperda* caspase-1 enzyme. In contrast, vilangin showed the lowest binding energy (-155.16 kcal.mol⁻¹) with the target enzyme *Spodoptera frugiperda* caspase-1 (Table 3).

The binding energy results showed the following order: azadirachtin (-504.85 kcal.mol⁻¹), < coenzyme Q_{10} (-434.56 kcal.mol⁻¹), < idebenone (-292.08 kcal.mol⁻¹), < 5-O-Methylembelin (-258.03 kcal.mol⁻¹), < potassium embelate (-246.62 kcal.mol⁻¹), < amitraz (-236.96 kcal.mol⁻¹), < embelin (-210.73 kcal.mol⁻¹), < vilangin (-155.16 kcal.mol⁻¹).



Note: \downarrow Down arrow mark represents the Histidine (His) amino acid at position 142 of the *Spodoptera frugiperda* beta glycosidase enzyme interacting with the ligand (potassium embelate). The dotted lines represent the hydrogen bonds.

Fig. 1: Interaction of potassium embelate with the target enzyme Spodoptera frugiperda beta glycosidase.



Note: \downarrow Down arrow mark represents the Glycine (Gly) amino acid at position 137 of the *Spodoptera frugiperda* caspase-1 enzyme interacting with the ligand (vilangin). The dotted lines represent the hydrogen bonds.

Fig. 2: An interaction of potassium embelate with the target enzyme Spodoptera frugiperda caspase-1.



| S.No. | Ligand names | -ACE [*] (-kcal.mol ⁻¹) | Interaction of amino acid residue | Bond distance (Å) |
|-------|--------------------|--|-----------------------------------|---------------------------|
| 1. | Coenzyme Q 10 | 434.56 | No interactions | - |
| 2. | Dopaquinone | 187.98 | Arg40 Tyr202 Ile204 | 3.5 1.6 and 3.3 2.5 |
| 3. | Embelin | 210.73 | Arg203 | 2.3. 2.4 and 3.2 |
| 4. | Idebenone | 292.08 | Ile204 | 3.1 and 3.4 |
| 5. | 5-O-Methylembelin | 258.03 | No interactions | - |
| 6. | Potassium embelate | 246.62 | Arg203 Ile204 | 3.2 3.1, 3.1 and 3.4 |
| 7. | Vilangin | 155.16 | Gly137 | 2.6 and 3.3 |
| 8. | Azadirachtin | 504.85 | Arg203 | 2.5 |
| 9. | Amitraz | 236.96 | No interactions | - |

Table 3: The interaction energy analysis of nine selected ligands with the Spodoptera frugiperda caspase-1 using the PatchDock method.

Note; -ACE*- Atomic contact energy

In the present study, three ligands such as embelin, potassium embelate, and azadirachtin were shown to interact with the Arg 203 amino acid residue of the *Spodoptera frugiperda* caspase-1 enzyme. Interestingly one ligand (vilangin) was shown to interact with the Gly 137 amino acid residue (Fig. 2) of the *Spodoptera frugiperda* caspase-1 enzyme. This result is on par with the previous report (Forsyth et al. 2004 and Wang et al. 2021).

Secondly, metabolites from *Azadirachta indica* have been known to possess antifeedant and repellent activity against *Spodoptera frugiperda* (Paredes-Sanchez et al. 2021). *Embelia ribes* has been reported as one of the plants used in crop disease management practices in ancient medieval and premodern India (Nene 2003). Similarly, *E. ribes* leaf extracts have shown to possess growth inhibition and feeding deterrence on *Spodoptera litura* (Noosidum & Chandrapatya 2015). To the best of our knowledge, no docking reports are available for the *S. frugiperda* enzymes (beta glycosidase and caspase-1) till date.

CONCLUSION

In the present study, all the nine selected ligands have been shown to dock with both the target enzymes. To our understanding, we are the first to describe the docking behavior of *S. frugiperda* enzymes (beta glycosidase and caspase-1) with that of nine selected ligands even though *E. ribes* crude extract has been known to possess antifeedant activity. These results provide new insight into understanding their inhibitory activities and pave way for further *in vitro* investigation of these 9 selected ligands as possible inhibitors against both the *Spodoptera frugiperda* enzymes (beta glycosidase and caspase-1).

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