

RESEARCH ARTICLE

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## ***Caesalpinia bonducella* Seeds Extracts are Non-toxic to the Gut Bacteria *Lactobacillus rhamnosus*, as Substantiated by *In vitro* and *In silico* Studies**

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### **Abstract**

The seed kernels of *Caesalpinia bonducella*, a traditional medicinal plant in India, are widely used to treat various disorders, including polycystic ovary syndrome. The seed kernel possesses anti-bacterial properties against many pathogenic bacteria. However, their impact on *Lactobacillus* spp., a prominent gram-positive gut bacterium, has not been studied till date. The present study employed both *in vitro* and *in silico* methods to illustrate the effect of seed extract of *C. bonducella* against *Lactobacillus rhamnosus* GG. For this, disc diffusion assay was performed with 100, 500, and 1000 µg/ml of aqueous and methanolic seed extract against *L. rhamnosus* and *E. coli*, and the zone of inhibition was measured. While both the extracts inhibited the growth of *E. coli*, it did not show any zone of inhibition against *L. rhamnosus*. The latter possess surface layer proteins, SlpX and SlpA, which prevented the influx of the phytochemicals of *C. bonducella*, as demonstrated by molecular docking using Autodock Vina. Docking results showed that the binding of the phytochemicals to the SlpX and SlpA proteins was not in the active pockets. These findings conclude that *C. bonducella* seed kernel extracts are safe against the gut bacteria *L. rhamnosus*.

**Keywords:** Antibacterial Activity, Molecular Docking, Polycystic Ovary Syndrome, Phytochemicals, Surface Layer Protein

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#These authors contributed equally to this work

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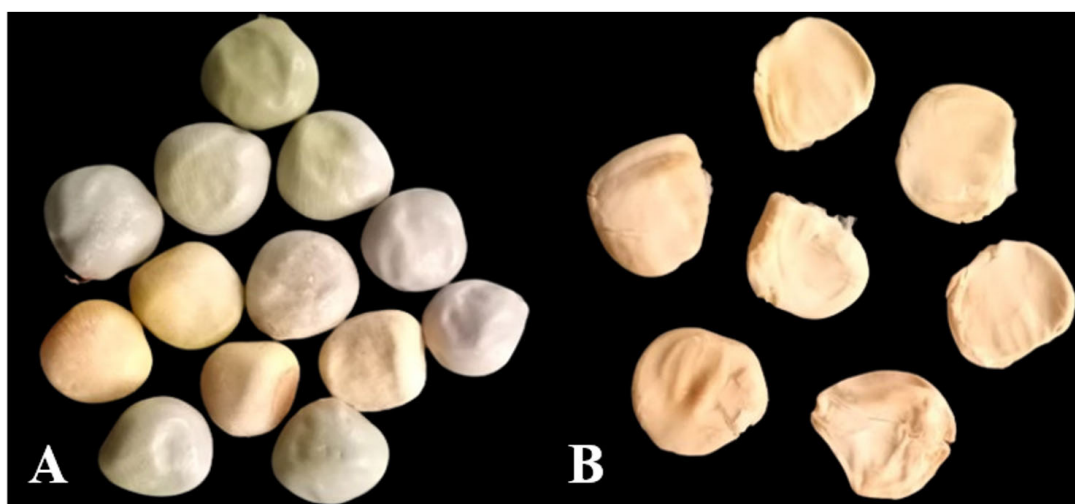
## INTRODUCTION

*Caesalpinia bonduc* (L.) Roxb., a traditional medicinal plant belonging to the family Caesalpiniaceae, is found in Africa and South Asia, particularly in the tropical regions of India. This plant possesses various secondary metabolites like alkaloids, flavonoids, glycosides, saponins, tannins, and triterpenoids. Major phytocompounds found in the seed kernels are bonducellin, citrulline,  $\alpha$ -caesalpin,  $\beta$ -caesalpin,  $\gamma$ -caesalpin, oleic acid, palmitic acid, stearic acid, aspartic acid, and arginine.<sup>1-3</sup> *C. bonducella* seed kernel (Figure 1) has numerous therapeutic properties, including anti-bacterial, anti-pyretic, anti-diuretic, anthelmintic, antioxidant, analgesic, anti-diarrhoeal, anti-anaphylactic, anti-asthmatic, anti-viral, anti-amoebic, and anti-cancer. It also possesses anti-diabetic, anti-inflammatory, anti-estrogenic, and anti-androgenic properties; hence, it is widely used in the treatment of polycystic ovary syndrome (PCOS) in Indian women.<sup>4-9</sup>

PCOS is an endocrine disorder that affects women of childbearing age.<sup>10</sup> Research on human trials has revealed that there is a significant change in the taxonomic diversity of gut bacteria in PCOS patients.<sup>11</sup> It has been shown that dysbiosis in the gut is directly related to PCOS and obesity.<sup>12</sup> Alternative medicine for PCOS is popular in India, and *C. bonducella* seed kernel with equal parts of

pepper mixed with ghee or honey for 48 days is prescribed by Siddha practitioners. Although there is a plethora of evidence that *C. bonducella* seeds are toxic to human pathogens like *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Mycobacterium smegmatis*, *Salmonella typhi*, *Escherichia coli*, *Proteus mirabilis*, *Klebsiella pneumoniae*, and *Vibrio cholerae*,<sup>13-15</sup> its effect on probiotic gut bacteria has not been investigated.

The gut microbiota is a complex biological community, comprising more than thousand microbial species.<sup>16</sup> The microbiota in our gut typically sustains our health, which ensures resistance to pathogen colonization, produces short-chain fatty acids (SCFAs) that fuel epithelial cells, regulates gene expression, and produces vitamins and toxins, in addition to regulating cholesterol metabolism and bile deconjugation, all of which are vital functions for human existence.<sup>17</sup> The gut microbiota is composed primarily of the phyla Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria, Fusobacteria, and Verrucomicrobia. Among these phyla, 90% are composed of Bacteroidetes and Firmicutes. More than two hundred distinct genera comprise the Firmicutes phylum, including *Ruminococcus*, *Bacillus*, *Lactobacillus*, and *Clostridium*.<sup>18</sup> The most significant probiotic bacteria in the gut microbiome belong to the genus *Lactobacillus*, which is a member of the phylum Firmicutes.



**Figure 1.** A) *Caesalpinia bonducella* seed; B) *Caesalpinia bonducella* seed kernels

*Lactobacillus*, a frequently consumed probiotic, makes up 6% of the total bacteria in the human duodenum and 0.3% in the human colon.<sup>19</sup> It kills the pathogens by producing lactic acid, acetic acid, propionic acid, bacteriocins, and reactive functional niches in the gut.<sup>20</sup>

*Lactobacillus* species also influence the functions and behaviors associated with the central nervous system, where species like *Lactobacillus helveticus* NS8 reduce depression, anxiety, and cognitive dysfunction and increase serotonin and neuropeptides in the hippocampus.<sup>21</sup> *Lactobacillus rhamnosus* regulates the GABA receptors that reduce anxiety and depression.<sup>22</sup> Dysbiosis in the gut microbiota results in the alteration of the beneficial and harmful bacterial ratio and is associated with many diseases and disorders, especially obesity, insulin resistance, and diabetes, that are directly associated with PCOS.<sup>23</sup> To balance gut barrier integrity and mucosal barrier defense and improve host immunological responses, these gut-dwelling *Lactobacillus* species converse not only with one another but also with the gut epithelial lining.<sup>24</sup> Hence, it is essential to know if the phytochemicals consumed for treating various disorders alter the gut bacterial community.

In this study, we investigated the effects of methanolic and aqueous extracts of *C. bonducella* seed kernels on *L. rhamnosus*, the most prevalent gut bacteria. Further, we performed molecular docking of the bioactive compounds in the seed kernel against the surface layer proteins of *Lactobacillus* spp., (SlpX and SlpA), as these proteins play a crucial role in protecting the bacteria from the outer environment.

## MATERIALS AND METHODS

### Bacterial culture

Two strains of bacteria were used in this research. *E. coli* TOP10 M15 was procured from the Microbial Type Culture Collection (MTCC). *L. rhamnosus* GG was isolated from kimchi (fortified food) by spread-plating the serially diluted food powder. Both cultures were validated using 16S rDNA sequencing. The forward primer -5'AGGCTACGCTAACCGATGTC 3' and reverse primer -5'AACGGCATACATTAACGCGC 3' were used in the 20 µL reaction containing 100 ng of isolated

genomic DNA as a template, two primers (10 pmol each) described by Scarpellini *et al.*<sup>25</sup>, 0.2 mM of dNTPs, 6.0 units of Taq polymerase, and 10 x buffer with 3 mM MgCl<sub>2</sub>. The reaction protocol was: 94°C for 5 mins, 30 cycles of 94°C for 1 min, 58°C for 2 mins, 72°C for 2 min, and then 72°C for 10 mins, carried out in a thermal cycler (Aligent Sure cycler 8800). Purified PCR products of about 1500 bp were sequenced, and BLAST was performed to identify the strains. All strains were stored at -20°C in glycerol until use.

### Composition of culture medium

*E. coli* TOP10 M15 was grown in Luria-Bertani broth (LB) agar composed of tryptone (10 g/L), yeast extract (5 g/L), sodium chloride (10 g/L), and agar (15 g/L) with a pH adjusted to 7.5 ± 0.2 and incubated at 37°C for 24 hours. *L. rhamnosus* GG was grown in De Man-Rogosa-Sharpe (MRS) agar, composed of proteose peptone (10 g/L), HM peptone B (10 g/L), yeast extract (5 g/L), dextrose (glucose) (20 g/L), polysorbate 80 (Tween 80) (1 g/L), ammonium citrate (2 g/L), sodium acetate (5 g/L), magnesium sulfate (0.1 g/L), manganese (II) sulfate (0.05 g/L), di-potassium hydrogen orthophosphate (2 g/L), agar (12 g/L), adjusted to pH 6.5 ± 0.2, and incubated at 37°C for 48 hours.

### Seed extraction

Fresh seeds of *C. bonducella* Roxb. were collected from the National Institute of Siddha, Chennai, India (11° 15' 42.9984 N; 78° 23' 8.5668 E) and stored at 4°C. Prof. P. Jayaraman, a taxonomist from Presidency College in Chennai, India, validated the seeds. The collected seeds were shade-dried for 2 weeks, and the seed coats were broken to collect the seed kernels, which were shade-dried for 10 more days and pulverized into a fine powder. The powder was then air-dried for 30 minutes. About 5 g of the seed powder was measured and dissolved in 50 ml of methanol and water, sealed, and incubated for 12 hours at 28 ± 2°C in a shaking incubator at 125 rpm. After 12 hours, the entire mixture was filtered using Whatman filter paper grade 1 (90 mm), and the same process was repeated for 3 subsequent days to extract most of the active ingredients. The methanol and aqueous extracts were dried and stored at 4°C until further analysis.

### Disc diffusion assay

The effect of methanol and aqueous crude extracts of the seed kernel (100, 500, and 1000 µg/ml) were screened against *L. rhamnosus* GG and *E. coli* using the disc diffusion method. Sterile discs (6 mm diameter, Himedia) were saturated with the above-mentioned concentrations of the extracts and placed on the MRS agar and LB agar medium, uniformly spread with *L. rhamnosus* GG, and *E. coli*, respectively. The inoculum was approximately  $10^6$  cfu/ml. A standard antibiotic (Ampicillin, 30 µg/disc) was imbedded in the sterile disc and was used as a positive control. The plates were then incubated at 4°C for one hour, which is efficient for the diffusion of the test material. Then the plates were incubated at 37°C and checked for zones of inhibition after 24 and 48 hours.

### Selection and preparation of target proteins

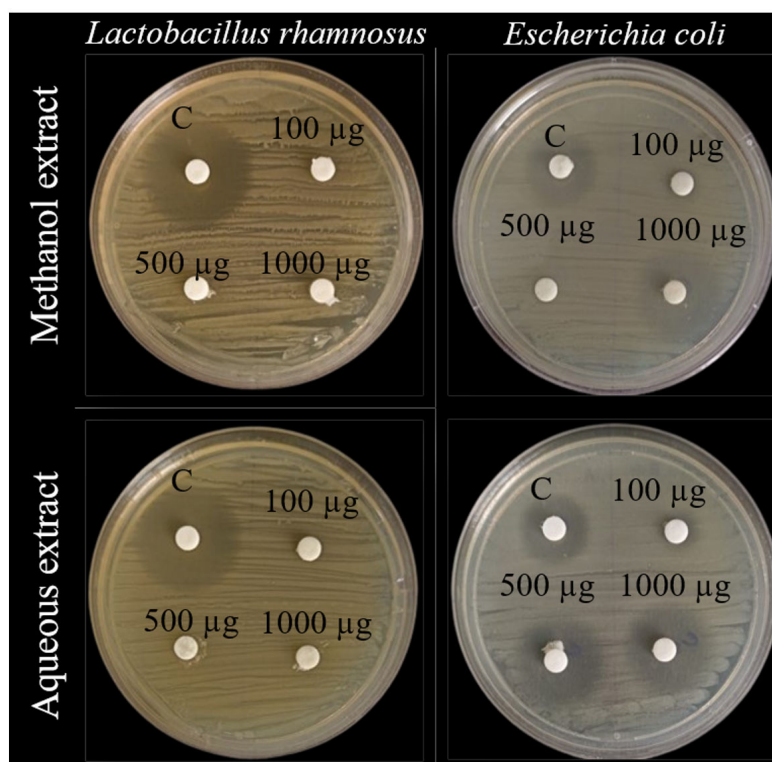
Surface layer proteins play a crucial role in the communication between the cell and the environment. Surface layer proteins SlpX and SlpA,

which are essential for protecting *Lactobacillus* spp. against the external environment, were selected as target proteins for docking against the phytochemicals of *C. bonducella* seeds.

The three-dimensional structures of the surface layer proteins, SlpX (PDB ID: 7QFJ) with a resolution of 2.50Å determined with X-ray diffraction and SlpA (PDB ID: 7QFG) with a resolution of 1.65Å determined with X-ray diffraction were obtained from the protein data bank (PDB) (<https://www.rcsb.org/>). Any associated groups, including  $\text{PO}_4^{2-}$  and water molecules, were eliminated from the proteins in PyMol software, and the protein structures were saved in pdbqt format for docking.<sup>26</sup> The binding pockets of the proteins were predicted by an online tool CASTp (<http://sts.bioe.uic.edu/castp/>) by uploading the protein pdb files and setting the radius to 1.4Å.<sup>27</sup>

### Selection and preparation of ligands

A comprehensive literature search was



**Figure 2.** *In-vitro* disc diffusion assay for aqueous and methanol extracts of *Caesalpinia bonducella* seed kernel. The zones of inhibition are observed on the cultured plates

conducted to gain insights into the bioactive compounds that are found in *C. bonducella* seed kernels. All relevant information was gathered from well-known databases, such as PubMed, Scopus, Google Scholar, and EMBASE; associated articles were located by looking up their references. Bioactive compounds of *C. bonducella*, secondary metabolites, bonduc nut, LC-MS, GC-MS, and additional pertinent terms were the keywords used in the literature search. The search did not exclude any specific region, period, or language. The structures of the compounds retrieved from the literature were obtained from the PubChem database (<https://pubchem.ncbi.nlm.nih.gov>). The structures were uploaded to PyRx and converted from the spatial data file (SDF) to PDB format using Open Babel (<https://www.cheminfo.org/>), an open-source software. The 2D structure of the derived bioactive compounds was drawn using ChemSketch version 2022.1.2 (<https://www.acdlabs.com/>). The Universal Force Field was applied to all the selected ligands before the molecular docking procedure.

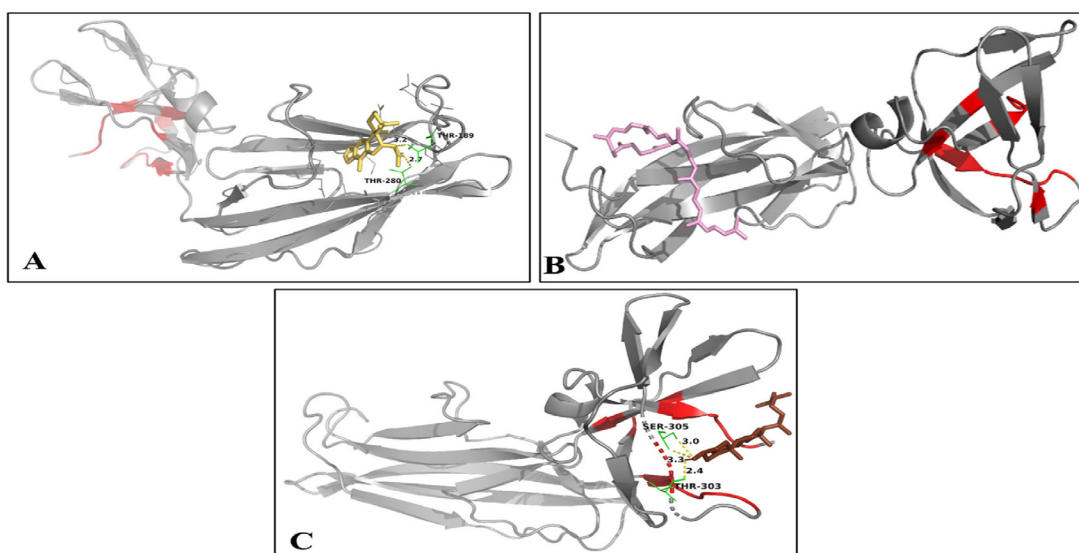
### Molecular docking

For molecular docking, the National Biomedical Computation Resources PyRx open-source software for virtual screening, which

incorporates Autodock Vina, was utilized. The Vina Wizard software was utilized to bind two different surface layer proteins (SlpA and SlpX) against 54 compounds from the seeds. The docking site of SlpA was defined at the active site with a grid box size of 80x80x80, a grid center of -26.055Å, -6.121Å, 33.527Å, grid space of 0.375Å. Similarly, for SlpX, a grid box size of 80x80x80, a grid center of 10.524Å, 0.441Å, 7.755Å, grid space of 0.375Å. The binding energy scores were used to predict the efficiency with which the compounds would interact with the target proteins.<sup>26</sup> Visualization of the docked protein-ligand complex was processed by PyMOL 2.3 software.

**Table 1.** Effect of the seed extracts against *E. coli* and *L. rhamnosus*

Sample	Concen. (µg/disc)	<i>E. coli</i> (mm)	<i>L. rhamnosus</i> (mm)
Ampicillin	30	16 ± 1	25 ± 2
Methanolic extract	100	-	-
	500	-	-
	1000	24 ± 1	-
Aqueous extract	100	10 ± 1	-
	500	22 ± 1	-
	1000	23 ± 2	-



**Figure 3.** Binding of protein SlpX with compound A) Cassane furano-diterpene B) Lycopene C) Campesterol. (Red indicates active sites of protein; yellow indicates hydrogen bond; grey indicates the protein; yellow indicates Cassane furano-diterpene; pink indicates Lycopene; brown indicates Campesterol)



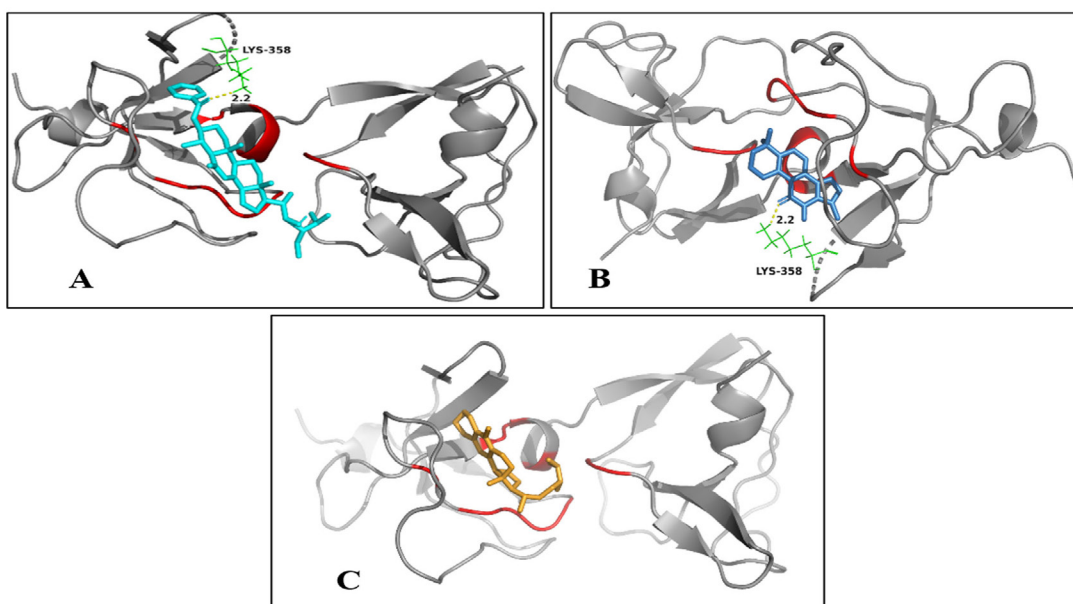
**Table 2.** The active pockets of the proteins SlpA and SlpX predicted with CASTp tool

Protein	Area (Å <sup>2</sup> )	Volume (Å <sup>3</sup> )	Binding pockets
SlpA (PDB:7QFG)	64.462	50.394	His323, Asn324, Ala325, Tyr326, Tyr328, Asn375, Ala377, Asn378, Gly415, Ala416
SlpX (PDB:7QFJ)	134.916	69.305	Gly294, Thr295, Leu296, Tyr297, Gly298, Asn299, Ile304, Val329, Ser342, Val344, Val359, Lys360, Thy361, Ser362

## RESULTS AND DISCUSSION


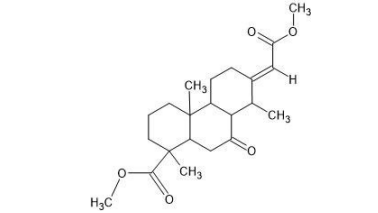

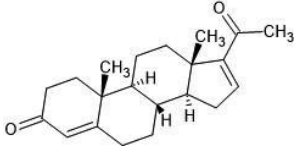
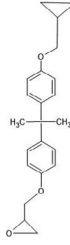
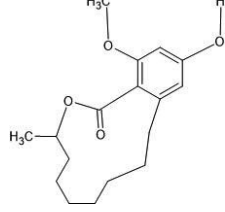
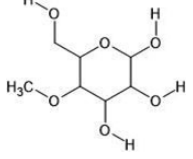
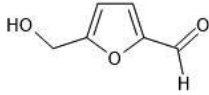
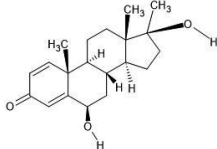
*C. bonducella* has been widely used to manage disorders like PCOS, Diabetes mellitus, insulin resistance, bacterial infections, diarrhea, and urinary tract infections. Prior research has examined the seed kernel extract's ability to combat pathogenic bacteria, including gram-positive bacteria like *Bacillus subtilis*, as well as gram-negative bacteria such as *P. aeruginosa*, *E. coli*, and *P. mirabilis*.<sup>28,29</sup> However, the impact of the seed extract on the human gut bacteria has not been studied yet. Our study focused on the effect of *C. bonducella* seed against *L. rhamnosus* GG, the most prominent bacterium in the human gut.

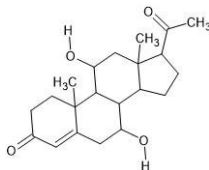
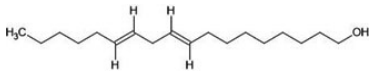
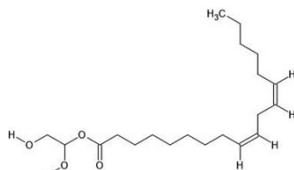
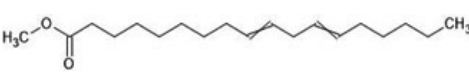
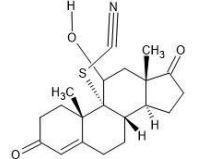
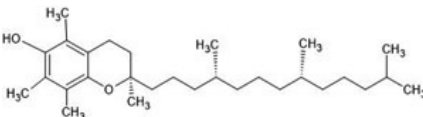
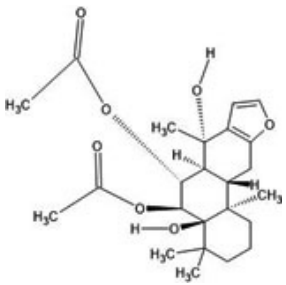
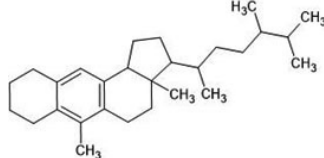
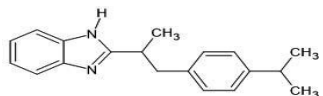
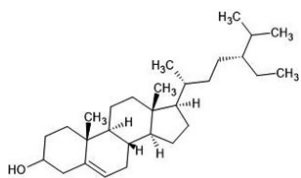
The antibacterial assay was performed for *L. rhamnosus* GG and *E. coli* with 3 different concentrations of the methanolic and aqueous extracts of *C. bonducella* seed kernel (100, 500, and 1000 µg), with ampicillin (30 µg) as the positive control (Table 1). No zone of inhibition was observed for *L. rhamnosus* GG in both methanolic and aqueous extracts, whereas *E. coli* showed a distinct zone of inhibition for 1000 µg of methanolic extract and all 3 concentrations of aqueous extract, with an increase in the zone size in proportion to the concentration of the extracts (Figure 2). This states that growth of *L. rhamnosus* GG is not affected by both the seed extracts, whereas that of *E. coli* is affected.



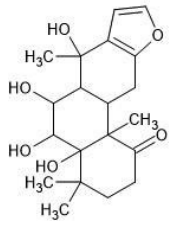
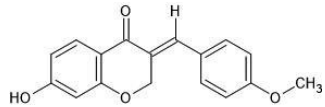
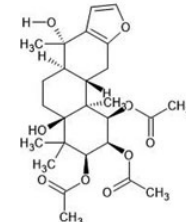
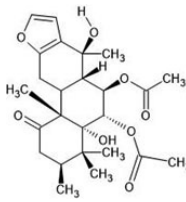
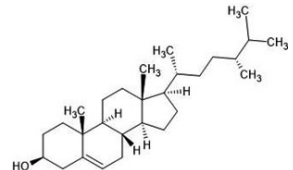
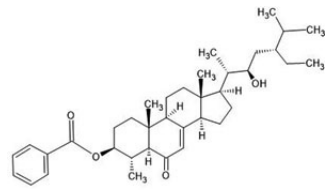
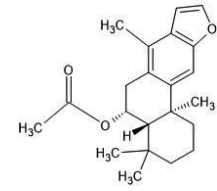
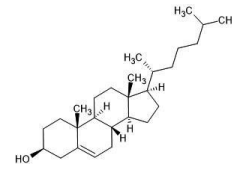
**Figure 4.** Binding of Protein SlpA with Compounds A) Carpesterol, B) Tanshinone IIA, and C) Anthraegostatrine. (Red indicates active sites of protein; yellow indicates hydrogen bond; gray indicates the protein; turquoise indicates carpesterol; blue indicates tanshinone IIA; orange indicates anthraegostatrine)

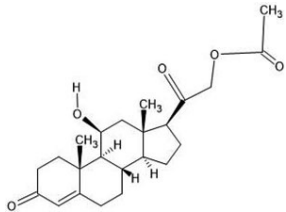
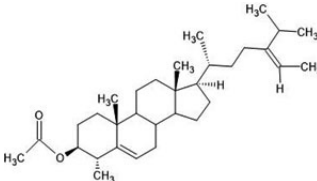
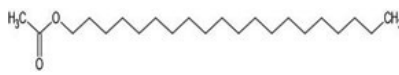
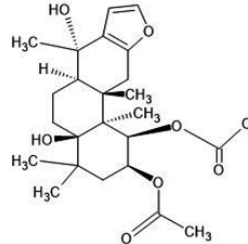
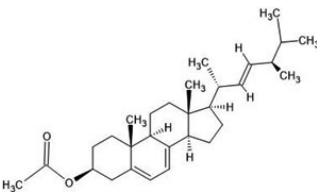
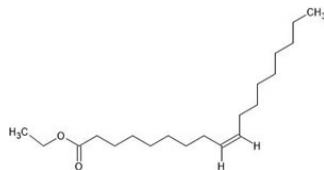
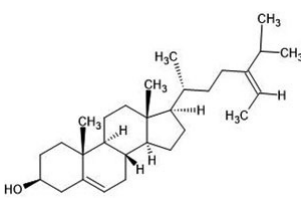
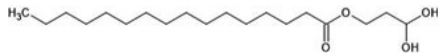
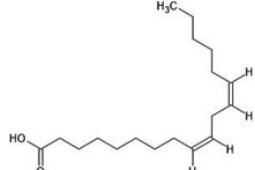
**Table 3.** Binding affinity of 54 phytocompounds of *Caesalpinia bonducella* seeds against SlpX and SlpA

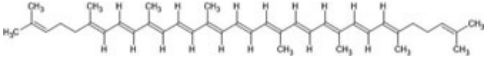
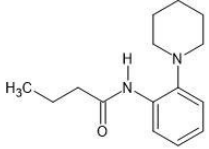
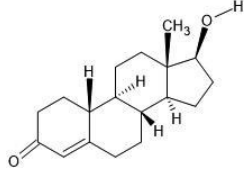

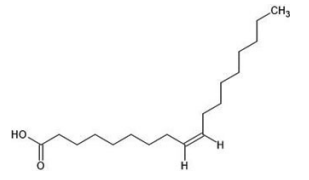
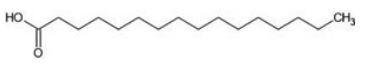
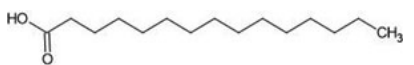
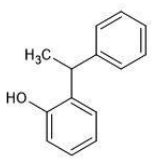
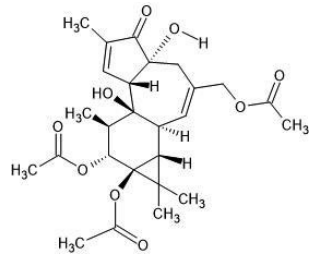
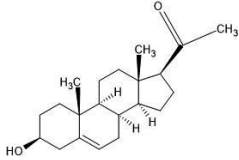
No.	Compound Name	Structure	Binding affinity	
			SlpX	SlpA
1.	1-undecanol (8184)		-4.1	-4.3
2.	1-Phenanthrenecarboxylic acid tetradecahydro 7-(2-methoxy-2-oxoethylidene)-1,4a,8-trimethyl-9-oxo-methyl ester (5379250)		-6.5	-4.5
3.	15,17,19,21-Hexatriacontatetrayne (537054)		-3.3	-4.1
4.	16-dehydroprogesterone (101964)		-6.3	-7.1
5.	2,4 bis (1 methyl 1 phenyl ethyl phenol (102877)		-6.4	-6.9
6.	2-Hydroxy-4-methoxy-7-methyl-7,8,9,10,11,12,13,14-octahydro-6-oxabenzocyclododecen-5-one (602765)		-6.7	-6.2
7.	4-o-methylmannose (345716)		-4.9	-4.9
8.	5-hydroxymethyl-furfural (237332)		-4.3	-4.5
9.	6b-Hydroxymethandienone (13241205)		-6.6	-7

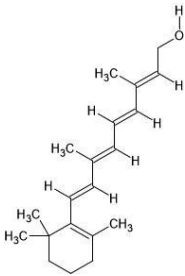
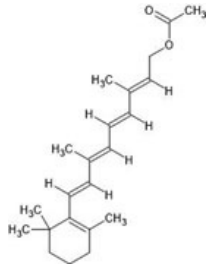
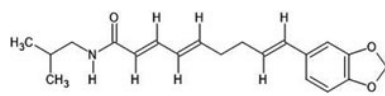
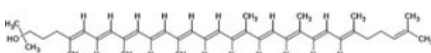
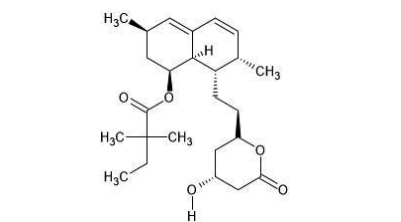
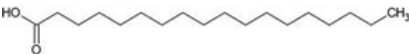
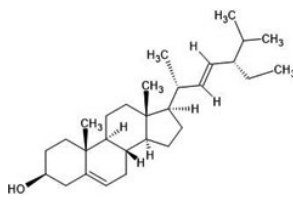
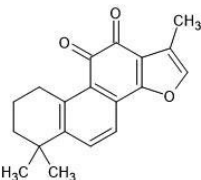
10.	7,11-Dihydroxyprogesterone (539326)		-6.9	-6.6
11.	9,12-octadecadien-1-ol (5462912)		-3.9	-5
12.	9,12-Octadecadienoic acid (Z, Z) 2-hydroxy-1-(hydroxymethyl) ethyl ester (5365676)		-4.1	-4.4
13.	9,12-Octadecadienoic acid methyl ester (8203)		-4.5	-5.2
14.	Androst-4-en-11-ol-3,17-dione- 9-thiocyanato- (91694000)		-6.7	-4.6
15.	Alpha-tocopherol (57393415)		-5	-6.4
16.	Alpha-caesalpin (21679154)		-6.4	-6.2
17.	Anthraegostatrine (313024)		-6.2	-7.3
18.	Benzimidazole 2-[1-(4-isopropylbenzyl) ethyl] (589515)		-6.6	-7.1
19.	Beta-sitosterol (222284)		-6.2	-6.2



20.	Beta-caesalpin (71440416)		-6.6	-6.5
21.	Bonducellin (14079439)		-6.1	-6.5
22.	Caesalpin F (101937720)		-5.7	-6.4
23.	Caesalpinin (15329770)		-6.3	-6.5
24.	Campesterol (173183)		-7	-6.7
25.	Carpesterol (21155918)		-6.7	-8.1
26.	Cassane furano-diterpenes (102286656)		-7.3	-7.2
27.	Cholesterol (5997)		-6	-6.6

28.	Corticosterone 21 acetate (255846)		-6.4	-6.3
29.	D5-avenasterol (91753899)		-6.5	-6.5
30.	Eicosyl acetate (110347)		-3.5	-3.7
31.	Epsilon-caesalpin (21679153)		-6.2	-7.2
32.	Ergosterol (6436903)		-6.9	-7
33.	Ethyl oleate (5363269)		-3.8	-4
34.	Fucosterol (5281328)		-6.7	-6.6
35.	Hexadecanoic_acid_2-hydroxy-1-(hydroxymethyl)_ethyl_ester (129853056)		-4.5	-4.1
36.	Linolei acid (5280450)		-4.7	-5.3

37.	Lycopene (446925)		-7.2	-6.7
38.	N-nonadecanol-1 (890281)		-4.4	-3.6
39.	Nandrolone (9904)		-6.5	-6.8
40.	Octacosane (12408)		-3.8	-3.3
41.	Oleic acid (445639)		-4.2	-4.2
42.	Palmitic acid (985)		-4.2	-4.5
43.	Pentadecanoic acid (13849)		-3.9	-3.8
44.	Phenol,2_(1-phenyl-ethyl) (95322)		-6.8	-7
45.	Phorbol 12,13,20 triacetate (499954)		-6	-6.4
46.	Pregnenolone (8955)		-6.2	-6.8

47.	Retinol (445354)		-6.2	-6.4
48.	Retinyl acetate (638034)		-6.3	-6.1
49.	Retrofractamide A (11012859)		-5.7	-6
50.	Rhodopin (5365880)		-5.1	-4.9
51.	Simvastatin (54454)		-6.6	-7.3
52.	Stearic acid (5281)		-4.1	-4.9
53.	Stigmasterol (5280794)		-6.4	-6.7
54.	Tanshinone IIA (164676)		-6.7	-7.8

The result shows that the seed kernel does not affect the growth of *L. rhamnosus* while inhibiting that of *E. coli*. We speculated that the exclusive surface layer proteins present

in *Lactobacillus* species may be responsible for *L. rhamnosus* GG's protection against the phytochemicals. These surface layer proteins have been found in many *Lactobacillus* spp.,

including *L. brevis*, *L. buchneri*, *L. helveticus*, *L. hilgardii*, *L. acidophilus*, *L. amylovorus*, *L. crispatus*, *L. gallinarum*, and *L. rhamnosus*.<sup>30,31</sup> Numerous strains of *Lactobacillus* are capable of inhibiting pathogen adhesion to the intestinal epithelial cells and mucus with the help of their surface layer proteins, SlpX and SlpA, with molecular weights ranging from 30-130 kDa.<sup>30,32</sup> These proteins also assist these gut microbes to survive in a hostile gut environment that is rich in digestive enzymes and bile salts.<sup>33</sup>

*In silico* analyses were performed to investigate if the phytochemicals bind to the active binding pockets of the Slps. For this, the 3D structure of the two Slps were derived from the Protein Data Bank and was used to predict the binding pocket with the CASTp tool. The tool predicted 10 amino acid sites for SlpA protein and 14 amino acid sites for SlpX as binding pockets (Table 2). These two proteins were docked with the 54 phytochemicals in the seed kernel of *C. bonducella* that were retrieved from the previously reported literature and their binding affinity is listed in Table 3.

SlpA showed a higher binding affinity with compounds, including Carpesterol, tanshinone IIA, and anthraegostatine, with a binding score of -8.1, -7.8, and -7.3 kcal/mol, respectively. The hydrogen bond interaction between the complex of both Carpesterol and tanshinone IIA with SlpA is at Lys358 with a length of 2.2Å, whereas anthraegostatine did not show any hydrogen bond interaction with the protein (Figure 3). SlpX showed a higher binding affinity with compounds cassane furano-diterpenes, lycopene, and campesterol, with binding scores of -7.3, -7.2, and -7 kcal/mol, respectively. The hydrogen bond interaction between the complexes of cassane furano-diterpenes is with Thr189 and Thr280, with a length of 3.2Å and 2.7Å, respectively. Campesterol showed two hydrogen bond interactions at Thr303 with a length of 2.4Å and Ser305 with a length of 3.0Å, whereas lycopene had no hydrogen bond interaction with SlpX (Figure 4).

Although these compounds showed higher binding scores with the Slp proteins, their interaction with the Slp amino acid residues did not match the amino acid residues at the active binding pocket (Table 2). Thus, it shows that

the phytochemicals do not bind tightly to the Slps and are hence prevented from entering the bacterial cell.

*E. coli* lacks these proteins and may be susceptible to the phytochemicals, thereby inhibiting its growth. Likewise, *Clostridium* spp., having huge potential as a probiotic by producing metabolites including secondary bile acids, butyrate, acetic acid, and propionic acid, helps in strengthening and energizing intestinal epithelial cells and intestinal barrier,<sup>34</sup> and *Enterococcus* spp., produces small peptides that are bacteriocin, having antimicrobial properties inhibiting the growth of *E. coli*, *P. aeruginosa*, *L. monocytogenes*, and *V. cholerae* in the human gut.<sup>35</sup> These *Clostridium* spp. and *Enterococcus* spp. families in the gut also possess Slp<sup>35,36</sup> that the seed's phytochemicals may not kill, and thus the gut microbiota will not be disturbed by consuming the seed kernel as a medicine. However, pathogenic bacteria like *S. aureus*, *P. aeruginosa*, *M. smegmatis*, *S. typhi*, *P. mirabilis*, *K. pneumoniae*, and *V. cholerae* lack Slps, making them vulnerable to and inhibited by the phytochemicals. Our finding put forth that *C. bonducella* seed extract affects those bacteria without Slp proteins and is safe against probiotic gut bacteria.

### Limitations of this study

The study's scope is confined to only *L. rhamnosus*, hence, requires further validation with other gut bacteria to ascertain the safe use of *C. bonducella* seed for various disorders.

### CONCLUSION

*Caesalpinia bonducella* seeds are used to treat various disorders, notably fever, edema, malaria, diabetes, and PCOS, and are shown to possess antibacterial properties against several pathogens. *Lactobacillus* is a prominent probiotic bacterium colonizing the human intestinal tract and plays a crucial role in preventing intestinal damage caused by certain bacterial infections. In our research, the impact of the seed extract of *C. bonducella* against *Lactobacillus rhamnosus* was tested where seed extract did not hinder the growth of the bacteria. Molecular docking of the surface layer proteins, SlpX and SlpA, to the phytochemicals of *C. bonducella* seed kernel,

revealed no binding to active binding pockets. This suggests that *C. bonducella* seed extracts are not toxic to *Lactobacillus* spp., which is prevalent in the gut microbiome.

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None.

## CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

## AUTHORS' CONTRIBUTION

BU contributed to the study's conception and design. AP and MK contributed equally to material preparation, data collection, and analysis. SMH performed molecular docking studies. AP and MK wrote the manuscript. BU edited the manuscript. All authors read and approved the final manuscript for publication.

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## DATA AVAILABILITY

All datasets generated or analyzed during this study are included in the manuscript.

## ETHICS STATEMENT

This article does not contain any studies on human participants or animals performed by any of the authors.

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