



RESEARCH ARTICLE

CURRENT SCENARIO OF VACCINE DEVELOPMENT AGAINST A NEGLECTED
DISEASE: VISCERAL LEISHMANIASIS

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ABSTRACT

Visceral leishmaniasis (VL) or kala-azar, a vector-borne protozoan disease, shows endemicity in larger areas of the Asia, Africa, South America, and the Mediterranean basin. WHO report suggested that an annual incidence of VL is nearly 200,000 to 400,000 cases, resulting in 20,000 to 30,000 deaths per year. Treatment with available anti-leishmanial drugs are not cost effective, with varied efficacies and higher relapse rate, which poses a major challenge to current kala-azar control program in Indian subcontinent. Therefore, a vaccine against VL is imperative and knowing the fact that recovered individuals developed lifelong immunity against re-infection, it is feasible. Vaccine development program, though time taking, has recently gained momentum with the emergence of omic era, i.e., from genomics to immunomics. Classical as well as molecular methodologies have been overtaken with alternative strategies wherein proteomics based knowledge combined with computational techniques (immunoinformatics) speed up the identification and detailed characterization of new antigens for potential vaccine candidates. This may eventually help in the designing of polyvalent synthetic and recombinant chimeric vaccines as an effective intervention measures to control the disease in endemic areas. This review focuses on such newer approaches being utilized for vaccine development against VL.

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INTRODUCTION

Visceral leishmaniasis (VL), synonymously known as kala-azar, is caused by obligate intra-macrophage protozoan parasite and is characterized by both diversity and complexity (Chappuis *et al.*, 2007). The disease is prevalent in larger areas of tropical, subtropical, and the Mediterranean countries. As per WHO report, nearly 200,000 to 400,000 new cases of VL (with an average duration of several months to more than one year) occur annually with 20,000 to 30,000 deaths per year which is lesser than by malaria among parasitic diseases, although its exact impact has been underestimated as an exact number of cases were never recorded. Ninety percent of the VL cases occur in Bangladesh, Brazil, India, Nepal, and Sudan. In India, 80% VL cases were only from the state of Bihar (Hasker E *et al.*, 2012). The arthropod vector – female phlebotomine sandflies, nocturnal, and telmophagous, are responsible for the transmittance of the disease. Two species – *Leishmaniadonovanidonovani* (in East Africa and the Indian subcontinent) and *L. donovaniinfantum* (in the Mediterranean

region of Europe, North Africa, and Latin America) are the main causative organisms for VL (Lukes, 2007). The parasite bears two distinct life forms: promastigote, a flagellar form, found in the gut of the vector, which is inoculated into the dermis where it is internalized by dendritic cells and the macrophages and eventually is transformed into an aflagellated amastigote form, which thrives and multiply within the phagolysosomes through a complex parasite–host interaction (Mauricio and Jonatan, 2015). Current control strategies for VL rely on anti-leishmanial drugs such as pentavalent antimonials, amphotericin B (AmB), miltefosine, paromomycin, etc., but they are far from satisfactory because of their cost, toxicity as well as unpleasant side effects, longer dose schedule with variable efficacies (Lodge *et al.*, 2006). The situation has further worsened with the emergence of resistance against current anti-leishmanial drugs in various regions of endemicity (Kedzierski, 2010). Hence, in the present situation, there is an urgent need to develop an effective vaccine against VL. Although vaccination against VL has received limited attention as compared to cutaneous leishmaniasis (CL), till date, there is no commercial vaccine against any human parasitic disease including leishmaniasis (Croft *et al.*, 2006). *Leishmania* parasite follows a digenetic life cycle it results in significant antigenic diversity, which

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ultimately hampered the passage of vaccine development against VL, therefore, the knowledge of such antigenic diversity is of utmost importance (Kumari, 2008). Several approaches utilized for identification of potential antigens, which can be targeted as suitable vaccine candidate (Figure 1).

Strategies for Vaccine Development against Visceral Leishmaniasis	
1	Classical Approach Whole Parasite Vaccine Native protein Based vaccine
2	Molecular Approach DNA Vaccine Polyprotein Vaccine Recombinant Vaccine Liposomal Vaccine Salivary Antigen based vaccine
3	Alternative Approach Mutant Vaccine Synthetic Vaccine

Figure 1. Approaches to develop vaccines against visceral leishmaniasis

Among them, proteomics attract the most since it addresses several unanswered questions related to microbial pathogens, including its development, evolution, and pathogenicity. Recent advancement in computational biology further simplifies our knowledge regarding the in-depth study of parasite. T-cell epitope prediction via bioinformatics analysis of protein sequences has been proposed as another alternative for rationale vaccine development (Lundegaard, 2007). The concept that CD8+ T lymphocytes could be important in protection and long-lasting resistance to infection has opened up a new strategy in *Leishmania* vaccine design known as “polytope vaccine” (Palatnik de Sousa, 2008). Its major advantages include greater potency, can be controlled better, can be designed to break tolerance, can overcome safety concerns associated with entire organisms or proteins, etc. *Leishmania* species employ distinct mechanisms to elude effector arms of the immune system, including inhibition of NO- and ROS-mediated macrophage killing and phagolysosomal fusion, inhibition of cell-mediated immunity via blocking of antigen presentation and cytokine production, and recruitment of regulatory T cells or other interleukin-10 (IL-10)-producing cells (Nylen *et al.*, 2007).

Various approaches to develop vaccines against Visceral Leishmaniasis

Live/killed whole parasite vaccine

As the researchers started culturing promastigote form of parasite in artificial media, the concept of live vaccination came into existence. A number of large-scale vaccination trials were conducted during the 1970s and 1980s in Israel, Iran, and the Soviet Union with a higher success rate. However, standardization and quality control are the major issues associated with live vaccines because parasites used for vaccination losses its infectivity due to repeated sub-culturing. Therefore, the focus of vaccine development program was shifted toward killed organisms in the early 90s (Handman, 2001). Use of whole killed parasites with or without adjuvant was proposed for both therapeutic as well as for prophylactic purposes (Basyoni, 2012). The vaccination trial conducted in a Brazilian population showed excellent protection with up-regulation of IFN- γ and absence of IL-4, an indicator of long-lasting Th1-type immune response (Castellano *et al.*, 2009).

Protein fractions based vaccine

Selection of suitable vaccine candidates seems to be a difficult task due to the multitude of antigens that has been evaluated with varied success rate depending on their formulation and the type of animal model used (Sinha, 2011). Complete protection has not been achieved so far due to the complexity of the parasite, which generates poly-specific response (Campos, 2001).

Recombinant protein vaccine

With the advancement in recombinant DNA technology, several leishmanial molecules, either species or life cycle stage specific, were extensively studied as a promising vaccine candidate in the form of recombinant proteins. The major advantages associated with these proteins are in terms of purity as well as yield. Recombinant proteins, either alone or combined with adjuvant or with bacteria/recombinant virus as a delivery vehicles (Maroof, 2012). Have also been tested as vaccines in preclinical studies. There have been significant efforts in recent time to identify recombinant antigens that can protect against *Leishmania* infection in experimental models. Some of these antigens include kinetoplastid membrane protein-11, (Agallou, 2011) sterol 24-c-methyltransferase (Goto, 2007) amastigote specific protein A2, (Ghosh, 2001) cysteine proteinase B, (Rafati, 2006). *Leishmania*-activated C kinase, promastigote surface antigen 2, (Benhmini, 2009) nucleoside hydrolase (Al-Wabel, 2007) and surface expressed glycoprotein gp63 (Connell, 1993). Although most of these recombinant antigens have been tested in animal models for their immunogenicity and protective efficacy, only a few have progressed to clinical trials in non-human primates, dogs or in preclinical human studies

Polyprotein vaccine

Due to the genetic polymorphism in the mammalian immune system, a multicomponent vaccine thought to elicit a better protective immune response (Goto, 2011). Therefore, multicomponent or polyprotein preparations such as Q protein, Leish-111f, Leish-110f, KSAC, etc., came into existence that had been demonstrated to afford better protection against experimental VL. Among these, Q protein containing five genetically fused antigenic determinants from Lip2a, Lip2b, H2A and P0 proteins, was initially assessed along with either BCG or CpG-ODN in mice and dogs (Molano, 2003), against *L. donovani* challenge (Parody, 2004).

DNA vaccines

Besides proteins, DNA had also been extensively utilized as a means of vaccine delivery, which reformed the area of vaccinology. Here, genes encoding the target proteins are cloned into a mammalian expression vector, which is injected either intradermally or intramuscularly leading to induction of Th1 responses, resulting in strong cytotoxic T-cell immunity. Safety, stability, long-term protection, ease of administration, and cost effectiveness are the major issues associated with this form of vaccine delivery. Several molecules were evaluated using this approach such as A2, PapLe22, P36LACK, ORFF, KMP-11 proteophosphoglycan (PPG), etc., in different animal models with significant level of protection. A2 (Ghosh, 2001) and ORFF (Sukumaran, 2003) when administered as a DNA vaccine were found to be significantly protective in BALB/c

mice against VL, which induced both humoral and cellular immune responses. Zanin *et al.* (Zanin, 2007). immunized mice with a NH/A2 DNA vaccine resulted in increased IFN- γ , IL-4, and IL-10 levels associated with edema and increased parasite loads. Das *et al.* (Das, 2014) very recently have developed a DNA vaccine using conserved proteins from various *Leishmania* species and found to be immunogenic inducing CD4⁺ and CD8⁺ T-cell responses in genetically diverse human populations of different endemic regions.

Heterologous prime boost vaccine

Different researchers utilized another strategy known as heterologous DNA-prime protein-boost (HPB) approach for some VL vaccine antigens such as cysteine proteinases, GP63, etc., which have also shown success but are yet to reach the level of clinical trials. Rafati *et al.* (Rafati *et al.*, 2005 and 2006) observed that vaccination mainly elicited antigen-specific IgG2a antibodies, suggesting the induction of a Th1 immune response. Liposomal delivery of parasite protein Liposome formulations have been adopted as a drug delivery system against *Leishmania* infection so as to induce an elevated immune response owing to their adjuvant property (Bhowmick S, 2010) thus can offer a new approach to the development of VL vaccines wherein it may induce a sustained Th1 immune response. This approach using *L. donovani* promastigote membrane antigens (LA_g) encapsulated in positively charged liposomes were found to induce significant protection against experimental VL by Afrin *et al.* (Afrin, 2002). In another study, using liposomal recombinant membranous protein – GP63 of *L. donovani*, there was a long-term protection against VL in BALB/c mice (Bhowmick, 2008)

Sandfly's salivary antigen as vaccine

Salivary proteins of vector-sandfly also fetch attraction as suitable anti-VL vaccine candidates. They received little attention in spite of the fact that salivary proteins from the vector are also delivered to the host during natural transmission of the pathogen and sometimes found immunomodulatory for the host (Basyoni, 2012). Several salivary proteins of *Phlebotomus* spp. and *Lutzomyia* spp. such as PpSP15, maxadilan, LJM17, LJM19, and LJM143 have been reported as potent immunogens inducing lymphocytic infiltration with up-regulation of IFN- γ and IL-12 (Gomes, 2008 and Collin, 2009). Similarly, immunization with other two salivary proteins – LJM143 and LJM17 generated strong Th1 responses in dogs with distinct cellular infiltration of CD3⁺ lymphocytes and macrophages (Collin, 2009). Therefore, these proteins may further be explored in conjunction with potent parasite proteins for vaccination studies. Despite these different approaches offer a variable degree of efficacy, several problems still hampers its feasibility due to variations in immunogenicity and due to genetic variation in host as well as in pathogen (Kumar R and Engwerda, 2014). Therefore, despite of numerous recombinant proteins that have been suggested as potential vaccine candidates, to date barely few have reached to clinical trials (Duthie, Reed, 2014).

Newer Alternative Strategies for Developing Anti-Leishmanial Vaccine

Live mutant vaccine: Attenuation of virulent *Leishmania* parasites through defined genetic alteration is a new area in

vaccine research since the perception of vaccination suggests that the more similar a vaccine is to the natural disease, better is the generation of protective immune response (Silvestre, 2008). Poor long-term immunity is the major issue with various recombinant vaccines tested so far while whole cell killed vaccines showed variable efficacy. Consequently, live-attenuated vaccine attracts the immunologists, since, it offers a complete milieu of antigens to the antigen presenting cells (APCs), therefore, providing an optimal polarization of CD4⁺ T-cells, resulting in better immune response (Sporri, 2005). Also, they assure persistence of antigen that may allow the generation of antigen-specific effector and memory cells, which react immediately following infection (Foulds, 2006). Centrin, a growth regulated gene was deleted from the amastigote stage of the *L. donovani* parasite and was subjected to evaluation of its prophylactic potential (Silvestre, 2008). The LdCen^{-/-} parasite was found to be safe and protective in mice and hamsters against virulent challenge (Selvapandiyan A, 2009) and is under exploration for further development as potential vaccine against VL. Very recently, Dey *et al.* (Dey, 2013) have demonstrated another knock out – Ldp27 (-/-) parasites to be safe and can provide protective immunity against both homologous and heterologous challenge with stimulation of both Th1-type CD4⁺ and CD8⁺ T-cells. Since, effector T-cell population requires continuous stimulation for excellent protection; it can be well accomplished through live-attenuated vaccines.

Synthetic peptide vaccine

Recent developments in blending of bioinformatics with vaccinology has revolutionized and expedited this area. Sequencing of large number of pathogen genome and increase in nucleotide and protein sequence databases accelerate the pace of vaccine development program. Although, killed or attenuated parasites are utilized for most of the existing vaccines, protective immune response is more often triggered by small amino acid sequence (peptides). More recent bioinformatic approaches utilizes number of algorithms for predicting epitopes, HLA-binding, transporter of antigen processing (TAP) affinity, proteasomal cleavage, etc., in order to explore the use of peptide epitopes with the highest probability of inducing protective immune responses. Synthetic peptide vaccines offer several advantages over other vaccine types like absence of any potentially infectious material, ability to include multiple epitopes, minimization of the amount and complexity of an antigen, economical scale up and decreased chance of stimulating a response against self-antigens.

Conclusion

The main scientific issues in the design of a *Leishmania* vaccine are no different from those for any other vaccine. They include specificity, the class or type of response induced, and the induction of long-term immunological memory. On a more positive note, there is currently rapid progress in our understanding of the molecular nature of potential vaccine candidates and of the mechanisms that determine disease-preventing immune responses. Several strategies such as genomic databases, evolutionary relationships, three-dimensional structure of proteins, presence of specific protein domains, primary structure of proteins, etc., have been applied to know novel interacting partners in order to validate the presumed interactions. Notwithstanding, there is a feeling of

renewed optimism in the scientific community that a Leishmania vaccine is achievable.

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