The antiplasmodial and spleen protective role of crude *Indigofera oblongifolia* leaf extract traditionally used in the treatment of malaria in Saudi Arabia

Mohamed A Dkhil\(^1\)\(^2\), Mahmoud Y Lubbad\(^1\)\(^3\), Esam M Al-Shaebi\(^1\), Denis Delic\(^4\), Saleh Al-Quraishy\(^1\)

\(^1\)Department of Zoology, College of Science, King Saud University, Riyadh, Saudi Arabia; \(^2\)Department of Zoology and Entomology, Faculty of Science, Helwan University, Helwan, Egypt; \(^3\)General Directorate of Environmental and Occupational Health, Public Health Agency, Ministry of Health, Riyadh, Saudi Arabia; \(^4\)Boehringer-Ingelheim Pharma, Biberach, Germany

Abstract: Malaria is one of the most serious natural hazards faced by human society. Although plant leaves of *Indigofera oblongifolia* have been used for the treatment of malaria in Saudi Arabian society, there is no laboratory-based evidence for the effectiveness and safety of the plant. This study therefore was designed to investigate the antimalarial and spleen protective activity of *I. oblongifolia* leaf extract (IOLE) in mice. Three doses (100, 200 and 300 mg/kg) of IOLE were used to treat mice infected with *Plasmodium chabaudi*-parasitized erythrocytes. The suppressive effect produced by the 100 mg/kg dose on parasitemia was highly significant compared to the infected nontreated group. This dose was also able to repair the change in the thickness of the mice spleen and significantly lower the number of apoptotic cells in the spleen. Moreover, *I. oblongifolia* also altered gene expression in the infected spleen. On day 7 postinfection, the mRNA expression of six genes – with immune response functions – was upregulated by more than twofold, while that of 24 other genes was downregulated. Among the differentially up- and downregulated genes under the effect of IOLE, we quantified the expression of *Ccl8, Saa3, Cd209a*, and *Cd209b* mRNAs. The expression data, determined by microarrays, were largely consistent with the expression analyses we performed with several arbitrarily selected genes using quantitative polymerase chain reaction (PCR). Based on our results, *I. oblongifolia* exhibits antimalarial activity and could protect the spleen from *P. chabaudi*-induced injury.

Keywords: spleen, malaria, *Indigofera oblongifolia*, apoptosis, microarray

Introduction

Malaria is a life-threatening disease caused by parasites that are transmitted to people through the bites of infected mosquitoes.\(^1\) According to the latest estimates by the World Health Organization, there were approximately 198 million cases of malaria in 2013 and an estimated 584,000 deaths.\(^2\)

Although malaria can be treated with numerous commercially available antimalarial drugs, drug resistance is a continual problem. Indeed, resistance against currently used drugs is increasingly being reported.\(^3\) Parasite resistance results in a delayed or incomplete clearance of parasites from the patient’s blood when the person is being treated with an antimalarial agent.\(^4\) Novel agents possessing antimalarial activity, and that are safe for use in humans, are therefore urgently required.

People have used medicinal plants for the treatment of malaria since ancient times, and such plants remain promising sources for identifying candidates for novel anti-malaria agents.\(^5,6\) These products do not necessarily target only the plasmodium, but may also show organ-protective properties in the plasmodium-infected hosts.\(^7,8\)
For example, our recent work has showed that pomegranate peel extract and berberine could be used as antimalarial and hepatoprotective agents.7

In the case of Saudi Arabia, Indigofera oblongifolia (family Fabaceae) is cultivated in areas with a high prevalence of malaria, such as Jazan and Nagran.5 Despite the fact that this plant is used informally for the treatment of malaria in Saudi Arabian society, there is no laboratory-based evidence for its effectiveness or safety. This study was therefore designed to investigate the antimalarial and spleen protective activity of I. oblongifolia leaf extract (IOLE) in a murine model.

Materials and methods
Preparation of I. oblongifolia leaf extract
The leaves of I. oblongifolia were collected from Jazan, Saudi Arabia. The plant was identified by Dr Pandalayil (Department of Botany, College of Science, King Saud University). The leaves were air dried and then ground into a powder. The constituents of the powdered leaves were extracted with 70% methanol.9

Animals
Nine- to twelve-week-old female C57BL/6 mice were obtained from the animal facility of the research center at King Faisal Specialist Hospital in Riyadh, Saudi Arabia. The mice were bred under specified pathogen-free conditions and fed a standard diet and water ad libitum. The experiments were approved by the state authorities at King Saud University for the project number PRG-02, and followed Saudi Arabian rules on animal protection.

Mice infection
Following the method of Wunderlich et al.,10 female mice were inoculated at weekly intervals with blood-stage infections of Plasmodium chabaudi by intraperitoneally injecting them with 1×106 P. chabaudi-parasitized erythrocytes. Parasitemia was detected in Giemsa-stained smears from tail blood. Cell numbers were counted in a Neubauer chamber.

Experimental design
Animals were divided into five groups with ten mice in each group. The first group, with uninfected mice, served as a vehicle control. This group was gavaged only with 100 µL distilled water. The second, third, fourth, and fifth groups were intraperitoneally infected with 1×106 P. chabaudi-infected erythrocytes, as described earlier. Then, after 60 minutes, mice of the third, fourth, and fifth groups were gavaged with 100 µL of IOLE at a dosage of 100, 200, and 300 mg/kg body weight of IOLE, respectively, once daily for 7 days. The average percentage of suppression by IOLE was calculated using the formula:

\[
\text{%suppression} = \frac{\text{Parasitemia in negative control} - \text{Parasitemia in test group}}{\text{Parasitemia in negative control}} \times 100
\]

Preparation of spleen tissue
Both noninfected and P. chabaudi-infected spleens were aseptically removed from mice on day 7 pi. Half of the spleen was fixed in 10% neutral buffered formalin for histological and immune histochemical investigations, and the other half was kept in RNAlater storage solution (Qiagen, Hilden, Germany) for the molecular study.

Spleen index and capsule thickness
The spleen index was determined as the ratio of the weight of the spleen to the weight of the mouse. To evaluate the spleen capsule thickness, the paraffin sections of the spleen were prepared according to standard protocols.11 Sections with a thickness of 5 µm were stained with hematoxylin and eosin. Capsule thickness was determined in five different mice spleen sections from each group.

TUNEL apoptosis detection
Terminal deoxynucleotidyl-transferase-mediated dUTP nick end labeling assay (TUNEL) staining was performed using a TUNEL Apoptosis Detection Kit (GenScript, Piscataway, NJ, USA) according to the manufacturer’s protocol. Briefly, sections of paraffin-embedded spleens were deparaffinized and then rehydrated in graded ethanol solutions before digestion with proteinase K. Slides were mounted with 4′,6-diamidino-2-phenylindole. Nuclei of the apoptotic cells appeared dark brown. Sections were counterstained with hematoxylin. The number of TUNEL-positive cells was counted in ten different areas per section.

RNA isolation and quality testing
Total RNA was isolated with TRizol (Qiagen). The quality and integrity of RNA were determined using the Agilent RNA 6000 Nano Kit on the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). RNA was quantified by measuring the absorbance at 260 nm on the ND-1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA).12
Labeling of RNA
Equal amounts of RNA prepared from individual spleen tissues of three mice were pooled. Labeling was performed as detailed in the protocol for the One-Color Microarray-Based Gene Expression Analysis (version 5.5, part number G4140-90050). Briefly, 1 µg of total RNA was used for amplification and labeling using the Agilent Low RNA Input Linear Amp Kit (Agilent Technologies) in the presence of cyanine 3-CTP and cyanine 5-CTP (PerkinElmer, Waltham, MA, USA). Yields of complementary RNA (cRNA) and the dye-incorporation rate were measured with the ND-1000 spectrophotometer (NanoDrop Technologies).

Hybridization of Whole Mouse Genome Oligo Microarray
The hybridization procedure was performed according to the One-Color Microarray-Based Gene Expression Analysis protocol (version 5.5, part number G4140-90050) using the Agilent Gene Expression Hybridization Kit (Agilent Technologies). Briefly, 825 ng of the corresponding Cy3- and Cy5-labeled cRNA was combined and hybridized overnight at 65°C to Agilent Whole Mouse Genome Oligo Microarrays 8x60 K using the hybridization chamber and oven recommended by Agilent. The used microarrays contained 55,681 gene-specific oligo spots including 39,430 Entrez Gene RNAs and 16,251 lincRNAs. After hybridization, the microarrays were washed once with 6x SSPE buffer at 37°C containing 0.005% N-lauroylsarcosine for 1 minute at room temperature, followed by a second wash with preheated 0.06x SSPE buffer at 37°C containing 0.005% N-lauroylsarcosine for 1 minute. Acetonitrile was used for the last washing step for 30 seconds.

Scanning and data analysis
Fluorescence signals of the hybridized microarrays were monitored using Agilent’s Microarray Scanner System G2505B and the Scan Control Software (Agilent Technologies). The Agilent Feature Extraction Software (FES) version 10.2.1.3 was used to read out and process the microarray image files. For the determination of differential gene expression, the FES derived output data files were further analyzed using the Rosetta Resolver® Gene Expression Data Analysis System (Rosetta Biosoftware, Seattle, WA, USA). The local signal of each spot was measured inside a 300 µm diameter circle. The local background was determined within 40 µm wide rings approximately 40 µm distant from the signal. Then, local background was subtracted from the local signal intensity to calculate the net signal intensity and the ratio of Cy5 to Cy3. The ratios were normalized to the median of all ratios, considering only those spots with fluorescence intensities three times larger than that of the control herring sperm DNA and spotting buffer negative controls. The values represent the means of four single spots and standard deviations. Cutoff was chosen at > twofold expression with P<0.01.

Quantitative PCR
All RNA samples were treated with DNase (Applied Biosystems, Darmstadt, Germany) for at least 1 hour and were then converted into cRNA using the Reverse Transcription Kit following the manufacturer’s protocol (Qiagen). Quantitative real-time PCR (RT-qPCR) was performed using the ABI Prism 7500HT sequence detection system (Applied Biosystems) with SYBR green PCR master mix from Qiagen. Genes were investigated by encoding the mRNAs for the following proteins: serum amyloid a3 (Saa3) (Mm_Saa3_1_SG), chemokine (C–C motif) ligand 8 (CCL8) (Mm_Ccl8_1_SG), cluster of designation 209a (CD209A) (Mm_Cd209a_1_SG), cluster of designation 209b (CD209B) (Mm_Cd209b_1_SG), and glyceraldehyde-3-phosphat-dehydrogenase (GAPDH) (Mm_Gapdh_1_SG). All primers used for RT-qPCR were obtained commercially from Qiagen. PCRs were conducted as follows: 2 minutes at 50°C to activate uracil-N-glycosylase (UNG); 95°C for 10 minutes to deactivate UNG; and 40 cycles at 94°C for 15 seconds, 60°C for 35 seconds, and 72°C for 30 seconds. Reaction specificity was checked by performing dissociation curves after PCR. For quantification, mRNA levels were normalized to those of GAPDH. The threshold cycle (Ct) value was the cycle number, selected from the logarithmic phase of the PCR curve, in which an increase in fluorescence above background could be detected. ΔCt was determined by subtracting the Ct of GAPDH from the Ct of the target. The fold change of mRNA expression was determined using the 2−ΔΔCT method.

Statistical analysis
One-way ANOVA was carried out, and the statistical comparisons among the groups were performed with Duncan’s t-test using a statistical package program (SPSS version 17.0). P≤0.05 was considered as significant for all the statistical analyses in this study.

Results
The in vivo antiplasmodial activity study revealed that the methanolic extract of I. oblongifolia produced suppression of parasitemia in a dose-dependent manner when compared
Table 1  Indigofera oblongifolia-induced suppression of parasitemia in mice infected with Plasmodium chabaudi on day 7 pi

<table>
<thead>
<tr>
<th>Group</th>
<th>Dose of IOLE (mg/kg)</th>
<th>Parasitemia (%)</th>
<th>Suppression of parasitemia (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Infected (− IOLE)</td>
<td>−</td>
<td>38±6</td>
<td>−</td>
</tr>
<tr>
<td>Infected (+ IOLE-100)</td>
<td>100</td>
<td>12±3*</td>
<td>68.4±8</td>
</tr>
<tr>
<td>Infected (+ IOLE-200)</td>
<td>200</td>
<td>34±8</td>
<td>10.5±3</td>
</tr>
<tr>
<td>Infected (+ IOLE-300)</td>
<td>300</td>
<td>22±5*</td>
<td>42.1±6</td>
</tr>
</tbody>
</table>

Notes: Values are means ± SD. *Significance against infected (− IOLE) group at P<0.05.
Abbreviations: pi, postinfection; SD, standard deviation; IOLE, I. oblongifolia leaf extract.

A higher number of TUNEL-positive cells were shown in spleen sections of mice infected with P. chabaudi-parasitized erythrocytes on day 7 pi (Figures 4 and 5). I. oblongifolia was able to reduce the number of TUNEL-positive cells in the spleen of mice treated with a dose of 100 mg IOLE/kg (Figures 4 and 5). However, the spleen of mice treated either with 200 or 300 mg IOLE/kg showed no significant difference in the number of TUNEL-positive cells compared to the infected group (Figure 5).

To detect possible molecular changes induced in the spleens by P. chabaudi infections, we compared spleen gene expression in noninfected control mice with that of mice infected with P. chabaudi on day 7 pi, and we also compared infected mice with mice treated with 100 mg IOLE/kg after infection. Specifically, we isolated the total RNA from the individual spleens of five mice in each group, and pooled equal amounts of RNA before subjecting the samples to Agilent 2-color microarray analysis. Among the total 55,680 oligo spots on the microarray, 4,037 spots were upregulated and 3,126 spots were downregulated (comparing the microarray of the infected group with that of the infected treated group) (Figure S1A). We also categorized the genes according to function into: immune response genes and genes concerned with metabolism, signaling, transport, gene expression, and erythrocytes function (Figure S1B). In this article, we concentrate only on those genes that are related to immune response, with their expressions being altered by more than twofold. It is clear from our data that IOLE was able to upregulate six genes (Table 2) and downregulate 24 genes (Table 3).

Among the differentially up- and downregulated genes under IOLE, we quantified the expression of four genes (Ccl8, Saa3, Cd209a, and Cd209b). The expression data determined by microarrays were largely consistent with the expression analyses we performed with several arbitrarily selected genes using quantitative PCR (Figure 6).

Discussion

Our previous studies revealed that clearance of malarial parasites appears to be mediated by both acquired and innate immune responses.13–15 Also, female C57BL/6 mice were able to heal infections with P. chabaudi and develop long lasting immunity against homologous rechallenge.15 I. oblongifolia extract was able to significantly lower the infection-induced parasitemia. This may be due to the presence of the active compounds of I. oblongifolia, such as saponins (steroids or triterpenes), phenol, quinines, and coumarin.16
The antiplasmodial and spleen protective role of crude I. oblongifolia

Figure 2 Indigofera oblongifolia-induced changes in mouse spleen capsules infected with Plasmodium chabaudi at day 7 pi.

Notes: (A) Noninfected spleen with normal capsule. (B) Infected spleen with thin capsule. (C) Infected I. oblongifolia treated (100 mg/kg) spleen with moderate thickness. (D) Infected I. oblongifolia treated (200 mg/kg) spleen with more thickened capsule. (E) Infected I. oblongifolia treated (300 mg/kg) spleen with thickened capsule. Sections are stained with hematoxylin and eosin. Scale bar =25 µm.

Abbreviation: pi, postinfection.

Figure 3 Changes in capsule thickness of spleens of uninfected, Plasmodium chabaudi-infected, and infected I. oblongifolia treated mice on day 7 pi.

Notes: Values are means ± SD. aSignificant against noninfected group at P ≤0.05. bSignificant against infected (−IOLE) group at P ≤0.05.

Abbreviations: pi, postinfection; SD, standard deviation; IOLE, I. oblongifolia leaf extract.

The differentiation of the spleen to an antimalarial effector organ is associated with splenomegaly and reorganizations of the spleen at maximal parasitemia. The change in spleen thickness during malaria has been reported in many studies and may be due to stretching of splenic parenchyma. There is an apparent enlargement of white pulp areas preceding the disappearance of white and red pulp segregation. This coincides with an increase in the number of leukocytes. Also, Helmy et al reported that malarial infection is characterized by both major activation and suppression of the immune system during different phases of the disease. Our results support Khare’s observation that all parts of the plant are used in treating enlargements of the liver and spleen.

Apoptotic cells have been found in the spleen among macrophages, T cells, and B cells, as was increased Fas expression; this indicates that P. chabaudi-induced apoptosis is, at least in part, a Fas-mediated event. In our study,
IOLE could significantly decrease the infection-induced apoptosis in the mice spleen.

The antimalarial activities of *I. oblongifolia* are associated with changes of gene expression induced by parasites in the *P. chabaudi*-infected mouse spleen. In particular, it is remarkable that *I. oblongifolia* upregulates, by more than twofold, the mRNA expression of genes encoding a transmembrane receptor (*Cd209a*, *Cd209b*, *Cd209d*, and *Cd209e*). These genes are often referred to as DC-SIGN because of their expression on the surface of dendritic cells and macrophages. The encoded proteins are involved in the innate immune system and recognize divergent pathogens ranging from parasites to viruses.23

Also, *I. oblongifolia* affects expression of the genes *Cr2* and *Fcer2a*, which code for B-lymphocyte activation.24 In addition, *Timd4* in the spleen was upregulated after treatment with *I. oblongifolia*. This gene enhances the engulfment of apoptotic cells and is also involved in regulating T-cell proliferation and lymphotxin signaling.25

The chemokine (C–C motif) ligand 8 (*Ccl8*) was highly expressed. This gene is located on chromosome 17 and is responsible for the immunoregulatory and inflammatory processes.26 *P. chabaudi* was able to upregulate the expression of *Ccl8*. This cytokine displays chemotactic activity for monocytes, lymphocytes, basophils, and eosinophils, and is responsible for immunoregulatory and inflammatory processes,26 but *I. oblongifolia* was able to downregulate the expression of this gene.

Finally, *I. oblongifolia* was able to alter the expression of *Saa3* from 34-fold to 3.5-fold. Zhang et al27 reported that this gene is highly expressed during infection and its transcription is induced in many organs, including the spleen.

Collectively, *I. oblongifolia* has antimalarial activity and can protect the spleen from *P. chabaudi*-induced injury.
Table 2 Expression of upregulated genes in spleen of *Plasmodium chabaudi*-infected mice treated with *Indigofera oblongifolia* compared to noninfected and *P. chabaudi*-infected mice without treatment

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Sequence description</th>
<th>Function related to EntrezGene</th>
<th>Accession #</th>
<th>Sequence code</th>
<th>Inf/Cont</th>
<th>Tre-inf/Inf</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ccl8</td>
<td>Chemokine (C–C motif) ligand 8</td>
<td>This cytokine displays chemotactic activity for monocytes, lymphocytes, basophils, and eosinophils</td>
<td>NM_021443</td>
<td>A_51_P464 703</td>
<td>41.3</td>
<td>−7.6</td>
</tr>
<tr>
<td>Igv10-3</td>
<td>dC1 anti-poly(dC) monoclonal antibody heavy chain variable region</td>
<td></td>
<td>AF045483</td>
<td>A_66_P114 537</td>
<td>39.6</td>
<td>−3.1</td>
</tr>
<tr>
<td>Saa3</td>
<td>Serum amyloid A 3</td>
<td>Major acute phase reactant</td>
<td>NM_011315</td>
<td>A_55_P195 3169</td>
<td>34.0</td>
<td>−3.5</td>
</tr>
<tr>
<td>Igv5-12</td>
<td>CB17 SCID immunoglobulin heavy chain variable region</td>
<td></td>
<td>U23092</td>
<td>A_55_P214 1105</td>
<td>30.6</td>
<td>−9.1</td>
</tr>
<tr>
<td>Il10</td>
<td>Interleukin 10 (IL-10)</td>
<td>Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF, and GM-CSF produced by activated macrophages and by helper T cells</td>
<td>NM_010548</td>
<td>A_51_P430 766</td>
<td>26.9</td>
<td>−2.0</td>
</tr>
<tr>
<td>Mcpt1</td>
<td>Mast cell protease 1</td>
<td>Can enhance the production of IgE and IgG (PMID: 11722648)</td>
<td>NM_008570</td>
<td>A_51_P169 476</td>
<td>22.6</td>
<td>−20.2</td>
</tr>
<tr>
<td>Mageb16</td>
<td>Melanoma antigen family B, 16</td>
<td></td>
<td>NM_028025</td>
<td>A_55_P195 7154</td>
<td>14.1</td>
<td>−2.4</td>
</tr>
<tr>
<td>Igkv9-129</td>
<td>Immunoglobulin kappa light chain</td>
<td></td>
<td>AY498738</td>
<td>A_51_P516 322</td>
<td>13.4</td>
<td>−3.3</td>
</tr>
<tr>
<td>Tigit</td>
<td>T-cell immunoreceptor with Ig and ITIM domains</td>
<td>Binds with high affinity to the poliovirus receptor (PVR) which causes increased secretion of IL-10 and decreased secretion of IL-1β and suppresses T-cell activation by promoting the generation of mature immunoregulatory dendritic cells</td>
<td>NM_001146</td>
<td>A_55_P202 6903</td>
<td>11.4</td>
<td>−2.0</td>
</tr>
<tr>
<td>Ccl24</td>
<td>Chemokine (C–C motif) ligand 24</td>
<td>The cytokine encoded by this gene displays chemotactic activity on resting T lymphocytes, a minimal activity on neutrophils, and is negative on monocytes and activated T lymphocytes</td>
<td>NM_019577</td>
<td>A_51_P322 640</td>
<td>10.1</td>
<td>−3.2</td>
</tr>
<tr>
<td>Il1r1</td>
<td>IL-1 receptor-like 1</td>
<td>Receptor for IL-33, its stimulation recruits MYD88, IRAK1, IRAK4, and TRAF6, followed by phosphorylation of MAPK3/ERK1 and/or MAPK1/ERK2, MAPK14, and MAPK8. Possibly involved in helper T-cell function</td>
<td>NM_010743</td>
<td>A_51_P339 793</td>
<td>7.7</td>
<td>−2.2</td>
</tr>
</tbody>
</table>

**Abbreviations:** SCID, severe combined immunodeficiency; Ig, immunoglobulin; ITIM, immunoreceptor; IFN, interferon; TNF, tumor necrosis factor; GM-CSF, granulocyte macrophage colony-stimulating factor; Tre-inf, treated-infected; Inf, infected; Cont, control; PMID, PubMed identifier.
<table>
<thead>
<tr>
<th>Gene name</th>
<th>Sequence description</th>
<th>Function related to EntrezGene</th>
<th>Accession #</th>
<th>Sequence code</th>
<th>Inf/Cont</th>
<th>Tre-inf/Inf</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cd209a</td>
<td>CD209a antigen</td>
<td>These genes encode a transmembrane receptor and are often referred to as DC-SIGN because of their expression on the surface of dendritic cells and macrophages. The encoded proteins are involved in the innate immune system and recognize divergent pathogens ranging from parasites to viruses.</td>
<td>NM_133238</td>
<td>A_55_P201806</td>
<td>-100</td>
<td>24.81105</td>
</tr>
<tr>
<td>Cd209b</td>
<td>CD209b antigen</td>
<td></td>
<td>NM_001037800</td>
<td>A_52_P267717</td>
<td>-100</td>
<td>62.567</td>
</tr>
<tr>
<td>Cd209d</td>
<td>CD209d antigen</td>
<td></td>
<td>NM_130904</td>
<td>A_55_P205598</td>
<td>-44.1</td>
<td>9.7</td>
</tr>
<tr>
<td>Cd209e</td>
<td>CD209e antigen</td>
<td></td>
<td>NM_130905</td>
<td>A_55_P196037</td>
<td>-13.6</td>
<td>3.4</td>
</tr>
<tr>
<td>Clec4g</td>
<td>C-type lectin domain family 4, member g</td>
<td></td>
<td>NM_029465</td>
<td>A_51_P145662</td>
<td>-100</td>
<td>26.9</td>
</tr>
<tr>
<td>Il22ra2</td>
<td>Interleukin 22 receptor, alpha 2</td>
<td>The encoded soluble protein specifically binds to and inhibits interleukin 22 activity by blocking the interaction of interleukin 22 with its cell surface receptor. The encoded protein may be important in the regulation of inflammatory response, and has been implicated in the regulation of tumorigenesis in the colon.</td>
<td>NM_178258</td>
<td>A_55_P204606</td>
<td>-55.6</td>
<td>5.9</td>
</tr>
<tr>
<td>Il9r</td>
<td>Interleukin 9 receptor</td>
<td>The functional IL-9 receptor complex requires this protein as well as the interleukin 2 receptor and gamma (IL2RG), a common gamma subunit shared by the receptors of many different cytokines.</td>
<td>NM_00113458</td>
<td>A_55_P221453</td>
<td>-50.1</td>
<td>17.4</td>
</tr>
<tr>
<td>Hamp2</td>
<td>Hepcidin antimicrobial peptide 2</td>
<td>The product encoded by this gene is involved in the maintenance of iron homeostasis, and it is necessary for the regulation of iron storage in macrophages, and for intestinal iron absorption. These peptides exhibit antimicrobial activity.</td>
<td>NM_183257</td>
<td>A_52_P21486</td>
<td>-46.3</td>
<td>4.8</td>
</tr>
<tr>
<td>Skint3</td>
<td>Selection and upkeep of intraepithelial T cells 3</td>
<td>Immunglobulin superfamily gene cluster, positively selects epidermal gammadelta T cells.</td>
<td>NM_177578</td>
<td>A_55_P197889</td>
<td>-46.0</td>
<td>12.5</td>
</tr>
<tr>
<td>Siglech</td>
<td>Sialic acid binding immunoglobulin (Ig)-like lectin H</td>
<td>In the immune response, may act as an inhibitory receptor upon ligand-induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules.</td>
<td>NM_178706</td>
<td>A_55_P216579</td>
<td>-27.2</td>
<td>10.1</td>
</tr>
<tr>
<td>Kllb1</td>
<td>Kallikrein B, plasma 1</td>
<td>Plasma kallikrein is a glycoprotein that participates in the surface-dependent activation of blood coagulation, fibrinolysis, kinase generation, and inflammation.</td>
<td>NM_008455</td>
<td>A_55_P199811</td>
<td>-24.6</td>
<td>2.3</td>
</tr>
<tr>
<td>Cr2</td>
<td>Complement receptor 2</td>
<td>Receptor for complement C3Dd, for the Epstein-Barr virus on human B cells and T cells, and for HNRP. Participates in B-lymphocyte activation.</td>
<td>NM_007758</td>
<td>A_55_P197172</td>
<td>-23.9</td>
<td>9.3</td>
</tr>
<tr>
<td>Pigr</td>
<td>Polymorphic immunoglobulin receptor</td>
<td>This receptor binds polymeric IgA and IgM at the basolateral surface of epithelial cells.</td>
<td>NM_011082</td>
<td>A_51_P239737</td>
<td>-22.9</td>
<td>2.2</td>
</tr>
<tr>
<td>Fcer2a</td>
<td>Fc receptor, IgE, low</td>
<td>The protein encoded by this gene is a B-cell specific antigen, and a low-</td>
<td>NM_013517</td>
<td>A_55_P211734</td>
<td>-22.7</td>
<td>4.8</td>
</tr>
<tr>
<td>Gene</td>
<td>Description</td>
<td>Accession</td>
<td>Start</td>
<td>End</td>
<td>Source</td>
<td></td>
</tr>
<tr>
<td>-------</td>
<td>-----------------------------------------------------------------------------</td>
<td>-------------</td>
<td>-------</td>
<td>-------</td>
<td>-----------</td>
<td></td>
</tr>
<tr>
<td>Klr2</td>
<td>Killer cell lectin-like receptor family 1 member 2 (Designated KLRG (NKG2))</td>
<td>XM_003946193</td>
<td></td>
<td></td>
<td>A_55_P203248</td>
<td></td>
</tr>
<tr>
<td>Klr12</td>
<td>Killer cell lectin-like receptor subfamily A, member 12</td>
<td>NM_010646</td>
<td></td>
<td></td>
<td>A_55_P216771</td>
<td></td>
</tr>
<tr>
<td>Mug1</td>
<td>Murinoglobin 1 (The encoded protein acts as an inhibitor for several proteases, and has been reported as the p170 antigen recognized by autoantibodies in the autoimmune disease paraneoplastic pemphigus (PMID: 20805888).)</td>
<td>NM_008645</td>
<td></td>
<td></td>
<td>A_55_P210541</td>
<td></td>
</tr>
<tr>
<td>Mug2</td>
<td>Murinoglobin 2</td>
<td>NM_008646</td>
<td></td>
<td></td>
<td>A_55_P207476</td>
<td></td>
</tr>
<tr>
<td>Plg</td>
<td>Plasminogen (The protein encoded by this gene is a secreted blood zymogen that is activated by proteolysis and converted to plasmin and angiostatin. It activates the urokinase-type plasminogen activator, collagenases, and several complement zymogens, such as C1 and C5.)</td>
<td>NM_008877</td>
<td></td>
<td></td>
<td>A_52_P662013</td>
<td></td>
</tr>
<tr>
<td>Clec4a4</td>
<td>C-type lectin domain family 4, member a4 (Members of this family share a common protein fold and have diverse functions, such as cell adhesion, cell-cell signaling, glycoprotein turnover, and roles in inflammation and immune response.)</td>
<td>NM_001005860</td>
<td>A_55_P210388</td>
<td>15.7</td>
<td>3.7</td>
<td></td>
</tr>
<tr>
<td>Prg3</td>
<td>Proteoglycan 3 (Possesses similar cytotoxic and cytostimulatory activities to PRG2/MBP.)</td>
<td>NM_016914</td>
<td></td>
<td></td>
<td>A_51_P363729</td>
<td></td>
</tr>
<tr>
<td>Fcamr</td>
<td>Fc receptor, IgA, IgM, high affinity (In vitro, stimulates neutrophil superoxide production and IL-8 release, and histamine and leukotriene C4 release from basophils. Functions as a receptor for the Fc fragment of IgA and IgM. Binds IgA and IgM with high affinity and mediates their endocytosis. May function in the immune response to microbes mediated by IgA and IgM.)</td>
<td>NM_001170632</td>
<td>A_55_P228882</td>
<td>13.7</td>
<td>10.3</td>
<td></td>
</tr>
<tr>
<td>Ccr3</td>
<td>Chemokine (C–C motif) receptor 3 (This receptor binds and responds to a variety of chemokines, including eotaxin (CCL11), eotaxin-3 (CCL26), MCP-3 (CCL7), MCP-4 (CCL13), and RANTES (CCL5). It is highly expressed in eosinophils and basophils, and is also detected in TH1 and TH2 cells, as well as in airway epithelial cells.)</td>
<td>NM_009914</td>
<td>A_52_P661044</td>
<td>12.6</td>
<td>5.4</td>
<td></td>
</tr>
<tr>
<td>Timd4</td>
<td>T-cell immunoglobulin and mucin domain containing 4 (Phosphatidylserine receptor that enhances the engulfment of apoptotic cells. Involved in regulating T-cell proliferation and lymphotxin signaling.)</td>
<td>NM_178759</td>
<td>A_52_P609868</td>
<td>12.6</td>
<td>5.2</td>
<td></td>
</tr>
</tbody>
</table>

**Abbreviations:** Inf, infected; Cont, control; Tre-inf, treated-infected; PMID, PubMed identifier.
Further studies are required to evaluate the mechanism of *I. oblongifolia* action as well as the effect of active components in the plant extract.

**Acknowledgment**

The authors extend their appreciation to the Deanship of Scientific Research at King Saud University for funding the work through the research group project No PRG-1436-02.

**Author contributions**

All authors contributed toward data analysis, drafting, and critically revising the paper and agree to be accountable for all aspects of the work.

**Disclosure**

The authors report no conflicts of interest in this work. The authors alone are responsible for the content and writing of this paper.

**References**


---

**Figure 6** Expression of selected genes determined by quantitative RT-PCR and microarray analysis.

**Notes:** Quantitative RT-PCR of SAA3, CCL8, CD209A, and CD209B in the spleens of mice infected with *Plasmodium chabaudi* was performed. Expression of mRNAs was determined in spleens from uninfected and infected mice on day 7 pi, normalized to GAPDH mRNA expression, and relative expression is given as fold change compared to the uninfected control mice. *Significant against infected (~ IOLE) group at P<0.05.

**Abbreviations:** RT-PCR, reverse transcription polymerase chain reaction; GAPDH, glyceraldehyd-3-phosphate-dehydrogenase; pi, postinfection.
Supplementary material

Figure S1 Gene expression in spleens of Plasmodium chabaudi-infected mice treated with Indigofera oblongifolia leaf extract.

Notes: (A) Scatter plot of signal intensities of all spots. As an example, the data of one array experiment is shown. The signal intensities of each feature represented by a dot are shown in double logarithmic scale. X-axis: control-log signal intensity; Y-axis: sample-log signal intensity. Red diagonal lines define the areas of twofold differential signal intensities. Blue cross: unchanged genes; red cross: significantly upregulated genes (P-value < 0.01); green cross: significantly downregulated genes (P-value < 0.01); gray cross in legend: summary of significantly up- and downregulated signatures. (B) Summary of percentage change in gene regulation according to function. Data for Plasmodium chabaudi-infected vs infected-treated (+ IOLE-100) spleen.

Abbreviation: IOLE, I. oblongifolia leaf extract.