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# Invitro studies for immuno stimulant activity of Cuttle fish ink

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#### Abstract

In the Marine organisms were isolated the 10,000 of new compounds were being discovered every year. Huge innovations were obtained from the waste, by product of the marine sources to discover the new compounds to the consumers. In the 21<sup>st</sup> century, people are interested in healthy eating that shift towards the potential health benefits beyond basic nutrition. Cuttle Fish Ink was evaluated for Immunostimulant activity by using invitro studies. Phagocytic index and cell count in Immunomodulatory assay, molecular docking studies of the compounds such as Phenyl thiazole, Boldenone using Insilico docking analysis. Our results showed the Cuttle Fish Ink possess Immunostimulant activity and molecular docking score produces with appreciable and better therapeutic effect in the ADME properties.

Keywords: Cuttle Fish Ink, Immunomodulatory, Molecular docking, Insilico docking, Phagocytic index.

# Introduction

In recent years, great attention towards the potential pharmacological utilization of bioactive natural products<sup>1</sup>. Mollusca is the 2<sup>nd</sup> largest phylum in the marine environment around 1,00,000 species found in all over the world<sup>2</sup>. Huge innovations were obtained from the waste by product of the marine sources to discover the new compounds to consumers<sup>3</sup>.

The ink sac with its ink gland produces a black ink containing melanin, the funnel shaped organ containing mucus producing gland. Cuttlefish is mainly used in homeopathic medicine. It is also used namely such as food products, antiseptic, antibacterial and antitumor agent<sup>4</sup>.

Antibody molecule consists of two light and two heavy chains composed of different domains i. Fab fragment, ii. Fc fragment. Fab fragment serves as the antigen binding site. Fc fragment is relatively constant and determines the effect or function of the antibody<sup>5</sup>. Many bacterial products are PAMPs, they strongly stimulate inflammation by triggering cytokine production in APCs. These in turn, stimulate the adaptive immunity and overall increase leukocytes number by boosting hematopoiesis<sup>6</sup>. Immunization is the administration of antigen to the host in order to induce antibody production. Vaccines are used for active immunization, they impart active immunity, which takes some time to develop and therefore used prophylactically. The antibodies so developed destroy the specific microorganism when it enters the body<sup>7</sup>. An immune response required the both innate immunity and the more powerful flexible acquired immunity<sup>8</sup>.

## Materials and methods

Extraction: The fresh Cuttle fish was collected directly from the Muthupettai region of Nagapattinam and dissected the fish

collected the Ink Sac and transferred immediately in ice box to extract the Ink. The Ink was dissolved with equal volume of Phosphate Buffer Saline (pH-7) immediately ultrasonicated the extract and then the extract was centrifuged at 5000rpm for 10 minutes, and the supernatant liquid was stored at -20°C until use it should freeze<sup>9</sup>.

**Preparation of Phosphate Buffer Saline (PBS):** 2.38g – Disodium Hydrogen Phosphate, 0.19g – Potassium Hydrogen Phosphate, 0.8g – Sodium Chloride weighed and mixed with distilled water to produce 1000ml, pH adjusted at 7.



Figure-1: Dissection of Cuttle fish.



Figure-2: Cuttle Fish Ink sac.

**Invitro Immunostimulant assay:** By finger prick method the blood was collected and placed to the blood to the glass slide and spread upto  $1.5 \times 1.5$  cm. Blood was allowed to clot at  $37^{\circ}$ C for 25 min. By using sterile normal saline the blood clot was removed from the slide. The polymorph nuclear leukocytes (PMN's) were found on the glass surface, the rest of the blood components are washed away. Duplicate slides were prepared and used for the Cuttle fish ink extract.

0.1ml of Cuttle fish ink extract was flooded over the slides, the slides were incubated at 37°C for 15 min followed by the addition of 100µl of *C. albicans* cell suspension. The slides were incubated at 37°C for 60 min. After incubation period, washed the film for twice with normal saline. By using the methanol to fixed the film for 5 min. Diluted Giemsa stain was flooded over the film for 25 min. The excess stain was removed using PBS and air dried. The slides were observed under the oil immersion (×100) objective. In microscopically to determined the number of *Candida cells* phagocytosed to detect the morphological criteria. This number was taken as the phagocyte index (PI) and was compared with the PI of the control. Immuno stimulation (%) was calculated by using the following Equation<sup>10,11</sup>.

Stimulation (%) =  $\frac{PI (test) - PI (control)}{PI (control)} \times 100$ 

**Molecular docking** *for Immunostimulant:* Tool: autodock vina 1.2 was used for docking analysis<sup>12-14</sup>.

**Receptor protein:** In the RCSB Brookhaven Protein Data Bank [PDB entry code 1M48 and 1PW6] were retrieved the Crystal structures of the IL-2 and used for docking studies. The structure 1M48 with was used for docking. All water molecules, except HOH357, and ligand were removed and hydrogen were added to the original protein data bank file.

**Ligand**: The ligands from squid ink (4-phenyl thiazole, Boldenone) were constructed by using standard bond lengths and angles from the SYBYL 7.3 fragment library. Geometry optimizations were performed and Gasteiger–Huckel charges were used for the ligands.

**DOCKING:** The entire docking study was determined by Autodock vina equipped with UCSF chimera and the ligands were focused on the active site of the viral protein receptors to perform site-specific docking to procure potential inhibitors. The residues of the binding sites were manually determined for the possible flipped orientation, protonation, and tautomeric states with Pymol 1.3 (Delano Scientific, San Carlos, USA) side-chain wizard script. The binding sites were defined as all the amino acid residues encompassed within a 10.0 a radius sphere centered on catalytic. The successful ligands obtained from screening analysis were further investigated for ADMET (absorption, distribution, metabolism, excretion and toxicity) properties<sup>15</sup>.

### **Results and discussion**

**Immunomodulatory** *assay: Invitro* evaluation of phagocytosis, extract of Cuttle fish Ink at  $10\mu$ l,  $50\mu$ l and  $100\mu$ l showed, morphological changes in the granulocytes given in (Figure-3). Maximum phagocytic activity was recorded as 71% at  $100\mu$ l followed by 28% at  $50\mu$ l. In this study dose-dependent shift on neutrophils in *invitro* phagocytosis was noted. At  $10\mu$ l no stimulation was recorded but at the high concentration elevation of the phagocytic index.





D: Untreated Phagocytic. Figure-3: Immunostimulatory effect of Cuttle fish ink.

Immunostimulation (%) was calculated by using the equation

Stimulation (%) =  $\frac{PI (test) - PI (control)}{PI (control)} \times 100$ 

**Table-1:** Immunostimulation (%).

| Sample      | PI | Stimulation (%) |  |
|-------------|----|-----------------|--|
| Control     | 28 | Sumulation (%)  |  |
| Test 10 µL  | 28 | 0               |  |
| Test 50 µL  | 36 | 28              |  |
| Test 100 µL | 48 | 71              |  |

Molecular Docking for Immunostimulant: ADME properties of GCMS–NIST matched compounds: Pharmacokinetics, bioavailability, drug-likeness of Cuttle fish Ink in studied by ADME properties. Out of 16 different compound from cuttle fish ink GCMS analysis 4 compounds are poorly soluble, two are moderately soluble, five are soluble and 4 are highly soluble in nature with permitted range of Log S (not exceed +6).The prediction of bioavailability revealed that same bioavailability scores were obtained for 13 small molecules (0.55) and 0.85 for three molecules. All the 16 obeyed Lipinski's 'rule of five' further BBB absorption reveals 9 compounds were found to be positive result on BBB barrier. Based on pharmacokinetics **Phenyl thiazole and Boldenone were selected for docking**<sup>16</sup>.

Sequence similarity analysis of selected target receptor: Pair wise Sequence Alignment by EMBOSS Needle algorithm of receptor 1M48 (001) and 1PW6 (002) is given below (Figure-4), Out of 133 residues similarity percentage was 99.2% and the fealty gap was 0.8% was given in (Figure-5)<sup>17,18</sup>.

| EMBOSS_001 | 1 -PTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKA  | 49  |
|------------|---|-----|
| EMBOSS_002 | 1 APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKA  | 50  |
| EMBOSS_001 | 50 TELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE | 99  |
| EMBOSS_002 | 51 TELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE | 100 |
| EMBOSS_001 | 100 TTFMCEYADETATIVEFLNRWITFCQSIISTLT 132             |     |
| EMBOSS 002 | 101 TTFMCEYADETATIVEFLNRWITFCQSIISTLT 133             |     |

Figure-4: Similarity analysis of selected target receptor.

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Aligned_sequences: 2

1: EMBOSS_001

2: EMBOSS_002

Matrix: EBLOSUM62

Gap_penalty: 10.0

Extend_penalty: 0.5

Length: 133

Identity: 132/133 (99.2%)

Similarity: 132/133 (99.2%)

Gaps: 1/133 (0.8%)

Score: 676.0
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Figure-5: Residues Similarity percentage.

| Table-2: ADME | properties | of NIST    | matched  | compounds. |
|---------------|------------|------------|----------|------------|
|               | properties | 01 1 110 1 | materiea | compounds. |

| Comp. Name  | Mol.wgt | Numb<br>Hydr | oer of<br>ogen | er of<br>ogen Water<br>Donor | GI<br>absorption | Bioavailability<br>score | BBB<br>absorption | Lipinski | Log  | Log  |
|---|---------|--------------|----------------|------------------------------|------------------|--------------------------|-------------------|----------|------|------|
|   | (g/mol) | Accept       | Donor          |                              |                  |                          |                   |          | Р    | S    |
| Docosanoic acid   | 340.58  | 2            | 1              | Poorly<br>soluble            | Low              | 0.85                     | No                | Yes,4.15 | 9.19 | 7.05 |
| Hexadecanoic acid   | 256.42  | 2            | 1              | Moderate soluble             | High             | 0.85                     | Yes               | Yes,4.15 | 7.23 | 5.80 |
| 1,2-Benzene dicarboxylic acid                                     | 164.11  | 4            | 0              | Very<br>soluble              | High             | 0.85                     | Yes               | Yes,0    | 1.22 | 1.73 |
| Phthaic acid, 6 ethyl oct-3-<br>yl phenyl ester                   | 373.42  | 4            | 0              | Poorly soluble               | High             | 0.55                     | Yes               | Yes,4.15 | 6.92 | 6.14 |
| Dimethyl 3-(2-thienyl)-4,5-<br>isoxazoledi carboxy late           | 268.27  | 6            | 0              | soluble                      | High             | 0.55                     | No                | Yes, 0   | 2.03 | 3.45 |
| 2-(2-methyl piperidino)<br>ethyl p-chloro benzoate                | 281.78  | 3            | 0              | Moderate soluble             | High             | 0.55                     | Yes               | Yes, 0   | 3.44 | 3.34 |
| Cyclononasiloxaneoctadeca methyl                                  | 667.39  | 9            | 0              | Poorly soluble               | Low              | 0.55                     | N0                | Yes, 500 | 5.56 | 6.21 |
| Glutaric acid, di(2-methoxy phenyl) ester                         | 344.36  | 6            | 0              | Soluble                      | High             | 0.55                     | Yes               | Yes, 0   | 3.30 | 4.53 |
| Fumaric acid, 3-<br>fluorophenyl hexadecyl<br>ester               | 434.58  | 5            | 0              | Poorly<br>soluble            | Low              | 0.55                     | No                | Yes,4.15 | 8.49 | 7.15 |
| Phenyl thiazole   | 161.22  | 1            | 0              | Soluble                      | High             | 0.55                     | Yes               | Yes, 0   | 2.72 | 2.58 |
| 1-(4-Pyrimidinyl) ethanone  | 122.12  | 3            | 0              | Very<br>soluble              | High             | 0.55                     | Yes               | Yes,0    | 0.01 | 0.09 |
| Boldenone   | 286.41  | 2            | 1              | Soluble                      | High             | 0.55                     | Yes               | Yes,0    | 3.08 | 4.04 |
| 6H Purin-6-one, 2 amino-<br>1,7 dihydro                           | 169.14  | 4            | 4              | Very<br>soluble              | High             | 0.55                     | No                | Yes, 0   | 0.66 | 0.33 |
| 2,2-dimethyl 2 (2,3,5,6-<br>tetramethyl) ethanol                  | 206.32  | 1            | 1              | Soluble                      | High             | 0.55                     | Yes               | Yes, 0   | 4.39 | 3.73 |
| Dicyclohexylphosphinic acid                                       | 230.28  | 2            | 1              | Soluble                      | High             | 0.55                     | Yes               | Yes,0    | 3.48 | 2.23 |
| 6 hydroxy 5- (methyimino)<br>methyl-2,4(1H,3H)<br>pyrimidinedione | 169.14  | 4            | 3              | Very<br>soluble              | High             | 0.55                     | No                | Yes,0    | 1.64 | 1.64 |

*In silico* docking of 4-phenylthiazole with 1PW6-L: The co-crystallized ligands, namely 1PW6-L, is docked into active site by multipose docking with 4-phenylthiazole and Boldenone. Crystal Structure of Human IL-2 1PW6-L Complexed with (R)-N-[2-[1-(Aminoiminomethyl)-3-piperidinyl]-1-oxoethyl]-4-

(phenylethynyl)-L-phenyl alanine methyl ester was given in (fig.6) and ligand is given in (Figure- 7).

Interaction with 4-phenylthiazole (Figure-8) formed 3 major hydrogen bonds with ARG 81 residues at pose v13, v14 and V27 with the distance of 3.287, 2.585 and 3.189A° (Table-3). V13 and V27 Arginine Residue interacted with S1 atom of 4phenylthiazole whereas V14 residues form bonding with N1 of ligand. All the three poses showed same amino acid with docking score of -5.

#### Table-3: In silico docking of 4-phenylthiazole with 1PW6-L.

| Pose      | Docking<br>score | Energy  | Amino acid       | H bond<br>Distance A |
|-----------|------------------|---------|------------------|----------------------|
| V13/2     | -5.352062        | 4.78002 | ARG81-<br>LIG S1 | 3.287                |
| V14-<br>1 | -5.9690866       | 3.22708 | ARG81-<br>LIG N1 | 2.585                |
| V27/2     | -5.295699        | 6.08042 | ARG81-<br>LIG S1 | 3.189                |



Figure-6: Crystal structure of 1PW6-L.







Figure-8: Interaction of 4-phenylthiazole.

*In silico* docking of 4-phenylthiazole with 1M48-L: The co-crystallized ligands, namely 1M48, is docked into active site by multipose docking with 4-phenylthiazole and Boldenone. Crystal Structure of 1M48 Complexed with (R)-N-[2-[1-(Aminoiminomethyl) – 3 - piperidinyl] – 1 - oxoethyl] - 4-(phenylethynyl)-L-phenylalanine methyl ester was given in (Figure-9) and Interaction of ligand with 4-phenylthiazole (Figure-10) formed 2 major hydrogen bonds with ARG 81 residues at pose V28/1 and V31/1 with the distance of 2.407 and 2.735A (Table-4). V28 Arginine Residue interacted with N1 atom of 4-phenylthiazole whereas V31 residues form bonding with S1 of ligand. All the two poses showed same amino acid with docking score of -5 and -4.

#### Table-4: In silico docking of 4-phenylthiazole with 1M48-L.

| Pose   | Docking   | Enorate  | Amino said   | H bond     |
|--------|-----------|----------|--------------|------------|
| rose   | score     | Ellergy. | Allillo aciu | Distance A |
| V20/1  | -         | 2 78726  | ARG81-       | 2 407      |
| V 20/1 | 5.4773726 | 5.76250  | LIG N1       | 2.407      |
| 21/1   | -         | 4 70026  | ARG81-       | 2 725      |
| 51/1   | 4.8410544 | 4.79050  | LIG S1       | 2.755      |



Figure-9: Crystal structure of 1M48-L.



Figure-10: Interaction of ligand with 1M48-L.

*In silico* docking of Boldenone with 1PW6-L:The structure of ligand given in (Figure-11) and predicted binding pose between Boldenone and 1PW6-L was in good and found 11 stable hydrogen bond possibilities (Figure-12). Table-5 shows number of hydrogen bond, distance and residues take part in interaction. Boldenone interacted with ARG81, LEU70 and GLN74. The maximum docking score was -7.02649 formed by LEU70 with 2.617A° long hydrogen bond followed by ARG81 have score of -6.8500466 and 2.714A° hydrogen bond. The docking score of GLN is -5.45621735 and the distance of H bond is 2.210A°.

*In silico* docking of Boldenone with 1M48-L: The interaction of ligand given in (Figure-13) and predicted binding pose between Boldenone and 1M48 was in good and found 6 stable hydrogen bond possibilities. Table-6 shows number of hydrogen bond distance and residues take part in interaction. Boldenone interacted with ARG81 and ARG81H. The maximum docking score was -6.9702897 formed by ARG81H with 2.362A and it also have a long hydrogen bond. The docking score of ARG81 is -6.943564 and the distance of H bond is 1.922A.

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| Dees    | Docking    |         | Amino   | H bond     |
|---------|------------|---------|---------|------------|
| Pose    | score      | Energy: | acid    | Distance A |
| V1/1    | 5 084672   | 17 0627 | ARG81H- | 2 255      |
| V 1/1   | -3.984072  | 17.9027 | LIG H47 | 2.233      |
| V1/1    | 5 7518616  | 10 6081 | ARG810- | 2 234      |
| V 1/1   | -5.7518010 | 19.0901 | LIG S1  | 2.234      |
| V1/1    | 6 0700845  | 25 7505 | ARG81H- | 2.038      |
| V 1/1   | -0.9709843 | 25.7595 | LIG O   | 2.038      |
| V1/1    | 6 705144   | 27.8    | ARG81H- | 2 211      |
| V 1/1   | -0.703144  | 27.0    | LIG O   | 2.211      |
| V2/2    | -7.02649   | 11 2959 | LEU70   | 2 617      |
| V 2/2   | -7.020+7   | 11.2757 | LIG H47 | 2.017      |
| V3/1    | -6 8500466 | 10 3027 | ARG810- | 2 714      |
| V 3/ 1  | -0.0500+00 | 10.3027 | LIG H47 | 2.714      |
| VA/1    | -6.015827  | 21 1666 | ARG810- | 2 350      |
| V 4/ 1  | -0.013027  | 21.1000 | LIG O25 | 2.550      |
| V16/1   | -5 6501822 | 22.889  | ARG81H- | 2 649      |
| V 10/ 1 | 5.0501022  | 22.007  | LIG O14 | 2.077      |
| V22/1   | -5 7811737 | 21 2966 | LEU70-  | 2 389      |
| v 22/ 1 | 5.7011757  | 21.2700 | LIG H47 | 2.307      |
| V24/1   | -          | 22 1716 | GLN 74- | 2 210      |
| v ∠+/ 1 | 5.45621735 | 22.4740 | LIG H47 | 2.210      |

**Table-5:** In silico docking of boldenone with 1PW6-L.



Figure-11: Boldenone ligand.



Figure-12: Interaction of ligand with 1PW6-L IL receptor.

Table-6: In silico docking of boldeone with 1M48-L.

| Pose  | Docking<br>score | Energy  | Amino acid        | H bond<br>Distance A |
|-------|------------------|---------|-------------------|----------------------|
| V0/1  | -6.943564        | 13.0824 | ARG81-<br>LIG O14 | 1.922                |
| V0/2  | -<br>6.8775163   | 15.1162 | ARG81H-<br>LIGO14 | 2203                 |
| V0/2  | -6.822891        | 15.613  | ARG81H-<br>LIGO14 | 1.980                |
| V0/1  | -<br>6.1994705   | 14.9614 | ARG81H-<br>LIGO14 | 1.965                |
| V2/1  | -<br>6.9702897   | 13.9473 | ARG81H-<br>LIGO14 | 2.362                |
| V35/1 | 5.4658237        | 17.5381 | ARG81H-<br>LIGO25 | 2.346                |



Figure-13: Interaction of boldenone with 1M48-L.

# Conclusion

From the results it was concluded that the Cuttle Fish Ink have a Immunostimulant activity, it showed that the Phagocytosis of cells were counted and the morphological changes in the granulocytes was recorded as it possess the better effects, and the Molecular docking of *Insilico* models the compounds are Phenyl thiazole and Boldenone interaction with the Interleukin receptors produced more effect, docking score -5 to -7 hence its produces the better therapeutic effect of Immunostimulant activity.

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