Expression, purification, and characterization of the *Necator americanus* aspartic protease-1 (*Na*-APR-1 (M74)) antigen, a component of the bivalent human hookworm vaccine

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Over 400 million people living in the world's poorest developing nations are infected with hookworms, mostly of the genus *Necator americanus*. A bivalent human hookworm vaccine composed of the *Necator americanus* Glutathione S-Transferase-1 (*Na*-GST-1) and the *Necator americanus* Aspartic Protease-1 (*Na*-APR-1 (M74)) is currently under development by the Sabin Vaccine Institute Product Development Partnership (Sabin PDP). Both monovalent vaccines are currently in Phase 1 trials. Both *Na*-GST-1 and *Na*-APR-1 antigens are expressed as recombinant proteins. While *Na*-GST-1 was found to express with high yields in *Pichia pastoris*, the level of expression of *Na*-APR-1 in this host was too low to be suitable for a manufacturing process. When the tobacco plant *Nicotiana benthamiana* was evaluated as an expression system, acceptable levels of solubility, yield, and stability were attained. Observed expression levels of *Na*-APR-1 (M74) using this system are ~300 mg/kg. Here we describe the achievements and obstacles encountered during process development as well as characterization and stability of the purified *Na*-APR-1 (M74) protein obtained from representative 5 kg reproducibility runs performed to qualify the *Na*-APR-1 (M74) production process is also presented. This process has been successfully transferred to a pilot plant and a 50 kg scale manufacturing campaign under current Good Manufacturing Practice (cGMP) has been performed. The 50 kg run has provided a sufficient amount of protein to support the ongoing hookworm vaccine development program of the Sabin PDP.

Introduction

New estimates from the Global Burden of Disease Study 2010 (GBD 2010) indicate that 439 million people residing in impoverished areas of South and Southeast Asia, Oceania, Africa, and Latin America live with hookworms in their gastrointestinal tracts.^{1,2} The most prevalent human hookworm species is *Necator americanus*, which has the ability to cause intestinal blood loss leading to anemia.³ GBD 2010 has further determined that hookworms are now a leading cause of anemia in many developing countries,⁴ especially affecting children⁵ and pregnant women.⁶

Adult hookworms cause anemia by ingesting human blood at their site of attachment in the small intestine. In order for the parasite to utilize blood as a source of nutrition, its gut is lined with proteases which catalyze the hydrolysis of host hemoglobin.^{7,8} A major enzyme involved in the process of hemoglobin hydrolysis is *N. americanus* Aspartic Protease-1 (*Na*-APR-1), a 45 kDa protein member of the cathepsin D aspartic protease family. The *Na*-APR-1 protein is expressed in the gut of the adult *N. americanus* parasites where it functions in concert with the cysteine protease *Na*-CP-3 and the metalloprotease *Na*-MEP-1 to digest the hemoglobin tetramer.^{7–9} Due to its role

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in hemoglobin digestion, Na-APR-1 was selected as a candidate for the development of a hookworm vaccine since neutralization of this crucial enzyme would result in starvation of the parasite and concomitantly could lead to parasite death and the prevention of blood loss in the infected host. In support of this hypothesis, vaccination of dogs with the canine homolog of the wild type Na-APR-1 (Ancylostoma caninum-APR-1) resulted in the production of neutralizing antibodies against the hookworm hemoglobinase and thus, higher level of hemoglobin in the blood of vaccinated dogs compared to the non-vaccinated control group, as well as a reduction in both egg counts and adult parasite burden in the gut of the infected host.¹⁰ Likewise, hamsters immunized with Ac-APR-1 also showed a significant reduction in worm burden.¹¹ These findings led to the development of an experimental human hookworm vaccine comprised of Na-APR-1, together with N. americanus glutathione S-transferase 1 (Na-GST-1) a unique hookworm enzyme that functions in heme binding and detoxification.¹²⁻¹⁵ The goal of the vaccine strategy is to elicit neutralizing antibodies to both enzymes which would inhibit the parasites ability to detoxify and eliminate heme as well as utilize host hemoglobin for survival.

During development of the aspartic protease based component of the human hookworm vaccine, the catalytic active site of *Na*-APR-1 was inactivated by mutating the aspartic acid residues at positions 113 and 300 to alanine residues (*Na*-APR-1 (M74)). The rationale for the change was to circumvent potential toxicities of immunizing humans with an active proteolytic enzyme. Vaccination of canines with *Na*-APR-1 (M74) followed by a heterologous challenge with the canine hookworm *Ancylostoma caninum* resulted in a significant reduction in both parasite egg burden and weight loss.⁹ In addition, vaccination with *Na*-APR-1 (M74) induced antibodies that not only bound to the native enzyme in the parasite gut, but also neutralized enzymatic activity of both wild type *Na*-APR-1 as well as APR-1 orthologues from 3 other hookworm species that infect humans.⁹

The production of Na-APR-1 (M74) protein at high yields and with adequate stability, however, has been challenging due to the very low expression levels observed in *P. pastoris* and the lack of solubility of the Escherichia. coli expressed protein. Attempts to solubilize Na-APR-1 (M74) with chaotropic agents followed by refolding the protein proved difficult to achieve. In contrast to P. pastoris and E. coli, evaluation of the tobacco plant N. benthamiana as a potential expression system resulted in both acceptable yields and stability of the aspartic protease. In support of using this expression system for process development and ultimately scale up, plants have been shown to be a good alternative for recombinant protein production due to their ability to generate a high biomass with the potential for high protein expression.¹⁶ Being a eukaryotic system, plants are able to perform post-translational modifications to the target protein, thus making the protein more similar to the native protein. Furthermore for the purpose of vaccine manufacturing and safety concerns, plants do not harbor pathogens which can endanger humans.¹⁷⁻¹⁹ The cost of producing a recombinant protein in transgenic plants as compared to E. coli or other expression hosts could be 10-50 fold lower depending on the

plant strain used.²⁰ There are many examples of recombinant proteins manufactured in plants which are being used as effective vaccines for diseases such as influenza, anthrax, and plague.^{21,22,24,28} However, heterologous protein expression in plants does face many hurdles that must be overcome. Recombinant proteins which express at low levels in plants require considerable effort to isolate from the milieu of total plant proteins. Recovery can be compromised when isolating a low abundance target as described herein. While no products transiently expressed in tobacco have yet been approved by the FDA, Taliglucerase alfa which is produced in transgenic carrot cells at commercial scale by Protalix BioTherapeutics was approved in 2012. Facilities which utilize controlled plant growth and infiltration processes for heterologous protein expression in whole plants that conform to current Good Manufacturing Practice (cGMP) guidelines have been described.^{32,33} Although our system is using a non-transgenic plant which does not require the permits and strict containment plans required for transgenic plants,³¹ the system has yet to be tested at commercial manufacturing scale. With plant expression technology, there are additional hurdles which must be overcome including issues related to safety of potential contaminating proteins, cultivation, and downstream processing.34

Fraunhofer USA Center for Molecular Biotechnology (FhCMB; Newark, DE) has developed a transient plant-based hybrid expression system for the production of vaccine antigens by infiltration of N. benthamiana with Agrobacterium tumefaciens which harbor an expression vector containing viral vector sequences for controlling target gene expression. The FhCMB system has been successfully implemented and utilized to produce Phase 1 material for 5 human clinical trials. Na-APR-1 (M74) without the native pro-sequence (residues 1-73) was codon optimized for expression in N. benthamiana and engineered to include a PR-1a signal sequence at the N-terminus for protein secretion and a C-terminal 6-HIS tag to ease purification. Na-APR-1 (M74) was then cloned into the hybrid vector system and used to express Na-APR-1 (M74) at \sim 300 mg protein per kg plant biomass with approximately 60% solubility. Purification of the target protein resulted in final yields of 7-10 mg per kg biomass with a purity of >90%. Here, we describe the process development and characterization strategy of the in process and purified protein samples obtained from representative 5kg scale reproducibility runs performed to qualify the Na-APR-1 (M74) production process. In addition, we present data from the stability assessment of Na-APR-1 (M74) purified at the 5Kg scale. The process reported here was successfully transferred to a pilot plant and a 50 kg scale manufacture has been performed under current Good Manufacturing Practice in support of Phase I trials.

Results

Expression and purification of *Na*-APR-1 (M74) from *N. benthamiana*

The general structure of the Na-APR-1 (M74) expression cassette and the amino acid sequence is shown in Figures 1A-B, respectively. The time between infiltration of N. benthamiana with the Agrobacterium and harvesting of the plants was 6 days as determined by analyzing the accumulation of Na-APR-1 (M74) between 5 to 7 days post infiltration (Table 1). Western blot analysis indicate similar target protein levels at 5 or 6 days post infiltration as well as similar levels of total soluble target protein for 2 different agrobacteria clones screened. A reduction in both total target protein and total soluble target protein levels were observed for clone 1 on 7 days post infiltration, thus 6 days was chosen for biomass harvest. Na-APR-1 (M74) expression level was based on the relative intensity between the extracted Na-APR-1 (M74) and an arbitrary 6-His tagged protein by Western analysis using an anti-histidine antibody. The estimation of total Na-APR-1 (M74) expression (300 mg/kg) is

based on quantitative Western blot analysis (data not shown). After expression in N. benthamiana followed by extraction and clarification, Na-APR-1 (M74) was purified using a 3 column chromatography method composed of an immobilized metal affinity chromatography step (IMAC) followed by anion exchange (AEX) and finally a size exclusion chromatography (SEC) step. During process development, IMAC was incorporated as the first capture step to significantly enrich for the target protein due to the low percentage of Na-APR-1 (M74) in comparison to the contaminating plant proteins. Additional downstream methods were investigated which included various ion exchange and size exclusion chromatographic methods as well as various binding conditions and solubilizing agents to further increase the purity of the target protein. The process overview of the final Na-APR-1 (M74) production process is shown in Figure 2A and the basic processes performed at each step is given in Figure 2B. During development of the production process, purification was performed using Na-APR-1 (M74) extracted from plant biomass at the 1 and 5 kg scale. SDS-PAGE analysis of Na-APR-1(M74) samples collected throughout the purification process is shown in Figure 3. The protein migrates as a doublet with a molecular weight of approximately 42 kDa. Analysis of in-process and purified Na-APR-1(M74) samples using rabbit anti Na-APR-1 polyclonal antibodies and commercial anti-HIS antibodies suggests that the doublet observed on SDS-PAGE may be the result of C-terminal truncation. In fact, it was observed that while both bands reacted with the anti Na-APR-1 antibody, only the higher molecular weight band reacted with the anti-HIS antibody (data not shown), indeed suggesting the loss of the His tagged C-terminal. SDS-PAGE analysis of a nonreduced IMAC elution sample from a 5 kg preparation is shown in Figure 3, Lane I. A significant reduction in contaminating host proteins is present in the IMAC elution as expected (Fig. 3,

A PR1a Na-APR-1(M74)								
Residues 74-446 Na-APR-1								
= 6His-KDEL								
В								
MGFVLFSQLP	SFLLVSTLLL	FLVISHSCRA			-30			
ASKLQSANEI	DELLRNYMDA	QYYGVIQIGT	PAQNFTVIFA	TGSSNLWVPS	50			
RKCPFYDIAC	MLHHRYDSGA	SSTYKEDGRK	MAIQYGTGSM	KGFISKDIVC	100			
IAGICAEEQP	FAEATSEPGL	TFIAAKFDGI	LGMAFPEIAV	LGVTPVFHTF	150			
IEQKKVPSPV	FAFWLNRNPE	SEIGGEITFG	GVDTRRYVEP	ITWTPVTRRG	200			
YWQFKMDMVQ	GGSSSIACPN	GCQAIAATGT	SLIAGPKAQV	EAIQKYIGAE	250			
PLMKGEYMIP	CDKVPSLPDV	SFIIDGKTFT	LKGEDYVLTV	KAAGKSICLS	300			
GFMGMDFPEK	IGELWILGDV	FIGKYYTVFD	VGQARVGFAQ	AKSEDGFPVG	350			
TPVRTFRQLQ	EDSDSDEDDV	FTFHHHHHHK	DEL		383			

Figure 1. Expression construct for Na-APR-1 (M74). (A) Schematic of the expression construct for Na-APR-1 (M74), and (B) Na-APR-1 (M74) amino acid sequence. The PR-1a signal peptide is shown in bold.

Lane I vs. Fig. 3, Lane H). The average yield of Na-APR-1 (M74) at the IMAC step from 3 independent experiments performed at the 5 kg scale was 79 \pm 7 mg/kg biomass (data not shown). After elution from the IMAC column, the protein was stored at 2-8°C until the sample was prepared for ion exchange chromatography. Prior to ion exchange chromatography, the IMAC eluate was equilibrated to room temperature and an equal volume of Q Solution A was added to maintain the conductivity at <17 mS/cm to allow for target binding. After equilibration to room temperature, the adjusted IMAC elution pool was loaded onto the Q Sepharose (QFF) column followed by washing with 56 mM NaCl and elution with 560 mM NaCl. The Q Sepharose elution fractions with a cumulative concentration >1.8 mg/ mL were analyzed by reducing SDS-PAGE and fractions enriched with Na-APR-1 (M74) were pooled (Fig. 3, Lane Q). SDS-PAGE analysis of the pooled Q elution fraction (QP)

Table 1. Expression and solubility screening for *Na*-APR-1(M74) agrobacteria clone. Expression level and solubility of *Na*-APR-1 (M74) 5–7 days post infiltration (DPI) based on Western analysis

Days Post Infiltration	Clone 1		Clone 2		
	Expression (mg/kg)	Solubility	Expression (mg/kg)	Solubility	
5 DPI TST	44	59%	42	48%	
5 DPI TP	75		88		
6 DPI TST	40	54%	42	48%	
6 DPI TP	74		88		
7 DPI TST	31	80%	42	48%	
7 DPI TP	39		88		

DPI - days post infiltration

TST – total soluble target

TP – Target protein, total

Harvest & Clarification	Extraction / Clarification Harvest fresh biomass at 4°C	IMAC at 4°C Chelating Sepharose Big Beads
MAC Chromatography	 Triton extraction at 4°C for 20 minutes Centrifugation Depth filtration 	 5.5 min residence time Triton wash after loading Tris/ Borate/ EBB wash to remove Triton and National Nation
AEX Chromatography	• 0.2 µm filtration	150 mM imidazole elution300 mM imidazole strip
SEC Chromatography	AEX - Q Sepharose FF at RT	4°C hold until Q FF step SEC - Superdex 200 at RT
↓ Bulk Storage	IMAC-E warmed to R1 Dilution with Q Solutin A Sample pH and conductivity confirmation O FF loading	 Fractionation based on chromatogram Aggregate (A1/A2), pre-monomer (M1), main monomer (M2) and monomer tail (MT) pooling 0.2 µm filtration of main monomer (M2) pool
	 Q Wash with 56 mM NaCl Q Elution with 560 mM NaCl O Strip with 1 M NaCl 	Shipment of final bulk purified protein

Figure 2. Process Schematic Overview. (A) Schematic of the purification process of Na-APR-1 (M74). (B) Summary of the process steps for the harvest/clarification and for each chromatography step.

indicated a QFF yield of approximately $17 \pm 4 \text{ mg } Na$ -APR-1 (M74) per kg biomass as determined by densitometric comparison to BSA standards of known concentrations (data not shown). Based on the quantitative SDS-PAGE analysis, the Q pool contained 91 \pm 15 mg of Na-APR-1 (M74) (average from 3 5kg preparations). Prior to performing SEC chromatography, the Q pool was divided into equal fractions in order to keep the SEC load volume between 3.4 - 4.0% of the CV for each of the SEC runs to ensure sufficient resolution and separation of proteins. Fraction collection during each SEC run was based on 1) separation of the Na-APR-1 (M74) monomer from the aggregate

contaminants and 2) a cumulative concentration of not less than 0.2 mg/mL to provide a final acceptable concentration for later formulation. The SEC fractions observed consisted of an aggregate upslope (A1), aggregate downslope (A2), pre-monomer (M1), main monomer (M2) and post monomer tail (MT) portions (Fig. 4A). Separation of the monomer from aggregate was determined by non-reducing SDS-PAGE analysis of the first SEC run fractions (Fig. 4B). Division points were determined by examining each fraction for the presence of high molecular weight contaminants that could be seen in the aggregate downslope (A2) and pre-monomer (M1) fractions (Fig. 4B; lanes 2).





(A2) versus lanes 3-8 (M1)). Fractions containing high molecular weight contaminants were not used for SEC pooling. The endpoint for the SEC M2 fraction (main monomer) was based on maintaining the cumulative pooled concentration above 0.2 mg/mL. Reduced SDS-PAGE analysis of the final purified Na-APR-1 (M74) protein is shown in Figure 5. Analytical SEC of the IMAC elution pool (IMAC), the Q elution pool (AEX), and the final purified Na-APR-1 (M74) protein (Final) is shown in Figure 6. Data indicates that the SEC step significantly reduces the aggregate peak resulting in enrichment of the Na-APR-1 (M74) target monomer. The final yield of purified bulk Na-APR-1 (M74) after the SEC step was 8.6 ± 2.0 mg per kg biomass based on the average of 3 runs.

Characterization of the *Na*-APR-1 (M74) and accelerated stability studies

The recombinant Na-APR-1 (M74) was characterized after purification to

ensure purity and integrity of the sample prior to vaccine formulation. Characterization included visual inspection, determination of the pH, measurement of the protein concentration by absorbance at 280 nm (Table 2), evaluation of the separation profile by SEC-HPLC, SDS-PAGE followed by Coomassie Blue staining, Silver Staining and Western blot (Fig. 7). Immediately after elution, the protein sample was analyzed and aliquots were placed at 2–8°C, 25° or 37°C for a time period of 30 days for accelerated stability studies. At days 7, 15 and 30, samples were removed from the storage temperatures and tested for the same parameters as described above. Although the pH and protein concentration of

these samples did not vary significantly across the storage conditions tested, degradation products were detected by SDS-PAGE followed by Coomassie Blue staining and Silver Staining after 7 days (Fig. 8A,B), and increasingly after 15 (Fig. 8D,E) and 30 days (Fig. 8G,H). Similar degradation products were observed when the samples were analyzed by Western blot after 7 days, 15 days, and 30 days (Fig. 8C,F,I). The SEC-HPLC elution profiles for the different time points are shown in Figures 9A–I.

Protein stability after freeze/thaw (F/T)

The study was carried out as described in Curti et al., 2014. After each freeze/thaw cycle, Na-APR-1 (M74) was characterized by the analytical methods previously described. The data indicated a progressive, but subtle degradation of the molecule after each freezethaw cycle. The samples maintained their color and appearance properties as well as pH, but a subtle increase of the absorbance reading was observed upon the last freeze/thaw cycle (Table 2B). When SDS-PAGE, only analyzed by traces of Na-APR-1 (M74) degradation products were observed at each freeze thaw cycle (Fig. 10D) which were detected by Western blot (Fig. 10E) and SEC-HPLC (Fig. 10A-C). While the samples still retained an SEC-HPLC elution time of approximately 13 minutes, the overall SEC-HPLC elution profiles of the samples after the second and third freeze/thaw cycles indicated increasing signs of degradation, with a reduction in the sample peak area (μV^*sec) and peak height (μV) (Table 2C). The performance of Na-APR-1 (M74) upon freeze/thaw was assessed across multiple lots and the data gathered were comparable (data not shown).

Long term stability testing of Na-APR-1 (M74) protein

A real time stability study was also performed on Na-APR-1 (M74) and data have been collected for up to 24 months from the date of purification. Samples were removed from the -80° C freezer and characterized at specified time points. For all time points tested, the samples maintained the color and appearance properties as colorless homogenous solutions free of particles (data not shown). In addition, the pH as well as the concentration of the protein solution did not vary significantly



Figure 4. Representative elution profile for preparative SEC. Fractions include aggregate upslope (A1), aggregate downslope (A2), pre-monomer (M1), main monomer (M2) and monomer tail (MT). (**B**). SDS-PAGE (non-reducing, denatured) analysis of selected SEC fractions including A2, M1 with sub-fractions, and the leading edge of M2. The clearance of high molecular species eluting in A2 and M1 fractions was the impetus for limiting M2 as the main product peak.

between time points tested demonstrating that the protein retained its release specifications and characteristics at manufacture for the entire time of the study when stored at -80° C. When analyzed by SDS-PAGE and by SEC-HPLC, degradation of *Na*-APR-1 (M74) was not observed which confirmed that *Na*-APR-1 (M74) could be stored for a period of time up to 24 months at -80° C (Fig. 11).

Long-term stability of the Na-APR-1 (M74) vaccine

The long-term plan for the Human Hookworm vaccine is to co-formulate Na-APR-1(M74) with a second hookworm antigen (Na-GST-1) which is currently in Phase 1 studies. Both antigens are intended to be formulated with Alhydrogel[®] adjuvant. The isoelectric point (pI) of Na-APR-1 (M74) is 5.26 and the pH of the Imidazole buffer used for formulation is 7.4. Therefore, to







Figure 6. Analytical Fast Pressure Liquid Chromatography-SEC of the IMAC eluent, the anion exchange (AEX) eluent, and the final purified *Na*-APR-1 (M74) protein.

maximize the electrostatic interaction between the aluminum salt and the protein, aluminum hydroxide (Alhydrogel[®]) was chosen as the most suitable adjuvant. In addition, Alhydrogel[®] is already considered safe and approved for human use by the regulatory agencies. To validate the choice of the adjuvant, long-term binding and stability of Na-APR-1 (M74) to Alhydrogel® was examined. Following storage of the formulated Na-APR-1 (M74)/ Alhydrogel[®] vaccine at 2–8°C, its stability was investigated by assessing the color and appearance, pH, protein content by the O-phthaldialdehyde (OPA) assay, percent of protein bound to Alhydrogel[®], and the identity by SDS-PAGE after desorption of the protein followed by Coomassie Blue staining (data not shown). Samples were withdrawn and tested at specific time points up to a maximum of 24 months. While the color, appearance, and pH were evaluated as previously described, the OPA assay was used to quantify the amount of protein bound to the Alhydrogel[®] surface by separating the surface bound protein fraction of the formulation from the unbound fraction in the supernatant by centrifugation. As shown in Figure 12, when the Na-APR-1 (M74)/Alhydrogel® formulation was centrifuged to separate the pellet fraction from the supernatant, the Na-APR-1 (M74) protein segregated in the pellet fraction and only a very faint band was visible in the supernatant fraction, indicating a tight binding of the molecule to the surface of the Alhydrogel[®].

Discussion

Na-APR-1, the N. americanus Aspartic Protease-1, is being developed together with Na-GST-1, N. americanus Glutathione S-Transferase-1, as lead candidate antigens in a bivalent human hookworm vaccine by the Sabin Vaccine Institute Product Development Partnership (Sabin PDP). Establishment of an expression system as well as a robust purification process for *Na*-APR-1 (M74) proved, however, to be more difficult than for *Na*-GST-1 (produced in *P. pastoris*).

After screening a number of expression systems including *P. pastoris* and *E. coli* for their ability to produce *Na*-APR-1 (M74), *N. benthamiana* was ultimately selected as the expression host based on the potential scalability of the system and its ability to provide adequate amounts of pure soluble protein to support early clinical development. Even with the successful implementation of this system into the *Na*-APR-1 (M74) development program, some aggregation of the target protein as well as lower than expected yields, persisted. The final selected purification process developed for *Na*-APR-1 (M74) included an extraction and clarification step followed by several chromatographic steps including an immobilized metal affinity (IMAC) step, an ion exchange (QFF) step, and finally a size exclusion (SEC) polishing step.

Mass analysis was performed throughout process development not only to identify the sources and key steps of major protein loss, but also to evaluate the benefit of changing parameters within each step in order to improve product recovery and quality. During the early phase of the development process, the extraction as well as the IMAC purification processes resulted in a significant loss of the target product. This obstacle was partially resolved by changing the extraction buffer from phosphate to Tris allowing for direct loading of the IMAC eluate onto the AEX resin without addition of an ultrafiltration/diafiltration step. In addition, the pH of the IMAC buffers was increased from 7.5 to 8.0 to allow for the AEX step to be performed at room temperature rather than 4°C, which is more suitable for later scale up. For the AEX step, both strong (QFF) and weak (DEAE) anion exchangers were screened for binding efficiency and the QFF matrix was selected based on its greater Na-APR-1 (M74) binding capacity compared to the DEAE matrix, at all pH conditions screened.

Despite these optimizations, the overall process recovery remained surprisingly low, with approximately 80% of the IMAC elution being lost through the following QFF step. Further evaluation of the process revealed that the product loss observed at the QFF step was due in part to some product loss during the wash step, but primarily due to the collection of a narrow portion of the relatively broad QFF elution peak. This minimal collection window, however, was necessary in order to 1) maintain the target concentration at >1.8 mg/mL in order to minimize the SEC load volume and/or the number of SEC cycles and 2) to ensure that the Na-APR-1 (M74) eluted from the SEC at a concentration sufficient for downstream formulation (>0.2 mg/ml). In addition to the loss of target protein from the QFF step, a substantial percentage of Na-APR-1 (M74) in the QFF eluate was detected as high molecular weight protein suggesting the presence of aggregates (Fig. 6) which supports the narrow fraction window collected.

As a means to reduce aggregation, a number of detergents including anionic, cationic and several zwitterionic detergents were

Table 2: A: Color and appearance, pH measurement and protein content by absorbance at 280nm of *Na*-APR-1 (M74) samples at day 0 and hold at 2–8°C, 25°C, and 37°C for 7, 15 and 30 days; B: Color and appearance, pH measurement and protein content by absorbance at 280nm of Na-APR-1 (M74) samples subjected to the 3 freeze/thaw cycles; C: SEC HPLC elution parameters of *Na*-APR-1 (*M74*) subjected to the 3 freeze/thaw cycles

	Parameter			C: SEC HPLC Elution parameters			
Sample	Color and Appearance	рН	Protein content by A280	RT (min)	Peak area (μV*sec)	Peak (μV)	
A. Protein Stability	prior to Freeze Thaw						
Day 0	2–8°C	Clear, colorless, particle free, homogeneous, non-viscous	7.42	0.231 mg/mL	ND	ND	ND
	25°C	ND	ND	ND	ND	ND	ND
	37°C	ND	ND	ND	ND	ND	ND
Day 7	2–8°C	Clear, colorless, particle free, homogeneous, non-viscous	7.47	0.218 mg/mL	ND	ND	ND
	25°C	Clear, colorless, particle free, homogeneous, non-viscous	7.47	0.212 mg/mL	ND	ND	ND
	37°C	Clear, colorless, particle free, homogeneous, non-viscous	7.48	0.253 mg/mL	ND	ND	ND
DAY 15	2–8°C	Clear, colorless, particle free, homogeneous, non-viscous	7.47	0.235 mg/mL	ND	ND	ND
	25°C	Clear, colorless, particle free, homogeneous, non-viscous	7.47	0.230 mg/mL	ND	ND	ND
	37°C	Clear, colorless, particle free, homogeneous, non-viscous	7.48	0.234 mg/mL	ND	ND	ND
DAY 30	2–8°C	Clear, colorless, particle free, homogeneous, non-viscous	7.42	0.263 mg/mL	ND	ND	ND
	25°C	Clear, colorless, particle free, homogeneous, non-viscous	7.41	0.272 mg/mL	ND	ND	ND
	37°C	Clear, colorless, particle free, homogeneous, non-viscous	7.41	0.300 mg/mL	ND	ND	ND
B. Protein Stability	after Freeze-Thaw						
Freeze/Thaw 1	Clear, colorless, particle free, homogeneous, non-viscous	7.43	0.222 mg/mL	13.009	822293	16851	
Freeze/Thaw 2	Clear, colorless, particle free, homogeneous, non-viscous	7.40	0.239 mg/mL	13.018	792084	15169	
Freeze/Thaw 3	Clear, colorless, particle free, homogeneous, non-viscous	7.47	0.248 mg/mL	13.035	742475	13425	

tested. Among these, Empigen[®] BB was determined to be the most effective at disrupting the *Na*-APR-1 (M74) aggregation observed in the QFF eluate while not interfering with the downstream chromatography or protein analysis methods. During process scale up, incorporation of Empigen[®] BB resulted in a significant increase in

the ratio of monomer relative to aggregate throughout the entire purification process and also improved the stability of the monomer at -80° C. Furthermore, the introduction of Empigen[®] BB throughout the purification process provided an additional benefit as it allowed for the reduction in the imidazole concentration



Figure 7. Evaluation of the purity profile of the *Na*-APR-1 (M74). (A): Analytical SEC HPLC chromatogram of the final purified *Na*-APR-1 (M74); (B): SDS-PAGE followed by Coomassie Blue Staining of *Na*-APR-1 (M74) and respective gel loading scheme (D), (C): Western Blot of *Na*-APR-1 (M74) probed with primary rabbit anti-WT-APR-1 antibodies and AP Goat Anti-Rabbit secondary antibodies and respective loading scheme (D); (D): Gel loading scheme for SDS-PAGE and Western Blot shown in (B and C).



Figure 8. Electrtophoretic analysis of *Na*-APR-1 (M74) samples collected during accelerated stability study. *Na*-APR-1 (M74) was analyzed by SDS-PAGE followed by Coomassie Blue staining (left column), silver staining (center column) and Western Blot (right column) probed with anti-APR-1 antibodies. *Na*-APR-1 (M74) was incubated at 2–8°C, 25°C or 37°C for 7 (**A**, **B**, **C**), 15 (**D**, **E**, **F**) and 30 days (**G**, **H**, **I**). Gels were loaded as follows. Lane 1: Mark 12TM unstained standards, lane 2: *Na*-APR1 (M74) (reduced) 2–8°C, lane 3: *Na*-APR1 (M74) (reduced) 25°C; lane 4: *Na*-APR1 (M74) (reduced) 37°C, lane 5: Mark 12TM unstained standards, lane 6: *Na*-APR1 (M74) (non-reduced) 2–8°C, lane 7: *Na*-APR1 (M74) (non-reduced) 25°C; lane 8: *Na*-APR1 (M74) (non-reduced) 37°C.

required for *Na*-APR-1 (M74) elution from the IMAC column from approximately 500 mM to 150 mM. This process change, as well as earlier modifications to the buffer salts, contributed to the evolution of a simple dilution of the IMAC eluate rather than performing a buffer exchange step prior to AEX chromatography which further streamlined the downstream process.

Despite these improvements, the overall yield of Na-APR-1 (M74) obtained after the final size exclusion chromatography step was only ~50% of the AEX recovery. This was attributed to the low resolution of the SEC chromatography and thus the difficulty in separating the pre- and main monomer fractions (M1 and M2, **Fig. 4A**). The main efforts of the work described was to isolate the Na-APR-1 (M74) monomer from the aggregate, as the monomer species has been the main focus of preclinical efficacy and safety studies. Monomer isolation was performed at a great sacrifice to the overall process recovery, but was deemed necessary since preliminary immunogenicity data from studies carried out in Balb/c mice indicated that the monomeric form once formulated with Alhydrogel[®] resulted in higher Na-APR-1

antibody titers than the aggregated form (data not shown). If the aggregate had been shown to be immunogenic, the improvement in overall SEC yield by combining the monomer with the aggregate would not be significant since the yield could not be greater than that of the preceding QFF step, or 17 ± 4 mg/kg biomass. Finally, from a manufacturing perspective, the presence of aggregates in the final product may be very problematic and difficult to control for batch to batch consistency. Therefore, efforts are currently ongoing to identify an alternative method to replace the size exclusion step in order to 1) reduce the overall manufacturing time, 2) reduce target protein loss while maintaining the same high purity, 3) ensure a better separation of monomeric and aggregated Na-APR-1 (M74) species without the loss observed using SEC, and 4) significantly improve the scalability of the Na-APR-1 (M74) manufacturing process. A simple terminal filtration process using a molecular weight cut off which would retain the aggregated species but allow the monomeric species to pass through is one option which can be explored. Such a change would significantly reduce manufacturing time,



Figure 9. Analytical HPLC SEC of Na-APR-1 (M74) samples collected during accelerated stability studies. Samples were, incubated at 2–8°C, 25°C and 37°C for 7 (A, D, G), 15 (B, E,H) and 30 days (C, F, I).



Figure 10. Freeze Thaw studies of *Na*-APR-1 (M74). A-C: Analytical HPLC SEC of *Na*-APR-1 (M74) after 3 (**A**, **B**, **C**) F/T cycles and reduced and non-reduced SDS-PAGE analysis followed by Coomassie Blue staining of the samples after 3 F/T cycles (**D**, Lane 2, and 4, respectively). Reduced and non-reduced western-blot analysis of the samples after 3 F/T cycles (**E**, lane 2 and 4, respectively), following the SDS-PAGE and western blot loading scheme defined in (**E**).



Figure 11. (**A**) Analytical HPLC SEC of *Na*-APR-1 (M74) after 24 month hold at -80° C and SDS-PAGE analysis followed by Coomassie Blue staining of *Na*-APR-1 (M74) after 24 months at -80° C. Lane 1 Mark12TM Marker, lane 2 and 3 *Na*-APR-1 (M74) non reduced, lanes 4 and 5 *Na*-APR-1 (M74) reduced.

cost, and eliminate the need to pool which is required for multiple SEC steps.

Based on the production process described herein, a final yield of *Na*-APR-1 (M74) of 8.6 \pm 2.0 mg per kg plant biomass has been achieved. The process described has provided an initial platform for successfully transferring a *Na*-APR-1 (M74) production process to pilot scale manufacturing in support of ongoing clinical development. The final yield of *Na*-APR-1 (M74) per kg biomass after purification is, however; significantly lower when compared to other referenced vaccine candidate antigens expressed in *Nicotiana* (60–380 mg/kg biomass). This lower yield is likely due to 1) difficulty in expressing non-aggregated *Na*-APR-1 (M74) in most



Figure 12. SDS-PAGE analysis followed by Coomassie Blue staining of the *Na*-APR-1 (M74) pellet and supernatant fractions after desorption from the Alhydrogel[®] adjuvant. After storage for 37 months at 2–8°C, the vaccine was treated with desorption buffer and separated into a pellet (lanes 2 and 3) and supernatant (lanes 5 and 6) fraction by centrifugation. Lane 1, Mark12TM molecular weight standards, lane 2 and lane 3 non-reduced pellet of *Na*-APR-1 (M74) after desorption, lane 4 nonreduced *Na*-APR-1 (M74) protein controls, lanes 5 and 6 non-reduced supernatant of *Na*-APR-1 (M74) once desorbed from the Alhydrogel[®].

systems which is likely due to the insoluble nature of the protein, and 2) the inclusion of a size exclusion chromatography step which reduces the final *Na*-APR-1 (M74) yield by 50% when compared to the yield at the previous QFF step. Due to the low yield of the current process, we have ongoing studies to investigate other strategies to improve yield by 1) exploring potential optimization steps to the current process, and 2) to re-evaluate the use of the *E. coli* expression system.

For the current plant-expressed product, several efforts are underway to elucidate the process weaknesses and implement improvements. Experiments have suggested that filters used in the current clarification procedures may retain target prior to the IMAC step. Use of membranes with alternate or low charge in combination with other extraction techniques may increase Na-APR-1 (M74) available for IMAC capture. In addition, Western blot analysis of the IMAC strip fraction has shown significant amount of protein remaining bound to the column after elution. Formation of Na-APR-1 (M74) aggregates trapped within the matrix of the resin or suboptimal elution conditions may both account for this loss. Furthermore, preliminary studies have suggested that the actual Na-APR-1 (M74) binding capacity of the QFF is greater than originally determined, thus allowing for a reduction in the OFF bed volume used, and consequently a reduction of the QFF eluate. This optimization should improve the overall QFF step recovery since protein concentration is being used as the pooling criteria. As previously suggesting, the use of Ultrafiltration (UF) after the QFF step rather than SEC could also broaden the acceptable fractions for pooling which would improve the overall product yield. However, because the final Na-APR-1 (M74) protein within the vaccine is to be without a tag, significant improvement to the overall expression level will be required. If we are successful in improving the yield using the plant system to the point where we can use a tagless version of Na-APR-1 (M74), then pre-clinical bridging studies will need to be performed to confirm potency and equivalency to the original HIS-tagged version. There are however additional hurdles which must be resolved by industry in general for production of pharmaceutical proteins in plant systems.³⁴ For example, unlike bacterial and mammalian expression systems, the nature and safety of potentially

contaminating proteins has not been well established. In addition, Industry standards concerning plant strains and methods of cultivation must be identified. Also, robust downstream processes must be identified and standardized since processing of plant material is unique when compared to other expression systems. However, these challenges have not slowed the drive to produce vaccines and biotheraputics under GMP in plants as reviewed in the same article.³⁴ Specifically for transiently expressed plant produced recombinant proteins, a number of facilities have opened in the last 2 decades to drive these processes at manufacturing scale. To address upstream challenges in plant production, Fraunhofer Center for Molecular Biotechnology (Newark, DE) has built a fully automated cGMP facility for pilot-scale production of transiently expressed protein. This facility handles all aspects from seeding to harvest in a nearly lights-off manner.³⁵ Concerns of containment and compatibility of using plants for cGMP process has been advanced by tightly controlled and contained indoor environments.³² In addition to the Fraunhofer facility, the large-scale plant expressed protein manufacturers of Kentucky BioProcessing (Owensboro, KY), Medicago Inc. (North Carolina) and Caliper Biotherapeutics (College Station, Texas) all have manufacturing facilities with various levels of robotic and flexible use facilities. To address the hurdle of generating industry standards, US regulatory bodies (FDA, USDA and APHIS) have drafted guidelines describing unique aspects of plant produced pharmaceuticals, the responsibilities of regulatory agencies and their expectations of manufacturer's in this area.³⁶ The draft guidance includes the use of plant transient expression systems, reviews expectations for characterizing and maintaining host plants and generally guides the manufacturer to the same Federal Regulations applied to any biological intended for human use.

A second option is to re-explore the use of the *E. coli* expression system and test several new strategies to achieve a soluble *Na*-APR-1 (M74) product which include 1) use of high throughput screening tools to screen a wider array of different buffer conditions to identify optimal salts and buffer conditions to achieve greater solubility and stability, 2) testing alternative *E. coli* vectors and host strains, and 3) consider addition of the native pro sequence since recent data suggests that this sequence may be necessary to achieve a soluble product. However as with the above scenario in the plant system, switching expression systems would also require bridging studies be performed to show potency and equivalency to the plant derived *Na*-APR-1 (M74) which was used for the Phase 1 studies.

Characterization of the *Na*-APR-1 (M74) protein and accelerated stability studies were performed during the product development cycle for a number of reasons, including the establishment of release criteria and storage conditions, and the development of a formulation which best stabilized the product. In addition, accelerated studies represent a means to ensure that the analytical methods selected for release are stability indicating assays. Freezing of protein biologics is often included in the manufacturing processes as it allows prolonged storage over time. The impact of freezing, thawing and cold storage over a prolonged time however may be protein dependent; therefore, a stability study was designed to include freeze/thaw cycles. The goal of stability evaluation for a bulk intermediate is to establish whether the material can be maintained at a specified temporary storage condition (for example at 2–8°C) for a given period of time without a negative impact on the quality of the final product. In addition, it is important to demonstrate that storage of the purified protein has negligible impact on the final product stability. The ongoing stability studies have shown that the purified *Na*-APR-1 (M74) has maintained its biochemical features when stored at -80° C, with no signs of degradation or aggregation up to 24 months. Accelerated stability conditions were used to increase the rates of degradation and enhance the likelihood of observing significant differences in the stressed sample compared to the unstressed sample. Development of analytical methods able to detect these differences was essential to monitor both degradation and aggregation events during the long term stability testing of the protein.

The stability data collected to date indicate that the Na-APR-1 (M74) is stable at 2-8°C only for approximately 7 days after which signs of degradation were observed. Although, the pH and the overall A280 were not significantly affected by the 7 days hold, SDS-PAGE analysis indicated a reduction in density of the 42 kDa band corresponding to Na-APR-1 (M74) as well as the appearance of low molecular weight degradation products. These data indicate that any refrigerated hold times during post-manufacture must be kept to a minimum. The degradation observed was more rapid at the higher temperature tested, but was also evident when the material was stored at 2-8°C for period of times longer than 7 days. In just 7 days, at 25°C or 37°C the density of the main bands corresponding to the Na-APR-1 (M74) protein decreased from 80 to 10%. Increase in aggregation was not observed during the length of this study. Similar protein degradation was observed by SEC-HPLC, supporting the use of both SDS-PAGE and SEC-HPLC assay methodologies for monitoring stability. Taken together, these data also support the conclusion that the final Na-APR-1 (M74) protein can only be held at elevated temperatures for a short time without risking a detrimental impact on the integrity of the protein. In contrast, the stability of the protein was maintained when the samples were stored at -80° C for longer periods of times. As indicated by the ongoing long-term stability studies, the protein has maintained its properties for all time points up to 2 years.

In order for the vaccine to be effective, the use of immunostimulatory agents (or adjuvants) is critical for most recombinant protein vaccines because proteins are usually weakly immunogenic. The most widely used vaccine adjuvants are aluminum salts and there is extensive data regarding the safety of these adjuvants. The most common are aluminum phosphate (Adju-Phos[®]) and aluminum hydroxide (Alhydrogel[®]). The adsorption of a protein on aluminum compounds heavily depends on electrostatic forces between the protein and the adjuvant. Based on the pI of Na-APR-1 (M74) as well as the pH and salts present in the formulation buffer, Alhydrogel[®] was selected as the most suitable adjuvant in order to maximize the electrostatic interaction between the aluminum salt and the protein. Binding studies and a Langmuir binding isotherm further supported the rationale for the Aluminum/protein ratio of the vaccine formulation. Ongoing stability studies have validated this selection since the formulated product, i.e., the protein bound to Alhydrogel[®], has been shown to maintain its properties at the intended storage conditions of 2–8°C so far for up to 3 years. No variation in pH, in protein content and percentage of protein adsorbed to Alhydrogel[®], or protein identity has been detected during this time. The long term stability of both the *Na*-APR-1 (M74) protein as well as the formulated product is to be monitored for a minimum of 5 years. The implementation of optimal storage and formulation protocols based on the described stability data has allowed the Sabin PDP to successfully move *Na*-APR-1 (M74) formulated with Alhydrogel[®] into phase 1 clinical testing.

Materials and Methods

Cloning of *Na*-APR-1 (M74) into launch vector and expression in *N. benthamiana*

The DNA sequence encompassing amino acids 74–446 of the N. americanus Aspartic Protease-1 (Na-APR-1, NCBI accession number CAC00543.1), without the pro-sequence, was optimized for expression in plants and synthesized by Geneart. The synthesized sequence was cloned into the Tobacco Mosaic virus (TMV)based launch expression vector pGRD4 23,24 with a PR-1a signal peptide of Nicotiana tabacum (BAA14220) replacing the native Na-APR-1 signal peptide at the N-terminus.²⁵ A His tag (6xHIS), as well as ER retention sequence (KDEL), was inserted at the C-terminus (Fig. 1) of the protein to aid purification. Additional modifications to the Na-APR-1 (M74) sequence included the D113A and D300A mutations to eliminate the hemoglobinase activity. The resulting construct and the helper plasmid, pSoup, which provides replication functions in trans, were then introduced into Agrobacterium tumefaciens strain GV3101 by electroporation in order to generate the Research Cell Bank.

Preparation of Master and Working Cell Banks for Agrobacterium tumefaciens (GV3101) Na-APR-1 (M74)

Master and Working Cell Banks (MCB/WCB) of Agrobacterium tumefaciens Na-APR1 (M74) were prepared following cGMP practices as follows: For production of the Master Cell Bank, a vial of Research Cell Bank was thawed and used to inoculate 1L of alternative protein source LB broth containing Kanamycin (50 μ g/ml). The culture was grown at 28 + 1°C for 16–24 hours. The culture was centrifuged and re-suspended in media to an OD₆₀₀ of >5 and glycerol was added to a final concentration of 20–25% to create the Master Cell Bank. Aliquots of the Master Cell Bank glycerol stocks were prepared in cryovials at 1.0 mL per vial and stored at \leq –70°C. A vial of the MCB was thawed and used to create the WCB using the same procedure as described above.

Preparation of Agrobacterium and infiltration

One vial of WCB was thawed and used to inoculate a 2L shake flask containing 250 mL sterile LB medium with 50 μ g/mL Kanamycin. Fermentation was performed at 28°C. Air was supplied and agitation was gradually increased to maintain the O₂ saturation. The pH was maintained at 7.0. Directly after inoculation of the fermenter, a glucose feed was initiated to maintain the carbohydrate source. Fermentation was carried out for at least 15 hours. Cell density was monitored during fermentation and the run was terminated when the OD₆₀₀ reached a cell density greater than 5. For dilution of the *Agrobacterium* and infiltration, Milli-Q water was added to the culture to reduce the cell density to OD₆₀₀ of 0.5 (range 0.3–1.0). Hydroponically grown 29–32 day old *N. benthamiana* seedlings were vacuum infiltrated with the Agrobacterium as described previously.^{24,26} Briefly, the plant trays were drained and manually inverted into the diluted *Agrobacterium* solution. After vacuum infiltration the plants were submerged in a tank with Milli-Q water for rinsing and subsequently grown for 6 days to accumulate recombinant *Na*-APR-1 (M74). On day 5, approximately 50 g of plant biomass was sampled to determine the IMAC recovery of target protein per gram of plant tissue (based on SDS-PAGE, data not shown)

Plant harvesting, dicing, homogenization and clarification prior to chromatography

N. benthamiana plants transiently expressing Na-APR-1 (M74) were harvested at 6 days post-infiltration by clipping at the base of the stem. Aerial plant tissue of the post-infiltration plants were then collected and separated from the trays. Approximately 5 kg of tissue was used for Na-APR-1 (M74) extraction at a 5 kg scale. The aerial tissue was diced, mixed with extraction buffer and passed twice through a Comitrol 1500 homogenizer. Triton X-100 was added to 0.5% and the homogenate mixed for 20 minutes at 4°C. The majority of solids were removed from the Triton extracted homogenate by continuous flow disk stack centrifugation (12,000 rpm). Residual solids were removed by passage first through a 0.27 m² depth filter (3M Cuno Zeta Plus series) followed by a 0.2 µm dead end filter (3M Cuno LifeAssure PDA series). Immobilized Metal Affinity Chromatography (IMAC) load buffer was used as a filter chase ($\sim 10\%$ total homogenate volume) and the resulting clarified extract was held in a sterile bioprocess bag (Sartorius Stedim, Flexboy) at 2-8°C until chromatography.

Purification of Na-APR-1 (M74)

Na-APR-1 (M74) purification consisted of 3 column chromatography steps: first an Immobilized Metal Affinity Chromatography (IMAC) purification step was performed in order to capture the Na-APR-1 (M74) from the crude plant extraction supernatant. The IMAC eluate was then purified using a Q Sepharose FF anion exchange column (AEX), followed by a Superdex 200 (size-exclusion) column. IMAC purification was performed at 2-8°C. An IMAC column (7 × 22 cm packed bed) with a bed volume of 843 mL resin was first washed with Milli-Q water followed by equilibration with 3 column volumes (CV) of 50 mM Tris, 0.5 M Sodium Chloride, 20 mM Imidazole, 0.5% Triton X-100, pH 7.0 (Capture Buffer A1) at a flow rate of 240 cm/hr. After equilibration with Capture Buffer A1, the clarified harvest was loaded at 240 cm/hr. onto the IMAC column followed by washing with 4 CV of Capture Buffer A1 at 240 cm/hr. to allow residual, unbound material to flow through. The IMAC column was then washed with a minimum of 5 CV of 10 mM Tris, 0.1 M Sodium Borate, 0.3% Empigen BB, pH 8.0 (Capture Buffer A2) at a flow rate of 335 cm/hr. until the absorbance at 280 nm (A_{280}) returned to a stable baseline. Finally, the Na-APR-1 (M74) was eluted from the column with approximately 2 CV of 10 mM Tris, 0.1 M Sodium Borate, 150 mM Imidazole, 0.3% Empigen BB, pH 8.0 at a flow rate of 218 cm/hr. while monitoring the A280. The IMAC elution fractions containing Na-APR-1 (M74) was stored at 2-8°C. A Q Sepharose FF (GE Healthcare) column (9 \pm 3 \times 7 cm) with a packed to bed volumes of 238-423 mL of resin was sanitized with a 2.5 CV wash of 0.5 N Sodium Hydroxide (NaOH) followed by a 60 minute hold and an additional 2.5 CV wash of 0.5 N NaOH. Residual base was removed from the column with a 9 CV Milli-Q water wash. After sanitization, the column was stored in 20% ethanol until use. Prior to chromatography, the resin was washed with Milli-Q water, equilibrated with 3 CV of 10 mM Tris, 60 mM Sodium Borate, 560 mM Sodium Chloride, 0.3% Empigen BB, pH 8.0 (Q Solution C) and then equilibrated with 5 CV of 10 mM Tris, 100 mM Sodium Borate, 0.3% Empigen BB, pH 8.0 (Q Solution A). Prior to loading the column, the Na-APR-1 (M74) containing IMAC eluent was equilibrated to room temperature and an equal volume of Q Solution A was added to ensure the conductivity was <17 mS/cm. The sample conductivity and pH were then confirmed to be within acceptable ranges of 16.5-19.0 mS/cm and 7.8-8.4, respectively. The diluted IMAC eluate was loaded onto the Q Sepharose FF column for a targeted 4 minute media contact time. After loading, the resin was washed with at least 5 CV of Q Solution A followed by 5 CV of 10 mM Tris, 96 mM Sodium Borate, 56 mM Sodium Chloride, 0.3% Empigen BB, pH 8.0 (Q Solution B). Finally the Na-APR-1 (M74) was eluted using Q Solution C while monitoring the A_{280} . Individual elution fractions were analyzed by SDS-PAGE. Fractions which were enriched with Na-APR-1 (M74) (> 1.8 mg/mL) were pooled and stored overnight at 2-8°C prior to SEC.

SEC (Superdex 200)

SEC provides a polishing step (removal of high molecular weight species) as well as a buffer exchange step for the QFF ion exchange elution pool. SEC was performed at room temperature over tandem Superdex S200 Prep grade columns (50×30.5 cm, GE Healthcare) packed to a total bed volume of 1215 mL. The columns were sanitized with 1.0 N NaOH at a flow rate of 31 cm/hr., washed with Milli-Q water at the same flow rate, then equilibrated with 10 mM Imidazole, 150 mM Sodium Chloride, 0.3% Empigen BB, pH 7.4 (SEC running buffer) for 4 CV overnight. The Na-APR-1 (M74) pool eluate from the Q Sepharose FF column was divided into 2 or 3 equal aliquots based on the total volume. Each aliquot was processed separately on the Superdex S 200 column using the same process parameters as described above, and separating each run with an equilibration step. For each run, one aliquot was loaded onto the pre-equilibrated Superdex S200 column (3.4-4.0% bed volume) and allowed to flow through the column in SEC running buffer while monitoring the A₂₈₀ of the eluate. The eluate was collected in fractions comprising 5 main elution sections: an aggregate upslope (A1), an aggregate downslope (A2), a pre-monomer peak (M1), the main monomer peak (M2), and monomer tail (MT). Fractions enriched for *Na*-APR-1 (M74) were stored overnight at 2–8°C until pooling. Pooling provided a means of excluding high molecular weight contaminants from the leading side of the main monomer peak (M2) while maintaining a target concentration of ≥ 0.2 mg/mL, as determined by UV₂₈₀, for the trailing side of the M2 peak. The final pooled product was sterile filtered through a 0.22 µm filter, aliquoted into sterile Nalgene cryovials, and frozen at $\leq -70^{\circ}$ C. The final *Na*-APR1 (M74) concentration was determined by densitometry of *Na*-APR1 (M74) bands after SDS-PAGE and Coomassie Blue staining and comparison to BSA standards, and by absorption at 280 nm (A_{0.1%} = 1.16) for the final purified protein.

SDS-PAGE/Western Analysis

For the Na-APR-1 (M74) samples collected during purification, SDS-PAGE analysis was performed on 10% acrylamide gels stained with Coomassie (Gel Code Blue, Pierce Rockford, IL). Western blot analysis on the same samples was performed as follow: SDS-PAGE separated samples were transferred to PVDF membranes, blocked with I-Block (Applied Biosystems, Carlsbad, CA) and developed using either anti-4X HIS (Qiagen, Valencia, CA) or rabbit anti-Na-APR-1 (M74) antibodies. Excess primary antibodies were removed by washing the blots with 1xPBS containing 0.1% Tween 20 (PBST) followed by an antirabbit or mouse HRP conjugated secondary antibody (1:10,000 dilution, Jackson ImmunoResearch, West Grove, PA) and by detection with a chemiluminescent substrate (SuperSignal West Pico, Thermo Fisher). Images were captured using either a flatbed scanner or a Genome chemiluminescence detector (Syngene Corp.). For characterization of the purified protein, the presence of residual host cell proteins was assessed by SDS-PAGE and Western blot analysis on reduced and non-reduced 4-20% Trisglycine gels. A mouse primary antibody recognizing host cell proteins was used to detect the presence of host contaminants at a 1:3000 dilution. Alkaline phosphatase conjugated goat anti rabbit IgG and goat anti mouse secondary antibodies (KPL) were used for colorimetric detection at 1:3000 or 1:10000 dilution, respectively. The blots were developed using a BCIP/NBT (KPL) membrane phosphatase substrate system. 4-20% Tris glycine gels and 4-12% Bis-Tris gels were used for evaluation of sample purity and electrophoresis was performed following the manufacturer's recommendations. For the reduced samples, β-mercaptoethanol was added to the 2X Tris-glycine sample-loading buffer to a final concentration of 10% and to the 4X Bis-Tris sample-loading buffer to a final concentration of 20%. Approximately 2 µg of non-reduced or reduced protein was loaded for each lane. Gels were stained, de-stained and scanned as described above. Identity of the protein was confirmed by Western blot with target specific antibodies raised in rabbits and used to detect Na-APR-1 (M74) at a 1:1000 dilution.

Analysis by SEC

SEC analysis of in process samples was performed using a Superdex 200 10/300 GL column with effluent monitored at A_{280} . Samples were injected with a 50% sample loop overfill at a

flow rate of 0.5 mL/min. The running buffer used was PBS (pH 7.4) supplemented with 0.3% Empigen BB.

Purity by SEC-HPLC

Purity of stability samples was analyzed by SEC-HPLC. All samples were injected in a 50 μ L volume at a flow rate of 0.6 mL/min onto a Tosoh TSK gel G3000SWxl column using a Shimadzu Prominence UFLC with a PDA detector. The column was run at room temperature at a flow rate of 0.6 mL/min for 30 min, using 1X PBS + 0.3% Empigen[®] BB pH 7.4 as the mobile phase. To determine the percent purity, the area of the main peak was compared to the area of all other peaks on the chromatograph (excluding sample buffer peaks).

Freeze/thaw studies of the Na-APR-1 (M74) protein

Three 1 mL aliquots of Na-APR-1 (M74) were placed in liquid nitrogen for 10 minutes followed by a thaw step at room temperature. The three vials were exposed respectively to 1, 2 or 3 freeze/thaw cycles. After each cycle, samples were tested for color and appearance by visual inspection on both a white and black background, for pH by a Thermo Scientific Orion Versa StarTM pH meter using standard manufacturer recommendations, and for protein content by the absorbance at 280 nm (Ultrospec 6300pro). The identity, and purity of the sample was also tested by SEC-HPLC using a Waters Alliance® HPLC system with the Empower[®] 2 software for data analysis. 50 µg of Na-APR-1 (M74) at 1 µg/µL were loaded on a TSK gel G3000SWxl column with 1X PBS + 0.3% Empigen[®] BB pH 7.4 as the mobile phase and at a flow rate of 0.6 mL/min and run time of 30 min. SDS-PAGE analysis was performed using 4-20% Tris-glycine gels with a protein load of 2 µg of each sample per lane under both reducing and non-reducing conditions. Gels were stained with Coomassie Blue or Silver Stain following conventional procedures.

Accelerated and long-term stability studies of the Na-APR-1 (M74) protein

For the accelerated stability studies, the Na-APR-1 (M74) protein was placed at 3 different temperatures, 2-8°C, 25°C and 37°C for a maximum time period of 30 days and then characterized. At time zero, 1 mL protein aliquots were placed at the above specified temperatures and analyzed after 7, 15, and 30 days for color and appearance, pH measurement, and protein content by absorbance at 280 nm, as performed for freeze/thaw analysis. Identity and purity by SEC-HPLC, as well as identity by SDS-PAGE followed by Coomassie Blue staining and silver staining, were also performed following the same procedures as described above. For long term stability studies, the Na-APR-1 (M74) protein was maintained at it is storage temperatures of -80° C and then characterized after 3, 6, 9, 12, 18, 24 months and every year thereafter, for a total of 5 years (ongoing). Color and appearance, pH measurement, and protein content by absorbance at 280 nm, Identity and purity by size exclusion HPLC, as well as identity by SDS-PAGE followed by Coomassie Blue staining was performed at each time point following the same procedures as described above.

Preparation of the Na-APR-1 (M74) formulation

The *Na*-APR-1 (M74) protein stock solution and the Alhydrogel[®] were combined in 10 mM imidazole, 150 mM Sodium Chloride buffer, 0.3 % Empigen[®] BB, pH of 7.4 such that the final protein concentration was 0.1 mg/mL and the final Alhydrogel[®] concentration was 0.8 mg/mL. Upon formulation, adsorption of the protein to the Alhydrogel[®] surface was assessed by SDS-PAGE and OPA assay.²⁷

Stability testing of the formulated protein

Stability of the Na-APR-1 (M74)/Alhydrogel ® formulation was monitored 1, 3, 6, 9, 18, 24, 37 months post formulation. Color and appearance, pH measurement, protein content by OPA and identity by SDS-PAGE after desorption with 100 mM sodium citrate, 92 mM dibasic sodium phosphate, pH 8.9 followed by Coomassie Blue staining were evaluated at each time point. While the color and appearance and pH were evaluated as previously described, the OPA assay was used to quantify the total protein content of the vaccine. The OPA assay was performed using a Victor 3 multilabel counter with Wallac 1420 software (PerkinElmer). A series of dilutions of non-formulated Na-APR-1 (M74) protein ranging from 0 to 250 µg/mL were made in PBS pH 7.4 as the diluent and used to populate a standard curve. Over this range, the fluorescence intensity increased in a linear fashion with the concentration of the protein. 40 µl of each test sample and standard was dispensed into a 96 wells microplate to which 200 µL of OPA reagent solution was added. Samples were incubated for approximately 2 minutes with moderate shaking at room temperature and the fluorescence signal was measured using a Victor 3 multilabel counter plate reader with a 355 nm, 40 bandwidth, excitation filter and a 460 nm, 40 nm bandwidth, emission filter. The standard curve following the least means squared linear equation was generated using the Wallac 1420 software. The same assay was used to evaluate the percent protein adsorbed to Alhydrogel[®].

Disclosure of Potential Conflicts of Interest

All authors of this manuscript currently are involved in a program for the development of human hookworm vaccine. There are no other conflicts of interest to disclose.

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