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ORIGINAL ARTICLE

Expression and preliminary characterization of the potential vaccine candidate LipL32 of leptospirosis

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Abstract

Leptospirosis is a globally re-emerging infectious disease mainly for mammals. The infection is caused by the spirochete Gram-negative bacterium *Leptospira interrogans*, which affects animals and humans worldwide. In our previous studies, recombinant protein production has been obtained from the bacterial expression system. In this study, we have investigated the over expression of LipL32 and hGMCSF genes into yeast expression system for obtaining a high yield of recombinant protein production. Here, we described the yeast expression studies with several applications such as protein folding, fast growth, and post-translational modification. The expression studies were carried out in a novel protein expression system, the methylotrophic yeast *Pichia pastoris* KM71 strain. The LipL32, Green fluorescent protein (EGFP), and human granulocyte–macrophage colony-stimulating factor (hGMCSF) genes were cloned into pPIC9 yeast expression vector. The recombinant clones of pPIC9-EGFP-LipL32 and pPIC9-EGFP-hGMCSF-LipL32 were transformed into *Pichia pastoris* KM71 strain by electroporation. Media optimization and other physiological characters were studied for the transformed recombinant protein. The protein was then purified using a Ni–NTA column, meanwhile, the recombinant DNA constructs contain His-tag at the C- terminal end. Finally, the intracellular EGFP expression of pPIC9-EGFP-LipL32, and pPIC9-EGFP-hGMCSF-LipL32 in *Pichia pastoris* KM71 strain was confirmed by fluorescence microscopic analysis. Protein–protein dockings were done to study LipL32-Adjuvant (hGMCSF, hIgGFc and hC4) interactions. Furthermore, this docking analysis was shown better interaction between LipL32, and hGMCSF, which is also used for the enhanced vaccine potential against leptospirosis.

Keywords *Pichia pastoris* · Leptospirosis · LipL32 · hGMCSF · EGFP · BMMY

Introduction

Leptospirosis is an infection caused by a pathogenic bacterium from the genus of Leptospira (Zarantonelli et al. 2018). The disease was mostly found in the endemic areas with rainy season, close human contact, and poor sanitation. Leptospirosis is commonly observed worldwide, especially in rural and urban areas; mostly sewage workers, hunters, farmers, abattoir, veterinarians, and farmworkers will get infected (Benschop et al. 2009; Haake and Levett 2015). In humans, leptospirosis is caused due to direct and indirect contact with water and soil contaminated by the urine of infected animals (Torgerson et al. 2015). Leptospira causes severe disabilities like body pain, headache, fever, and severe symptoms with neurological complications and hepatic and renal failure (Faine 1994; Marquez et al. 2019). A recent analysis showed that the health risk in emergency evolved and evolving countries,

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mainly European countries, particularly people in this environment involved in water sport activities (Haake et al. 2002; Dupouey et al. 2014). The pathogenic Leptospira species, comprised of 23 serogroups and 250 serovars, are commonly present in wild and domestic animal reservoirs. This corresponded to the infection of farm animals (cows, pigs, horses) and humans inhabit with them (Costa et al. 2015). Globally, about one million people were affected by this disease. Nowadays, the number of incidents has amplified in tropical areas; it causes a death rate in region 6.85%, based on the prevalent serovars (Garba et al. 2017). Penicillin and doxycycline are the antibiotics used for the treatment of human leptospiral infections. The crucial need for a novel vaccine has motivated many research groups to evaluate the protective immune response stimulated by recombinant vaccines. Significant protection has been analyzed with many potential outer membrane proteins, including LipL32 and other leptospiral immunoglobulin-like proteins (Grassmann et al. 2017). In general, Outer membrane Protein (OMP) can be used to identify leptospiral virulence factors and OMP components attached to the host cell and initiate the infectious cycle. Surface exposure ability and conserveness across pathogenic serovars of leptospiral OMP genes are considered potential virulence factors (Shang et al. 1996; Cullen et al. 200[illegible] King et al. 2013; Lucas et al. 2011). Accordingly, these potential vaccine candidates are focusing on the evaluation of new vaccines against leptospirosis.

Mainly LipL32 is present in the interior leaflet of the outer membrane protein of pathogenic leptospira species. (Guerreiro et al. 2001; Haake et al. 2000). The most pathogenic leptospira species involves 7[illegible]% of LipL32 in the outer membrane protein. Till now, approximately 95% of patients identified with leptospirosis produced antibodies against LipL32. The pathogenic leptospira expresses a huge quantity of LipL32. Because of the antigenic properties of LipL32, many researchers have been used the LipL32 as a target gene for vaccine trials and observed partial protection against leptospira infection in some animal models. LipL32 is mostly bound with the extracellular matrix protein (Branger et al. 2001; Seixas et al. 2007; Hauke et al. 2008; Tung et al. 2010). LipL32 is one of the most leading sero reactive antigens absorbs during severe and convalescent leptospirosis. It plays an essential function in stimulating the host inflammatory reaction during infection and stimulating an innate immune response through TLR 2 (Yang et al. 2006). Currently, vaccines for leptospirosis based on cellular and molecular studies have been found on lipoprotein, lipopolysaccharide, bacterial motility, and outer membrane proteins (OMPs). Though, it is still an insufficient knowledge-based explanation for many researchers in the area of Leptospirosis vaccine development. Thus, it has aimed us to explore the development of the recombinant leptospiral vaccine by using a yeast expression system.

The expression systems have been established and widely used to produce various types of therapeutic recombinant proteins that comprise cell cultures of bacterial, yeast, mammalian origin, and insect (Rogan and Babiuk 2005). From the expression mentioned above systems, yeast is a suitable expression system for the expression of both endogenous and heterologous recombinant protein productions. Because the yeast expression system was easy to operate genetically. There is a high yield of recombinant protein production, accessible fermentation, proteolytic processing, proper folding, post-translational modification, fast growth, and simple genetic manipulation. The most critical nontoxic pathogen-free recombinant protein production is less expensive and a large-scale culture that can only be performed in yeast; however, it is not present in the bacterial expression systems (Narayanan et al. 2021a, b, c). The most commonly working yeast species in the research laboratories are *Pichia pastoris* and *Saccharomyces cerevisiae* (Cregg et al. 2000; Nielsen 2013; Yu et al. 2014; Han and Yu 2015; Kim and Kim 2017).

Yeast expression systems are excellent hosts for recombinant protein production with various applications such as medical and industrial. The main concern has been developed on yeasts due to the crucial advantages and novel development in this host cell. For each specific recombinant protein production, a suitable expression system should be found and improved on scalable fermentation and simple genetic manipulation levels, including the vector, host, and expression approaches. They are also used in several advantages, including fast growth, post-translational modification, safe pathogen-free recombinant production, and increase biomass concentrations (Nielsen 2013; Han and Yu 2015; Kim and Kim 2017) *Pichia pastoris* is an outstanding expression host for the recombinant protein production of heterologous foreign proteins with biopharmaceuticals and industrial enzymes. Up to now, this methylotrophic yeast expression system has been effectively used for the production of many eukaryotic recombinant proteins such as human serum albumin, human monoclonal antibody 3H6 Fab fragment human erythropoietin, human superoxide dismutase, phytase, trypsin, collagen, and phospholipase C (Looser et al. 2015; Irani et al. 2016).

Currently, above 5000, recombinant protein production has been effectively produced in the methylotrophic yeast *P. pastoris* expression system. Although the prospect of the *P. pastoris* is tightly packed of PAOX1 expression to some restrictive conditions, the circumstance of repressing carbon sources expressively small amount of recombinant protein expression during the methanol-induction phase (Kandasamy et al. 2021). The remaining carbon sources can be eliminated by medium, additionally key to methanol induction, though this procedure was not

suitable for large-scale recombinant protein production. Finally, methanol can be used as a sole carbon source for energy and recombinant protein growth in the expression system of *P. pastoris* (Tan et al. 1995; Cregg et al. 2000; Macauley-Patrick et al. 2005; Liu and Liu 2008; Chang et al. 2018).

This study has expressed LipL32 as a fusion construct with the adjuvant human granulocyte macrophage colony-stimulating factor (hGMCSF) and green fluorescent protein gene (GFP) into pPIC9 yeast expression vector along with AOX1 promoter and then the overexpressed recombinant proteins were purified. Hence, this yeast-based expression system is amenable to produce the LipL32 in higher quantity as a native form. Further, it can be directly used for vaccines, and purified protein will diagnose leptospiral infection.

Materials and methods

Chemicals required

The Gram-negative bacteria, *E. coli* DH5α strain, can be used as a vector host for this study. All the recombinant DNA cloning were followed by standard procedures (Sambrook and Russell 2006). All the chemicals, reagents, and antibiotics were purchased from Himedia labs, Mumbai, India. Molecular biology chemicals, pTZ57R/T vector, and restriction enzymes were bought from MBI Fermentas Inc., USA. All the sequencing and primers were designed and procured from Xcelris labs, Ahmedabad, India. For selective growth, bacteria (*E.coli* DH5α) were raised in Luria Bertani (LB) broth, which also contains the required concentration of various antibiotics such as 100 µg/mL of Ampicillin or 50 µg/mL of kanamycin sulfate (Sigma Aldrich, St Louis, MO, USA). The plasmid purification kit was bought from Sigma-Aldrich, and the methods were followed as per the Sigma-Aldrich manual instructions.

Construction of pPIC9-EGFP-LipL32 and pPIC9-EGFP-hGMCSF-LipL32 plasmid

The source of full-length LipL32 gene was amplified from the clone, which contains the pXCM-LipL32 plasmid (gift from Dr. T. Jebasingh, Department of Plant Science, School of Biological Sciences, Madurai Kamaraj University, Madurai, Tamil Nadu). The LipL32 gene was encoding the outer membrane lipoprotein of Leptospira, and it was amplified from recombinant pXCM-LipL32 using the pairs of gene-specific primers. The primers were constructed forward primer (FP) flanked with ATG as Start codon and restriction enzymes like *Avr*II, *Eco*RI, *Nhe*I, and reverse primer (RP) flanked with the *Stu*I and *Xho*I recognition site. The polymerase chain reaction (PCR) limitation was: initial denaturation at 94 °C for 2 min; 30 cycles of (94 °C for 1 min, 53 °C for 45 s, 72 °C for 1.5 min); keep on 72 °C for 8 min (Final extension). Then the PCR product was confirmed in 1% agarose gel electrophoresis (AGE), and PCR amplicons 0.8 kb of LipL32 was purified, and the DNA concentration was checked using AGE and Nanodrop method.

Then the resulting PCR product, LipL32, was ligated into pTZ57R/T as a T-tail vector. The recombinant pTZ-LipL32 construct was transformed into competent cells (*E. coli* DH5α) than the recombinants were investigated with LB agar plate supplemented with 40 µg/mL concentration of X-gal, 100 mM concentration of IPTG and with Ampicillin (100 µg/mL) antibiotics. The recombinant colonies (pTZ-LipL32) observed white colour indicating recombinant colonies and blue colour showing non-recombinant colonies. Further, the recombinant plasmid (pTZ-LipL32) was checked by colony PCR and restriction digestion with specific enzymes.

The EGFP (pEGFP-C3) and hGMCSF genes were amplified using pairs of gene-specific primers flanked with the restriction enzyme as a recognition site, and PCR parameters were followed by Tables 1 and 2. The PCR product was checked via electrophoresis using 0.8% agarose gel, and the PCR products were purified and introduced into pTZ57R/T. The ligation mixture was transformed into *E. coli* DH5α

Table 1 Gene specific primers

S no	Primer sequence description	Sequence	DNA restriction enzyme site present
1	LipL32 forward	5′CTAGCGAATCCGATATCATGAAAAAACTTTCGATTTTGGC3′	*Eco*RV
2	LipL32 reverse	5′TCTAGAAGATCTTTCCTCGAGCTTAGTCGCGTCAGAAGCAGC3′	*Xho*I
3	EGFP forward	5′GTTACTAAGCTTATGGTGAGCAAGGGCGAGGAG 3′	*Hind*III
4	EGFP reverse	5′TATTATGCTAGCACCGATTCCACCCTTGTACAGCTCGTC 3′	*Xba*I
5	Human GMCSF forward	5′GGAGCTAGCATGTGGCTGCAGAG 3′	*Nhe*I
6	Human GMCSF reverse	5′CTCGATATCCTCCTGGACTGGC 3′	*Stu*I

Table 2 PCR condition for EGFP, hGMCSF, LipL32

Temperature (°C)	Time	Number of cycles
94	2 min	1
94	1 min	28
61	1 min	
72	55 s	
72	8 min	1
12	∞	1

competent cells and picked recombinant colonies were confirmed by colony PCR. The recombinant DNA was digested with primers flanked restriction enzymes, and then 717-bp of EGFP, 453-bp of hGMCSF genes release was observed in the 1% agarose gel electrophoresis. The recombinant clones (pTZ-LipL32, pTZ-EGFP and pTZ-hGMCSF) were transformed into the pPIC9 yeast expression vector, and the constructs were named as pPIC9-EGFP-LipL32 and pPIC9-EGFP-hGMCSF-LipL32. Finally, all the recombinant plasmids were sequenced, and sequence data were analyzed with Sequencer version 4.10 (Xcelris labs, Ahmedabad, India) and aligned with Clustal W Omega.

Culture medium for yeast

For the growth of yeast cells, YPD media was used, which consists of yeast extract (*w*/*v* of 1%), peptone (*w*/*v* of 2%), dextrose (*w*/*v* of 2%), and YPDS medium (YPD medium plus 1 M concentration of sorbitol). The yeast cells were grown at 30 °C for 24 h. The transformation of target genes into *P. pastoris* was done by electroporation using MD (Minimal dextrose): 1.34% yeast nitrogenous base (YNB) 4 × 10–5% biotin and 2% dextrose MM (minimal methanol media for replacement of dextrose into 1% methanol). For the expression of the protein in *P. pastoris,* it was grown by using BMMY (Buffered Methanol-complex) Medium composed of 1 M potassium phosphate buffer, pH 6.0, 10X YNB (13.4% Yeast Nitrogen Base with Ammonium Sulphate without amino acids), 500X B (0.02% Biotin), 10X M (5% Methanol). BMGY medium composed of (Buffered Glycerol-complex Medium similar to BMMY) 5% Methanol was replaced with 10% Glycerol, 1.5% *w*/*v* of agar.

Transformation of yeast by electroporation

A single colony of KM71 strain *P. pastoris* was inoculated into 150 mL conical flask containing 10 mL YPD growth medium, incubated in the Orbitek rotatory shaker at 30 °C with 250 rpm agitation for 24 h. The culture was then moved into a new 225 mL of YPD growth medium, and the conical flask was incubated above the similar condition (at 30 °C with 250 rpm), waiting for the optical density (OD) of yeast to reach 1–1.5 at 600 nm. Then the culture was transferred into 50 mL centrifuge tubes and centrifuged at 1500 rpm for 15 min at 4 °C subsequent two or three times for washing with the help of 40 mL of sterile ice-cold Molecular grade water. The pellets were dissolved in 30 mL of ice-cold 1 M sorbitol and centrifuged at 1500 rpm for 10 min. Finally, the pellets were resuspended in 1.5 mL ice-cold 1 M sorbitol. Subsequently, yeast recombinant plasmid such as pPIC9, pPIC9-EGFP-LipL32, and pPIC9-EGFP-hGMCSF-LipL32 were single digested with *Sac*I in both plasmids. For electrotransformation, electrocompetent KM71 cells were prepared from a log phase culture of *P. pastoris*. It was mixed with 5–30 µg of suitably linearized pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSF-LipL32 and control (pPIC9) expression plasmids and was transferred into 0.2 cm electroporation cuvette. The cells present in the cuvette were pulsed for approximately 10 min with a field strength of 1500 V cm^{-1} using a Gene Pulser. After the cells in the cuvette were transferred into 15 mL centrifuge tube and mixed with 1 mL of YPD media. Then these tubes were incubated in a shaker at 30 °C (190 rpm) for 3–4 h. After incubation, the 100 µL of transformant cells were spread into different media (YPD, MD, and MM supplemented with 100 µg/mL Ampicillin). After inoculation, the plates were incubated at 30 °C overnight. The next day the transformant colonies were observed and were used for further studies.

Selection of multiple insertions

P. pastoris (KM71) transformants containing the methanol-inducible pPIC9-EGFPLipL32 and pPIC9-EGFP-hGMCSF-LipL32 expression plasmids were selected on MM and MD plates (absent in the histidine), then it is screened for Muts /Mut + phenotype.

Direct screening of multiple inserts

Pichia transformant colonies, found either by selection media such as YPD, MD, or MM, were investigated for the gene insert of EGFP, LipL32, and hGMCSF by DNA-based PCR explained previous report (Arora et al. 1998). Briefly, the DNA was isolated from Pichia transformants. Overnight cultures were centrifuged at 1.5 mL centrifuge tubes at 12,000 rpm for 2 min, and the pellets were resuspended with 985 µL of lysis buffer by repeated pipetting. Then 15 µL of proteinase K was added and mixed vigorously and incubated in the heating block (Rivera instrument) at 65 °C for 1 h. After incubation, the same volume of phenol: chloroform (24:1) was added and mixed by inverting tubes for 10–15 times, and then the tubes were centrifuged at 12,000 rpm for 10 min. The uppermost layer of supernatant was transferred into 1.5 mL fresh centrifuge tubes. With that equal volume of isopropanol and 0.2 volume of 10 M, ammonium acetate

concentration was added and incubated for 30 min at − 20 °C to precipitate the genomic DNA. After incubation, the centrifuge tubes were centrifuged at 12,000 rpm for 20 min. The supernatant was discarded, and 500 µL of 70% ethanol was added. The tubes were centrifuged at 12,000 rpm for 25 min and removed the supernatant; the pellets were allowed to air dry. Finally, 50 µL of Milli-Q water was added to dissolve the air-dried pellet. The genomic DNA was used as template DNA for the amplification of inserts. The 717-bp of EGFP, 453-bp of hGMCSF gene, and 0.8-kb of LipL32 gene were amplified using the gene-specific primers, and these gene specific primers are represented in Table.1, and PCR condition was described in Table 2.

Production of recombinant EGFP-LipL32 and EGFP-hGMCSF-LipL32 protein

In a 500 mL conical flask, a single colony of these recombinant *P. pastoris* (pPIC9-EGFP-LipL32 and pPIC9-EGFP-hGMCSF-LipL32) were inoculated in 25 mL BMGY medium and the conical flask was incubated in a shaker overnight for 30 °C with 250 rpm with intermittent shaking until the reach OD (1.5–2.0) at 600 nm which was achieved at a log phase growth. Then the log phase cells were then centrifuged at 5000 rpm for 10 min at room temperature. After centrifugation, the supernatant was discarded. The pellets were washed with molecular grade water twice and the washed cell pellets were resuspended in 20 mL of BMMY medium. Again, the cells were centrifuged at 5000 rpm for 5 min at 37 °C, and the supernatant was discarded. Finally, the cell pellets were resuspended approximately 100 mL of BMMY medium to induce protein expression and transferred the culture in a 1 L baffled flask. Then the baffled flask was incubated at 30 °C to continue the growth. Then the filter-sterilized methanol (0.5% *w/v*) was supplemented every 24 h to maintain the process of protein induction. At a particular time of focus next to the start of the protein expression, 2 mL of the culture was transferred into a 2 mL microcentrifuge tube, and tubes were centrifuged at 1200 rpm for 4 min at 37 °C. The supernatant was collected into a fresh 2 mL microcentrifuge tube. The pellet and supernatant were stored at − 80 °C up to further investigation. The protein samples were taken from different time intervals (12, 24, 36, 48, and 60 h) to determine the optimal time phase for protein expression after methanol induction.

Further, the growth was maintained for four days. Then the best time interval changes between different proteins were expressed. Finally, the samples of supernatants and cell pellets were analyzed for protein expression using SDS-PAGE analysis. Further, the cell pellets were analyzed for the intracellular expression of pPIC9-EGFP-LipL32, pPIC9 EGFPhGMCSF-LipL32 in *P. pastoris*.

Analysis of SDS-PAGE and protein purification

The cell lysate (pellet and supernatant) was collected and separated on 12% acrylamide gel. The eighty microlitres of different time interval samples and mixed twenty microlitres of sample buffer were boiled (heating block) at 90 °C for 10 min. The protein sample mixture was individually loaded onto the 12% acrylamide gel. Finally, the samples were compared with the protein ladder (Thermo scientific, USA). Further, the over expressed recombinant protein samples were purified using Ni-NTA-HIS-Tagged Protein Purification Kit (Hi-media, Mumbai, India). The protein purification protocols were followed as per the instructions mentioned in the user manual.

Physiological characteristics

In 1L baffled flask, the log phase cells were raised on 150 mL of different growth mediums such as YPD, BMMY, and BMGY. The cell culture biomasses were observed at 0, 9, 12, 24, 36, 48, 60 h after culture. The cells were incubated at 30 °C in a shaker for 250 rpm with intermittent shaking. 0.5% filter-sterilized methanol was used at a final concentration and induced for every 3 h to provide a constant methanol induction. This potential recombinant protein medium was used for further optimization as below.

The recombinant protein-producing colonies were selected for further characterization in terms of temperature's effect, which was assessed at 20 °C, 25 °C, 30 °C, and 37 °C. The range of pH used in this analysis was between 4.0, 5.0, 6.0, and 7.0. The cultures were incubated using similar cultural conditions that were explained before. The samples were harvested every 12 h for further investigation.

Intracellular expression of pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSF-LipL32 in *P. pastoris*

The methanol-induced cell pellets were washed with phosphate buffer saline (PBS; pH 7.4), which consist of Na_2HPO_4 (14.4 g), KCL (2 g), KH_2PO_4 (2.4 g), and NaCl (80 g). The tubes were then centrifuged at 1200 rpm for 3 min, and then the supernatant was removed. Then 20 µL of PBS was added to dissolve the cell pellet. After that, the cells were placed on the microscopic slide. The yeast cells were observed for their fluorescence using an Olympus CKX53 inverted fluorescence microscope with universal GFP settings at a 515–550 nm wavelength, and the images were taken at 10X objective.

Protein–protein docking

To make a comparative study on LipL32 protein and their binding efficiency, three important glycoproteins/cytokines

Table 3 Protein–protein docking of LipL32 against three cytokines

Protein 1	Protein 2	PDB ID of Protein 2	Resolution (Å)	Interaction energy (Kcal/mol)	Number of hydrogen bonds
LipL32 (PDBID: 2ZZ8_A with 2.01 Å resolution)	hGMCSF	2GMF_A	2.4	−880.6	256
	hC3D	1C3D_A	1.8	−768.5	221
	MCO	Model	Nil	−676.7	160

(GMCSF, hC3d, and hIgGFC) were used. The PDB ID and resolution of the cytokines are given in Table 3. To study the interaction strength of LipL32 with cytokines, Cluspro 2.0 (Kozakov et al. 2017) tool is used. Cluspro uses a PIPER method, an FFT-based docking program that uses a pair-wise interaction potential as part of its scoring function. Cluspro docking has provided good results for many complexes used as targets in the Critical Assessment of Predictions of Interactions experiment (Ponniah et al. 2021). The residue–residue interactions between LipL32 and cytokines were further found using the protein interaction calculator server (PIC) (Tina et al. 2007). PIC server calculates the number of hydrogen bonds formed within a protein or between proteins in a complex.

Results

Construction of yeast expression plasmid pPIC9-EGFP-hGMCSF-LipL32

The EGFP, LipL32, and hGMCSF genes were amplified by PCR using gene-specific primers; the PCR amplified EGFP, LipL32, and hGMCSF genes were inserted to T-Tail vector pTZ57R/T, yielding recombinant plasmids DNA, namely pTZ-EGFP, pTZ-LipL32, and pTZ-hGMCSF, respectively. The gene fragments corresponding to EGFP, LipL32, and hGMCSF genes from recombinant pTZ57R/T were subcloned into the yeast expression vector pPIC9. Each construct was determined by restriction analysis with vector backbone and specific target bands of which 0.8-kb for LipL32, 0.7-kb for EGFP, 1.4-kb for hGMCSF, and 9.5-kb for pPIC9-EGFP-LipL32, and 9.9-kb for pPIC9-EGFP-hGMCSF-LipL32, respectively showed in Figs. 1 and 2. PCR further determined with respective primers showed in Table1.

Production of recombinant *P. pastoris*

The recombinant DNA constructs pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSFLipL32 were linearized using the *Sac*I restriction enzyme and then electro-transformed into KM71 strain of *P. pastoris*. Then recombinant plasmids were grown on different growth mediums (MM, YPD, MD). Based on the growth condition analysis, YPD and MM media showed good growth, compared with MM, which showed reduced growth. Then the recombinants were confirmed by direct Polymerase Chain Reaction (PCR), and it has demonstrated successful insertion of the EGFP, LipL32, hGMCSF gene into the genome of *P. pastoris* (Fig. 3).

Secretary mutants of growth were observed in the three plates, such as YPD, MM, and MD, as shown in Fig. 3i, ii.

It can grow on an MD medium plate (Muts), and MD medium cannot give alcohol oxidase (the product of the

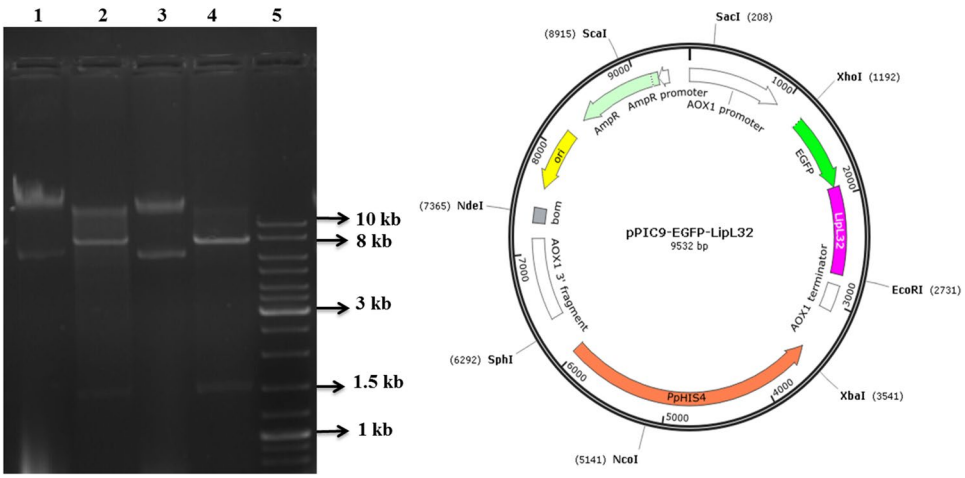

Fig. 1 Confirmation of pPIC9-EGFP-LipL32 by restriction digestion: Lane 1 and 3: pPIC9-EGFP-LipL32 uncut; Lane 2 and 4: pPIC9-EGFP-LipL32 digested with *Eco*RI and *Xho*I; Lane 5: Gene Ruler (100-bp to 10 kb)

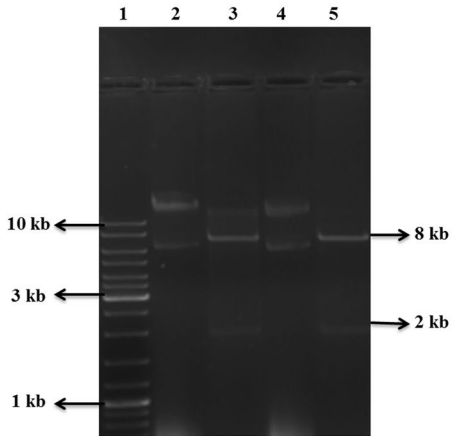

Fig. 2 Confirmation of pPIC9-EGFP-hGMCSF-LipL32 by restriction digestion: Lane 1: Gene Ruler (100-bp to10-kb); Lane 2 and 4: pPIC9-EGFP-hGMCSF-LipL32 uncut; Lane 3 and 5: pPIC9-EGFP-hGMCSF-LipL32 digest with *Eco*RI and *Xho*I

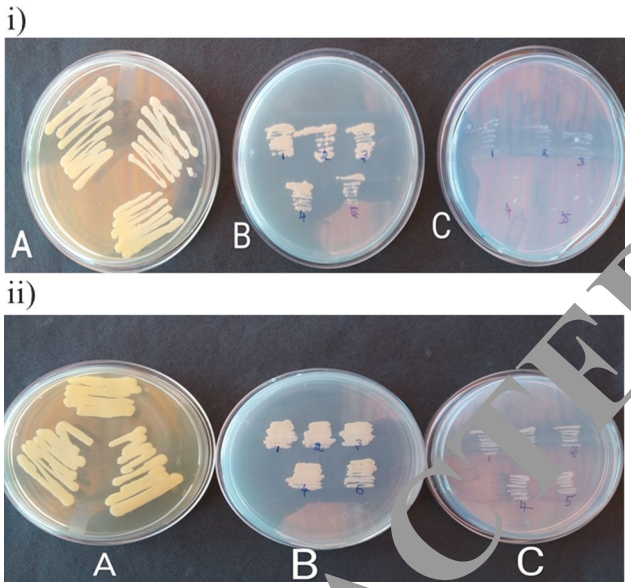

Fig. 3 **i** Screened Secretary mutants from electroporated pPIC9-EGFP-LipL32: ***A*** pPIC9-EGFP-LipL32 in YPD medium, ***B*** pPIC9-EGFP-LipL32 in MM and ***C*** pPIC9-EGFP-LipL32 in MD. **ii** Screened Secretary mutants from electroporated pPIC9-EGFP-hGMCSF-LipL32: ***A*** pPIC9-EGFP-hGMCSF-LipL32 in YPD medium, ***B*** pPIC9-EGFP-hGMCSF-LipL32 in MM and ***C*** pPIC9-EGFP-hGMCSF-LipL32 in MD

AOX1 gene). Most importantly, it cannot effectively absorb methanol as a carbon source. It can only absorb dextrose as a source of energy. Therefore, they can grow slowly (MD) was observed in plate C. In the plate, B was observed in the slow growth on methanol induced medium MM. It can differentiate His^+transformants in which the promoter of the AOX1 gene has been interrupted (His + Muts) from His^+transformants with an intact 3AOX1 gene (His^+ Mut^+).

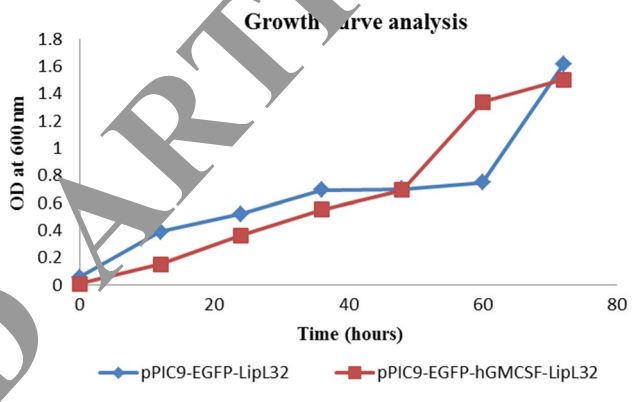

Fig. 4 A time course of growth of pPIC9-EGFP-LipL32 and pPIC9-EGFP-hGMCSF-LipL32 yield by the recombinant *P. pastoris*

Growth curve analysis for pPIC9-EGFP-LipL32, and pPIC9-EGFP-hGMCSF-LipL32 production in recombinant *P. pastoris*

The recombinant plasmid (pPIC9-EGFP-LipL32, and pPIC9-EGFP-hGMCSF-LipL32) of *P. pastoris* KM71 growth curve was observed as a rapid lag phase, durable for a limited time hour for monitoring the exponential growth, before getting the stationary phase 10 h later (Fig. 4). The graphs show that the first growth of pPIC9-EGFP-LipL32, pPIC9- EGFP-hGMCSF-LipL32 was observed after 3 h from starting culture, i.e., presently after being induced in the methanol at 12 h. The expression of pPIC9-EGFP-LipL32, pPIC9- EGFP-hGMCSF-LipL32 production appeared parallel with a rise in the growth. Above this condition, the pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSF-LipL32 were repeatedly produced even after the culture achieved its stationary phase. All data are repeated twice, and it was performed in triplicate.

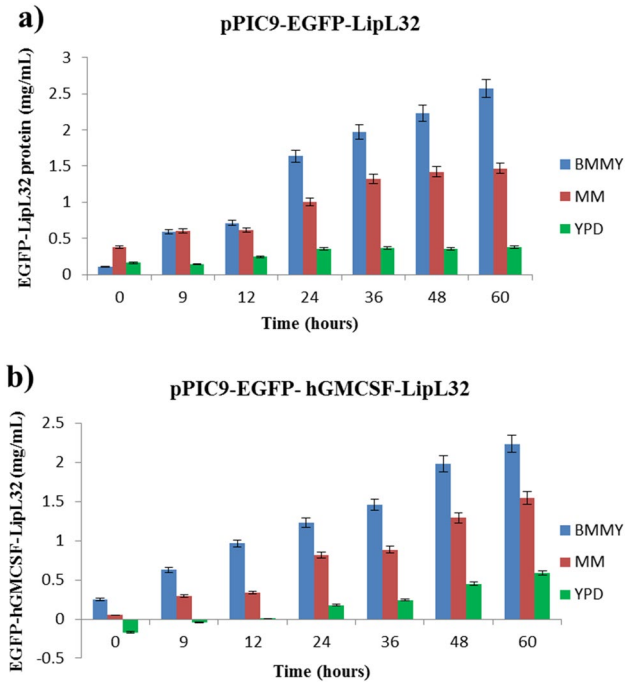

Fig. 5 Graph shows that **a** pPIC9-EGFP-LipL32 and **b** pPIC9-EGFP-hGMCSF-LipL32 protein production and cell biomass accumulation by the recombinant *P. pastoris* on various growth media

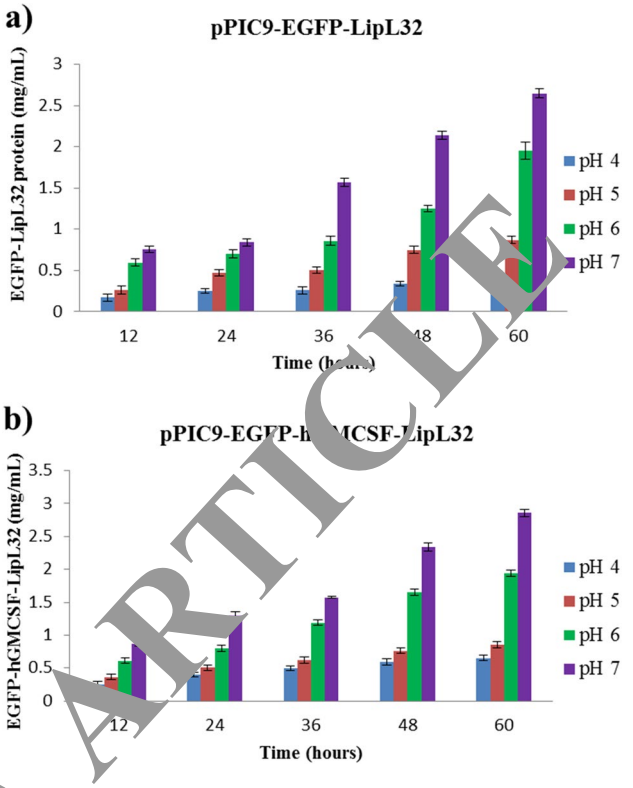

Fig. 6 Effect of pH on cell biomass **a** pPIC9-EGFP-LipL32 and **b** pPIC9-EGFP-hGMCSF-LipL32 protein produced by the recombinant *P. pastoris*

The studying of different cultural conditions on growth for transformants

The different growth mediums observed production of recombinant proteins (pPIC9-EGFP-LipL32, pPIC9-EGFP hGMCSFLipL32) and biomass accumulation (BMMY, YPD, and MM) Fig. 5. In this work, the biomass of protein production, the entire growth medium was found to promote the proper growth of the cells observed. Although the highest cell biomass of recombinant protein production was observed in the BMMY medium and the remaining two of this medium (YPD and MM) slow growth and a small amount of protein production was observed in the both recombinant DNA constructs pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSF-LipL32, and significant production was observed in BMMY medium. Finally, BMMY media was used for future studies.

Recombinant protein purification of pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSF-LipL32

The *P. pastoris* transformed construct pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSF-LipL32 were grown overnight, and it was sub-cultured until the culture reaches 1.0 OD at 600 nm. For induction, it was initially optimized by different pHs such as 4, 5, 6, and 7 conditions (Fig. 6) and different concentrations of methanol such as 0.0, 0.25, 0.5, and 1%, respectively, (Fig. 7) for various time intervals such as 12, 24, 36, 48, and 60 h, respectively. Finally, the constant concentration of pH-7 media with 0.5% methanol concentration in 60 h of time interval was observed high protein yield. The EGFP-LipL32 protein size was 56-kDa, and the EGFP-hGMCSF-LipL32 protein size is 72-kDa, and all bands were observed in the 12% SDS-PAGE gel. The expressed protein bands were also noticed at approximately 56-kDa, and 72-kDa was showed in Fig. 8.

Intracellular expression of pPIC9-EGFP-LipL32, pPIC9-EGFP- hGMCSF-LipL32 in *P. pastoris*

P. pastoris KM71 strain was used for the analysis of the expressed recombinant protein of pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSF-LipL32. This study investigates the intracellular GFP (Green fluorescent protein) protein expression of two plasmids (pPIC9- EGFP-LipL32 pPIC9-EGFP-hGMCSF-LipL32) having EGFP along with a hexa-histidine tag, and it is present in the C-terminal end. The pPIC9 and recombinant plasmids pPIC9-EGFP-LipL32 and pPIC9-EGFP-hGMCSF-LipL32 were transformed into *P. pastoris* KM71 strain and the transformants were plated into different media such as in BMMY, YPD, MM. In BMMY, media can generate recombinant proteins

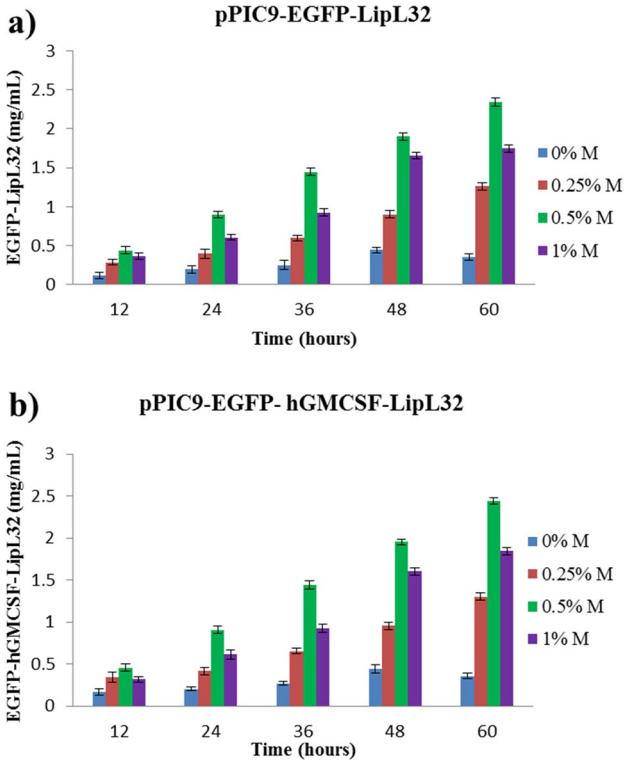

Fig. 7 Effect of various concentration of methanol on **a** pPIC9-EGFP-LipL32 and **b** EGFP-hGMCSF-LipL32 protein produced by the recombinant *P. pastoris*

because methanol is used as a supply of carbon and energy. Figure 9b and c clearly shows that both DNA constructs, EGFP expression were observed. Whereas Fig. 9a shows no fluorescence, the pPIC9 can be used as a negative control. Finally, both recombinant plasmids were effectively expressed, and GFP was observed in this study.

Docking

Using the Cluspro tool, LipL32 was docked with three cytokines to form the complex structure. The output of Cluspro gave the best10 docked structures, and they were ranked according to the binding energy. We considered a docked confirmation with the least binding energy for our further analysis, shown in Table 3. Our docking results observed LipL32 interacts strongly with GMCSF with the interaction energy of − 880.6 kcal/mol by forming 256 hydrogen bonds. The interaction energy of hC3-LipL32 is − 768.5, forming 221 hydrogen bonds, whereas the interaction energy of hIg-GFC-LipL32complex is − 676.7 kcal/mol with 260 hydrogen bonds. The least binding energy conformation of GMCSF-LipL32 from Cluspro was selected and shown in Fig. 10. While comparing the interaction energy of all the three complexes, the GMCSF-LipL32 complex had the least binding energy, proving its better binding efficiency, which means it is firmly bound. The Q means a score of the GMCSF-LipL32 (0.66) is higher than the other two cytokines.

Discussion

Leptospirosis has occurred worldwide and is the most important communicable diseases (Bharti et al. 2003). Leptospirosis has appeared worldwide as the main transmissible disease, and it is caused by the genus of Leptospira (Gram-negative bacteria). It is mainly happening in rural regions and occurs in the municipality environment of

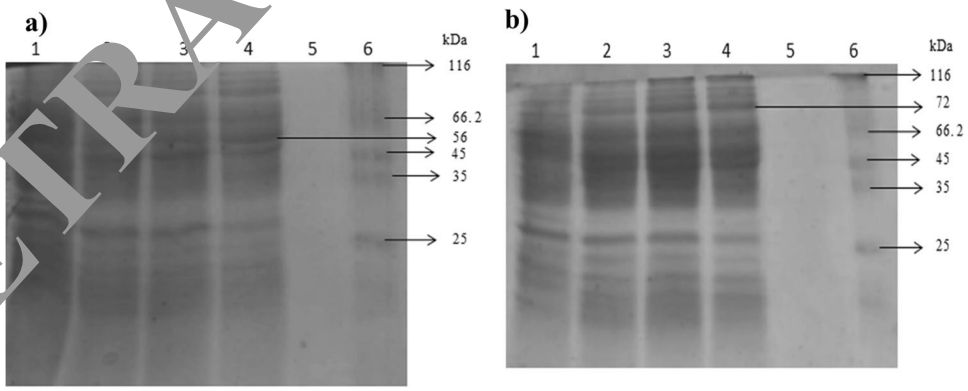

Fig. 8 **a** SDS-PAGE (12%) analysis of the expressed recombinant EGFP-LipL32 protein in *P. pastoris* which was induced by 0.5% Methanol at different time period: Lane 1: induced (12 h) cell lysate. Lane 2: induced (24 h) cell lysate. Lane 3: induced (36 h) cell lysate. Lane 4: induced (48 h) cell lysate. Lane 5: Un induced cell lysate. Lane 6: Unstained protein molecular weight marker (kDa), (Thermo, scientific). **b** SDS-PAGE (12%) analysis of the expressed recombinant EGFP-hGMCSF-LipL32 protein in *P. pastoris* which was induced by 0.5% Methanol at a different time period: Lane 1: induced (12 h) cell lysate. Lane 2: induced (24 h) cell lysate. Lane 3: induced (36 h) cell lysate. Lane 4: induced (48 h) cell lysate. Lane 5: Un-induced cell lysate. Lane 6: Unstained protein molecular weight marker (kDa), (Thermo, scientific)

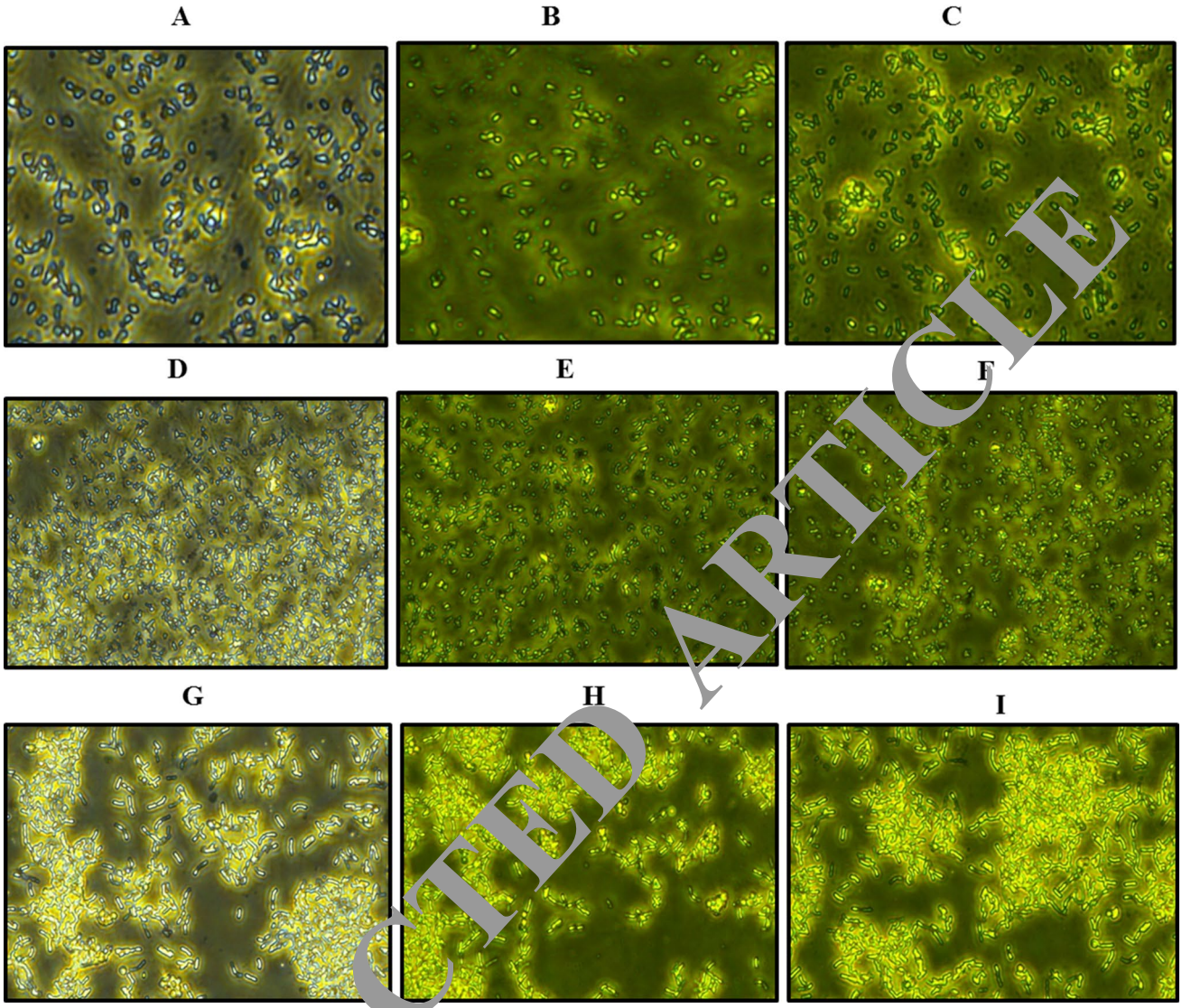

Fig. 9 Fluorescence microscopy of *P. pastoris* (KM71) cells transformed with plasmid DNA. **a** pPIC9 (12 h); **b** pPIC9-EGFP-LipL32 (12 h); **c** pPIC9-EGFP-hGMCSF-LipL32 (12 h); **d** pPIC9 (24 h); **e** pPIC9-EGFP-LipL32 (24 h); **f** pPIC9-EGFP-hGMCSF-LipL32 (24 h); **g** pPIC9 (48 h); **h** pPIC9-EGFP-LipL32 (48 h); **i** pPIC9-EGFP-hGMCSF-LipL32 (48 h);

industrialized and developing nations. It is mostly infected in humans, and mammalian species are grown in both via an indirect or direct link with urine having the causative bacterial pathogens (Whangchai et al. 2021). Leptospirosis exhibits a variant symptom in the range of clinical symptoms (subclinical illness such as fever, headache, and body pain) to complication symptoms like kidney injury, hepatic failure, and pulmonary hemorrhage syndrome (Hartwig et al. 2014; Sánchez-Montes et al. 2015; Sanhueza et al. 2015). Leptospira has multiple vaccine candidates such as OMP, LipL32, LipL21, LipL41, and others (Vijayachari et al. 2015). During the Leptospira infection in humans, the LipL32 protein binds to the host extracellular matrix (ECM) (Murray 2015). The major three outer membrane proteins (OMPs: LipL32, LipL41, and OMPL1) usually induce a humoral immune response to leptospirosis. These OMPs are highly immunogenic and also conserved across the pathogenic Leptospira species. Therefore, these OMPs have been mainly focused on developing potential vaccines for heterologous protection in Leptospiral disease (Yan et al. 2003; Martinez et al. 2004; Laurichesse et al. 2007; Niloofa et al. 2015; Silveira et al. 2017).

The increasing frequency of leptospiral infection found a severe clinical issue globally that requires to be appropriately directed. The high incidence of leptospiral infection points out the demand for diagnosing and treating the disease. Thus, there is an urgent need for more studies to understand the leptospiral infection, followed by developing

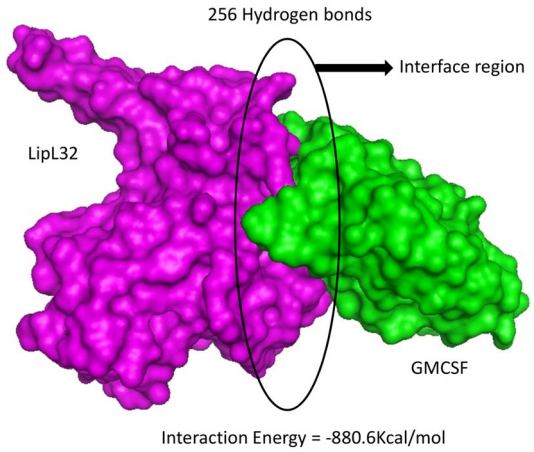

Fig. 10 The surface diagram of the GMCSF-LipL32 complex generated from cluspro docking. The LipL32 is shown in purple color and the GMCSF structure is shown as green color. The interface region is marked as a black oval line

accurate and particular diagnostic methods and suitable strategies for leptospiral treatment.

Nowadays, vaccine availability against leptospirosis is used in bacterins to eliminate the suspension's bacterial cells in the human body, and bacterins like vaccines are used for human vaccination in several countries like Japan, France and Cuba. In contrast, in China, people have utilized the purified Leptospiral outer membrane protein as a vaccine. Subsequently, the purified outer membrane protein has been used as a vaccine against Leptospiral infection (Yan et al. 2003; Martinez et al. 2004; Laurichesse et al. 2007; Niloofa et al. 2015; Silveira et al. 2017).

In general, the prokaryotic expression system (*E. coli*) involves developing inclusion bodies of improperly folded aggregates that require refolding, making the purification of recombinant proteins that were functionally and structurally active. This yeast expression system helps post-translational modifications like glycosylation. Simultaneously, the yeast expression system (*P. pastoris*) is overcoming by the problems mentioned above. To date, *P. pastoris* is the best expression system, and it produces approximately above 420 heterologous recombinant proteins (Eckart and Bussineau 1996; Sreekrishna et al. 1988; Macauley-Patrick et al. 2005; Jahic et al. 2006; Hamilton and Gerngross 2007; Böer et al. 2007; Lin-Cereghino et al. 2008). The *Pichia pastoris* is a methylotrophic yeast and mostly used for the expression of heterologous recombinant protein production. *P. pastoris* yeast has various benefits, comprising alcohol oxidase I promoter (AOX1), protein purification method is easy for heterologous protein production, the cells are cultivated in high proficiency, and modifications of recombinant proteins. KM71 strain is the derivative of GS115 strain. These two strains (KM71 and GS115) are mainly used to express recombinant protein production and are also used in medicine and industry (Näätsaari et al. 2012).

In this present study, we use LipL32 as a diagnostic tool; The LipL32, EGFP, and hGMCSF gene sequences were amplified using gene-specific primers, cloned unidirectionally into the T-tail vector of pTZ57R/T vector and characterized. The pTZ clones were cloned into pPIC9 as a yeast expression vector, and clones were confirmed by further analysis. The recombinant DNA constructs pPIC9-EGFP-LipL32, pPIC9-EGFP-hGMCSF-LipL32 were linearized by *Sac*I restriction enzymes and electrotransformed into *P. pastoris* KM71 strain. (Scorer et al. 1994).

The recombinant colonies were grown on different growth mediums (YPD, MD, and MM). Based on the growth condition analysis, YPD and MM media have shown good growth, and MD media has shown slow growth. Colony PCR result shows EGFP, LipL32, and hGMCSF gene into the pPIC9 vector (*P. pastoris* genome). The time-course growth pPIC9, pPIC9-EGFP-LipL32, and pPIC9-EGFP-hGMCSF-LipL32 by the recombinant production of *P. pastoris* on various media and different conditions like YPD, BMGY, and BMMY. In the BMMY media was showed suitable biomass of protein.

Here we attempted to enhance the maximum recombinant protein production by *P. pastoris* expression system. An efficient method was necessary to improve the yield of recombinant pPIC9-EGFP-LipL32 and pPIC9-EGFP-hGMCSF-LipL32 protein production. Previous reports demonstrated that the culture condition and other inducer concentrations were essential in recombinant protein production (Batra et al. 2014; Yu et al. 2014). Then, the most important factors such as pH, temperature, and methanol concentrations were chosen to investigate the recombinant protein expression.

The quantity of recombinant protein secreted into the growth medium was established for involvement by the optimum condition. The culture condition is one important factor for enhancing recombinant protein production in strains of yeast. The first step of optimizing the recombinant protein production using the shaken flask method and this method has produced tenfold lower than fermenter because so many factors are affected, such as culture density and limited aeration and another important factor for choosing the culture condition (Barr 1992; White et al. 1994; Romanos 1995; Daly and Hearn, 2005). In this study, we have used different media such as YPD, BMMY, and MM medium to produce the highest-level protein production. Methanol plays another central role in the production of recombinant protein. Methanol is present in these media (BMMY and MM), and it can perform as the exclusive (yeast) in the carbon source (energy), and along with, it is used as an inducer for the protein expression. The low level of methanol concentrations is not sufficient for the initiate transcription of recombinant DNA (Lin-Cereghino et al. 2008). In this study,

different concentration of methanol was used (in *w*/*v*) such as 0%, 0.25%, 0.5%, and 1% for measurement recombinant protein production. Compared with previously reported recombinant protein production in *P. pastoris* strain (Hong et al. 2002). These are general factors for producing the maximum production level of recombinant protein, and mainly the recombinant protein production is directly proportional to cell density (Cregg et al. 2000; Zhang et al. 2000; Gou et al. 2012). However, the YPD growth medium has produced the lowest level of recombinant protein production. Finally, BMMY media and 0.5% methanol concentration are suitable for recombinant protein production.

The reporter gene is most commonly used for Green fluorescent protein (GFP) isolated from the Aequorea Victoria (jellyfish). Both species-independent eukaryotic and prokaryotic cells (Chalfie et al. 1994; Kain et al. 1995). Early the GFP has expressed using *P. pastoris* in plasmid pPICZB, and pPIC3, which carry the AOX1 strong promoter to determine intracellular gene expression (Sears et al. 1998; Gellissen 2000; Zupan et al. 2004; Hisiger and Jolicoeur 2005). Nowadays, GFP has been most widely used for the reporter gene, and their main advantage of the GFP reporter gene is species independence, stability, and easy detection in UV light. GFP can be mainly observed non-invasively in living cells and fused into the C and N terminus of the proteins. The EGFP is an appropriate *invivo* marker for gene expression and protein localization studies (Logan and Leaver 2000).

In this current work, the GFP has conjugated to the DNA constructs used in this study. The GFP showed correct processing for proper protein folding and its presence in the cytoplasm. Some of the protein is transferred into peroxisomes, methanol induced into *P. pastoris* cells (Zupan et al. 2004; Papakonstantinou et al. 2009).

Conclusions

The current results of this work show the manipulation of *P. pastoris* as the best expression system for the production of recombinant LipL32 from *L. interrogans*. The attractiveness of our outcome was the BMMY media with 0.5% (*w*/*v*) of methanol induction for the excellent recombinant LipL32 protein production. Therefore, future studies of recombinant LipL32 protein for optimization and confirmation of ELISA for diagnosing leptospirosis. Finally, recombinant LipL32 has been used for diagnostic purposes of leptospirosis.

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Declarations

Conflict of interest The authors declare no conflict of interest.

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