

Review

Application of biotechnological tools for coccidia vaccine development

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Coccidiosis is a ubiquitous intestinal protozoan infection of poultry seriously impairing the growth and feed utilization of infected animals. Conventional disease control strategies have relied on prophylactic medication. Due to the continual emergence of drug resistant parasites in the field and increasing incidence of broiler condemnations due to coccidia, novel approaches are urgently needed to reduce economic losses. Understanding the basic biology of host-parasite interactions and protective intestinal immune mechanisms, as well as characterization of host and parasite genes and proteins involved in eliciting protective host responses are crucial for the development of new control strategy. This review will highlight recent developments in coccidiosis research with special emphasis on the utilization of cutting edge techniques in molecular/cell biology, immunology, and functional genomics in coccidia vaccine development. The information will enhance our understanding of host-parasite biology, mucosal immunology, and host and parasite genomics in the development of a practical and effective control strategy against *Eimeria* and design of nutritional interventions to maximize growth under the stress caused by vaccination or infection. Furthermore, successful identification of quantitative economic traits associated with disease resistance to coccidiosis will provide poultry breeders with a novel selection strategy for development of genetically stable, coccidiosis-resistant chickens, thereby increasing the production efficiency.

Key words: Chicken, *Eimeria*, coccidiosis, vaccine, biotechnology

Introduction

Intestinal infections such as coccidiosis, salmonellosis, and cryptosporidiosis are prevalent in commercially bred chickens and inflict severe economic losses on the poultry

industry [78,85,88]. Many avian diseases are currently controlled by chemoprophylaxis in ways that promote development of drug resistant pathogens and at great cost to the poultry industry. Prophylactic drug usage also creates unnecessary anxiety in a consuming public already concerned with chemical residues in food. Consequently, the past two decades have witnessed great interest in alternative strategies to control avian diseases. Among the more promising of these are development of new vaccines based upon in depth analysis of the genomes and proteomes of multiple *Eimeria* species, and the characterization of host effector molecules which impact the development of resistance to infection with *Eimeria* species.

Because the life cycle of *Eimeria* comprises intracellular, extracellular, asexual, and sexual stages, it is not surprising that host immunity is also complex and involves many facets of non-specific and specific immunity, the latter encompassing both cellular and humoral immune mechanisms [82,86,128]. Chickens infected with *Eimeria* produce parasite-specific antibodies in both the circulation and mucosal secretions, but humoral immunity plays only a minor role in protection against this disease. Rather, studies conducted at our laboratory implicate cell mediated immunity (CMI) as the major factor conferring resistance to coccidiosis. It is anticipated that increased knowledge on the interaction between parasites and host will stimulate the development of novel immunological and molecular biological concepts in the control of intestinal parasitism crucial for the design of new approaches against coccidiosis.

Life cycle

Eimeria are obligate intracellular parasites that carry out their life cycle in epithelial cells of the intestinal mucosa, often causing serious damage to the physical integrity of the gut. Oocysts ingested by feeding birds excyst to generate invasive sporozoites and sporogony ensues within 24 hours. Sporozoites are first seen within intestinal intraepithelial lymphocytes (IELs), primarily CD8⁺ cells, shortly after invasion [116]. Sporozoites undergo merogony resulting in the release from one sporozoite of about 1,000 merozoites,

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sometimes repeating this stage 2-4 times before merozoites differentiate into the sexual stages, gamonts and gametes. Microgametes (male) fertilize macrogametes (female) to produce oocyst encased by a thick wall impervious to the harshest of environmental conditions and subsequently excreted. Once outside the host, oocysts sporulate and can remain viable for long periods of time before being ingested and starting the life cycle over again.

Host cell invasion and parasite proteins associated with invasion

Invasion of host epithelial cells or cultured cells by sporozoites follows a conserved but complex scheme initiated by contact between the anterior end of the sporozoite and the cell surface [8,38]. The initial contact is followed by internalization of the membrane eventually enclosing the parasite within a vacuole. The invasion is driven by the parasite and is entirely dependent on gliding motility thought to be actin-myosin dependent. Apical organelles of the parasite, the rhoptries and micronemes, are involved in the invasion process. Micronemes are excyctosed during initial contact with the host cell and provide the formation of a moving junction with the host cell membrane. The rhoptries are excyctosed while the parasitophorous vacuole is expanding and are integrated into the vacuole membrane. In some apicomplexans, dense granules are also secreted into the vacuolar space.

Some of the parasite proteins involved in host cell invasion have begun to be characterized by using antibodies [108,118] and by selective labeling with ricin [52]. Micronemes from *E. tenella* contain at least 10 major proteins secreted into culture medium during cell invasion [14,17]. Rhoptries from *Eimeria* contain at least 60 independent polypeptides that can be resolved by 2D-electrophoresis. However, rhoptries from three species of *Eimeria* share few antibody cross-reactive epitopes [113]. Sequencing of genes coding for organelle proteins has shown several domains and motifs conserved among the apicomplexa, particularly the microneme proteins [114]. Several antibodies against surface proteins of *E. tenella* and *E. acervulina* sporozoites blocked invasion of sporozoites into host cells *in vitro* [108,118]. For analysis of protective immunity against *Eimeria in vivo*, chicken monoclonal antibodies with chicken B cell line were made [108] and recombinant single chain variable fragment (scFv) antibodies were constructed to circumvent the problems associated with chicken hybridoma [65,98]. The ability to develop an *in vitro* culture system for other *Eimeria* species would facilitate genomic analysis of developmental stages of *Eimeria* species such as *E. acervulina* and *E. maxima*. High throughput expressed sequence tag (EST) sequencing of *Eimeria* will facilitate functional genomics studies of *Eimeria* to identify parasite genes involved in host invasion.

Immunopathology and pathobiology

Most major enteric parasites, including coccidia, invade the intestinal mucosa and induce a certain degree of epithelial cell damage and inflammation. Extensive damage leads to diarrhea, dehydration, weight loss, rectal prolapse, dysentery, serious clinical illness and, at times, mortality [28]. Reduced weight gains and increased feed conversions are major characteristics of avian coccidiosis, and are the main contributors to the cost of this disease to the poultry industry. Nutrient malabsorption can account for some of the reduced weight gain [106]. However, reduced feed intake due to anorexia is also involved. Klasing *et al.* [66] was among the first to show that growth depression in chickens could be mediated by inflammatory cytokines such as IL-1, and was related to decreased feed intake. Recent investigations [58-60,62,63] have strengthened the concept that the immune, neuroendocrine, and central nervous systems are linked through networks of common receptors and ligands, and that they work together to modulate disease resistance, metabolism, and growth. In particular, it is now known that the expression of leptin, a peptide that homes to the hypothalamus and causes depressed feed intake and reduced energy expenditure, is upregulated by inflammatory cytokines. Finck and Johnson [43] have suggested that hyperleptinemia induced by cytokines is an integral part of the acute phase response, and necessary for comprehensive immunocompetence. Chicken leptin has been cloned [103] and its quantitation methods have been developed [104,105]. Following the leptin response during infections with the separate *Eimeria* species should provide insight into the regulation of weight gain during coccidia infections as well as measuring markers for muscle protein turnover, 3-methylhistidine [41] and growth, IGF-1 [20].

Host defense mechanisms, acute phase proteins and oxidative stress

Cells of the host immune system, commonly macrophages, produce superoxide as a product of phagocytosis and nitric oxide when stimulated by interferon (IFN) or other cytokines. Both superoxide and nitric oxide, as well as peroxy-nitrite, a reaction product, are toxic to parasites. In order to survive, parasites must detoxify these reactive oxygen and nitrogen species. Some utilize antioxidant enzymes such as superoxide dismutase (SOD), catalase and glutathione peroxidase. These enzymes are electrophoretically distinct from homologous host enzymes [54]. Of the avian *Eimeria*, only unsporulated oocysts of *E. tenella* have high levels of SOD [97]. The sporozoites have only low levels. The existence of glutathione-based defense mechanisms for avian *Eimeria* has not been investigated as yet, although they are present in parasites such as trypanosomes [29]. However, *E. tenella*, and presumably other avian *Eimeria*

species, have a mannitol cycle which may serve the purpose of keeping the parasite protected from an oxidative environment [109]. Knowledge of the intermediary metabolism of avian *Eimeria* has come mainly from analyses of *E. tenella* that develops in the relatively anaerobic environment of the intestinal cecum, and some investigators have concluded that avian *Eimeria* are facultative anaerobes [29].

Alpha-1-acid glycoprotein [22], hemopexin [48] and ovotransferrin [53] also are known to be acute phase response proteins in chickens. These proteins may vary characteristically with the infecting species of *Eimeria* and could serve as biomarkers of resistance and susceptibility. Some metal binding proteins (metallothionein and ceruloplasmin) are apparently differentially elevated in acute infections with *E. acervulina* and *E. tenella* [102].

There is an increased recognition of the importance of oxidative stress as an initiator of signal transduction in biological processes [42,44,111]. Externally or internally generated free radicals such as superoxide and nitric oxide [18,100], or changes in the redox potential of cells [37,67, 101,110], can lead to production of second messengers and transcription factors that up-regulate genes expressing antioxidant factors, including enzymes that counteract the oxidative stress [42]. Oxidative stress is an important regulator of immunity [30,36,70] and an important component of host-parasite interactions [7,40,54,99]. Production of free radical species accompanies infection by murine coccidia and all species of avian coccidia [1-3]. Furthermore, recent experiments showed that major alterations in whole body thiol balance, as illustrated by significant reductions in both reduced and oxidized whole blood glutathione, occur from days 3-10 post-infection with *E. acervulina* and *E. tenella*. Reduced glutathione is one of the major cellular components maintaining a reduced intracellular environment in normal cells [5]. Expression of enzymes that control glutathione and other cellular antioxidant components are regulated by cytokines and other biological messenger molecules elaborated during the immune response. Application of genomic analyses over time courses of infection to investigate the enzymes catalyzing both the oxidative response to parasite invasion as well as the host enzymes that counteract oxidative stress could provide important clues to innate resistance and development of immunity to coccidiosis.

Gut-associated lymphoid tissues (GALT)

The mucosal immune system is composed of the mucosal-associated lymphoid tissues (MALT) of the nasal passage, bronchial organs, mammary glands, genital tract, and gut-associated lymphoid tissues (GALT) [13,94,95]. The most important role of the MALT is to destroy invading pathogens at their port of entry to prevent dissemination and

systemic infection throughout the host. This function is accomplished in a number of different ways. Non-specific barriers such as gastric secretions, lysozyme and bile salts, peristalsis, and competition by native microbial flora provide an important component of the first line of defense in the MALT [107]. Specific defense mechanisms are mediated by antibodies and lymphocytes. The specific mechanisms for elimination of harmful pathogens involve complex interactions among humoral and cellular immunity utilizing both antigen specific and antigen independent processes that have evolved to detect and neutralize invading microorganisms.

More than half of the total lymphocyte pool of the MALT is contained within the GALT. Histologically, the outer layer of the GALT consists of epithelial cells and lymphocytes situated above the basement membrane. Beneath the basement membrane is the lamina propria, also containing lymphocytes, and the submucosa. In chickens, a variety of specialized lymphoid organs (Peyers patches, caecal tonsils and bursa of Fabricius) and cell types (epithelial, lymphoid, antigen presenting and natural killer cells) have evolved in the GALT to defend against harmful pathogens. Other cell types in the GALT include macrophages, mast cells, fibroblasts, and dendritic cells. All of these cells are known to secrete and respond to cytokines. Cellular communication networks within the GALT, important for development of protective immunity, are bi-directional with lymphocytes secreting and responding to cytokines that stimulate or inhibit the activities of other lymphocytes and non-lymphoid, resident cells.

The mucosal immune system contains a number of unique cell types reflective of its evolution as the first line of immune defense [6]. T and B lymphocytes and plasma cells are located in the mucosa of the small and large intestines. T cells are predominantly CD4⁺ memory/effector T cells while B cells and plasma cells are largely of the IgA isotype. Within the intestinal mucosa, lymphocytes are present in two anatomic compartments, the epithelium (IELs) and lamina propria (lamina propria lymphocytes) [9]. As with mammals, chicken IEL T cells can be phenotypically separated into CD4⁺ and CD8⁺ subpopulations [23]. Molecular complexes similar to human and murine CD3, CD4, and CD8 antigens have been identified on chicken IELs [23,73]. The ontogeny of T cells bearing the two different T cell receptor (TCR) molecules has been studied [15,119].

Adaptive immune responses to *Eimeria*

In general, the GALT serves three functions in host defense against enteric pathogens, processing and presentation of antigens, production of intestinal antibodies and activation of CMI. The role of parasite specific antibodies both in serum and mucosal secretions has been

extensively studied in coccidiosis [46,47,72,115]. In infected chickens, production of specific antibodies, IgA and IgM in particular, was always significantly greater in parasitized areas of the intestine compared with areas devoid of parasites [46]. However, the ability of antibodies to limit infection is minimal, if any, since agammaglobulinemic chickens produced by hormonal and chemical bursectomy are resistant to reinfection with coccidia [71]. Nevertheless, IgA may attach to the coccidial surface and prevent binding to the epithelium by direct blocking, steric hindrance, induction of conformational changes, and/or reduction of motility. Mucosal IgA responses were regulated by T helper cells and cytokines [126].

It is clearly documented that CMI mediated by antigen specific and non-specific activation of T lymphocytes, natural killer (NK) cells and macrophages plays the major role in protection against coccidia [12,21,86,128]. The importance of T cells in acquired immunity to coccidia has been well documented [82]. For example, changes in intestinal T cell subpopulations in the duodenum following primary and secondary *E. acervulina* infections have been investigated and correlated with disease [75,79,82]. Following secondary infection, a significantly higher number of CD8⁺ IELs was observed in SC chickens, which manifested a lower level of oocyst production compared to TK chickens. In summary, these results identified variations in T cell subpopulations in the GALT as a result of coccidia infection and suggested that increase in $\alpha\beta$ TCR⁺CD8⁺ IELs in SC chickens may contribute to their enhanced immunity to *Eimeria* compared with TK chickens [77,80,81]. The immunological basis for the genetic difference in disease resistance has been addressed by recent studies, which showed different kinetic and quantitative response in local cytokine production between SC and TK chickens following *Eimeria* infection [130,131]. IFN- γ mRNA in caecal tonsils was higher in SC chickens following primary infection with *E. acervulina* [26]. Zhang *et al.* [132,133] investigated the effect of a cytokine with tumor necrosis factor activity on the pathogenesis of coccidiosis in SC and TK chickens. In summary, these results all emphasize the importance of CMI in protective immunity to coccidiosis.

Cytokine production during CMI to coccidiosis

In contrast to the plethora of mammalian cytokines, only a few chicken homologues have been described, the main ones being IFN- γ , TGF, TNF, IL-2 and IL-15 [82,89]. T lymphocytes and macrophages are the most likely sources of cytokine production in the intestine [79]. Intestinal lymphocytes have been observed in direct contact with parasitized epithelial cells promoting the hypothesis that they are producing cytokines and thereby modulating the immune response [80,116,117]. The availability of recombinant chicken IFN- γ and its monoclonal antibodies

has led to a better understanding of its physiologic and immunologic roles in chicken coccidiosis [83,90,91,129]. Administration of exogenous recombinant IFN- γ to chickens significantly hindered intracellular development of *Eimeria* parasites and reduced body weight loss [87]. When chicken fibroblast cells transfected with the IFN- γ gene were infected with *E. tenella* sporozoites, significant reductions in parasite intracellular development occurred although the ability of parasites to bind and invade host cells was not affected [87]. Although the biological function of this cytokine in the intestine requires further investigation, these results indicate a major role of CMI in protective immunity to pathogens in this organ.

Application of poultry genomics for control of coccidiosis

Tremendous success in the improvement of commercial chicken growth, reproduction and feed efficiency has been accomplished using classical genetic breeding techniques. However, selection of commercial poultry stocks for improved disease resistance using similar breeding techniques has been unsuccessful due to technical difficulties [45]. Although selection based on progeny tests may be used to avoid this negative impact, as demonstrated by selection of broiler strains with enhanced antibody responsiveness to *Salmonella enteritidis* [61], this is a labor-intensive, time consuming and costly approach. Moreover, lack of a clear understanding of the mechanisms of protective immunity against most avian diseases makes genetic selection of stocks with enhanced disease resistance very difficult [84]. DNA marker technology avoids many of these problems, making it easier to select animals with superior performance for resistance to particular diseases of commercial importance. In the DNA marker approach, phenotypic traits for disease resistance are measured in genetically diverse animals challenged with the pathogen of interest. DNA marker(s) associated with disease resistance are identified in particular genotypes and subsequently used for marker-assisted selection of breeding stocks.

Most of the economically important traits (quantitative traits) of food animals are regulated by multiple genes that manifest different effects and are continuously distributed in the population. The loci affecting these traits are referred to as quantitative trait loci (QTL) [4,92,93]. With DNA marker technology and statistical methodology, it is possible to map QTL on chromosomes. DNA marker-based methods have had a significant impact on both gene mapping and animal breeding [35]. Genetic mapping using DNA markers that cover the entire genome, with defined intervals between the markers is called whole genome scanning. Candidate genes that potentially affect traits of interest and are positively correlated with QTL can thus be mapped on the genome. To map QTL efficiently, a linkage map with high marker

density is required. Bumstead and Palyga [16] reported the first DNA marker linkage map of the chicken genome. Currently, more than 1,800 DNA-based genetic markers are available for chicken genotyping [51]. A large number of these markers have been mapped to chicken linkage groups [24,25,31-33,50,51,68,69]. The current chicken linkage map covers more than 95% of the entire genome and provides sufficient marker density for QTL mapping with an average interval of less than 20 cM [50]. QTL affecting animal growth [49,122], feed efficiency [123], carcass traits [124], and Marek's disease [120,121,125,127] have been reported.

In general, larger population sizes increase QTL detection power. Groenen *et al.* [50] suggested that with 100% genome coverage, the preferred distance between adjacent markers is 20 cM or less to map loci affecting quantitative traits in initial genetic mapping studies. Given the size of the chicken genome, approximately 200 evenly spaced markers are needed to cover the entire genome. The distance (m) of 20 cM is equal to 0.165 of the recombination fraction (r) according to Haldanes mapping function, $r = 0.5 (1 - e^{-2m})$. For example, in the broiler chickens used in our study, the marker MCW0058 affecting animal growth (selected trait) is 20 cM from the marker LEI0101 affecting coccidiosis resistance (non-selected trait). By computer simulation, a 50 cM marker interval was found to be optimal or close to optimum for initial studies in a variety of experimental designs, if experimental cost is a limiting factor [34].

The chicken genome comprises 39 pairs of chromosomes, 8 pairs of cytologically distinct chromosomes, one pair of sex chromosomes (Z and W), and 30 pairs of small, cytologically indistinguishable microchromosomes. The size of chicken genome is estimated to be 1.2 billion base pairs [11] and approximately 3,500 to 4,000 cM in genetic length. Therefore, 1 cM is equivalent to approximately 350 kb. There are several high capacity vectors available to clone chicken genomic DNA. These include cosmids (maximum insert size = 30-45 kb), bacteriophage P1 (70-100 kb), P1 artificial chromosomes (130-150 kb), bacterial artificial chromosomes (BAC, 120-300 kb), and yeast artificial chromosomes (250-400 kb). Among these, BAC are the most attractive vectors because they are stable, capable to propagate very large DNA fragments and easy to manipulate. Recently, two chicken genomic DNA libraries were constructed at the Texas A&M BAC Center. Both were derived from the Red Jungle fowl (UCD 001) with the intention of maximizing genetic heterogeneity in expressed clones. The first library was derived from *Hind* III-digested genomic DNA and inserted into the BAC vector pECBAC1. It contains 49,920 clones representing 5.4-times genomic coverage. The average insert size of this library was estimated to be 130 kb. The second library was created from *Bam* HI partial digests of UCD 001 genomic DNA cloned into pBeloBAC11. Its average insert size was estimated to be 150 kb. This library is also maintained at the University

of Michigan by Dr. Jerry Dodgson (Coordinator for NAGRP/NRSP-8). For these studies, both libraries will be used to construct BAC clone contigs covering the chromosomal region of interest.

DNA microarray for gene expression studies

In addition to DNA marker and cloning technologies, DNA microarray is another revolutionary tool for genomic study of interesting traits. By immobilizing thousands of DNA sequences in individual spots on a solid phase, DNA microarray allows simultaneous analysis of a large number of genes in a single step, thereby identifying genes whose expression levels are altered during natural biological processes or experimental treatments or vary due to genetic differences [39]. In one approach, the sample of interest, such as mRNA isolated from a certain tissue, is used to synthesize cDNA labeled with colored substances (e.g., fluorescent dyes like Cyanine). The labeled cDNA probes (both Cy3 and Cy5) are then hybridized to the array at 42°C for 16-18 h. and a post-hybridization image is scanned to capture fluorescence images using a ScanArray 4000 Microarray Analysis System (GSL Lumonics) and is analyzed using ScanAlyze software developed at Stanford University. The color density of individual nucleic acid species reflects the relative amount of labeled cDNA hybridized to the DNA immobilized at the known position of the array. By comparing samples tested in well-controlled conditions, change of expression levels of individual genes can be detected. The DNA sequences immobilized on an array are usually produced by PCR from genes whose sequences are partially or completely known. This technique has been widely used to detect gene mutations and polymorphisms, gene expression profiling, genetic linkage, sequence analysis, and single nucleotide polymorphism-based tests [96]. While only a small number of chicken genes have been cloned and completely sequenced, more than 5,000 chicken ESTs from mitogen-activated chicken T cell and macrophage cDNA libraries [112] are currently available for designing DNA microarrays. Using EST sequences from activated T-cell cDNA library, several genes associated with immune response have been identified using DNA array.

Several methods exist to quantify microarray signals and the best method to use is often based on how well each measurement correlates with the amount of DNA probe hybridized to each printed spot. Quantitation can be based on the following signal parameters: total (sum of intensity values of all pixels in a spotted area), mean, median, mode (most likely intensity value), volume (difference between signal mean and background multiplied by signal area), intensity ratio of two colors, or correlation ratio [134]. The best method for a particular experimental design can be determined by analysis of duplicate experiments. Data

normalization and transformation are other important processes to improve the quality of array data [134]. Many analysis methods have been implemented in commercial software. Differences in gene expression detected by DNA microarray have been demonstrated to be highly correlative with the results of Northern blot analysis [10].

Vaccines against *Eimeria*

Identification of parasite life cycle stages and development-specific antigens inducing protective immunity is a critical step in recombinant protein vaccine development. In the case of *Eimeria*, recombinant forms of both parasite surface antigens and internal antigens have been investigated as vaccine candidates. Sporozoites are the preferred parasitic form for preparation of recombinant vaccines because they are relatively easy to obtain and blocking their activities should theoretically prevent infection. Cell surface antigens are logical components of vaccines because of their direct role in host-parasite interactions. cDNAs encoding a 22 kDa surface protein and EAMZp30-47 protein of *E. acervulina* sporozoites were cloned and expressed [55,56,57]. The recombinant protein (MA1) induced significant *in vitro* activation of T lymphocytes obtained from chickens inoculated with *E. acervulina* [74]. A cDNA (MA16) from *E. acervulina* encoding an immunogenic region of a surface antigen shared between sporozoites and merozoites was cloned, expressed in *E. coli* and shown to activate T lymphocytes *in vitro* from *E. acervulina* immune chickens [19]. Intramuscular immunization with a recombinant p250 surface antigen of *E. acervulina* merozoites or oral inoculation with live *E. coli* expressing p250 resulted in antigen specific *in vitro* T cell and humoral responses and conferred significant reduction in mucosal parasitism [64,76]. Vaccination with *E. coli* expressing a recombinant protein is more effective than immunization with the protein alone since bacteria growing in the intestine continuously express the recombinant protein thus providing antigenic stimulation over an extended period of time.

DNA vaccines employ genes encoding immunogenic proteins of pathogens rather than the proteins themselves. They are administered directly in conjunction with appropriate regulatory elements (promoters, enhancers) permitting the encoded protein to be expressed in its native form and thereby recognized by the host's immune system in a manner that simulates natural infection. DNA vaccination requires gene transfer and expression of the antigen in tissues accessible to the immune system such as the skin, muscle or mucosal surfaces. Lillehoj *et al.* [87] observed immune protection manifested by significantly reduced fecal oocyst shedding in chickens vaccinated subcutaneously with a cDNA encoding an *E. acervulina* protein (3-1E). Further protection was obtained when the 3-1E cDNA was administered in conjunction with cDNAs

encoding chicken IFN- γ or IL-2 [27,87]. These results raise the exciting possibility of using IFN- γ and/or IL-2 immunoprophylactically to control coccidiosis in commercial poultry flocks. In spite of the advantages of DNA vaccines over conventional vaccines, the negative side factors such as the genetic background of the recipient must be considered [72,78,85].

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