An insect serotonin receptor mediates cellular immune responses and its inhibition by phenylethylamide derivatives from bacterial secondary metabolites

Md Ariful Hasan[1], Hyun-Suk Yeom[2], Jaewook Ryu[2], Helge B. Bode[3], Yonggyun Kim[1,*]

[1] Department of Plant Medicals, College of Life Sciences, Andong National University, Andong 36729, Korea. [2] Center for Eco-Friendly New Materials, Korea Research Institute of Chemicals Technology, Yuseong, Daejeon 34114, Korea. [3] Department of Biosciences, Molecular Biotechnology, and Buchmann Institute for Molecular Life Sciences (BMLS), Goethe-Universität Frankfurt am Main, Germany

* Corresponding author: hosanna@anu.ac.kr

Abstract

Serotonin (5-hydroxytryptamine: 5-HT) is a biogenic monoamine that mediates immune responses and modulates nerve signal in insects. *Se-5HTR*, a specific receptor of serotonin, has been identified in the beet armyworm, *Spodoptera exigua*. It is classified into subtype 7 among known 5HTRs. *Se-5HTR* was expressed in all developmental stages of *S. exigua*. It was expressed in all tested tissues of larval stage. Its expression was up-regulated in hemocytes and fat body in response to immune challenge. RNA interference (RNAi) of *Se-5HTR* exhibited significant immunosuppression by preventing cellular immune responses such as phagocytosis and nodulation. Treatment with an inhibitor (SB-269970) specific to 5HTR subtype 7 resulted in significant immunosuppression. Such immunosuppression was also induced by bacterial secondary metabolites derived from *Xenorhabdus* and *Photorhabdus*. To determine specific bacterial metabolites inhibiting Se-5HTR, this study screened 37 bacterial secondary metabolites with respect to cellular immune responses associated with Se-5HTR and selected 10 potent inhibitors. These 10 selected compounds competitively inhibited cellular immune responses against 5-HT and shared phenylethylamide (PEA) chemical skeleton. Subsequently, 46 PEA derivatives were screened and resulting potent chemicals were used to design a compound to be highly inhibitory against Se-5HTR. The designed compound was chemically synthesized. It showed high immunosuppressive activities along with specific and competitive inhibition activity for Se-5HTR. This study reports the first 5HT receptor from *S. exigua* and provides its specific inhibitor designed from bacterial metabolites and their derivatives.

Author Summary

Serotonin (5-hydroxytryptamine: 5-HT) plays a crucial role in mediating nerve and immune signals in insects. Interruption of 5-HT signal leads to malfunctioning of various insect physiological processes. Se-5HTR, a 5-HT receptor of beet armyworm, *Spodoptera exigua*, was identified and classified as subtype 7 (5-HT_7) of 5-HT receptors. A specific inhibitor (SB-269970) for 5-HT_7 highly inhibited immune responses such as phagocytosis and nodulation mediated by Se-5HTR. Two entomopathogenic bacteria, *Xenorhabdus* and *Photorhabdus*, could secrete potent inhibitors against immune responses mediated by 5-HTR. Bacterial secondary metabolites were screened against Se-5HTR-mediating immune responses. Most of resulting compounds shared phenylethylamide (PEA) chemical skeleton. Subsequent screening using PEA derivatives supported the importance of this chemical skeleton. Based on their relative inhibitory activities, a compound was designed and synthesized. This novel compound possessed high inhibitory activities against Se-5HTR-mediating immune responses and exhibited competitive inhibition with 5-HT.

Introduction

Serotonin or 5-hydroxytryptamine (5-HT) is a biogenic monoamine found across most phyla of life [1]. This indolamine compound is biosynthesized from tryptophan by successive catalytic activities of tryptophan hydroxylase and aromatic-L-amino acid decarboxylase [2-4] primarily in nervous systems [5,6]. In human and other vertebrates, serotonin is a well-known neurotransmitter involved in mood, appetite, sleep, anxiety, cognition, and psychosis [7-9]. Outside the nervous system, serotonin plays important roles as growth factor and regulator of hemostasis and blood clotting [10,11]. In plants, serotonin is basically involved in stress signaling [12]. Serotonin plays crucial role in physiological and behavioral processes in insects and other invertebrates [13,14]. In *Drosophila melanogaster*, there is evidence that serotonin is required for courtship and mating [15], circadian rhythm [16,17], sleep [18], locomotion [13,19], aggression [20], insulin signaling and growth [21], and phagocytosis [22]. Serotonin is also involved in olfactory processing [23], feeding behavior [19], heart rate [24], and responses to light [25] in *D. melanogaster* larvae.

Serotonin modulates physiological processes by binding to specific receptors. Seven main subtypes of serotonin receptors have been classified in vertebrates [26]. Except $5-HT_3$ receptor, the other six classes ($5-HT_1$, $5-HT_2$, $5-HT_4$, $5-HT_5$, $5-HT_6$, and $5-HT_7$ receptors) belong to G protein-coupled receptor family [27]. Among these receptors, $5-HT_1$ and $5-HT_5$ receptors can inhibit cAMP synthesis by preferentially coupling to a trimeric G protein $G_{i/o}$ [28]. $5-HT_2$ receptor uses $G_{q/11}$ to induce breakdown of inositol phosphates, resulting in an increase in cytosolic Ca^{2+} level [28]. Besides, $5-HT_4$, $5-HT_6$, and $5-HT_7$ receptors coupled to G_s can stimulate cAMP production [28]. However, $5-HT_3$ receptor is a ligand-gated cation channel that mediates neuronal depolarization [29].

Insects have at least three subtypes of 5-HT receptors. Five different 5-HT receptors as

orthologous to mammalian $5\text{-}HT_{1A}$, $5\text{-}HT_{1B}$, $5\text{-}HT_{2A}$, $5\text{-}HT_{2B}$, and $5\text{-}HT_7$ have been identified in

D. melanogaster [14]. In addition, partial sequences of two $5\text{-}HT_1$, two $5\text{-}HT_2$, and one $5\text{-}HT_7$

receptors have been identified in the field cricket *Gryllus bimaculatus* [30]. Two $5\text{-}HT_1$ receptors

and two $5\text{-}HT_1$ splice variants have been described in *Tribolium castaneum* and *Papilio xuthus*,

respectively [31,32]. As from *D. melanogaster* and *G. bimaculatus*, two $5\text{-}HT_2$ receptors have

been described from *Apis mellifera* while only one $5\text{-}HT_2$ receptor has been reported in other

insects such as *Periplaneta americana* and *Locusta migratoria* [33,34]. In a lepidopteran species,

Pieris rapae, four different 5-HT receptors including a novel subtype 8 have been reported

[35,36].

5-HT modulates various physiological processes via expression of different receptor types in

various tissues. 5-HT receptors are expressed highly in brain and ventral nerve cord of insects

[32]. $5\text{-}HT_1$ receptor in honey bee brain is involved in visual information processing [37].

Expression pattern of $5\text{-}HT_7$ receptor in honey bee nervous system suggests its possible roles in

information processing, learning, and memory [38]. 5-HT receptors might play roles in

neuroendocrine secretion and gut motility in cockroaches [29]. In salivary gland of several

insects, $5\text{-}HT_7$ receptor has been reported to be involved in salivary secretion mediated by cAMP

level elevation [33,39,40]. Moreover, $5\text{-}HT_7$ receptor mediates visceral muscle contraction in the

gastrointestinal tract of several insects including *A. aegypti* and *T. castaneum* [41,42]. 5-HT not

only has neurophysiological roles, but also mediates cellular immune responses in insects by

enhancing phagocytosis and nodulation [43]. Two different 5-HT receptors (1B and 2B) are

expressed in hemocytes of *P. rapae*, of which 5-HT receptor 1B mediates cellular immune

response [22]. In another lepidopteran insect, *Spodoptera exigua*, 5-HT mediates increase of total

circulatory hemocyte number by stimulating sessile hemocytes and mediating cellular immune

responses such as phagocytosis and nodule formation [44,45]. However, 5-HT receptor in *S.*

exigua has not been reported yet.

Two entomopathogenic bacteria, *Xenorhabdus* and *Photorhabdus*, can inhibit insect immune

responses to protect themselves and their symbiotic nematodes [46]. To accomplish host

immunosuppression, these bacteria can synthesize and secrete secondary metabolites to inhibit

immune signals and effectors [47]. Among these bacterial metabolites, tryptamine and

phenylethylamide derivatives have been identified with suggested function of interrupting 5-HT

signaling [48]. The objective of the present study was to determine bacterial secondary

compound(s) that could inhibit 5-HT signaling. To this end, we identified 5-HT receptor that

could mediate insect immunity in *S. exigua*. To determine a potent inhibitor of this receptor, we

screened bacterial secondary metabolites and their potent derivatives.

Results

Bioinformatics analyses reveal that *S. exigua* contains a 5-HT receptor

From a short read archive database (GenBank accession number: SRR1050532) of *S. exigua*, a

highly matched contig (accession number: GARL01017386.1) containing 3,308 bp nucleotide

sequence with an open reading frame (ORF) from 996th to 2,690th bp was identified. Prediction

of amino acid sequence by BlastP analysis revealed that its ORF sequence shared identities with

other insect 5-HT receptors: 99% with *Spodoptera litura* 5HTR (XP_022827337.1), 98% with

Helicoverpa armigera 5HTR (XP_021195909.1), 95% with *Trichoplusia ni* 5HTR

(XP_026729862.1), and 85% with *Manduca sexta* 5HTR (AGL46976.1). This novel 5-HT

receptor from *S. exigua* (Se-5HTR) encoded a sequence of 564 amino acids having a predicted

molecular weight of about 63.23 kDa. Phylogenetic analysis of its protein sequence indicated

that Se-5HTR was clustered with other 5-HT$_7$ receptors (Fig 1A). Predicted amino acid sequence

of Se-5HTR contained a signal peptide of 35 residues and attained GPCR character with seven

transmembrane domains. Consensus N-linked glycosylation sites are located in the N-terminus

(Asn^{48} and Asn^{53}), the third intracellular loop (Asn^{362}), and C-terminus (Asn^{534}). Several

consensus sites for phosphorylation by protein kinase A and/or protein kinase C were predicted

throughout the length of the sequence. A disulfide bond between two Cys residues at

extracellular matrix ('ECM', S1 Fig) is also predicted.

Se-5HTR sequence attains highly conserved amino acid residues (Fig 1B) found uniquely in

the biogenic monoamine receptor family [49-51]. Negatively charged Asp residue in TM3

(Asp^{163}) might interact with positively charged amino group of the ligand. A hydrogen bond

between the hydroxyl group of serine residue in TM5 (Ser^{247}) and the hydroxyl group of 5-HT

was predicted. In TM6, the consensus sequence unique to aminergic receptors (Phe^{444}-X-X-X-

Trp^{448}-X-Pro^{450}-X-Phe^{452}) is conserved. Like other GPCRs, a possible motif (Asn^{485}-Pro^{486}-X-X-

Tyr^{489}) that might participate in agonist-mediated sequestration and re-sensitization of Se-5HTR

is conserved in TM7. The C-terminus of the receptor contains two potential post-translational

palmitoylation cysteine residues (Cys^{508} and Cys-^{532}) and PDZ (post synaptic density protein,

Drosophila disc large tumor suppressor, and zonula occludens-1 protein)-domain binding motif

(Glu^{561}-Ser^{562}-Phe^{563}-Leu^{564}).

Se-5HTR is expressed in all developmental stages and larval tissues

Expression of *Se-5HTR* in different developmental stages of *S. exigua* was assessed by RT-PCR.

Results showed its expression from egg to adult stages (Fig 2A). RT-qPCR revealed variation in

its expression among developmental stages, with L5 larvae and adults showing the highest

expression levels. In L5 larvae, all tissues analyzed by RT-PCR showed its expression (Fig 2B).

RT-qPCR revealed that the midgut exhibited the highest expression level of *Se-5HTR*.

Hemocytes and brain also showed relatively high levels of its expression. Basal expression levels

of *Se-5HTR* were highly up-regulated in response to immune challenge (Fig 2C). *Se-5HTR*

expression was increased ~125-fold after challenge with fungus, *Beauveria bassiana* compared

to control (unchallenged). It was increased 60~90-fold after bacterial challenge compared to

naïve larvae.

Specific inhibitors against 5-HTR suppress hemocyte behaviors of *S. exigua*

A commercial inhibitor (SB-269970) specific to $5-HT_7$ was used to assess its effect on hemocyte

behaviors of *S. exigua* (Fig 3). Total hemocyte count (THC) of L5 larvae was ~1.2×10^7

cells/mL (Fig 3A). THC was significantly ($P < 0.05$) increased in response to 5-HT or bacterial

challenge. SB-269970 prevented the increase of THC in response to bacterial challenge. Its IC_{50}

value was estimated to be 1.925 μM. These results suggest that Se-5HTR can mediate hemocyte

mobilization in response to 5-HT upon bacterial challenge.

To determine the modulation effect of Se-5HTR on hemocyte-spreading behavior,

competitive inhibition between SB-269970 and 5-HT against Se-5HTR was assessed (Fig 3B).

Hemocytes were spread on slide glass with growth of F-actin. However, SB-269970 significantly

($P < 0.05$) suppressed such hemocyte-spreading behavior. The inhibitory effect of the inhibitor

was rescued by addition of 5-HT. A relatively low dose (SB-269970: 5-HT = 10:1) of 5-HT did

not rescue the inhibitory effect. However, a relatively high dose (1:10) of 5-HT significantly ($P <$

0.05) rescued such inhibitory effect, indicating a specific competition between inhibitor and

ligand against Se-5HTR.

RNA interference (RNAi) of Se-5HTR

To address the immunomodulatory effect of Se-5HTR on hemocytes, its gene expression was

knocked-down by RNAi (Fig 4). RNAi was performed using dsRNA specific to *Se-5HTR*.

dsRNA-injected larvae exhibited significant ($P < 0.05$) reduction of *Se-5HTR* expression. RT-

qPCR analysis showed that about 90% of *Se-5HTR* mRNA was suppressed by dsRNA treatment

at 24 h PI (Fig 4A). At 24 h PI of dsRNA, *Se-5HTR* expression was analyzed in four different

tissue samples. Compared to control tissues, dsRNA-treated larvae exhibited significant ($P <$

0.05) reduction of *Se-5HTR* expression in all tissues including hemocytes.

RNAi of Se-5HTR suppresses hemocyte behaviors of *S. exigua*

The effect of RNAi specific to Se-5HTR on hemocyte mobilization in response to bacterial

challenge was analyzed (Fig 4B). Upon bacterial challenge, THC increased by more than two

folds. However, RNAi treatment significantly ($P < 0.05$) suppressed such increase of THC. The

RNAi treatment also significantly ($P < 0.05$) influenced hemocyte-spreading behavior (Fig 4C).

On glass slide, hemocytes exhibited spreading behavior in 40 min by cytoskeletal rearrangement

through F-actin growth (see phalloidin staining). However, hemocytes collected from larvae

treated with RNAi specific to Se-5HTR lost such behavior.

Modulation of cellular immune responses by Se-5HTR

The influence of Se-5HTR on modulating hemocyte-spreading behavior suggested that it might

mediate cellular immune responses against bacterial infection. Phagocytosis against FITC-

labeled *Escherichia coli* was observed in hemocytes from control larvae. Labeled bacteria were

observed within hemocytes of control larvae (Fig 5A). However, hemocytes of larvae treated

with dsRNA specific to Se-5HTR significantly ($P < 0.05$) lost such phagocytosis, similar to that

found for hemocytes of larvae treated with SB-269970. Phagocytosis was decreased around 57%

or 78% after treatment with dsRNA or inhibitor, respectively. In response to bacterial challenge,

S. exigua formed ~78 hemocytic nodules per larva (Fig 5B). However, RNAi specific to Se-

5HTR or inhibitor treatment significantly ($P < 0.05$) reduced such cellular immune response.

Influence of bacterial secondary metabolites on immune responses mediated by Se-5HTR

RNAi or specific inhibitor assays indicated that 5-HTR could mediate both cellular immune

responses of phagocytosis and nodule formation in response to bacterial challenge. Bacterial

metabolites of two entomopathogens, *Xenorhabdus nematophila* (Xn) and *Photorhabdus*

temperata temperata (Ptt), were extracted from their culture broth using different organic

solvents and their inhibitory activities against cellular immune responses were then assessed (Fig

6). Organic solvent extracts of Xn- or Ptt-cultured broth exhibited significant ($P < 0.05$)

inhibitory activities against phagocytosis (Fig 6A) and nodulation (Fig 6B), although there were

variations in their inhibitory activities among extracts.

To identify bacterial secondary compounds that could inhibit Se-5HTR, 37 compounds (HB4

– HB602) derived from *Xenorhabdus* and *Photorhabdus* [47] were screened for their inhibitory

activities against hemocyte nodule formation and phagocytosis (Fig 7). More than three 75% (28

out of 37 compounds) of these test compounds exhibited significant ($P < 0.05$) inhibition against

phagocytosis (Fig 7A). In nodulation assay, all test compounds exhibited significant ($P < 0.05$)

inhibition (Fig 7B). Since Se-5HTR could mediate both cellular immune responses, bacterial

compounds that highly inhibited both phagocytosis (< 60%) and nodulation (< 30 nodules per

larva) were selected. As a result, 10 potent chemicals (HB 4, HB 5, H23, HB 30, HB44, HB 45,

HB 50, HB 223, HB 302, and HB 531) belonging to six chemical categories [phenylethylamide

(PEA), tryptamide, xenortide, xenocycloin, nematophin, and GameXPeptide] were found (S2

Fig). All these compounds exhibited median inhibitory concentration (IC_{50}) of 58~253 μM

against cellular immune response of hemocytic nodulation.

To support the specific inhibitory activity of these selected compounds against Se-5HTR,

competitive assay was performed between test compounds and 5-HT (Fig 8). With a constant

concentration of 5-HT, phagocytotic behavior of *S. exigua* hemocytes gradually decreased with

increasing amount of test compound (Fig 8A). On the other hand, increase of 5-HT amount

gradually decreased the phagocytotic behavior using a constant amount of test compound (Fig

8B).

Influence of PEA derivatives on phagocytosis mediated by Se-5HTR

These 10 selected compounds shared phenyl (or aromatic) ethylamide backbone except

xenocycloin (S2 Fig). Based on PEA backbone, 45 derivatives were selected from a chemical

bank and their inhibitory activities against the phagocytotic behavior of *S. exigua* hemocytes

were tested (Fig 9A). More than 66% (30 out of 45 compounds) of PEA derivatives exhibited

significant ($P < 0.05$) inhibition against phagocytosis. Three PEA derivatives (Ph15, Ph17, Ph33)

had inhibitory activities similar to a bacterial metabolite (HB 44), with IC_{50} at 1.8 ~ 5.6 μM

against phagocytosis (Fig 9B). These three PEA derivatives competitively inhibited the

phagocytosis mediated by Se-5HTR (Fig 9C).

Synthesis of a potent inhibitor and inhibitory efficacy against Se-5HTR

Potent compounds from 45 PEA derivatives were analyzed for their structures and activities

against phagocytosis mediated by Se-5HTR (S3 Fig). They shared the PEA backbone. However,

they had different side chains at 'X' and 'Y' (Fig S6A). When different X substituents were

compared for their inhibitory activities, methoxy was the most potent moiety (Fig S6B). When

different Y substituents were compared for their inhibitory activities with respect to identical X

groups, hexahydropyrrolo[1,2-a]pyrazine-1,4-dione was the most potent moiety (Fig S6C). This

analysis allowed us to design a hypothetical compound containing methoxy in X and

hexahydropyrrolo[1,2-a]pyrazine-1,4-dione at Y based on PEA backbone (Fig. S6D).

The designed compound ('PhX') was chemically synthesized and in its inhibitory activity

against phagocytosis was assessed compared with a specific 5-HT$_7$ inhibitor, SB269970, as a

reference (Fig 10). PhX was highly potent. It competitively inhibited cellular immune response

with 5-HT. Its inhibitory activity was more potent ($t = 14.9$; df $= 32$; $P < 0.0001$) than

SB269970.

Discussion

5-HT plays a crucial role in mediating cellular immune responses of *S. exigua* by stimulating

actin rearrangement [45]. Furthermore, it performs a functional cross-talk with eicosanoid

signaling via a small G protein Rac1 [52]. However, its signaling pathway leading to immune

responses remains unclear due to the lack of its receptor information in *S. exigua*. This study

identified a 5-HT receptor and showed its physiological function in mediating immune

responses.

Se-5HTR attains seven transmembrane domains and shares common molecular characters

with other 5-HT receptors. Like other GPCRs, Se-5HTR contains the canonical seven

transmembrane domains along with consensus glycosylation in the N-terminus (Asn^{48} and Asn^{53})

[53]. Additionally, its sequence contains a consensus aspartic acid residue in TM3 (Asp^{163}) and

a serine residue in TM5 (Ser^{247}) to interact with functional groups of biogenic monoamines [54].

At the intracellular border of TM3, the highly conserved Asp^{180}-Arg^{181}-Tyr^{182} motif is evident

for a strong ionic interaction with Glu^{430} residue adjacent to the intracellular end of TM6 that

plays a crucial role in GPCR signal transduction [55]. The sequence contains consensus Phe^{444}-

X-X-X-Trp^{448}-X-Pro^{450}-X-Phe^{452} motif in TM6 which is unique to biogenic monoamine GPCRs

[38]. Additionally, Se-HTR contains two potential post-translational palmitoylation cysteine

residues (Cys^{508} and Cys^{532}) [56] at the final intracellular region with a PDZ-domain binding

motif (Glu^{561}-Ser^{562}-Phe^{563}-Leu^{564}) at the C-terminus [57].

Se-5HTR is expressed in all developmental stages. It is expressed in immune-associated

tissues (hemocytes and fat body), digestive (gut) tissues, and nervous (brain) tissues at larval

stage. Three 5-HT receptors of *P. rapae* larvae are all expressed, although their expression levels

in tissues are different. Subtypes 1A and 1B receptor are highly expressed in nervous tissues

while subtype 7 receptor is mainly expressed in digestive tissue [36]. *Se-5HTR* was also highly

expressed in the gut like 5-HT_7 of *P. rapae*. Furthermore, our phylogenetic analysis of 5-HT

receptors showed that these two insect 5-HT_7s were closely related and clustered. Expression

levels of *Se-5HTR* in hemocytes were similar to those in the brain. This suggests that Se-5HTR is

associated with immune function as well as neurophysiological function. Indeed, bacterial or

fungal infection up-regulated the expression of *Se-5HTR*. The increase of *Se-5HTR* expression

might be explained by the up-regulation of *de novo* biosynthesis of its ligand, 5-HT, via increase

in expression of biosynthetic genes as seen in hemocytes of *P. rapae* larvae after immune

challenge [22].

The presence of 5-HT$_7$ receptor in hemocytes of *S. exigua* and its physiological function

associated with immune responses were supported by its sensitivity to specific 5-HTR inhibitors.

In response to 5-HT or bacterial challenge, *S. exigua* larvae exhibited significant increase of

THC. This up-regulation of THC was explained by mobilization of sessile hemocytes to

circulatory form by cytoskeletal rearrangement via a small G protein, Rac1 [45,52]. This

suggests that Se-5HTR can activate Rac1 to stimulate the hemocyte behavior. In vertebrates,

activation of 5-HT$_7$ receptor increases cAMP level via a trimeric G protein G$_s$ and small G

proteins of Rho family including Cdc42, RhoA, and Rac1 via another trimeric G protein G$_{12}$ [58].

This suggests that immune challenge can induce biosynthesis and release of 5-HT which then

binds to Se-5HTR on hemocytes and activates Rac1 to stimulate hemocyte behaviors. In addition,

the cAMP pathway triggered by Se-5HTR might activate Akt and ERK1/2 as seen in mammalian

cancer cells [59] to facilitate actin rearrangement to form cellular shape change of hemocytes.

These findings suggest that Se-5HTR plays a crucial role in hemocyte migration and cell shape

change during cellular immune responses. Indeed, RNAi of *Se-5HTR* expression resulted in

significant immunosuppression by exhibiting reduction in phagocytosis and nodulation.

Bacterial metabolites derived from two entomopathogens, *Xenorhabdus* and *Photorhabdus*,

inhibited cellular immune responses mediated by Se-5HTR. Especially, six chemical groups

(phenylethylamide, tryptamide, xenortide, xenocycloin, nematophin, and GameXPeptide) highly

inhibited both phagocytosis and nodulation, suggesting that they can inhibit Se-5HTR. This was

supported by their competitive inhibition with the ligand, 5-HT. Bacterial secondary metabolites

may be synthesized and released in the bacterium-nematode complex in order to defend immune

attack from target insect to compete with other microbes occurring in the insect cadaver and

facilitate host nematode development or bacterial quorum sensing [47]. It has been reported

phenylethylamides and tryptamides identified from *Xenorhabdus* can act as quorum quenching

activators by competitive binding to N-acylated homoserine lactone (AHL) receptor because

AHL accumulation drives gene expression of bioluminescence, virulence factor, and biofilm

formation in bacteria [60,61]. Xenortides are linear peptides consisting of 2-8 amino acids

synthesized from both *Xenorhabdus* and *Photorhabdus* [62]. They are synthesized in insect hosts

during infection with putative role in inhibiting prophenoloxidase activation to suppress insect

immunity [63]. Xenocycloins produced by *X. bovienii* are cytotoxic to hemocytes of *Galleria*

melonella [64]. Nematophin is synthesized by condensation of α-keto acid and tryptamine in *X.*

nematophila. It possesses a specific antibacterial activity against *Staphylococcus aureus* [65].

GameXPeptides are cyclic pentapeptides widely synthesized in both *Xenorhabdus* and

Photorhabdus. However, their biological functions remain unclear [66]. This current study

showed that these six compound classes could inhibit cellular immune responses by competitive

inhibition with 5-HT against Se-5HTR.

A novel phenylethylamide compound, PhX, was found to be highly inhibitory against Se-

5HTR. Derivatives of phenylethylamide compound (HB 4) exhibited different inhibitory

activities against cellular immune responses mediated by Se-5HTR. Especially, PhX containing

methoxy and hexahydropyrrolo[1,2-a]pyrazine-1,4-dione exhibited the highest inhibitory

activity. 5-HT receptors have been used for screening for potent insecticides with growth-

inhibiting or larvicidal activities against *Pseudaletia separata* [67]. Thus, PhX can be a candidate

for this application unless it shows mammalian or non-target species toxicity [68].

Materials and methods

Insect rearing and microbial culture

A laboratory strain of *S. exigua* was originated from Welsh onion field (Andong, Korea) and maintained for ~20 years. Larvae of this laboratory strain were reared on an artificial diet [69] at temperature of $25 \pm 1°C$ and relative humidity of $60 \pm 10\%$ with a photoperiod of 16:8 h (L:D). Under these conditions, larvae had five instars ('L1-L5'). Adults were reared with 10% sucrose solution. For immune challenge, *Escherichia coli* Top10 (Invitrogen, Carlsbad, CA, USA) was cultured in Luria-Bertani (LB) medium (BD Korea, Seoul, Korea) in a shaking incubator (200 rpm) at 37°C overnight (16 h).

Chemicals

Serotonin hydrochloride was purchased from Sigma-Aldrich Korea (Seoul, Korea). It was dissolved in distilled water. SB-269970 (a specific inhibitor to 5-HT receptor subtype 7, 5-HT$_7$) was purchased from Cayman Chemical Company (Korea). It was dissolved in desired concentrations with dimethyl sulfoxide (DMSO). Fluorescein isothiocyanate (FITC) [2-(6-hydroxy-3-oxo-3h-xanthen-9-yl)-5-isothiocyanatobenzoic acid] was purchased from Sigma-Aldrich Korea. It was dissolved in DMSO to make a solution at 10 mg/mL. Anticoagulant buffer (ACB) was prepared using 98 mM NaOH, 186 mM NaCl, 17 mM Na$_2$EDTA, and 41 mM citric acid at pH 4.5. Phosphate-buffered saline (PBS) was prepared at pH 7.4 with 50 mM sodium phosphate and 0.7% NaCl. Tris-buffered saline (TBS) was prepared using 150 mM NaCl, 50 mM Tris-HCl at pH 7.6. Hank's balanced salt solution (HBSS) was prepared with the following compositions: 8 g NaCl, 400 mg KCl, 40 mg Na$_2$HPO$_4$, 60 mg KH$_2$PO$_4$, 1 g glucose, 140 mg CaCl$_2$, 120 mg MgSO$_4$, and 350 mg NaHCO$_3$ in 1,000 mL distilled H$_2$O.

Bioinformatics to search for 5-HT receptor and sequence analysis

S. exigua 5-HT receptor (Se-5HTR) sequence was obtained from GenBank by manual annotation.

Briefly, a dopamine receptor sequence (AKR18180.1) of *Chilo suppressalis* was used to screen a

transcriptome (SRR1050532) of *S. exigua*. A blast contig (GARL01017386.1) was analyzed for

open reading frame (ORF) and the predicted amino acid sequence was used for analysis using

BlastP program against GenBank (www.ncbi.nlm.nih.gov). After confirming its high homologies

(E value < 10^{-20}) with other known insect 5HTRs, the resulting ORF sequence (= Se-5HTR) was

deposited at NCBI-GenBank (accession number: MH025798). Sequence alignment was

established using Clustal Omega tool (https://www.ebi.ac.uk/Tools/msa/clustalo/) provided by

European Bioinformatics Institution. Phylogenetic tree was generated with Neighbor-joining

method using Mega6 and ClustalW programs. Bootstrapping values were obtained with 1,000

repetitions to support branch and clustering. Protein domain was predicted using InterPro tool

(https://www.ebi.ac.uk/interpro/),   pfam   (http://pfam.xfam.org),   and   Prosite

(http://prosite.expasy.org/).

RNA extraction and cDNA preparation

Using Trizol reagent (Invitrogen), total RNAs were extracted from all developmental stages as

well as larval tissues (hemocyte, midgut, fat body, and brain) of *S. exigua* according to the

instruction of the manufacturer. Numbers of individuals used for RNA extraction for each

individual developmental stage were as follows: ~500 eggs, ~20 larvae for L1-L2, ~10 larvae for

L3, ~5 larvae for L4, one larva for L5, one pupa, and one adult. L5 larvae were used for RNA

extraction from different tissue samples. After extraction, total RNAs were resuspended in

nuclease-free water and cDNAs were synthesized from ~1 µg of RNAs using Maxime RT

Premix (Intron Biotechnology, Seoul, Korea) according to the manufacturer's instruction.

Expression pattern of Se-5HTR by RT-qPCR

A fragment of *Se-5HTR* was amplified with gene-specific primers (5'- CTT TAC CTT CGT

GTC TTC TC-3' and 5'- GGT GTC AGT CTT CTC ATT AC -3'). PCR was performed with 35

cycles of denaturation (94°C, 1 min), annealing (49°C, 1 min), and extension (72°C, 1 min). PCR

products were subjected to agarose gel electrophoresis to visually confirm their amplifications.

With the same gene-specific primers used in RT-PCR, RT-qPCR was performed in a qPCR

machine (CFX Connect™ Real-Time PCR Detection System, Bio-Rad, Hercules, CA, USA)

using SYBR Green Realtime PCR Master Mix (Toyobo, Osaka, Japan) under a guideline of

Bustin et al. [70]. The amplification used 40 cycles of 15 s at 95°C, 30 s at 60°C, and 45 s at

72°C. After PCR reactions, melting curves from 60 to 95°C were obtained to confirm unique

PCR products. A ribosomal protein, RL32, gene was used as a control with primers of 5'-ATG

CCC AAC ATT GGT TAC GG-3' and 5'-TTC GTT CTC CTG GCT GCG GA-3'. Each

treatment was independently triplicated. Relative quantitative analysis method ($2^{-\Delta\Delta CT}$) was used

to estimate mRNA expression levels of *Se-5HTR*.

RNA interference (RNAi)

Gene fragment of *Se-5HTR* was amplified from template DNA using gene-specific primers (5'-

CTT TAC CTT CGT GTC TTC TC-3' and 5'-GGT GTC AGT CTT CTC AT-3') possessing T7

RNA polymerase promoter sequence (5'-TAA TAC GAC TCA CTA TAG GGA GA-3') at 5'

ends. PCR was performed with 5 cycles of denaturation (94°C, 1 min), annealing (49°C, 1 min),

and extension (72°C, 1 min) followed by 30 cycles of denaturation (94°C, 1 min), annealing

(60°C, 1 min), and extension (72°C, 1 min) to synthesize DNA template for dsRNA synthesis.

Double-stranded RNA (dsRNA) against *Se-5HTR* ('dsSe-5HTR') was synthesized using

Megascript RNAi kit (Ambion, Austin, TX, USA) following the manufacturer's instruction. The

resulting dsRNA was blended with Metafectene PRO (Biontex, Plannegg, Germany) at 1:1 (v:v)

ratio and incubated at 25°C for 30 min for liposome formation. Two microliters of the prepared

mixture containing ~900 ng of dsRNA was injected twice into *S. exigua* larval hemocoel using a

microsyringe (Hamilton, Reno, NV, USA) equipped with a 26-gauge needle. The first injection

was at late L4 stage. It was repeated 12 h afterwards. RNAi efficacy at 0, 24, and 48 h post-

injection (PI) in reducing *Se-5HTR* expression was determined by RT-qPCR. At 24 h PI, treated

larvae were used for immune challenge experiments. Each treatment was replicated thrice using

10 larvae for each replication.

Total hemocyte count (THC)

Hemolymph was collected by cutting larval proleg and mixed with ACB (1:10, v/v). Hemocytes

were counted using a Neubauer hemocytometer (Superior Marienfeld, Lauda-Königshofen,

Germany) under a phase contrast microscope (BX41, Olympus, Tokyo, Japan) at 100×

magnification. Heat-killed (90°C, 30 min) *Escherichia coli* (5×10^5 cells/larva) and a test

chemical (5-HT or SB-269970) were co-injected into hemocoel through abdominal proleg of L5

larvae in a volume of 5 μL using a 10 μL micro-syringe (Hamilton) after surface-sterilization

with 70% ethanol. After 4 h of incubation at 25 ± 2°C, hemolymph of the insect was collected

and assessed for THC.

Hemocyte-spreading analysis

After hemolymph (~150 µL) was collected from five L5 larvae by cutting prolegs, it was mixed with three times volume of ice-cold ACB and incubated on ice for 30 min. ACB-treated hemolymph was then centrifuged at $800 \times g$ for 5 min at 4°C. The resulting pellet was re-suspended in 500 µL of filter-sterilized TC-100 insect cell culture medium (Welgene, Daegu, Korea). On a glass coverslip placed in a moist chamber, 10 µL of hemocyte suspension was applied and placed in a dark condition. Hemocytes were then fixed with 4% paraformaldehyde (filter-sterilized) at 25°C for 10 min and then washed thrice with filter-sterilized PBS. Cells were then permeabilized with 0.2% Triton-X dissolved in PBS at 25°C for 2 min and washed with PBS. After that, hemocytes were blocked using 10% bovine serum albumin (BSA) dissolved in PBS at 25°C for 10 min and washed again with PBS. Cells were then incubated with FITC-tagged phalloidin in PBS for 60 min and washed thrice with PBS. Hemocytes nuclei were then stained by incubating with 4′,6-diamidino-2-phenylindole (DAPI, 1 µg/mL) (Thermo Fisher Scientific, Rockford, IL, USA) dissolved in PBS and washed thrice with PBS. Hemocytes were then observed under a fluorescence microscope (DM2500, Leica, Wetzlar, Germany) at 400× magnification. Hemocyte-spreading was dictated by appendages of F-actin outward the hemocyte cell boundary.

To assess effect of *Se-5HTR* RNAi on hemocyte-spreading, hemocytes were collected at 24 h after injecting dsSe-5HTR (~900 ng/larva). In separate experiments, 5-HT and 5-HTR inhibitor SB-269970 were co-injected into dsRNA-treated larvae at ratios of 1:10 and 10:1 to check their influence on hemocyte-spreading. At 6 h after co-injection, hemolymph was collected from the treated larva and hemocyte-spreading was observed using the above-mentioned method.

Nodulation assay

Overnight culture of *E. coli* Top10 bacterial cells was washed with PBS and centrifuged at 1,120 $\times$ *g* for 10 min. L5 larvae were used to assess hemocyte nodule formation by immune-challenge with bacterial injection (~1.8 $\times$ 10^5 cells/larva) through the abdominal proleg into larval hemocoel using a microsyringe as previously described. To assess the effect of *Se-5HTR* RNAi on nodule formation, bacterial challenge was performed at 24 h after injecting dsSe-5HTR (~900 ng/larva). To check the influence of chemicals on nodule formation, 2 μg of ketanserin and/or 10 μg of 5-HT was co-injected along with the bacterial suspension. In separate experiment, 1 μg of the bacterial secondary metabolite was co-injected with the bacterial suspension to assess immune suppression activity of the test compound. After an incubation period of 8 h at 25°C, treated insects were dissected under a stereo microscope (SZX9, Olympus, Japan) to count melanized nodule numbers. Each treatment was triplicated independently using five insects for each replication.

Phagocytosis assay

Preparation of FITC-labeled bacterial cells followed the method described by Harlow and Lane (1998). Briefly, *E. coli* Top10 cells were cultured in 50 mL of Luria-Bertani broth (37°C, 16 h). These bacterial cells were then harvested by centrifuging 1 mL of the cultured broth at 1,120 $\times$ *g* for 10 min at 4°C. Bacterial cells (10^5 cells/mL) were washed twice with TBS and re-suspended in 1 mL of 0.1 M sodium bicarbonate buffer (pH 9.0). In the suspension, 1 μL of 10 mg/mL FITC solution was added and immediately mixed. The mixture was then incubated under darkness with end-over-end rotation at 25°C for 30 min. After the incubation, FITC-tagged bacteria were harvested by centrifugation at 22,000 $\times$ *g* for 20 min at 4°C. These bacterial cells

were washed thrice with HBSS to remove unbound dye and re-suspended in TBS.

To assess *in vivo* phagocytosis activity, 5 µL of FITC-tagged *E. coli* suspension was injected

into the hemocoel of L5 larva through the proleg. To assess the effect of *Se-5HTR* RNAi on

phagocytosis activity, bacteria were injected at 24 h after injecting dsSe-5HTR (~900 ng/larva).

To check the influence of a specific 5-HT$_7$ receptor inhibitor on phagocytosis, 2 µg of SB-

269970 was co-injected with the tagged bacterial suspension. To determine the effect of

secondary metabolite on phagocytosis, 1 µg of bacterial secondary metabolite was co-injected

with tagged bacterial suspension. After 15 min of incubation, treated larvae were surface-

sterilized using 70% ethanol. With a pair of scissors, the proleg was cut to collect hemolymph

sample (~50 µL) in 150 µL of cold ACB with gentle shaking of the tube to mix hemolymph and

ACB thoroughly. Hemocyte monolayers were made using 50 µL of hemocyte suspension (~5 ×

10^3 cells) and left in a moist chamber for 15 min for hemocytes to settle and attach to the glass

surface. After the incubation period, monolayers were washed with TBS to remove plasma.

These monolayers were overlaid with 1% trypan blue dye solution to quench non-phagocytosed

bacterial cells. After 10 min, monolayers were washed again with TBS and then fixed with 1.5%

glutaraldehyde solution to observe under a fluorescence microscope at 400× magnification.

Hemocytes undergoing phagocytosis were counted from a total of 100 hemocytes observed from

different areas of each slide. Each observation was triplicated with three different slides.

Preparation of organic extracts from bacterial culture broth

X. nematophila K1 (Xn) and *P. temperate temperata* ANU101 (Ptt) bacteria were cultured in

TSB at 28°C for 48 h. Culture broths were centrifuged at 12,500 × *g* for 30 min and supernatants

were used for subsequent fractionation. To obtain ethyl acetate extract, the same volume (1 L) of

ethyl acetate was mixed with the supernatant and separated into organic and aqueous fractions.

Ethyl acetate extract ('EAX') was dried using a rotary evaporator (Sunil Eyela, Seongnam,

Korea) at 40°C. The resulting extract (0.2 mg) was obtained from 1 L cultured broth and

resuspended with 5 mL of methanol. The aqueous phase was then combined with 1 L of butanol.

Butanol extract ('BX') was also dried using the rotary evaporator at 40°C and the resulting

extract (0.2 mg) was resuspended with 5 mL of methanol.

Secondary bacterial metabolites – biological activity against immune responses

Secondary metabolites (37 samples, S4 Fig) derived from *Xenorhabdus* and *Photorhabdus*

cultures were from the Bode lab compound collection named 'HB' compounds. Their biological

activities for suppressing *S. exigua* immunity were then determined. Individual chemicals were

dissolved in DMSO, diluted into desired concentrations with DMSO, and stored at -20°C.

For hemocyte nodulation inhibition assay, overnight culture of *E. coli* bacterial cells was

washed with PBS. Test compound (1 µg/larva) was injected into larval hemocoel along with the

bacterial suspension (~1.8×10^5 cfu/larva) using a microsyringe as previously described. Insects

were then incubated at 25°C for 8 h. After the incubation period, insects were dissected and

nodule numbers were counted as described above. Each treatment was triplicated independently

using five insects for each replication. For phagocytosis inhibition assay, 5 µL of FITC-tagged *E.*

coli suspension along with 1 µg of test compound was injected into L5 larval hemocoel. After 15

min of incubation period, hemocytes undergoing phagocytosis were counted as previously

described.

Secondary bacterial metabolites – competitive assay with 5-HT

To determine effects of bacterial secondary metabolites on nodulation and phagocytosis, 10

potent chemicals were selected based on their common inhibitory activity on both phagocytosis

and nodulation and their median inhibition concentration (IC_{50}) values were calculated.

Percentages of phagocytosis against increasing concentrations of HB chemicals were calculated

and their IC_{50} values were calculated using Probit analysis

(https://probitanalysis.wordpress.com). To assess a competitive inhibitory activity between test

compound and 5-HT, HB chemicals were injected in different doses (0, 0.01, 0.1, 1 and 10

µg/larva) along with a fixed 5-HT concentration (1 µg/larva) and FITC-tagged bacteria (500

cells/larva). In a separate experiment, different doses of 5-HT were injected into the larvae with a

fixed HB compound content (1 µg/larva). At 15 min after bacterial injection, hemocytes from

treated larvae were collected in ACB and phagocytosis assay was performed as described above.

Chemical derivatives and their inhibitory activities against Se-5HTR

Based on potent phenylethylamide (PEA) HB compounds, 45 additional PEA samples (S5 Fig)

were obtained from Korea Chemical Bank of the Korea Research Institute of Chemical

Technology (KRICT). Derivative compounds were dissolved in DMSO, diluted into desired

concentrations with DMSO, and stored at -20°C. These PEA chemicals were then tested for their

abilities to suppress nodule formation and phagocytosis in *S. exigua* as described above. For

nodulation inhibition assay, each chemical (150 ng/larva) was injected into larval hemocoel

along with bacterial suspension (~1.8 × 10^5 cfu/larva). Each treatment was triplicated

independently using five insects for each replication. For phagocytosis inhibition assay, 5 µL of

FITC-tagged *E. coli* suspension along with 150 ng of each chemical was injected into L5 larval

hemocoel of *S. exigua*. After incubating for 15 min, hemocytes undergoing phagocytosis were

counted using previously described method.

Chemical synthesis of PhX

A potent chemical was designed as PhX ((*S*)-2-(1,4-dioxohexahydropyrrolo[1,2-*a*]pyrazin-

2(*1H*)-yl)-*N*-(4-methoxyphenethyl)acetamide) and chemically synthesized according to a method

described in S6 Fig.

Statistical analysis

All studies were triplicated independently. Results are expressed as mean ± standard error.

Results were plotted using Sigma plot (Systat Software, San Jose, CA, USA). Means were

compared by least squared difference (LSD) test of one-way analysis of variance (ANOVA)

using POC GLM of SAS program [71] and discriminated at Type I error = 0.05.

Funding

This work was supported by a grant (No. 2017R1A2133009815) of the National Research

Foundation (NRF) funded by the Ministry of Science, ICT and Future Planning, Republic of

Korea. This work was also supported by a project (No SI1808, Development of crop protection

agents leading the future market). The chemical library used in this research was provided by

Korea Chemical Bank (http://www.chembank.org) of the Korea Research Institute of Chemical

Technology (KRICT).

Acknowledgments

We appreciate Youngim Song for ordering and arranging materials and Malsook Cho for rearing

insects. Work in the Bode lab was supported by the LOEWE Center Translational Biodiversity

Genomics funded by the state of Hesse, Germany.

Author Contributions

Conceptualization: Yonggyun Kim.

Formal analysis: Ariful Hasan, Yonggyun Kim.

Investigation: Hyun-Suk Yeom, Jaewook Ryu, Helge B. Bode, Yonggyun Kim.

Project administration: Yonggyun Kim.

Supervision: Hyun-Suk Yeom, Jaewook Ryu, Helge B. Bode, Yonggyun Kim.

Writing – original draft: Ariful Hasan, Yonggyun Kim.

Writing – review & editing: Ariful Hasan, Hyun-Suk Yeom, Jaewook Ryu, Helge B. Bode,

Yonggyun Kim.

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 Figure captions

 Fig. 1. Bioinformatics analysis of a novel 5-HTR$_7$ identified from *S. exigua* (Se-5HTR:

 MH025798). (A) Phylogenetic analysis of 5HTRs. Amino acid sequences were retrieved from

 GenBank: Hs5HTR1D (NP_000855.1), Ss5HTR1D (NP_999323.1), Rn5HTR1D

 (NP_036984.1), Oc5HTR1D (NP_001164624.1), NP_000854.1 Hs5HTR1B (NP_000854.1),

 Dr5HTR1D (NP_001139158.1), Hs5HTR1F (NP_000857.1), Hs5HTR1E (NP_000856.1),

 Cp5HTR1E (NP_001166222.1), Hs5HTR1A (NP_000515.2), Ap5HTR1B (ABY85411.1),

 Ms5HTR (ABI33827.1), Pr5HTR1B (XP_022120028.1), Am5HTR1 (NP_001164579.1),

 Dm5HTR1B (NP_001163201.2), Pa5HTR1 (CAX65666.1), Pr5HTR1A (XP_022129638.1),

 Ap5HTR1A (ABY85410.1), Hs5HTR7 (P34969), Rn5HTR7 (P32305), Pr5HTR7

 (AMQ67549.1), Am5HTR7 (NP_001071289.1), Dm5HTR7 (NP_524599.1), Ae5HTR7

 (Q9GQ54), Hs5HTR4 (Q13639), Cp5HTR4 (O70528), Rn5HTR4 (Q62758), Mm5HTR4

 (P97288), Hs5HTR6 (P50406), Pt5HTR6 (Q5IS65), It5HTR6 (XP_005317590.1), Rn5HTR6

 (P31388), Mm5HTR6 (Q9R1C8), Cp5HTR6 (XP_003471412.1), Pm5HTR2A (KPJ17794.1),

 Pr5HTR2A (XP_022112310.1), Bm5HTR2A (NP_001296483.1), Cl5HTR2A

 (XP_014254278.1), Rp5HTr2B (AKQ13312.1), Mq5HTR2A (KOX78271.1), Am5HTr2B

 (NP_001189389.1), Hs5HTR2A (NP_000612.1), Hs5HTR2C (NP_000859.1), Hs5HTR2B

 (NP_000858.3), Pt5HTR2C (XP_015921531.1), Mp5HTR2C (XP_022169104.1), Am5HTr2A

 (NP_001191178.1), Pr5HTR2C (XP_022122944.1), Ba5HTR2C (XP_023955125.1),

 Rn5HTR5B (P35365), Mm5HTR5B (P31387), Hs5HTR5A (NP_076917.1), Rn5HTR5A

 (P35364), Mm5HTR5A (P30966), Hs5HTR3C (NP_570126.2), Hs5HTR3E (NP_001243542.1),

 Hs5HTR3D (NP_001157118.1), Hs5HTR3B (NP_006019.1), Rn5HTR3B (NP_071525.1),

Hs5HTR3A (AP35868.1), Cp5HTR3A (O70212), Rn5HTR3A (NP_077370.2), Mm5HTR3A (P23979). The phylogenetic tree was constructed using neighbor-joining method. Bootstrap values on branch nodes were obtained after 1,000 repetitions. **(B)** Amino acid sequence alignment of Se-5HTR with orthologous receptors from *Homo sapiens* (Hs-5HTR7: P34969), *Drosophila melanogaster* (Dm-5HTR7: NP_524599.1), *Manduca sexta* (Ms-5HTR7: AGL46976.1), and *Pieris rapae* (Pr-5HTR7: AMQ67549.1). Identical residues among these five sequences are illustrated as white letters against black. Dashes within sequences indicate gaps introduced to maximize homology. Putative seven transmembrane domains (TM1-TM7) are shown as blue bars. Potential N-glycosylation sites (⊠), potential phosphorylation sites for protein kinase A and/or C (⊠), potential residue to interacts with 5-HT amino group (⊠) and 5-HT hydroxyl group (⊠), potential disulfide bond groups (⊠), and potential post translational palmitoylation sites (⊠) are indicated. Overbars indicate unique motif to aminergic receptor, agonist mediated sequestration and resensitization motif, and PDZ-domain binding motif, respectively. Conserved domains were determined using InterPro tool (https://www.ebi.ac.uk/interpro/) and Prosite (http://prosite.expasy.org/) whereas other residues and motifs were predicted using several tools from DTU bioinformatics (www.cbs.dtu.dk/services/).

Fig. 2. Expression profile of *Se-5HTR*. (A) Differential expression of *Se-5HTR* in different developmental stages: egg, larval instars ('L1-L5'), pupa ('Pu'), and adult ('Ad'). **(B)** Differential expression of *Se-5HTR* in different tissues of L5 larvae: hemocyte ('HC'), midgut ('GUT'), fat body ('FB'), and brain ('BR'). **(C)** Expression pattern of *Se-5HTR* in immune-challenged L5 larvae: *Escherichia coli* ('Ec'), *Xenorhabdus nematophila* ('Xn'), *Photorhabdus*

temperata temperata ('Ptt'), *Serratia marcescens* ('Sm'), and *Beauveria bassiana* ('Bb').

Immune challenge was performed by injecting each L5 larva with 1.8×10^5 cells of bacteria or 5

$\times 10^5$ conidia of fungi. After incubation at 25°C for 8 h, gene expression analysis was performed

using RT-PCR and RT-qPCR. As a constitutive expressional control, a ribosomal gene, *RL32*,

was used for expression analysis in RT-PCR and RT-qPCR. Each measurement was replicated

three times with independent biological samples. Histogram bars annotated with the same letter

are not significantly different at Type I error = 0.05 (LSD test).

Fig. 3. Effect of an inhibitor specific to 5-HT$_7$ receptor ('SB-269970') on hemocyte

behaviors of *S. exigua*. (A) Total hemocyte count (THC) analysis in L5 larvae. For the assay, 2

μg of 5-HT or 2 μg of SB-269970 was injected. THC was assessed with or without bacterial co-

injection (1.8×10^5 cells per larva). **(B)** Hemocyte-spreading behavior analysis. Hemocyte-

spreading was assessed with a 20 μL reaction mixture containing 1 or 2 μL test chemical with 18

or 19 μL hemocytes. 5-HT was co-applied with SB-269970 at ratios of 1:10 (2 μg 5-HT: 20 μg

SB-269970) and 10:1 (20 μg 5-HT: 2 μg SB-269970). Spread cells were stained with F-actin and

FITC-labeled phalloidin. Nuclei were stained with DAPI. Each treatment was independently

replicated three times. Histogram bars indicate percentages of spread hemocytes and error bars

indicate standard deviation. Histogram bars annotated with the same letter are not significantly

different at Type I error = 0.05 (LSD test).

Fig. 4. RNA interference (RNAi) of *Se-5HTR* and suppression of hemocyte behaviors. (A)

RNAi of *Se-5HTR* expression with a gene-specific dsRNA (dsSe-5HTR). About 900 ng of dsSe-

5HTR was injected to L5. At 0, 12, 24, and 48 h post-injection (PI), expression levels of *Se-*

5HTR were assessed from whole body. Expression levels of *Se-5HTR* in different tissue parts

were assessed at 24 h PI. As a constitutive expressional control, a ribosomal gene, *RL32*, was

used for expression analysis in RT-PCR and RT-qPCR. As a control RNAi (dsCON), dsRNA

specific to *CpBV-ORF302* (a viral gene) was used for expression analysis. In RT-qPCR, each

treatment was triplicated. **(B)** Influence of RNAi on up-regulation of total hemocyte count (THC)

in response to bacterial challenge. At 24 h PI of dsSe-5HTR, hemolymph was collected from L5

larvae for THC assessment. Each treatment was replicated three times. **(C)** Influence of RNAi on

hemocyte-spreading behavior. For spreading assay, hemocytes from larvae treated with dsRNA

were collected at 24 h. Each treatment was independently replicated three times. Spread cells

were stained with F-actin and FITC-labeled phalloidin. Nuclei were stained with DAPI.

Histogram bars indicate percentages of spread hemocytes and error bars indicate standard

deviation. Different letters above standard error bars indicate significant difference among means

at type I error = 0.05 (LSD test). Asterisks represent significant difference between control and

treatment in each tissue.

Fig. 5. RNA interference (RNAi) of *Se-5HTR* and suppression of cellular immune responses.

(A) Analysis of phagocytosis in L5 larvae of *S. exigua*. FITC-tagged *E. coli* were injected into

L5 larvae at 24 h post-injection of dsSe-5HTR. A specific inhibitor (SB-269970) to 5-HT$_7$

receptor was co-injected at a dose of 2 μg along with FITC-tagged bacteria. At 15 min after

injection, phagocytic cells were observed under a fluorescent microscope at 400 × magnification

and percentage of phagocytotic hemocytes was calculated from randomly chosen 100 cells. Total

hemocytes were observed from bright-field ('BF'). Each treatment was independently replicated

three times. **(B)** Nodulation assay. After RNAi, *E. coli* (1.8×10^5 cells/larva) was injected to L5

larvae. SB-269970 (2 μg/larva) was co-injected with bacteria. After 8 h incubation at 25°C,

treated insects were assessed for nodule formation. Histogram bars indicate percentages of

phagocytosis and error bars indicate standard deviation. Histogram bars annotated with the same

letter are not significantly different at Type I error = 0.05 (LSD test).

Fig. 6.   Immunosuppressive activities of organic extracts from culture broth of

***Xenorhabdus nematophila* ('Xn') and *Photorhabdus temperata temperata* ('Ptt') bacteria**

against L5 larvae of *S. exigua*. Each larva was injected with *E. coli* (10^5 cells) along with 1 μL

of ethyl acetate ('EAX') or butanol ('BX') extract. **(A)** Phagocytosis in L5 larvae. FITC-tagged

E. coli were injected to L5 larvae at 24 h post-injection of an organic extract. After 15 min,

phagocytic cells were observed under a fluorescent microscope at 400 × magnification and

percentage of phagocytotic hemocytes was calculated from randomly chosen 100 cells. Each

treatment was independently replicated three times. **(B)** Nodule formation. *E. coli* (1.8×10^5

cells/larva) was injected to L5 larvae. An organic extract was co-injected with the bacteria. After

8 h of incubation at 25°C, treated insects were assessed for nodule formation. Each treatment

was replicated with 10 larvae. Different letters above standard deviation bars indicate significant

difference among means at Type I error = 0.05 (LSD test).

Fig. 7. Screening 37 bacterial secondary metabolites derived from *X. nematophila* and *P.*

***temperata temperata* for their effects on cellular immune responses mediated by Se-5HTR in**

***S. exigua*. (A)** Screening with phagocytosis assay. FITC-tagged *E. coli* cells were injected to L5

larvae along with 1 μg of each test chemical. After 15 min, phagocytic cells were observed under

a fluorescent microscope at 400 × magnification and percentage of phagocytotic hemocytes was

calculated from randomly chosen 100 cells. Each treatment was independently replicated three

times. **(B)** Screening with nodule formation assay. *E. coli* (1.8×10^5 cells/larva) was injected to

L5 larvae along with 1 µg of each test chemical. After 8 h of incubation at 25°C, treated insects

were assessed for nodule formation. Each treatment was replicated with 10 larvae. Asterisks

above standard deviation bars indicate significant difference compared to control ('CON'

without inhibitor) at Type I error = 0.05 (*), 0.01 (**), and 0.005 (***) (LSD test).

Fig. 8. Competitive inhibition of 10 selected bacterial metabolites derived from *X.*

***nematophila* and *P. temperata temperata* with 5-HT against Se-5HTR mediating**

phagocytosis. FITC-tagged *E. coli* cells were injected to L5 larvae along with test chemicals.

After 15 min, phagocytic cells were observed under a fluorescent microscope at 400 $\times$

magnification and percentage of phagocytotic hemocytes was calculated from randomly chosen

100 cells. Each treatment was independently replicated three times. **(A)** Dose-response of

inhibitory compound (0, 0.01, 0.1, 1, and 10 µg/larva) with a fixed 5-HT concentration (1

µg/larva). **(B)** Dose-response of 5-HT (0, 0.02, 0.2, 2 and 20 µg/larva) with a fixed HB

compound concentration (1 µg/larva). 'CON' represents a positive control without any inhibitor.

Fig. 9. Validation of phenylethylamide (PEA) compounds for their inhibitory activities

against 5-HTR using derivatives with different side chains ('X' and 'Y' of PEA skeleton).

(A) Screening of 45 PEA derivatives for their effects on hemocyte phagocytosis of *S. exigua*

with HB 44, a potent bacterial metabolite, as reference. PEA compounds (300 ng/larva) were

injected into hemocoels of L5 larvae along with FITC-tagged bacteria. After incubating for 15

min, hemocytes were assessed for phagocytosis. Asterisks above standard deviation bars indicate

significant difference compared to control ('CON' without inhibitor) at Type I error = 0.05 (*),

0.01 (**), and 0.005 (***) (LSD test). **(B)** Chemical structures of three selected PEA compounds

and their median inhibitory doses (IC_{50}). **(C)** Competitive inhibition of the three selected PEA

derivatives with 5-HT against Se-5HTR mediated phagocytosis. For dose-response analysis of

inhibitory compounds (0, 0.3, 3, 30, and 300 ng/larva), a fixed 5-HT concentration (1 μg/larva)

was used. For dose-response of 5-HT (0, 2, 20, 200 and 2,000 ng/larva), a fixed HB compound

concentration (1 μg/larva) was used. 'CON' represents a positive control without any inhibitor.

Fig. 10. Specific inhibition of a designed compound (PhX) on Se-5HTR with a commercial

5-HTR$_7$ inhibitor (SB-269970) as reference in phagocytosis of *S. exigua*. FITC-tagged *E. coli*

cells were injected to L5 larvae along with test chemicals. After 15 min, phagocytic cells were

observed under a fluorescent microscope at 400 × magnification and percentage of phagocytotic

hemocytes was calculated from randomly chosen 100 cells. Each treatment was independently

replicated three times. **(A)** Dose-response of PhX and SB-269970 with a fixed 5-HT

concentration (500 ng/larva). **(B)** Dose-response of 5-HT (0, 0.002, 0.02, 0.2, and 2 μg/larva)

with a fixed inhibitor concentration (10 ng/larva). 'CON' represents a positive control without

any inhibitor.

(A)

(B)

```
Se-5HTR   MAT-------QSHNSYCS---------LPSFVALPSCLIVLAS-ILLQP------------------------------  32
Hs-5HTR7  -MMD-------VNSSGRP---------DLYGHLRSFLLPEVGRGLPDLS------------------------------  32
Dm-5HTR7  MALSGQDWRRHQSHRQFRNHRTQGNHQKLISTATLTLFVLFLSSWIAYAAGKATVPAPLVEGETESATSQDFNSSSAFLG  80
Ms-5HTR7  MAT-------QNHKSHS---------LPSFVALPSCLLILVSIILLQPN-----------------------------  33
Pr-5HTR7  MAS-------QNNSHYS---------RPSLVTLSSYLLIFVSLVLQADS-----------------------------  33
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                                          ▲       ▲                *              *
Se-5HTR   ALASVE---------------------IPSILSPEFNVSNPSTVNWTFLDDNSTFL--KHGHIKHSKYSI-------P  81
Hs-5HTR7  PDGGADP--------------------VAGSWAPHLLSEVTASPAPTWDAPPDNAS------GCGEQINYGR-------V  79
Dm-5HTR7  AIASASSTGSGSGSGSGSGSGSGSGSYGLASMNSSPIAIVSYQGITSSNLGDSNTTLVPLSDTPLLLEEFAAGEFVLPPL 160
Ms-5HTR7  AVDSVDC--------------------VDSLLASEYNYTNPNSTSNCTFRDTNST-----HKHIKHSKYST-------P  80
Pr-5HTR7  AFASFD--------------------FNSTFS-GVNTTNPNSTINWTFYDNNATVV--KHLHIKHLKYST-------L  81
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                    ▬▬▬▬▬▬▬ TM1 ▬▬▬▬▬▬▬              ▬▬▬▬▬▬▬ TM2 ▬▬▬▬▬▬▬        ▬▬
                                                *                            ↓
Se-5HTR   TTILLVTIFMIVIIGTIIGNVLVCVAVRLVRKLRRPSNYLIVSLAVSDLCVACIVMPVATVYDIMG-TWPFGPVICDFWV 160
Hs-5HTR7  EKVVIGSILTLITLLTIAGNCLVISVCFVKKLRQPSNYLIVSLALADLSVAVAVMPFVSVTDLIGGKWIFGHFFCNVFI 159
Dm-5HTR7  TSIFVSIVLLIVILGTVVGNVLVCIAVCMVRKLRRPCNYLIVSLAISDLCVALLVMPMALLYEVLE-KWNFGPLLCDIWV 239
Ms-5HTR7  VTIFLVILFLIVIVCTIVGNILVCVAVRLVRKLRRPSNYLIVSLAVSDLCVAIIVMPFATVYDIMG-TWPFGPVICDFWA 159
Pr-5HTR7  VTVLLAAIFMVVIFGTIVGNILVCVAVCLVRKLRRPSNYITVSLAVSDPCVAIMVMPVAMVYDLMG-SWPFGPVICDFWV 160
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              ▬▬▬▬▬▬▬ TM3 ▬▬▬▬▬▬▬                    ▬▬▬▬▬▬▬ TM4 ▬▬▬▬▬▬▬
              ●                              *                                    ↓ *
Se-5HTR   SSDVLSCTASILNLCMISVDRYYAITKPLEYGVKRTPRRMLFCVFIVWISAAFISLPPVLILGNEKTDTS----CSVSQN 236
Hs-5HTR7  AMDVMGCTASIMTLCVISIDRYLGITRPLTYPVRQNGKCMAKMILSVWLLSASITLPPLFGWAQNVNDDK---VCLISQD 236
Dm-5HTR7  SFDVLCCTASILNLCAISVDRYLAITKPLEYGVKRTPRRMLCVGIVWLAAACISLPPLLILGNEHEDEEGQPICTVCQN 319
Ms-5HTR7  SSDVLSCAASILNLCMISVDRYYAITKPLEYGVKRTPKRMLLCILIVWMSAAFISLPPVLILGNEKTETS----CSVSQN 235
Pr-5HTR7  SSDVLSCAASILNLCMISVDRYYAITKPLEYGVKRTPRRMLFCVFIVWMSAAFISLPPVLILGNEKSDTS----CSVSQN 236
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              ▬▬▬▬▬▬▬ TM5 ▬▬▬▬▬▬▬
                    *
Se-5HTR   QAYQIYATFGSFYIPLTVMIVVYYKIFRAARKIVKDEKR-AQSHLETHCYLEIN-------VKNGGAAEAKLLGNQP-AQ 307
Hs-5HTR7  FGYTIYSTAVAFYIPMSVMLFMYYQIYKAARKSAAKHKFPGFPRVEPDSVIALNGIVKLQKEVEECANLSRLLKHERKNI 316
Dm-5HTR7  FAYQIYATLGSFYIPISVMLFVYYQIFRAARRIVLEEKR-AQTHLQ---QALNG-------TGSPSAPQAPPLGHT---E 385
Ms-5HTR7  QVYQIYATLGSFYIPLTVMVVVYYKIFRAARKIVKDEKR-AQSHLETHCYLEIN-------VKNGGAAEAKLLGNQPAAQ 307
Pr-5HTR7  QGYQIYATFGSFYLPLTVMVVVYYKIFSAARKIVKDERR-AQSHLESHCYLEIN-------VKNGGAAEAKLLGNQP--Q 306
```

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              *          *                                *              ▲
Se-5HTR   PPPRGSTASTNTTCSVDKTESTIGRCFSGQRKSNESQC--PMLQQPKTPTKPIHTINRSPTQLVPGKLAVKERQRQPSES 385
Hs-5HTR7  SIFKREQKAATLGIIVGAFTVCWLPFFLLSTARPFICGTSCSCIPLWVERTFLWLGYANSLINPFIYAFFNRDLRTTYR 396
Dm-5HTR7  LASSGNGQRHSSVGNTSLTYSTCGGLSSG------------------------------------------------- 414
Ms-5HTR7  PPPRGSTASTNTTCSVDKAESGLGRCFSGQRKSNESQC--PMLQQPKTPTKPIHTINRSPTLTPNNKPIVKDRRRPSET 385
Pr-5HTR7  NPTRGSTASTNTTCSVDKAENSIGRCFSG-RKSNESQC--PMLQFPKTLTKPIHTINR-PASQNLNPDSNLKERRRPSSD 382
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                                                                    ▬▬▬▬▬▬▬ TM6 ▬▬▬▬▬▬
                *  *                                      *              ▬▬▬▬▬▬▬▬▬▬▬▬▬▬
Se-5HTR   SQKNTTNR---IRSSLSNFAHKSHIAKDLLHPQNAVHQKKLRFQLAKERKASTTLGIIMSAFVICWLPFFVLALIRPFVK 462
Hs-5HTR7  SLLQCQYRNINRKLSAAGMHEALKLAERPERPEFVLRACTRRVLLRPEKRPPVSVWVLQSPDHHNWLADKMLTTVEKKVM 476
Dm-5HTR7  ----------GGAIACHGSGGGVSGSTGLLG-SPHHKKLRFQLAKEKKASTTLGIIMSAFTVCWLPFFILALIRPFET 481
Ms-5HTR7  SNKMTTNR---IRSSLSNFAQKSHIAKDLFHSQ-SSHQKKLRFQLAKERKASTTLGIIMSAFIICWLPFFVLALIRPFVE 461
Pr-5HTR7  NQKQTS-R---IRSSLSTFAHKSHIAKDLLHPVNSPHQKKLRFHLAKERKASTTLGIIMSAFIVCWLPFFVLALIRPFVN 458
```

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              ▬▬▬▬▬▬▬ TM7 ▬▬▬▬▬▬▬
              ▬▬▬▬▬▬▬▬▬▬▬▬▬▬                     ▽                    ▽ ▲ *
Se-5HTR   EDAIPDAVSALFLWLGYLNSLLNPVIYATLNRDFRKPFQEILFFRCGNLNHMMREEFYHSQYGDPDQHYCVNNTTKMHNY 542
Hs-5HTR7  IHD                                                                    ------- 549
Dm-5HTR7  MH-VPASLSSLFLWLGYANSLLNPIIYATLNRDFRKPFQEILYFRCSSLNTMMRENYYQDQYGEPPSQRVMLG------- 553
Ms-5HTR7  EDAIPDAVSALFLWLGYLNSLLNPIIYATLNRDFRKPFQEILFFRCSNLNHMMREEFYHSQYGDPDQHYCGNNTTKLHNY 541
Pr-5HTR7  EDTIPDAVSALFLWLGYLNSLLNPIIYATLNRDFRKPFQEILFFRCSNLNHMMREEFYHSQYGGPEPHYCVNNS-KNQNY 537
```

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                                *      ▬▬▬▬
Se-5HTR   EEGVEIVSAVDREETRASESFL 564
Hs-5HTR7  ------- 564
Dm-5HTR7  -------D--ER--HGARESFL 564
Ms-5HTR7  DEGVEIVSAIDREETRASESFL 564
Pr-5HTR7  DEGVEIVSAVDREETRATESFL 564
```

Fig. 1

Fig. 2

(A)

(B)

Fig. 3

(A)

(B)

(C)

Fig. 4

(A)

(B)

Fig. 5

(A)

(B)

Fig. 6

(A)

(B)

Fig. 7

(A)

(B)

Fig. 8

(A)

(B)

Compound	Structure	IC$_{50}$ (μM)
Ph 15		1.862 ± 0.221[c]
Ph 17		2.746 ± 0.078[b]
Ph 33		5.587 ± 0.98[a]

(C)

Fig. 9

(A)

(B)

Fig. 10

Supplementary data

S1 Fig. Putative domain and motif structures of Se-5HTR. Putative seven transmembrane domains (TM1-TM7) are primarily marked by dark yellow bars and circles. Extracellular and cytosolic regions are denoted by green and light blue regions, respectively. Potential N-glycosylation sites and phosphorylation sites are marked by orange and red circles, respectively. Aspartic acid residue (dark blue circle) in TM3 and serine residue (light brown circle) in TM5 are putative residues that might chemically interact with 5-HT. The unique consensus sequence motif (PXXXWXPXF, dark brown circles) in aminergic receptors is conserved in TM6. The motif (NPXXY, dark blue circles) is conserved in TM7 like other GPCRs. Two possible post-translational palmitoylation cysteine residues (light yellow circles) and a PDZ-domain binding motif (ESFL, black circles) are also present in the C-terminal. Conserved motifs were determined using InterPro tool (https://www.ebi.ac.uk/interpro/) and Prosite (http://prosite.expasy.org/) whereas other residues and motifs were predicted using several tools from DTU bioinformatics.

S2 Fig. Potent screened chemicals from HB compounds with their chemical structures and respective median inhibitory concentrations (IC$_{50}$). HB chemicals were injected in different doses (0, 0.01, 0.1, 1, and 10 µg/larva) along with a fixed 5-HT concentration (1 µg/larva) and FITC-tagged bacteria (500 cells/larva). After 15 min of treatment, hemocytes from treated larvae were collected in ACB followed by phagocytosis assay as described above. Percentages of phagocytosis against HB chemical treatment with increasing concentrations were calculated. Their IC$_{50}$ values were determined using Probit analysis (https://probitanalysis.wordpress.com).

S3 Fig. Designing a potent chemical inhibitor from phenylehtylamide (PEA) derivatives.

Derivatives of PEA were tested for their nodulation inhibition percentages and sorted by their X and Y groups. Most potent residues inhibiting nodulation were selected and a hypothetical most potent PEA chemical was designed. (A) Core PEA structure with two variable hypothetical residues (X and Y). X belongs to the residue group attached with para position of the phenyl ring whereas Y belongs to the residue group linked to the amide group. (B) Comparative analysis between X residue groups with their mean percent inhibition of nodulation. (C) Comparative analysis between Y residue groups with their percent inhibition of nodulation. (D) A hypothetical PEA chemical compound structure having the most potent inhibition capability.

S4 Fig. Bacterial secondary metabolites (37 chemicals) derived from *Xenorhabdus* and *Photorhabdus*

S5 Fig. Phenylethylamide (PEA) derivatives (45 chemicals) based on HB 44, a bacterial metabolite

S6 Fig. Chemical synthesis of PhX ((*S*)-2-(1,4-dioxohexahydropyrrolo[1,2-*a*]pyrazin-2(*1H*)-yl)-*N*-(4-methoxyphenethyl)acetamide)

S1 Fig

Groups	ID	Structure	IC$_{50}$ (μM)
Phenylethylamide	HB 4		253.2 ± 38.0
	HB 5		217.8 ± 43.6
	HB 44		103.7 ± 18.7
Tryptamide	HB 23		103.9 ± 15.6
	HB 50		90.6 ± 16.3
	HB 531		124.9 ± 23.7
Xenortide	HB 30		59.1 ± 9.5
Xenocyloin	HB 45		82.1 ± 14.8
Nematophin	HB 223		134. 6 ± 22.9
GameXPeptide	HB 302		58.4 ± 11.7

S2 Fig

(A)

(B)

X	N	Inhibition of nodulation
4-OCH$_3$	2	80.9%
3,4-di-OCH$_3$	1	53.4%
4-Cl	3	49.6%
4-F	1	72.1%
4-CF$_3$	1	66.9%
4-H	2	62.7%

(C)

Y	Inhibition of nodulation
(X=4-Cl)	
	84.1%
	36.3%
	35.1%
(X=3,4-di-OMe)	
	77.7%
	77.3%
	53.4%
(X=4-F)	
	72.1%
(X=4-CF$_3$)	
	66.9%
(X=4-H)	
	64.1%
	61.4%

(D)

S3 Fig

HB compound	Structure	HB compound	Structure
HB 4		HB 250	
HB 5		HB 251	
HB 23		HB 254	
HB 30		HB 255	
HB 44		HB 261	
HB 45		HB 272	
HB 50		HB 280	
HB 51		HB 302	
HB 52		HB 314	
HB 55		HB 343	
HB 56		HB 351	
HB 58		HB 352	

HB 62

HB 64

HB 167

HB 169

HB 170

HB 171

HB 223

HB 354

HB 372

HB 378

HB 528

HB 531

HB 602

S4 Fig

PEA compound	Structure	PEA compound	Structure
Ph 1		Ph 24	
Ph 2		Ph 25	
Ph 3		Ph 26	
Ph 4		Ph 27	
Ph 5		Ph 28	
Ph 6		Ph 29	
Ph 7		Ph 30	
Ph 8		Ph 31	
Ph 9		Ph 32	
Ph 10		Ph 33	
Ph 11		Ph 34	
Ph 12		Ph 35	

Ph 13

Ph 14

Ph 15

Ph 16

Ph 17

Ph 18

Ph 19

Ph 20

Ph 21

Ph 22

Ph 23

Ph 36

Ph 37

Ph 38

Ph 39

Ph 40

Ph 41

Ph 42

Ph 43

Ph 44

Ph 45

S5 Fig

Step 1

Synthesis of (*S*)-(-)-*N*-(*t*-butoxycarbonyl)-prolylglycine methylester (**3**)

To a solution of (S)-(-)-N-(t-butoxycarbonyl)-proline **1** (5.00 g, 23.0 mmol) in CH$_2$Cl$_2$ (150 mL), amino acid methyl ester hydrochloride **2** (2.89 g, 23.0 mmol), 1-[3-(dimethylamino)propyl)]-3-ethylcarbodiimide hydrochloride (5.34 g, 28.0 mmol), and 1-hydroxybenzotriazole monohydrate (3.77 g, 28.0 mmol) triethylamine (6.50 mL, 46.6 mmol) were added and the reaction mixture was stirred for 24 h at room temperature. The solvent was removed under reduced pressure. The residue was taken up in ethyl acetate (200 mL) and washed successively with water (200 mL), 1N HCl aqueous solution (200 mL), and sat. NaHCO$_3$ aqueous solution (200 mL). The solvent was removed under reduced pressure to give (*S*)-(-)-*N*-(*t*-butoxycarbonyl)-prolylglycine methylester **3** as a white solid (4.82 g, 73%).

Step 2

Synthesis of (*S*)-Hexahydropyrrolo[1,2-*a*]pyrazine-1,4-dione (**5**)

To a solution of (*S*)-(-)-*N*-(*t*-Butoxycarbonyl)-prolylglycine methylester **3** (4.80 g, 16.8 mmol) in CH$_2$Cl$_2$ (84 mL), trifluoroacetic acid (18.7 mL, 252.0 mmol) was added and the solution was stirred at room temp for 2 hr. The solvent was removed under reduced pressure. The residue was dissolved in MeOH (84 mL) and treated with triethylamine (9.3 mL, 67.2 mmol). The reaction mixture was kept under reflux overnight. The solvent was removed under reduced pressure and the oily residue was redissolved in *i*-propanol to give (*S*)-hexahydropyrrolo[1,2-*a*]pyrazine-1,4-dione **5** as a white solid (2.0 g, 78%).

Step 3

Synthesis of 2-chloro-*N*-(4-methoxyphenethyl)acetamide (**7**)

To a solution of 2-chloroacetic acid **6** (3.00 g, 31.8 mmol) in CH$_2$Cl$_2$ (160 mL), 2-(4-methoxyphenyl)ethylamine **7** (4.6 mL, 31.8 mmol) and *N,N*-diisopropylethylamine (8.45 mL, 63.5 mmol) were added and the reaction mixture was stirred for 15 min at room temperature. After addition of 1-[3-(dimethylamino)propyl)]-3-ethylcarbodiimide hydrochloride (7.30 g, 38.1 mmol) and 1-hydroxybenzotriazole monohydrate (5.14 g, 38.1 mmol), the reaction mixture was stirred for 24 h at room temp. The reaction mixture was washed successively with 1 N HCl aqueous solution (160 mL) and sat. NaHCO$_3$ aqueous solution (160 mL). The organic layer was dried over MgSO$_4$, filtered, and concentrated. The residue was washed with diethyl ether to give 2-chloro-*N*-(4-methoxyphenethyl)acetamide **8** as a yellow solid (4.60 g, 63%).

Step 4

Synthesis of (*S*)-2-(1,4-dioxohexahydropyrrolo[1,2-*a*]pyrazin-2(*1H*)-yl)-*N*-(4-methoxyphenethyl)acetamide (**9**)

To a solution of (*S*)-hexahydropyrrolo[1,2-*a*]pyrazine-1,4-dione **5** (1.00 g, 6.40 mmol) in THF (32 mL), portionwise 60 wt% NaH (260 mg, 6.40 mmol) at 0°C was added and the reaction mixture was stirred 15 min at room temperature. 2-chloro-*N*-(4-methoxyphenethyl)acetamide **7** was added slowly to the reaction mixture then the mixture was stirred overnight at 65°C. The reaction was monitored by TLC. The reaction mixture was quenched with sat. NH$_4$Cl aqueous solution (100 mL) and extracted with EtOAc (2 X 100 mL). Combined organic layers were dried over MgSO4, filtered, and concentrated. The crude product was purified by silica-gel column chromatography (eluent: MeOH 10% in CH$_2$Cl$_2$) to give (*S*)-2-(1,4-dioxohexahydropyrrolo[1,2-*a*]pyrazin-2(*1H*)-yl)-*N*-(4-methoxyphenethyl)acetamide **9** as a yellow foam (1.74 g, 79%).

S6 Fig