INTRODUCTION

Bacillary dysentery or shigellosis remains nowadays a major burden disease especially in developing countries; annual shigellosis mortality was estimated in 2010 at 123,000 deaths worldwide among 88.4 million cases, mainly children under the age of five [1]. Bacillary dysentery is associated with fever, abdominal cramps and rectal inflammation. Dysenteric stools characteristically contain erythrocytes, polymorphonuclear neutrophils (PMNs) and mucus. Although the etiologic agents, Shigella spp., have been identified more than a century ago, shigellosis represents a major threat to public health since no licensed vaccine is available.

Shigellas are a Gram-negative pathogenic enterobacteria infecting and colonizing specifically the human colon during shigellosis. Shigella encompasses four species (S. flexneri, S. sonnei, S. dysenteriae and S. boydii). Within each species, different serotypes were classified based on the structure of the O-antigen repeats that comprise the lipopolysaccharide moiety of the polysaccharides (reviewed in [1,2]). There is a large variety of serotypes among Shigella isolates: S. dysenteriae encompasses 15 serotypes, S. flexneri, 14 serotypes, S. boydii, 20 serotypes and S. sonnei a single serotype. Brutal epidemics of bacillary dysentery can be caused by S. dysenteriae, which produces the Shiga toxins, whereas the endemic forms of the disease are caused essentially by S. flexneri and S. sonnei [2]. The distribution of serogroups varies in different geographical regions; S. flexneri serotypes are most prevalent in India and in Asia [3,4]. In industrialized countries, S. sonnei is the prevalent serotype, which also recently emerged in China, Brazil, Vietnam or Bangladesh following the rapid industrialization of these countries [5-9]. The main causes of these changing geographical distributions remain elusive in some extents. Recent Global Enteric Multicenter Study (GEMS) confirmed the global threat of Shigella as a major cause of moderate-severe diarrhea among children under the age of five in sub-Saharan Africa and South Asia [10,11].

Shigella Vaccine Candidate Development

The design of a pan-Shigella vaccine protecting against all Shigella infections has been made difficult by the diversity of Shigella species and serotypes. In addition Shigella genome is continuously modified by the acquisition or deletion of genes mediated by mobile genetic elements (plasmids, transposons, insertion sequences and integrons). These modifications are the main cause of the generation of novel antibiotic resistant strains, but also the formation of novel Shigella serotype variants [12-15]. Main efforts have been focused on Shigella species and serotypes considered to be important causal agents of human shigellosis: S. sonnei, S. flexneri 2a, 2b and 6. Most Shigella vaccine candidates contain the specific Lipopolysaccharide-associated O-specific polysaccharide (O-SP) antigen, which is specific to one Shigella serotype and is highly antigenic: this is the case for cellular candidates (live-attenuated strains), glycoconjugate candidates (O-SP-protein conjugates) [16], novel antigen candidates, such as Generalized Modules for Membrane Antigens (GMMA) [17] or outer-membrane vesicles (OMVs) alone or encapsulated in
nanoparticles [18]. It has to be noticed that protein-based vaccine candidates in the presence of an adjuvant (i.e. dmLT or MPML) were also successfully evaluated using conserved cell-surface exposed antigen common to all Shigella species such as IpaB/IpaD [19] or PSSP-1 (pan-Shigella surface protein 1) [20]. Several Shigella vaccine candidates’ safety and efficacy were validated in pre-clinical trials and are currently evaluated in humans. Most candidates are in Phase I and II, including live-attenuated strains (S. flexneri 2a CVD 1204, S. flexneri 2a CVD 1200S, S. flexneri 2a SC602, S. sonnei WRSs1 and S. dysenteriae 1 WRSd1), conjugated antigenic molecules (S. flexneri 2a LPS-rEPA, S. sonnei PLS-rEPA, Invaplex, and O-antigen mimic-tetanus toxoid) (as recently reviewed in [21]).

The main difficulty for the assessment of Shigella vaccine candidates’ efficacy remains the lack of an ideal animal model of shigellosis. Shigellosis is characterized by the specific invasion and destruction of the human colonic mucosa by Shigella and rarely occurs in animals other than humans. Shigella are transmitted through the fecal-oral route, no animal reservoir has been described. However, several reports described sporadic shigellosis cases in experimental monkeys [22], pigs [23] or chicken [24]. Several animal models of Shigella infection have been described and used to replicate human shigellosis and assess Shigella virulence or Shigella vaccine candidates’ efficacy, although few of them allowed a step-by-step evaluation of Shigella virulence mechanisms from an oral infection to the colonic invasion and destruction. As a consequence, the evaluation of Shigella vaccine candidates’ protective action remains complicated. The potential and limits of the different animal models of shigellosis are hereafter described.

Animal Models of Shigelllosis

Sansonetti and colleagues went on to pioneer the characterization of the essential role of the Shigella flexneri virulence plasmid (pWRI110) in ligated rabbit ileal loops and in the guinea pig kerato conjunctivitis model (Sereny test) [25]. The attenuation of a Shigella dysenteriae 1 Tox- mutant was validated in ligated rabbit ileal loops and upon intragastric challenge of rhesus macaques (Macaca Mulatta) [26].

Until now the non-human primates rhesus macaque (Macaca Mulatta) model of Shigella infection is the one, which mimics best the shigellosis. It allows to follow Shigella adaptation to the gastric acidic environment, its survival to the small intestine-associated immune response and the invasion, colonization and destruction of the colonic mucosa, associated with bloody stools, intestinal ischemia and the infiltration of polymorphonuclear neutrophils [26,27]. However, this model of shigellosis is expensive and its use is now limited by regulatory and ethical constraints.

Among other large animal model of shigellosis, a young (4-week-old) domestic pig (Sus scrofa domesticus) model was evaluated, although no colonic colonization by Shigella strains (S. dysenteriae and S. flexneri) was observed upon oral administration of pathogens [23]. At the opposite, Shigella dysenteriae 1 oral administration in a piglet model lead to the gastrointestinal track epithelium invasion with a more profound destruction of the colonic mucosa and lamina propria, associated with high levels of IL-8 and IL-12 [28].

Rabbits have been widely used for Shigella infection studies, in particular the ligated rabbit ileal loop model of Shigella infection. This surgical model consists in ligating loops (between 8 and 10 per animal) along the rabbit ileum, allowing replicates of Shigella infections, potentially with different strains in one animal [29,30]. However, in this model the targeted organ is the ileum, not the colon as observed in humans. More specifically, it has been observed that M cells, located in the ileum Gut-associated lymphoid tissue (GALT) are preferentially invaded [29,31]. GALTs are composed of a specialized follicle associated epithelium (FAE), which overlies a subepithelial dome containing numerous macrophages, dendritic cells, T and B lymphocytes, and special antigen sampling microfold cells (M cells). The structure and the organization of M cells containing GALTs in the gut are diverse: Peyer’s patches (PPs) are found in the small intestine and isolated lymphoid follicles (ILFs) are present in the colon [32-34]. The invasion of M cells by Shigella in colonic ILFs remains elusive (as discussed in [35]). More recently a non-surgical rabbit model of enteric Shigella infection was characterized by oral administration of the pathogen. Consistently, the ileum, not the colon, was the major site of tissue infection and necrosis observed in this model [36]. However, this use of this model of shigellosis is now also limited by ethical constraints (moderate animal suffering) since alternative small animal models became available.

Mice are the experimental tool of choice for most host-pathogen interaction studies. However, adult mice do not develop shigellosis upon oral, intragastric or intrarectal challenge with Shigella, for reasons which remain elusive. Among other hypothesis, polymorphonuclear neutrophils, which play a central role during Shigella infection in humans, represents only 10-25% in mouse blood as compared to 50-70% circulating white blood cells in humans [reviewed in [37]]. Second, the gene coding for IL-8, a key chemokine mediating the polymorphonuclear recruitment during Shigella invasion [38] is absent in mice. Despite these limitations, several mouse models have been proposed and used exploiting different inoculation routes rather than oral and/or different targeting organs rather than the colon. Most of these alternative models do not mimic the step-by-step infectious process (from an oral infection to the colonic invasion and destruction). One exception is the newborn mouse model in which the colonic invasion and destruction are observed upon an oral challenge with Shigella strains [39]. However, the newborn mouse innate immune system is still immature: low IL-6 and G-CSF production lead to an inefficient granulopoiesis [40].

The most widely used mouse model of shigellosis is the lethal pulmonary infection (pulmonary pneumoniae model), consisting in an intranasal challenge of adult mice and the subsequent infection of lungs. Although, the targeted organ is not the colon and considering that the lung environment is drastically different from the colonic lumen, this model allowed the validation of glycoconjugate [41] or protein-based vaccine candidates [19]. An intraperitoneal infection mouse model of Shigella infection was proposed, leading to the colonic mucosa invasion, although the dissemination route was not clearly stated [42]. A last interesting mouse model described was the SCID mouse-human intestinal Xenograft model, which consists in the engraftment of human colonic tissue. This model mimics the interaction of Shigella with human intestine in vivo. Inflammation and tissue damages were observed and human intestinal production of IL-1β and IL-8 was
associated with a major influx of polymorphonuclear neutrophils into the graft [43].

Guinea pigs were originally used as the kerato conjunctivitis model, called the Sereny test, consisting in the inoculation of Shigella strains into guinea pigs eye. Conjunctivitis and keratitis occurred when virulent strains were inoculated [25]. More recently, a model of intraretal challenge of young guinea pigs with Shigella was described and validated by different groups [35]. Adult guinea pigs were not efficiently infected by Shigella. In young infected animals, an acute phase associated with the colonic mucosa invasion and destruction by Shigella and a major influx of polymorphonuclear neutrophils was observed (4-12h). Shigella infection was associated with a weight loss and tenesmus. Subsequently, infected animals naturally recover (2-3 days). Although the inoculation route is not oral as compared to shigellosis, the targeted organ is the colon, like in humans. This model has proven to be adapted for the characterization of early innate immune responses during Shigella infection, in particular focusing on the polymorphonuclear neutrophil recruitment at the infection site [44]. However, the potential validation of vaccine candidates’ safety or efficacy or the analysis of the adaptive immune response in this model remains limited, when animals naturally recover after few days.

Other animal models were previously described and deserve further confirmatory experiments, such as the intraperitoneal infection of young chicken [24], the oral challenge of rats with Shigella dysenteriae [45], or the intravenous microinjection of Shigella flexneri in zebrafish larvae [46].

PERSPECTIVES

Until now, in vitro experimentation (genetics, biochemistry, cell biology) and the use of various animal models described here allowed a comprehensive characterization of Shigella virulence mechanisms and the identification of most cell-surface exposed or secreted antigenic factors (Lipopolysaccharide, Peptidoglycan, Type Three Secretion Apparatus, auto transporters) [reviewed in [2,47]]. The colonic luminal environment and the inflammatory response are likely to modulate Shigella virulence mechanisms and the production of antigenic factors. Continuous efforts should be made to validate novel animal models of shigellosis allowing the assessment of Shigella virulence mechanisms from an oral infection to the colonic mucosa colonization and disruption. Several potential models such dedicated CRIPR-Cas9 genome edited mice [48-51] humanized mice or miniature pigs (mini pigs) should be evaluated for their susceptibility to Shigella infection. Taking into account the time (more than 10 years) and the cost of a vaccine development (estimated between US$200 million and US$500 millions per vaccine), characterizing a suitable animal model of shigellosis should be the priority for the evaluation of Shigella vaccine candidates.

REFERENCES

Shigella Vaccine Development: The Model Matters


Cite this article