Production of Recombinant Human Coagulation Factor IX by Transgenic Pig

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PRODUCTION OF RECOMBINANT HUMAN COAGULATION FACTOR IX BY
TRANSGENIC PIG

by

Weijie Xu

A DISSERTATION

Presented to the Faculty of

The Graduation College at the University of Nebraska

In Partial Fulfillment of Requirements

For the Degree of Doctor of Philosophy

Major: Chemical and Biomolecular Engineering

Under the Supervision of Professor William H. Velander

Lincoln, Nebraska

July, 2014
Hemophilia B is the congenital bleeding disorder caused by deficiency in functional coagulation factor IX (FIX) and about 28,000 patients worldwide in 2012. And current treatment is restricted to protein-replacement therapy, which required FIX concentrates for patients’ life-time. Approximately 1 billion units FIX were consumed in 2012. However, still about 70-80% patients, mostly in developing countries, received inadequate or no treatment because of the unavailable and/or unaffordable FIX concentrates. Considering safety reasons, e.g. transmission of blood-borne diseases, the recombinant human FIX (rFIX) is recommended other than the plasma-derived FIX. However, only one rFIX is currently available on the market. The complexity of the FIX protein and its post-translational modifications (PTMs) cause the limit quantity and unaffordable high price of the recombinant human FIX. We previously reported successfully expressing recombinant human FIX in the milk by mammary gland of transgenic pig (tg-FIX) and established a lab-scale purification protocol to achieve active tg-FIX. The expression of tg-FIX level was about 2-3 g/L and with 10-20% specific activity. The final purified high acidic tg-FIX had the specific activity closed to the normal human plasma derived FIX. In this study, efforts were aim to further increase the yield of the active tg-FIX from the transgenic pig. First, we investigated
degradation/activation of the tg-FIX in the milk by predominant milk-borne protease, plasmin. This provided us the data in decreasing the degradation and activation of final products. Then, to process the excessive non-active pro-peptide attached tg-FIX, we bio-engineered the mammary gland by introducing truncated human furin gene. The co-expressed recombinant furin cleaved pro-peptide of tg-FIX both in mammary epithelium, it also secreted and cleaved the pro-peptide in milk. This bio-engineering has been proved not interfering the over-expression of the tg-FIX and its specific activity. Finally, to mass producing active tg-FIX, we established the large scale purification protocol. The purified active tg-FIX was achieved within four chromatography steps with full specific activity. Not like the previous one, the active tg-FIX was further enriched and the contaminant activated tg-FIX was totally eliminated. This study made progress in producing recombinant human FIX economically.
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CHAPTER 1: INTRODUCTION

BACKGROUND

Coagulation factor IX and Coagulation Cascade

Coagulation Factor IX (FIX) gene is located on the X-chromosome at q27. Gene is expressed in hepatocytes with a highly tissue-specific manner as a pre-pro form (Fig.1) (1,2). The primary structure of FIX protein consist 40 amino acids γ-carboxyglutamate (Gla) domain, two Epidermal Growth Factor (EGF) domains (a.a. 47-127), activation peptide (a.a. 146-180) and the catalytic domain (a.a. 181-415). The first two domains compose the light chain (Mr. ~20 kDa) and the catalytic domain composes the heavy chain (Mr. ~28 kDa), in which His-221, Asp-269 and Ser-365 compose the serine protease catalytic triad. The nascent FIX is proceeded by several post translational modifications (PTM)s (Fig. 1), including the removal signal peptide, vitamin-K dependent gamma-carboxylation of first 12 glutamic acid(3,4), pro-peptide removal(5,6), glycosylation(7-10), beta-hydroxylation of Asp-64(11), sulfation of Tyr-155(12) and phosphorylation of Ser-158(13-15).

At the physiologic concentrations of Ca^{2+} (1.1 mM) and Mg^{2+} (0.6 mM), the core Gla domain of Vitamin K dependent (VKD) coagulation proteins like Protein C, Factor VII, Factor X and prothrombin have 4 Ca^{2+} and 2 Mg^{2+} specific sites and also 1 binding site that can accommodate either divalent cation. The FIX has 2 additional Gla than other VKD factors and one more Mg^{2+} specific sites. Binding of above cations to the Gla domain is required for its conformational rearrangement from a disordered form to an ordered and organized form(16,17); This conformational rearrangement is essential for
factor IX to bind to negatively charged phospholipid vesicles provided in vivo by activated platelets resulting in its local ionization and augmentation of activation (18). Gla domain also interacts with the C-terminal domain of TF in the TF/FVIIa complex during the FIX activation (19). In addition, it is essential for FX activation by binding of FVIIIa, co-factor of tenase complex (20).

Fig. 1. The Primary Structure of Nascent FIX, Zymogen, Activated FIX and their PTMs. S: signal Peptide; P: pro-peptide; Gla: γ-carboxylglutamate domain; EGF: epithelium growth factor domain; AP: activation peptide; ▼: signal peptide cleavage site; ▼: pro-peptide cleavage site; YY: γ-carboxylglutamates; ▲: O-link glycans; ▲: N-link glycans; □: disulfide bonds; ▼: activation cleavage sites.

The mature FIX secrets and circulates as a 55-57kDa zymogen form in the blood at a physiological concentration of 5 μg/ml (21). When tissue damage occurs, the blood coagulation cascade is initiated when the tissue factor (TF) comes in contact with activated factor VII (FVIIa). The TF-FVIIa complex initiates the coagulation cascade and finally forms the insoluble clot of activated platelets and fibrin polymers. Thrombin generated in the extrinsic pathway also activates the intrinsic pathway of blood
coagulation (Fig. 2) (22). Bauer, et. al. reported that FIXa generated in vivo mainly from the activity of the TF-FVIIa rather than the intrinsic pathway(23).

![Coagulation Cascade Diagram]

**Fig. 2. The Coagulation Cascade.** (Modified from Davie, E.W., et. al. The coagulation cascade: initiation, maintenance, and regulation. Biochemistry 30, 10363-70 (1991).

**Role of Pro-peptide in γ-carboxylation and Pro-peptide Processing**

Furie et. al. reported the deletion of the pro-peptide (residues -18 to -1) inhibiting vitamin K dependent carboxylation(24). Study of in vitro carboxylation indicated the carboxylase recognition sites was the pro-peptide (25,26). And in the study of pro-peptides between Vitamin K dependent proteins, the amino acids sequence showed highly homological at
Phe\textsuperscript{16} and Ala\textsuperscript{10}. Both mutation in pro-peptide, Phe\textsuperscript{16} to Ala and Ala\textsuperscript{10} to Glu completely inhibited the carboxylation (27,28). It is indicated that the role of pro-peptide in carboxylation, and the order in PTMs, the removal of pro-peptide should follow the gamma-carboxylation.

In addition, homology is shown in basic amino acids at residues -4, -2 and -1(29,30). Both FIX Cambridge (Arg\textsuperscript{-1} to Ser) and FIX San Dimas (Arg\textsuperscript{-4} to Glu) are partially carboxylated and having pro-peptide attached hemophilia FIXs (31,32). In studies of other hemophilia FIXs with the mutation in Arg\textsuperscript{-4} to Gln (FIX Seattle C), Leu (FIX Bendorf) or Trp (FIX Boxtel), although mutations do not affect gamma-carboxylation, the defective propeptide cleavage results in destabilizing the calcium-induced Gla domain conformation change and no pro-coagulation activity of pro-peptide attached FIX (33). Furin or paired basic amino acid cleaving enzyme (PACE), a Ca\textsuperscript{2+} dependent serine protease of the PC family, cleaves pro-peptides at dibasic sites with consensus sequence Arg-X-Lys/Arg-Arg (RXK/RR)(34). Furin undergoes an auto-activation, the 83-residue N-terminal propeptide is autoproteolytically excised in the endoplasmic reticulum (ER) at the consensus furin site, -Arg\textsuperscript{104}-Thr-Lys-Arg\textsuperscript{107}-. Then, the propeptide attached furin transport to the acidified TGN/endosomal compartments, furin cleaves the bound propeptide at P1/P6 Arg site (-Arg\textsuperscript{70}-Gly-Val-Thr-Lys-Arg\textsuperscript{75}-) resulting in propeptide dissociation and enzyme activation(35). The mature furin is localized primarily to the trans-Golgi network (TGN)(36-39), and also traffics between TGN and cell surface(40,41). The previous study also indicated that ER retention of furin blocked it activation resulting in no bioactivity. On the other hand, the vitamin K-dependent carboxylase is an integral membrane protein associated with endoplasmic reticulum(24).
The order in location of carboxylase (ER) and furin (TGN) in vivo assure the pro-peptide removal after the carboxylation formed.

**Hemophilia B and Protein Replacement Treatments**

Hemophilia B is the congenital bleeding disorders and is caused by deficiency in functional coagulation factor IX (FIX). Various mutations in FIX gene can impair the pro-coagulation activity of the FIX protein, resulting in bleeding-disorder(42). Since this an X-linked recessive chromosomal disorder, almost all Hemophilia B patients are male, 25,850 (92%) patients were male; only 719 (3%) patients were female (43). In absence or abnormal level of functional FIX, both the extrinsic and intrinsic coagulation pathway cannot be accomplished, patients experience frequent and recurrent bleeding episodes. Soft tissue hemorrhages and intracranial bleeding, potential to cause long-lasting damage to internal organs and can be life-threatening in some instances(44). Recurrent bleeding episodes are also associated with a range of longer-term clinical consequences, including musculoskeletal problems, which have the potential to restrict functional impairment in later life (45). The degree of impact associated with hemophilia is determined by the severity of the condition (46,47). Approximately 60–70% of hemophilia B patients have a moderate (defined as clotting factor concentration 0.05–0.40 IU/ml, experience prolonged bleeding responses to relatively minor trauma) or severe (<0.01 IU/ml, experience frequent spontaneous bleeds) form of the condition(48-50). Current treatment of hemophilia B is restricted to protein-replacement therapy, which centers on two distinct approaches: on-demand treatment and prophylaxis. The on-demand treatment offers short-term and immediate compensation of FIX to stop further hemorrhaging and minimize the impact of a bleeding episode. Conversely, prophylaxis focus upon
maintaining acceptable levels of baseline FIX, which decrease the frequency of acute hemorrhage and life-threatening bleeding episodes and is associated with better long-term outcomes (e.g. preventing joint damage and arthropathy)(51-53). In 2012, approximately 250 million units of FIX concentrate was consumed in U.S., and about 1 billion units worldwide(43). Currently, there are 15 FIX concentrates on the market (Table 1). 14 of them are plasma derived (pd-) FIX, although the purification protocols was improved in virus removal over the last 20 years, there are still some concerns regarding prions and non-capsulated viruses (54,55). Only one is recombinant (r-) human FIX (BeneFIX), which was introduced by 1988 to the market(56), and it has been proven to be safe and effective with low incidence of serious adverse effects(57).

<table>
<thead>
<tr>
<th>Brand Name</th>
<th>Company</th>
<th>Source</th>
<th>Fractionation</th>
<th>Viral Inactivation</th>
<th>Specific Activity (IU/mg)</th>
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<td>Aimafix®</td>
<td>Kedrion</td>
<td>Plasma</td>
<td>Anion exchange, DEAESephadex®/Sepharose®, Heparin-affinity chromatography</td>
<td>TNBP/polysorbate 80; dry heat, 100°C for 30 min; nanofiltration, 35 + 15 nm</td>
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<td>AlphaNine®</td>
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<td>Plasma</td>
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<td>Berinin® P</td>
<td>CSL Behring</td>
<td>Plasma</td>
<td>DEAE Sephadex, Heparin-affinity chromatography</td>
<td>Pasteurization at 60°C for 10 hours</td>
<td>146</td>
</tr>
<tr>
<td>Betafact®</td>
<td>LFB</td>
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<td>Precipitation, Multiple chromatography</td>
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<td>Sodium thiocyanate; ultrafiltration</td>
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<td>Brand Name</td>
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<td>Source</td>
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**Table 1. Factor IX Concentrates on Market** (Modified from Franchini, M., et. al. Treatment of hemophilia B: focus on recombinant factor IX. Biologics 7, 33-8 (2013)). Abbreviations: DEAE, diethylaminoethanol; S/D, solvent–detergent; TNBP, tri-n-butyl phosphate.

Although the in vivo activity recovery of r-FIX lower than the pd-FIX results in 1.5 to 2-fold increasing in r-FIX dosing(58,59), considering bio-safety reasons, the application of r-FIX products is widely recommended(60). In United States, 99% of consumed FIX concentrate was recombinant, while only 59% worldwide in 2012(43). The FIX concentrates account for up to 98% of the total cost of hemophilia care(61). Mean annual coagulation factor costs for on-demand treatment of haemophilia (A and B) ranging from € 24,771 ($34,184) in the United Kingdom to €92,918 ($128,227) in Germany, ranging from €112,727 ($155,563) in Netherlands to €182,075 ($251,264) in Germany for prophylaxis(62). Approximately 80% patients, mostly in the developing countries, received inadequate or no treatment because of the limited supplies and high costs of either r- or pathogen screened, pd-FIX concentrates(63,64).
Recombinant Therapeutics Production and Transgenic Livestock

The first therapeutic protein was the porcine insulin in 1920s, and recombinant human insulin prepared in bacteria was introduced in the market by early 1980s. By using the recombinant therapeutics, no more contamination of blood-borne pathogen needs to be worried about. Because of the complexity of the human protein and their in vivo post-translational modifications (PTMs), the bacteria had its limitation in producing recombinant proteins. Then, yeast, insect cells, mammalian cells, transgenic plants and animals were developed in producing complex therapeutics, which could not be produced correctly by bacteria. The Chinese Hamster Ovary (CHO) cells were widely used in current industrial scale manufacturing. All these therapeutic bioreactor systems has their advantages and limitations (Table 2)

<table>
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<tr>
<th>Points to consider</th>
<th>Bacteria</th>
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<th>Transgenic plants</th>
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<td>++</td>
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<td>Line stability</td>
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<td>modifications</td>
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</tbody>
</table>

Table 2. Comparison of the different systems to produce recombinant pharmaceutical proteins. (Modified from Houdebine, L. M. Production of pharmaceutical proteins by transgenic animals. 2009.)

Transgenic Livestock in Producing Recombiant Therapeutics

In 1985, Hammer and colleagues established the first transgenic livestock animals(65).

Since then, more and more pharmaceutical recombinant proteins were produced by using the transgenic animals (66-69). Mammary gland is currently the best available bioreactor
among all tissues in transgenic animals (66,68). The cell density of the gland is about $10^9$ cell mL$^{-1}$, which could be 2-3 orders of magnitude greater than density of mammalian cells culture (64); the milk production, pig as example is about 200-400 liters per lactation with 1-2 lactations per year; and more important, the mammary gland of transgenic animals could provide certain PTMs, like signal and pro-peptide removal, sulphation, glycosylation, carboxylation, which highly relate to the activity and recovery in vivo, to the recombinant proteins. And the transgenic pig was successfully in producing recombinant human PC(70,71), fibrinogen(72), FVIII(73) and FIX(74) in the milk.

The most successful example, ATryn, human antithrombin, is made from the milk of transgenic goats and approved by FDA in 2009 or treatment of patients with hereditary antithrombin deficiency(75). Only one transgenic goat produced same amount of antithrombin in a year as 90,000 blood donations (76). The cost and easy scaling up of therapeutics production is also the advantage of the transgenic livestock bioreactor. A previous study suggested that building a large-scale (10,000 liter bioreactor) manufacturing facility for mammalian cells takes 3–5 years and costs US$ 250–500 million, whereas a transgenic farm with a single purification facility should not cost more than US$80 million and would most likely cost less (66). So that, using the mammary gland of transgenic livestock as the bioreactor to express recombinant human FIX (tg-FIX) could be a promising source to produce FIX concentrates in a safe and more economical way. However, because of the complexity of the PTMs of human FIX, no all transgenic livestock are suitable for manufacturing this recombinant therapeutics. No active FIX had been detected in the transgenic sheep milk(77). Zhang et al reported
that >90% recombinant protein in milk appeared to be a gamma-glycosylated and biologically active but the expression level was only 13.7 ng/mL (78).

**Current Progress and Specific Aims**

Our lab has generated transgenic pigs that express high level (2-3 g/l) transgenic FIX (tg-FIX) in the milk, and also developed the protocol for purifying active tg-FIX by using the combination of heparin-affinity chromatography (whole tg-FIX population) and anion exchange (Mini Q) chromatography (high acidic/carboxylated tg-FIX subpopulation); the final purified tg-FIX had the specific activity at 197 U/mg (74). This tg-FIX was characterized in extent of γ-carboxylglutamate and N-glycosylation. Not like the plasma-derived human FIX, the tg-FIX has different extent of carboxylation subpopulations. At tg-FIX expression level was at 200 µg/L milk, it was highly carboxylated (≥10) (79). However, when the expression level increased about 1,000-fold (2 mg/ml), only 10-20% was highly carboxylated (74), this indicated the enzymatic PTMs were rate limited and block the yield of the active tg-FIX production. Van Cott et. al. reported the majority of the N-glycans of this tg-FIX were complex, bi-antennary, while pd-FIX N-glycans were highly branched (tri- and tetra-antennary), and highly sialylated. No detectable Neu5Gc nor Galα(1,3)Gal in tg-FIX, which is strongly antigenic in human (80). We also noticed, at this high tg-FIX expression level, approximately 10-30% of total tg-FIX population is pro-tgFIX (pro-peptide attached tg-FIX) that has no pro-coagulation activity. In addition, we noticed certain amount of degraded/activated tg-FIX in the high acidic tg-FIX subpopulation.

In this study, we were working on the following specific aims:
**Specific Aim#1:** Characterize the tg-FIX and its degraded species in purified high acidic tg-FIX subpopulation. And investigate the predominant milk-borne protease, plasmin, in degrading the tg-FIX and the extent of the Gla in protecting FIX being cleaved.

**Specific Aim#2:** Bioengineer pig mammary gland by introducing truncated human furin gene co-expressing with tg-FIX. Characterize the recombinant truncated human furin (r-furin) in processing the excessive pro-peptide and convert non-active tg-proFIX to active tg-FIX both in vivo and in vitro.

**Specific Aim#3:** Establish scaled-up purification protocol, using the more efficient, immunoaffinity chromatography FIX select column to capture whole tg-FIX population from transgenic milk; then enrich high acidic tg-FIX by anion exchange chromatography; finally isolate the active tg-FIX subpopulation by using HPLC-SEC.

**REFERENCE**

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CHAPTER 2:

PLASMIN PROTEOLYSIS OF RECOMBINANT HUMAN FACTOR IX MADE IN THE MILK OF TRANSGENIC PIGS


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ABSTRACT

The milk-borne plasmin, identical to the one in the plasma, is the predominant protease in the milk. Producing of recombinant human coagulation factor IX (tg-rhFIX) in milk by mammary gland of transgenic pig could also be proteolyzed by the plasmin as native milk borne protein. The previous study of proteolysis of plasma-derived (pd-) human FIX by pd-plasmin showed the yield of the activated and/or degraded tg-rhFIX. Tg-rhFIX expressed in the milk frequently has subpopulations with less than a full complement (12) of γ-carboxylated glutamic acid (Gla), which alters the divalent metal-dependant conformation of the Gla domain. We noticed the cleavage of tg-rhFIX was altered by the extent of γ-carboxylated in tg-rhFIX in the presence of Ca$^{2+}$. The low Gla content (≤10/12) tg-rhFIX subpopulations were frequently cleaved in the light chain at Gln$^{44}$ but not in tg-rhFIX with high Gla content (≥10/12). This cleavage was also seen in the tg-rhFIX with high Gla content (≥10/12) in a chelated environment. The conformation rearrangement of high extent Gla induced by Ca$^{2+}$ prevented the Gla domain being cleaved by plasmin.

Key words: factor IX, γ-carboxyglutamic acid, plasmin, proteolysis

INTRODUCTION

Factor IX (FIX) is a member of the vitamin K dependent family of proteins and a 56 kDa zymogen form of the serine protease activated FIX (FIXa) that contains several divalent metal binding domains including an amino-terminal region consisting of 12 γ-carboxyglutamic acid residues (Gla). At the physiologic concentrations of 1.1 mM Ca$^{2+}$
and 0.6 mM Mg$^{2+}$, the core Gla domain of Vitamin K dependent (VKD) coagulation proteins like Protein C, Factor VII, Factor X and prothrombin have 4 Ca$^{2+}$ and 2 Mg$^{2+}$ specific sites and also 1 binding site that can accommodate either divalent cation. The FIX has 2 additional Gla than other VKD factors and has one more Mg$^{2+}$ specific sites. Recombinant versions of FIX (rh-FIX) frequently contain subpopulations with less than 12 Gla residues (1,2). The difference in extent of γ-carboxylation causes subpopulations with a range of biological activity. The metal-dependent conformation of the Gla domain is essential for factor IX to bind to negatively charged phospholipid vesicles provided in vivo by activated platelets resulting in its local ionization and augmentation of activation (3) and interacts with the C-terminal domain of TF in the TF/FVIIa complex during the FIX activation (4), in addition, is essential for FX activation by binding of FVIIIa, co-factor of tenase complex (5). Thus, the Gla domain plays a large role in the nature of proteolysis that occurs with zymogen FIX and other VKD proteins by serine proteases that regulate coagulation.

Plasmin is the major source of protease activity in milk (6). Furthermore, plasmin and plasminogen in milk are essentially identical to those found in blood having similar heat and pH stabilities, pH optima for casein hydrolysis, inhibitor susceptibility (7-9) and primary structure (10). Human plasma derived plasmin has been shown to proteolyze FIX into four products having apparent molecular weights of 45 kDa, 30 kDa, 20 kDa and 14 kDa when analyzed by reduced SDS-PAGE and two products at 52 kDa and 14 kDa under non-reducing conditions (11). Sequence analysis demonstrated that cleavage occurred after Lys$^{43}$, Arg$^{145}$, Arg$^{180}$, Lys$^{316}$ and Arg$^{318}$. The conformational specificity of plasmin on FIX structure was indicated by the proteolysis at only 5 of the possible 43
plasmin sites within pd-FIX (12). The divalent metal induced conformational dependence of proteolysis (13) by plasmin has been shown in fully carboxylated pd-FIX but not partially carboxylated, biologically active rFIX. Plasmin proteolysis of FIX during circulation is normally inhibited by α₂-antiplasmin inhibitor (14).

We previously reported producing recombinant human FIX (tg-rhFIX) in the mammary gland of transgenic pig, this expression level was about 2-3 g/L in the milk (15). This contrasts previous studies on the expression of tg-rhFIX in the milk of sheep which was largely inactive and had low levels of Gla content and appeared proteolyzed (16). Like that of recombinant FIX made by CHO cells (CHO-rhFIX), which contains different extent of Gla subpopulations (2), we fractionated tg-rhFIX into active and inactive subpopulations based upon differences in Gla content. As human and porcine plasminogen closely related (17,18), we here study the proteolysis of tg-rhFIX, therapeutic grade CHO-rhFIX and fully carboxylated pd-hFIX by human plasma derived plasmin. We also compare this proteolysis to that found in tg-rhFIX made in milk. In contrast to previous proteolysis studies of pd-FIX, we report on the differential proteolysis by plasmin to tg-rhFIX with different extent of Gla.

MATERIALS AND METHODS

All buffer components were purchased from VWR International LLC (Radnor, PA) or Thermo Fisher scientific (Waltham, MA) or Sigma (St. Louis, MO) unless otherwise stated. Reference pd-FIX (Mononine, CSL Behring, USA) and CHO-rhFIX (BeneFIX, Pfizer Limited USA) were kind gifts from James Brown (Lincoln, NE). These stocks of
were expired for clinical use but exhibited full procoagulant activity by one stage clotting assay.

**Purifying High Acidic Tg-FIX from Transgenic Pig Milk**

The purification procedures were adapted from previous described (15). The collected milk was adjusted to 100 mM EDTA to dissolve the casein micelle, which recover more tg-rhFIX, and stored at -80°C. The milk was thawed and then centrifuged (12,800 X g for 20 minutes) to remove the insoluble fat contained in an upper layer and solid particulates that were contained in the lower layer. The decanted middle layer or clarified milk was mixed with 4 parts 20 mM Tris, 50 mM NaCl, pH 7.4. The diluted, clarified milk was then loaded onto a Heparin sepharose 6 Fast Flow (GE Healthcare Bio-Sciences AB, Sweden) column, 10 mm I.D. X 150 mm L (11.8 mL), with the flow rate at 150 ml/hr. Then the column was washed with 20 mM Tris, 200 mM NaCl, pH 7.4 to remove caseins then with 20 mM Tris, 500 mM NaCl, pH 7.4 to elute FIX. The eluate (EL) was exchanged into the equilibrium buffer (20mM potassium phosphate, pH 7.2) and loaded on the Ceramic Hydroxyapatite (CHT) (Macro-Prep Ceramic Hydroxyapatite Type II, 40 µm, Bio-Rad Laboratories, Inc., Hercules, CA) column, 10 mm I.D. X 150 mm L (11.8 mL), with the flow rate at 150 ml/hr. The tg-FIX was eluted with a linear gradient from 20 mM to 400 mM Sodium phosphate, pH 7.2. Latter portion (about 15%) of CHT eluate (EL) was collected. The purifications were performed on a BioCAD Vision chromatography station (Applied Biosystems, Grand Island, NY). In order to minimize degradation, purification processes were performed at 4°C.
Analyzing High Acidic FIX population by High Performance/Pressure Liquid Chromatography-Size Exclusion Chromatography (HPLC-SEC)

The high acidic tg-rhFIX was exchanged into SEC running buffer (20 mM Tris, 200 mM NaCl, 10 mM CaCl2, pH 7.4) by using the Minimate tangential flow filtration systems with 10 kDa molecular weight cut off (MWCO) membrane (Pall Corporation, Port Washington, NY) or Amicon tube (10 kDa MWCO) (EMD Millipore, Billerica, MA). Tg-FIX sample was loaded on a TSK gel G3000SWXL, 7.8 mm ID x 30 cm, 5 µm (particle size), equipped with a guard column, 6 mm ID x 4 cm, 7 µm (particle size), (Tosoh Bioscience, LLC). Columns was equilibrated and run with 20 mM Tris base, 200 mM NaCl, 10 mM CaCl2, pH 7.0. The flow rate was 0.5 ml per min and duration of the run was 45 min with all major peaks eluting before 35 min. The fractions of each peak were pooled together for further analysis.

Sodium Dodecylsulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE)

SDS-PAGE was performed using precast 12% Bis-Tris Novex acrylamide gels. The gels, 4x sample buffer, 10x reducing agent, molecular weight marker and 20x running buffer were all from Invitrogen (Carlsbad, CA). Samples were incubated with reducing or non-reducing sample buffer at 70 °C for 10 minutes prior to electrophoresis at 200 V using the Invitrogen XCell Surelock mini cell. Gels were stained with Colloidal Blue (Invitrogen).

Detecting Pig Plasmin in Transgenic Milk by Western Blot

Both human plasma derived (pd-) plasmin and plasminogen were purchased from Haematologic Technologies Inc. (Essex Junction, VT). And all milk samples were skimmed and loaded on the SDS-PAGE as described and then gels were electro-blotted onto poly vinylidene fluoride (PVDF) membranes using a BioRad Transblot SemiDry
Transfer Cell (Richmond, CA) for 30 min at 25 volts. For detecting both plasmin and plasminogen, the primary antibody, Chicken IgY anti-pig plasminogen (MBS560144, MyBioSource, Inc. San Diego, CA) and secondary antibody, Goat anti-Chicken IgY-HRP (SA114013, Thermo Scientific, Rockford, IL), were used. The chromogenic DAB substrate (Thermo, Rockford, IL) was used in color developing.

**NH2-terminal Sequencing of the Plasmin Cleavage Products of FIX**

Amino acid sequencing was performed at the University of Nebraska Medical Center, Protein Structure Core Facility. Protein samples were subjected to SDS-PAGE and transferred to PVDF membranes as described above. The membrane was stained with Colloidal Blue and bands excised and subjected to Edman degradation using Applied Biosystems Procise protein sequencer, a Hitachi 8800 Amino Acid Analyzer and a Michrom MAGIC HPLC equipped with a Diode Array Detector.

**Quantitation of Total Factor IX Activity**

Total FIX activity was determined using the activated partial thromboplastin time (aPTT) assay (19). Briefly, 50 µl each of PTT Automate 5 reagent (Diagnostica Stago, Inc., Parsippany, NJ), factor IX deficient plasma (George King Bio-Medical, Overland Park, Kansas, USA), and a sample of interest were added to a cuvette and incubated at 37 °C for 3 min. 50 µL of 25 mM CaCl$_2$ (Sigma) was then added and the clotting time was measured using the STart Hemostasis Analyzer (Diagnostica Stago, Inc., Parsippany, NJ). The normal human plasma (Diagnostica Stago, Inc., Parsippany, NJ) was used as the standard, assigning 1 unit of FIX clotting activity per milliliter of plasma. The concentration of purified tg-rhFIX was determined by measuring the optical density at 280 nm in a 1 cm quartz cuvette and using an extinction coefficient, $\varepsilon^{1\%}_{280}$ = 13.4.
Mass Spectrometry of Tg-rhFIX to Detect Gla Content

All tg-rhFIX samples were activated with Factor Xla (Haemtech, Essex Junction, VT) in order to separate the light chain domain containing the Gla domain from the heavy chain domain using a 1:100 (w:w) enzyme to substrate ratio in 5mM CaCl$_2$, 1X TBS, pH 7.4 at 37°C for 1.0 hour. After activation, the samples were quenched with 1.2 moles of EDTA per mole of calcium and stored at -80°C until further analysis. LC-ESI-TOF-MS analysis was performed on an Agilent 1200 capLC system with an Agilent 6210 ESI-TOF MS. Solvent A was 0.1% formic acid (Fluka) (v/v) in deionized water. Solvent B was 0.1% formic acid (v/v) in acetonitrile (Burdick and Jackson). The column was an Agilent 300SB-C8 Poroshell column: 7.5 cm L x 0.5 mm ID, 5 micron particle size. The samples were diluted in Solvent A in the HPLC vial and loaded in the autosampler. Approximately 35 pmol of sample was injected on the column in a 40 microliter injection volume. The column was pre-equilibrated with 5%B; the flow rate was 20 microliters/minute; the column oven was set at 37°C; the autosampler was set at 10°C. After injection, the column was washed for 5 minutes with 5%B, then a linear gradient up to 20%B over 10 minutes, followed by a linear gradient up to 55%B over 70 minutes. The column was then cleaned by ramping up to 95%B for 5 minutes and then a series of three cycles of 10%B to 70% B, and then the column was re-equilibrated for >10 CV with 0%B for the next injection. A blank injection was performed in between each sample. MS data were acquired with MassHunter in positive mode with the following parameters: 4000 V source voltage, 325°C nebulizing gas temperature, 7 L/min gas flow rate, internal reference mass of 922.01 m/z. MS data were analyzed using Agilent’s Qualitative Analysis (version B.01.03).
Activating FIX to Activated FIX by FXIa

CHO-rhFIX (BeneFIX, Pfizer Limited USA) and tg-rhFIX were activated to their activated forms by plasma derived human FXIa (Haematologic Technologies, Inc., Vermont, USA). The mass ratio of FIX to FXIa is 100:1 (w:w), and both were incubated in TBS (20 mM Tris, 0.15 M NaCl) pH 7.4 with 5 mM CaCl$_2$ at 37°C for 2 hours. The reaction samples were exchanged into SEC running buffer and loaded on the HPLC-SEC as above. The fractions of FIXa was collected and pooled.

Plasmin Digestion of FIX and Activated FIX

FIX samples, including pd-FIX (Mononine, CSL Behring, USA), CHO-rhFIX (BeneFIX, Pfizer Limited USA) and high/low Gla tg-rhFIX, and activated FIX samples, including pd-FIXa (Haematologic Technologies, Inc., Vermont, USA), CHO-rhFIXa and tg-rhFIXa, were used in the assay. FIX and FIXa samples were incubated with plasma derived human plasmin (Haematologic Technologies, Inc., Vermont, USA) at 37°C using a 1:100 (w:w) enzyme to substrate ratio in TBS (20 mM Tris, 0.15 M NaCl, pH 7.4) in the presence of 5 mM CaCl$_2$ or 10 mM EDTA. Aliquots were took out at time = 0, 10, 20, 40, 60, and 120 minutes and quenched with SDS sample loading buffer with reducing buffer (Invitrogen, Carlsbad, CA, USA), then analyzed by reduced and non-reduced SDS-PAGE. In addition, a negative control digest was analyzed with each sample by replacing the enzyme with water.
RESULTS AND DISCUSSION

Detecting Porcine Plasmin in Transgenic Milk

Transgenic milk samples, K75, K101, R175&179, R180 and R1014 lactation pools, were diluted and skimmed then loaded on the SDS-PAGE with the positive controls, human plasma derived (pd-) plasmin (83 kDa) and plasminogen (88 kDa). The antibody probing the plasmin as well. The ~ 83 kDa bands, shown in all transgenic milk samples, were porcine plasmin involving in proteolysis of tg-FIX in the transgenic milk. The amount of plasmin is about 2 µg (compared to the pd-plasmin) in 10 µL diluted milk sample, which has about 10 µg tg-FIX (Fig 1).

Figure 1. Non-reduced Western blot detecting porcine plasmin in the transgenic milk sample. Lane 1, human plasmin (83 kDa), 1 µg; lane 2, human plasminogen (88 kDa), 1 µg; lane 3-7, transgenic milk K75, K101, R175&179, R180 and R1014 lactation pool, diluted 1:1 (v/v) and skimmed, 10 µL.

State of Degradation of Biologically Active Tg-rhFIX Pool Isolated from Milk

We previously reported that only 10-20% of the total tg-rhFIX in the milk has FIX specific activity due to rate limitations in γ-carboxylation of the Gla domain (15). We quantitatively captured these biologically active subpopulations as a pool using a sequence of heparin affinity and Ceramic Hydroxyapatite (CHT) chromatography. The high acidic tg-rhFIX obtained from CHT column contained all of the specific activity
present in the clarified whey. Conversely, the low acidic tg-rhFIX contained no biologically active species.

**Figure 2. SDS PAGE of most acidic tg-rhFIX pool from CHT chromatography.** Panel A. Non-reduced and Panel B. Reduced SDS-PAGE of FIX samples. Lane 1. pd-hFIX reference; Lane 2. CHO-rhFIX reference; Lane 3. tg-rhFIX CHT most acidic pool. Each lane contains 7μg of protein sample. The tg-rhFIX was purified from pig K108 milk pool from lactation days 16-24.

Figure 2A compares a non-reduced Commassie Blue stained SDS-PAGE gel profile of the biologically active tg-rhFIX pool from CHT to highly purified, therapeutic grades of pd-hFIX and CHO-rhFIX. On the non-reduced SDS-PAGE, the majority of the tg-rhFIX appeared as a single band corresponding to the co-migration of both single chain and disulfide bridge-linked, two-chain species. The most common minor band in all samples was the proteolysis product termed FIXγ that results from a cleavage at Arg$^{318}$ and release of an 8 kDa carboxy-terminal peptide from the FIX parent (12). FIXγ and the released γ-peptide were present in all preparations. The MW of FIX and FIXγ species
present in pd-FIX and CHO-rhFIX were similar due to similar glycoforms and other post-translational modifications (2), but were about 2-3 kDa larger than the respective species found in tg-rhFIX. This might be due to the presence of quarternary and ternary N-linked glycoforms on the activation peptide of pd-FIX and CHO-rhFIX versus the smaller bianternary glycoforms observed in tg-rhFIX (20).

Reduced SDS-PAGE reveals the spectrum of two chain proteolytic products that were present in all FIX preparations where at least five bands appear in both reference and tg-rhFIX samples (Figure 2B). Other than the zymogen form of tg-FIX (MW 54 kDa), the predominant tg-rhFIX degraded species was FIXα, MW is about 40 to 42 kDa (Figure 2B Lane 3), which results from the cleavage at Arg\textsuperscript{145} and release of the light chain (LC) from the heavy chain (HC) attaching activation peptide (AP) (FIXα-HC). This intermediate of activated FIX (FIXa), which had additional cleavage at Arg\textsuperscript{180} and release of the AP, is still a biological active form of FIX if the light chain was properly carboxylated and the propeptide was removed (21).

**Proteolytic Cleavages Detected by NH2-terminal Sequencing**

Table 1 summarizes the amino-terminal sequence analysis of protein bands observed by reduced SDS-PAGE (Figure 2B) in pd-FIX, CHO-rhFIX and the biologically active pool (high acidic) tg-rhFIX obtained by CHT. These cleavages are consistent with those commonly attributable to that made by plasmin (12). The degraded species appearing within the therapeutic grade pd-FIX and CHO-rhFIX were detected at 56 kDa, 48 kDa, 40 kDa, 30 kDa, 18 kDa, and 8 kDa with amino terminal sequences corresponding to FIX zymogen, FIX\textgreek{y}, FIXα-HC, FIXα\textgreek{y}-HC, LC and the \textgreek{y}-peptide. The similar degraded species appeared in tg-rhFIX were 54 kDa, 46 kDa, 38-40 kDa, 30 kDa, 17-18 kDa and 8
kDa. In contrast to the more highly fractionated, therapeutic grade pd-hFIX and CHO-rhFIX preparations, only the tg-rhFIX pool contained the FIXαβ-HC, which is the activated FIX, also FIXa, that possessed a MW of about 28-29 kDa.

<table>
<thead>
<tr>
<th>Band #</th>
<th>M. W. (kDa)</th>
<th>N-terminal a.a. Sequence</th>
<th>Predicted FIX Species</th>
<th>FIX Sample</th>
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</thead>
<tbody>
<tr>
<td>1</td>
<td>56</td>
<td>YNSGK</td>
<td>FIX Zymogen</td>
<td>pd-FIX</td>
</tr>
<tr>
<td>2</td>
<td>48</td>
<td>YNSGK</td>
<td>FIXγ²</td>
<td>CHO-rhFIX</td>
</tr>
<tr>
<td>3</td>
<td>40</td>
<td>AETVF</td>
<td>FIXα-HC³</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>30</td>
<td>AETVF</td>
<td>FIXαγ-HC⁴</td>
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<td>YNSGK</td>
<td>LC</td>
<td></td>
</tr>
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<td>6</td>
<td>8</td>
<td>SALVL</td>
<td>γ-peptide</td>
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<td>56</td>
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<td>FIX Zymogen</td>
<td>tg-rhFIX</td>
</tr>
<tr>
<td>8</td>
<td>48</td>
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<td>FIXγ</td>
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<td></td>
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<tr>
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<tr>
<td>19</td>
<td>8</td>
<td>SALVL</td>
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</tbody>
</table>

Table 1. NH₂-terminal amino acids (a. a.) sequence of all bands on reduced SDS-PAGE of FIX samples and predicted FIX species. ¹The band number is according to the number shown on the reduced SDS PAGE of FIX samples (Figure 2B). ²The FIXγ is the FIX zymogen without the c-terminal γ-peptide ³The FIXα-HC is the FIX zymogen without the light chain (LC); it the heavy chain (HC) with activation peptide (AP) ⁴The FIXαγ-HC is the FIXα-HC without the c-terminal γ-peptide ⁵The FIXαβ-HC is the heavy chain alone.

The FIXα-HC retained the activation peptide but had the γ-peptide removed and was therefore inactivated (12). In contrast, pd-FIXa consists of a FIXαβ-HC having an intact protease domain where when paired with an intact light chain possesses a high specific activity of about 6000 U/mg (measured plasma derived human activated FIX). Zymogen forms of FIX typically has specific activity of about 150-200 U/mg. Thus, the high
specific activity of high acidic pool tg-rhFIX from CHT is seen to be caused by the presence of FIXa.

**Separate Active Tg-rhFIX Zymogen from CHT Eluate by HPLC-SEC**

The high acidic tg-FIX was loaded on the HPLC-SEC in the presence of calcium ion. Three peaks of species with different biological activity were isolated (Figure 3A, Table 2). Pool 1 (Figure 3B, lane 2) exhibited both a low biological activity by coagulation assay and low extent of γ-carboxylation (Table 3). Pool 2 (Figure 3B, lane 3) and Pool 3 (Figure 3B, lane 4) showed both a high specific coagulation activity (Table 2) and high extent of γ-carboxylation (Table 3) that was closed to that obtained for pd-FIX and CHO-rhFIX. Both SEC pool 1 and 2 contained primarily FIX and FIXα and very minor amounts of FIXαγ but not activated FIX. Fraction 3 showed the highest specific activity of any FIX preparation which correlated well with a high content of FIXa and the respective FIXαβ-HC and LC content identified by N-terminal sequencing. This confirmed the origin of the high overall activity seen in the starting CHT eluate.

<table>
<thead>
<tr>
<th>Samples</th>
<th>Retention Time (min)</th>
<th>Specific activity (Units/mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CHT Eluate</td>
<td>N/A</td>
<td>1681 ± 187</td>
</tr>
<tr>
<td>SEC Pool 1</td>
<td>16.5-20</td>
<td>11 ± 1</td>
</tr>
<tr>
<td>SEC Pool 2</td>
<td>20.5-22.5</td>
<td>155 ± 13</td>
</tr>
<tr>
<td>SEC Pool 3</td>
<td>23-28</td>
<td>3203 ± 890</td>
</tr>
<tr>
<td>Mononine</td>
<td>N/A</td>
<td>181 ± 8</td>
</tr>
<tr>
<td>BeneFIX</td>
<td>N/A</td>
<td>178 ± 14</td>
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</tbody>
</table>

**Table 2.** The tg-rhFIX CHT most acidic eluate SEC pools and their FIX specific activity.  

\(^1\)One International Unit is the amount of factor IX activity present in 1 mL of pooled, normal human plasma. The specific activity of plasma derived human FIX is greater than or equal to 200 IU per milligram of protein.
Figure 3. Fractionation by HPLC-SEC of high acidic tg-rhFIX population. Panel A. HPLC-SEC profile of most acidic tg-rhFIX pool. SEC Pool 1, 2, and 3 collected from HPLC-SEC are as indicated. Panel B. Reduced SDS-PAGE of SEC pools. Lane 1. Starting tg-rhFIX CHT eluate pool used for SEC fractionation; Lane 2, SEC pool 1; Lane 3, SEC pool 2; Lane 4, SEC pool 3. All samples loaded 2 ug.
### Table 3. Extent of γ-carboxyglutamic acid (Gla) of FIX samples.

<table>
<thead>
<tr>
<th>Gla Extent</th>
<th>pd-FIX</th>
<th>CHO-rhFIX</th>
<th>SEC Pool</th>
</tr>
</thead>
<tbody>
<tr>
<td>≥ 10</td>
<td>100%</td>
<td>100%</td>
<td>&lt; 20%</td>
</tr>
<tr>
<td>&lt; 10</td>
<td>0</td>
<td>0</td>
<td>≥ 80%</td>
</tr>
</tbody>
</table>

**In Vitro Plasmin Digestion of FIX Zymogen**

Time course plasmin digests of pd-FIX (Fig. 4A), CHO-rhFIX (Fig. 4B) and HPLC-SEC pool 1 (low Gla content) and 2 (high Gla content) of tg-rhFIX (Figures 4C and D) done with Ca\(^{2+}\) (lanes 2-6) or in a chelated environment (lanes 9-13) were evaluated by SDS-PAGE. In general, for all FIX species evaluated here, the pathway of proteolysis at α (Arg\(^{145}\)) and γ (Arg\(^{318}\)) sites by plasmin took place at a faster rate in the presence of calcium than in EDTA. The rate and pathway of proteolysis in the presence of Ca\(^{2+}\) for SEC pool 2 tg-rhFIX was similar to that of pd-FIX and CHO-rhFIX proceeding primarily to FIXαγ-HC. This showed that the origin of FIXαγ-HC in the high acidic tg-rhFIX was likely caused by endogenous porcine plasmin in the milk. However, no evidence of the cleavage at Arg\(^{180}\) and production of FIXa by plasmin were observed.

The proteolysis at α and γ sites in a chelated environment was also similar for pd-FIX, CHO-rhFIX, tg-rhFIX SEC pool 1 and 2 (Fig. 4C and D, lane 9-13). In contrast to that in the presence of Ca\(^{2+}\) (Fig. 4C and D, lane 1-6), the proteolysis of the most carboxylated FIX species in 10 mM EDTA all shifted to a pathway that generated a cleavage in the light chain at Lys\(^{43}\) and releasing the Gla domain. While FIXα was still made, but at a
slower mode, same as the proteolysis at Arg\textsuperscript{318}. The proteolysis of LC at Lys\textsuperscript{43} in less carboxylated tg-rhFIX, SEC pool 1, behaved similarly in either a Ca\textsuperscript{2+} or chelated environment. However, the proteolysis of the Arg\textsuperscript{180} and Arg\textsuperscript{318} in less carboxylated tg-rhFIX behaved same as the other three FIX samples in both environments. We show for the first time that a non-native conformation due to a low extent of γ-carboxylation results in a prominent presentation of Lys\textsuperscript{43} site in the light chain that results in cleavage after. Our findings with the highly carboxylated SEC pool 2 tg-rhFIX are consistent with the previous observations of (22).
Figure 4. Reduced SDS-PAGE of time course plasmin digestion of FIX in Ca2+ and in chelated environments. Panel A. pd-FIX; Panel B. CHO-rhFIX; Panel C. SEC Pool 2 tg-rhFIX; Panel D SEC Pool 1 tg-rhFIX. For all panels: Lane 1-6. plasmin treated sample in 5 mM CaCl2 at t = 0, 10, 20, 40, 60, and 120 minutes, respectively; lane 7, untreated sample at t = 120 minutes. Lane 8-13 plasmin treated sample in 10 mM EDTA at t = 0, 10, 20, 40, 60, and 120 minutes, respectively; No plasmin added sample in 10 mM EDTA at t = 120 minutes. All lanes have 3.75 µg of FIX sample loaded. NH2-amino terminal sequencing of each protein species as indicated.

**In Vitro Plasmin Digestion of Activated FIX**

We examined FIXa stability in the presence of plasmin. The pd-FIXa, and activated CHO-rhFIX and tg-rhFIX SEC pool 2 (activated by FXIa *in vitro*) all exhibited a similar resistance to proteolysis at Arg\(^{318}\) by plasmin in the presence of Ca\(^{2+}\) (Figure 5).
Figure 5. Reduced SDS-PAGE of time course plasmin digestion in Ca2+ and in chelated environments of activated FIX. Panel A. pd-FIXa; Panel B. CHO-rhFIXa; Panel C. Fraction 2 tg-rhFIXa; For all panels: Lane 1-6. plasmin treated sample in 5 mM CaCl2 at t = 0, 10, 20 40, 60, and 120 minutes, respectively; lane 7, untreated sample at t = 120 minutes. Lane 8-13 plasmin treated sample in 10 mM EDTA at t = 0, 10, 20, 40, 60, and 120 minutes respectively; Lane 9: no plasmin added sample in 10 mM EDTA at t = 120 minutes. All lanes have 3.75 µg of FIX sample loaded. NH2-amino terminal sequencing of each protein species as indicated.
The proteolytic product was FIXγ-HC. In a chelated environment, all FIXa species were rapidly proteolyzed at Lys$^{43}$. This pattern is opposite from the proteolysis of FIX zymogen, and the only difference between the substrates was the activation peptide.

**CONCLUSIONS**

Consistent with the previous findings for fully carboxylated pd-FIX, we observed that both highly carboxylated CHO-rhFIX and tg-rhFIX will undergo efficient plasmin cleavage at Arg$^{145}$ in the presence of calcium to form FIXα then FIXαγ. But we did not see the cleavage at Arg$^{180}$ which form the activated FIX. Although formation of FIXa from tg-rhFIX zymogen in milk was not directly caused by plasmin, the formation of the intermediate of activated FIX promotes the formation of the final activated tg-FIX by other protease, e.g. trypsin, in the milk. The proteolysis at Lys$^{43}$ in light chain of FIX was noticed in the chelated environment, it was also seen in the low γ-carboxylated tg-rhFIX even in the presence of Ca$^{2+}$. This indicated the Ca$^{2+}$ induced conformational change of the Gla domain prevented it being proteolyzed by the plasmin. In order to decrease or eliminate the proteolysis of plasmin, specific protease inhibitor, e.g. ε-aminocapric acid, and EDTA are required.

**REFERENCE**


CHAPTER 3

BIOENGINEERING OF THE MAMMARY GLAND OF PIG: INCREASED PRO-PEPTIDE PROCESSING OF FACTOR IX IN THE MILK OF TRANSGENIC PIGS BY CO-EXPRESSION OF FURIN

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ABSTRACT

28,008 patients worldwide had been diagnosed hemophilia B, which was congenital deficiency in coagulation factor IX (F9), and 1,005,358,368 IU F9 concentrates was consumed to treat those patients in 2012 (1). However, still about 70-80% patients received inadequate or no treatment because of unavailable and/or unaffordable factor concentrates (2). It is desired to manufacture safe and more economical F9. The higher cell density of the mammary gland, large quantity of milk production, and human-like post-translational modifications have been demonstrated to make bioactive recombinant (r) F9 at higher levels in mammary gland of transgenic pig than is currently done by using CHO cells. Cleavage of pro-peptide of nascent rF9, rate limit enzymatic modification, cannot be fully achieved by endogenous porcine furin at the high rF9 expression rate in transgenic mammary epithelium. Our data showed about 10-30% of whole rF9 population was inactive pro-peptide attached rF9 (pro-rF9). In this study, we constructed transgene with both the truncated human furin and F9 gene and generated the pig by somatic cell nuclear transfer (SCNT) technology. We demonstrate that recombinant (r) furin was co-expressed with rF9 more than 2000 U/ml milk, and it converted the inactive pro-rF9 into active rF9 both in vivo and in vitro. No evidence was shown the co-expressing rfurin interfered the over-express (≥ 2g/L milk) and γ-carboxylation of rF9.
INTRODUCTION

Hemophilia B is the congenital bleeding disorders and is caused by deficiency in functional coagulation factor IX (F9); by 2012, there were 28,008 patients worldwide (1,3). Prophylactic therapy, intravenous infusions of F9 per week, significantly reduces internal bleeding episodes (ie., into joints) and improves the quality of life (4,5). 1,005,358,368 IU F9 was consumed worldwide in 2012(1). However, about 70-80% patients, mostly in developing countries, received inadequate or no treatment because of the limited supplies and high costs of either recombinant(r) or pathogen screened, plasma-derived (pd-) F9 concentrates, whose average wholesale price is about US$1.18 per IU(2,6). Of 15 licensed F9 concentrates, 14 are pdF9 which may result in prion and virus transmission risks(7); while only one is mammalian cell expression derived, which is recommended because of the safety reason (5). Thus, more economical and pathogen safe ways to manufacture rF9 are desired.

Like other Vitamin K dependent proteins of the coagulation cascade, F9 is a complex protein made by the liver while occurring in plasma at trace levels of only 5 µg/ml(8). The complex biosynthesis of F9 begins with a precursor polypeptide that then undergoes a number of post-translational modifications (PTMs): proteolytic cleavage of the propeptide, γ-carboxylation, β-hydroxylation, phosphorylation, and glycosylation(9). Mammalian cells, like Chinese hamster ovary (CHO) cells can make certain PTMs essential to biological activity in a comparable way to hepatocytes such as propeptide removal and γ-carboxylation(10-12). Unfortunately, these are still very low rates of synthesis that impede the use of current bioreactor technology by developing countries to produce rF9 for biotherapeutic use (6,13).
The economical rF9 production is also hindered by the low expression rate and low mammalian cell concentrations, about $10^6$ cells/ml culture (6,14). To offset the restriction caused by low cell concentration in bioreactors, we and other groups have shown that the three orders of magnitude higher cell density of the mammary gland and demonstrated expressing bioactive rF9 at higher levels in pig milk than is currently done in the culture media of stainless steel bioreactors(6).

While the mammary gland is a prodigious vehicle for producing recombinant proteins at high concentrations, the combination of species specificity of the mammary gland to make certain PTMs while providing sufficient milk for production is still challenging. Transgenic animals, including mice and sheep, produced recombinant human F9 in their mammary glands, limited amount of bio-active F9 was secreted into the milk(14-16).

Importantly, our previous work has shown that the pig has combined capability to make a diversity of PTMs which include glycosylation, a high volume of milk production (200-400 liters per year) (6,17,18) and is also multiparous. These features make it an efficient livestock in which to do further multiple gene, bioengineering by using somatic cell nuclear transfer (SCNT) technology(19). Examples of the PTM capabilities of the pig has been demonstrated by the expression of human F8 (20), protein C (21) , von Willebrand factor (VWF) (22) and F9 (9,23). In addition, the pig has the advantage as a specific pathogen free source of human biotherapeutics because it is not sensitive to prion exposure. Other livestock such as cows may need the PRNP gene required for the development of prion diseases to be knocked out to help ensure a prion free condition (24).
In order to fully take advantage of the high translational and secretory throughput of the mammary gland, higher PTMs processing rates must be made by multiple enzymes engineered into the transgenic livestock. In perturbing the expression of rF9 ten-fold from 0.2 g/l to greater than 2 g/l, about 10-30% rF9 had pro-peptide attached. The defective propeptide cleavage results in destabilizing the calcium-induced Gla domain conformation change and no pro-coagulation activity of pro-peptide attached FIX (25).

Furin or paired basic amino acid cleaving enzyme (PACE), a Ca$^{2+}$ dependent serine protease of the PC family, is involved in processing pro-peptides at dibasic sites with consensus sequence Arg-X-Lys/Arg-Arg (RXK/RR) (26). This includes the precursors of hormone: pro-nerve growth factor β(27), pro-insulin, pro-albumin, pro-complement C3(28,29), pro-von Willebrand factor(30), pro-factor IX(31) and protein C (32). Furin is localized primarily to the trans-Golgi network (TGN)(33-36), and also traffics between TGN and cell surface, and ER retention of furin blocked it activation resulting in no bioactivity (37,38). The order in location of carboxylase (ER) and furin (TGN) in vivo assure the pro-peptide removal after the carboxylation formed.

In terms of bioengineering of the mammary gland of a mouse, Drews et al. used furin under the control of the murine Whey Acidic Protein (mWAP) to increase the proteolytic processing of internal dipeptides of protein C(32). We here present the bioengineering of the pig mammary gland to provide sufficient furin activity to completely remove the pro-peptide and convert the inactive pro-rF9 to mature and active rF9 zymogen form at expression rate of 2 g/L.
METHODS

All buffer components were purchased from VWR International LLC (Radnor, PA) or Thermo Fisher scientific (Waltham, MA) or Sigma (St. Louis, MO) unless otherwise stated. All of the following solutions and media used in fetal fibroblast collection, transgenic cells producing, oocyte maturation, SCNT, and embryo reconstruction were filtered by using a 0.22 µm filter. All animal procedures were performed with an approved University of Missouri Animal Care and Use (ACUC) protocol. Unless stated otherwise, the following purifications were performed on a BioCAD Vision chromatography station (Applied Biosystems, Grand Island, NY). In order to minimize degradation, purification processes were performed at 4°C. The pd-F9 (Mononine, CSL Behring, King of Prussia, PA) and CHO-rhF9 (BeneF9, Pfizer, New York City, NY) used in the study were expired for clinical use however when used in experiments, exhibited full pro-coagulant activity. Both were kind gifts from James Brown (Lincoln, NE)

Fetal Fibroblast Collection

Landrace fetal fibroblasts cells (FFCs) were collected as described(39) with some modifications. Briefly, after removing the head, intestine, liver, limbs, and heart, the fetus was minced and digested individually in 20 mL of digestion media (Dulbecco’s Modified Eagle Medium (DMEM) supplemented with 15% (v/v) FBS, 200 units/mL collagenase and 25 Kunitz/mL DNaseI) for 5 hrs at 38.5°C and 5% CO₂ in air. Digested cells were washed with DMEM, 15% fetal bovine serum (FBS) (Hyclone, Logan, UT) with 10 µg/mL gentamicin, cultured overnight, then collected and frozen at −80 °C in aliquots in FBS with 10% dimethyl sulfoxide (DMSO) and stored in liquid nitrogen.
Production of gene constructs

The production of the WAP6FIX and WAP5Furin transgenes has been described in detail previously (32,40) and showed in Fig. 1A. F9 and furin constructs were linearized by *NotI*. After enzyme digestion, constructs were gel purified and stored at -20°C until transfection.

**A**

Transgene constructs schematic for WAP6FIX and WAP5Furin. The cDNA for human FIX and truncated human furin cDNA were placed under control of the 4.1 or 2.5 kbp mammary specific Whey Acidic Protein (WAP) promoters, respectively.

**B**

Domain schematic of the primary structure of both native and truncated human furin. Domains indicated: Signal Peptide a.a.1-26 (SP); Propeptide a.a. 27-107 (PRO); Subtilisin-like Serine Protease domain a.a.132-447; activation maturation domain a.a.484-570 (P); Cystine-rich region (CRR); trans-membrane domain (TM); Cytoplasmic domain a.a. 759-762 (Cyt); Trans Golgi Network Signal domain (TGN).
Production of transgenic cells

Early passage number Landrace FFCs (1-2) were cultured in cell culture medium (DMEM supplemented with 15% (v/v) FBS, 2.5 ng/mL basic fibroblast growth factor (Sigma) and 10 μg/mL gentamicin) overnight and grown to 75–85% confluency. Media was replaced 4 hours prior to transfection. FFCs were washed for 1–2 min with phosphate buffered saline (Invitrogen) and harvested with 0.05% trypsin-EDTA (Invitrogen; 1 mL per 75cm² flask). Cells were resuspended in cell culture medium, pelleted at 600 × g for 10 min, resuspended in 10 mL Opti-MEM (Invitrogen), and then quantified by using a hemocytometer and repelleted. Cells were resuspended in transfection media (75% cytosalts [120 mM KCl, 0.15 mM CaCl₂, 10 mM K₂HPO₄; pH 7.6, 5 mM MgCl₂] (van den Hoff et al. 1992) and 25% Opti-MEM (Gibco BRL Grand Island, NY)) and quantified again and the cell concentration was adjusted to 1×10⁶ cells/mL. Two hundred microliters cells were co-transfected by electroporation with linearize F9 (2μg), furin (2μg) constructs. Each electroporation utilized three consecutive 250-V, 1-ms square wave pulses administered through a BTX ECM 2001 (BTX, San Diego, CA) in 2 mm gap cuvettes. After electroporation, cells were plated in 100 mm dish at the concentration of 3000 cells per dish in cell culture medium. After 36 hours, cells were selected by the addition of geneticin (G418; 400 μg/mL) for 10-14 days until the formation of cell colonies. Genomic DNA from the cell colonies was used to verify the presence of all two genes by PCR. These cells then were stored in liquid nitrogen until used as donor cells for somatic cell nuclear transfer (SCNT).
Oocyte Maturation, SCNT, and Embryo Reconstruction

Fibroblast cells identified to have integration of both F9 and furin transgenes were used as donor cells for SCNT into enucleated oocytes followed by electrical fusion and activation (39). In brief, cumulus-oocyte cell complexes (COCs) were received in Phase I maturation medium from ART Inc. (Madison, WI) approximately 24 hours after harvest. COCs were then cultured in fresh Phase II maturation medium for 16 h. Maturation was in a humidified atmosphere of 5% CO₂ at 38.5°C. Expanded COCs were then vortexed in 0.1% hyaluronidase in Hepes-buffered Tyrode’s medium containing 0.01% polyvinyl pyrrolidone for 4 min to remove the cumulus cells. Only oocytes having a visible first polar body (PB) with uniform cytoplasm were selected and placed in fresh manipulation medium (25 mM Hepes-buffered TCM199 with 3 mg/mL bovine serum albumin (BSA)) containing 7.5 μg/mL cytochalasin B overlaid with warm mineral oil. SCNT was conducted (39) by removing the PB, MII chromosomes and a small amount of surrounding cytoplasm of the oocyte by using a beveled glass pipette with an inner diameter of 17-20 μm. After enucleation, a donor cell was injected into the perivitelline space and placed adjacent to the recipient cytoplasm. The reconstructed embryos were fused and activated with 2 DC pulses (1 sec interval) of 1.2 kV/cm for 30 μsec provided by a BTX Electro-cell Manipulator 200 in fusion medium (0.3 M mannitol, 1.0 mM CaCl₂, 0.1 mM MgCl₂, and 0.5 mM Hepes, pH adjusted to 7.0–7.4). After fusion and activation, only the fused embryos were cultured into four well plates (Nunc, Denmark) containing 500 μL of PZM3 with 0.3% BSA and 500 nM Scriptaid at 38.5 °C and 5% CO₂ in humidified air for 14 to 16 hours, until embryo transfer (41).
Embryo Transfer and piglet production

More than 100 SCNT zygotes were surgically transferred to the oviducts of each surrogate on the day of, or one day after, the onset of estrus. Ultrasound was used to monitor the pregnancy. Piglets were delivered via cesarean section from surrogates by day 114-116 of gestation. Piglets are processed immediately and tissue samples were collected for establishment of cell lines and PCR genotyping. Piglets were then hand-raised until weaning (3-4 wks of age). After confirming genotype and reaching sexual maturity, the founders with both F9 and furin cDNA were mated to wild type pigs for production of animals for milking and phenotyping.

PCR Genotyping Assays

The integration of transgenes in the founders and offspring was conducted by using 10 ng of genomic DNA for each 25 µL PCR reaction (Mastercycler Pro; Eppendorf, Hauppauge, NY). GoTaq polymerase (Promega, Madison, WI) was used as recommended by the manufacturers. PCR primers (Table 1) were used in under PCR cycling conditions of: 95°C for 3 minutes followed by 30 cycles at 95°C for 15 seconds, 58°C for 30 seconds, and 72°C for 45 seconds.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primers</th>
<th>Fragment size</th>
</tr>
</thead>
<tbody>
<tr>
<td>F9</td>
<td>Forward: 5’-TACCTCTTTGGCCGATTCAG-3’&lt;br&gt;Reverse: 5’-GCTCCTTCATTTTCTCCGCT-3’</td>
<td>430bp</td>
</tr>
<tr>
<td>Furin:</td>
<td>Forward: 5’-GCGAGAGGACCCGCTTATCAAAGA-3’&lt;br&gt;Reverse: 5’-TGGAAATCACCTGTGGCTGTCTTGC-3’</td>
<td>293bp</td>
</tr>
<tr>
<td>eNOS</td>
<td>Forward: 5’-ACGAGCCTCCAGAACCTCCTTGCTT-3’&lt;br&gt;Reverse: 5’-TTTCCAGCAGCATGTTGGACACTG-3’</td>
<td>243 bp</td>
</tr>
</tbody>
</table>

Table 1. PCR Genotyping primers and fragments size for transgenic pigs
Content and quality of genomic DNA loaded in the PCR reaction was confirmed by amplification of the endogenous swine eNOS gene using the following PCR conditions: 95°C for 3 minutes followed by 30 cycles at 95°C for 15 seconds, 59°C for 30 seconds, and 72°C for 45 seconds.

**Pig milking**

Transgenic pig milk was collected as previously described (42). Milk samples were collected twice daily on the following days (D5-10, then every three days until D35). Piglets were removed from the mother 30 minutes before milk sample collection and returned following sample collection. An injection of Oxytocin was given to the sow 10-15 minutes before sample collection.

**Sodium Dodecylsulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE)**

Samples were analyzed by SDS-PAGE stained with colloidal Blue gel stain (Invitrogen, Carlsbad, CA, USA) using Invitrogen 12% Bis-Tris Novex acrylamide precast gels and the Invitrogen Surelock XL apparatus (200 Volts for 1 hour). Briefly, samples were mixed with 4x LDS sample buffer (Invitrogen) and deionized water followed by heating at 74 °C for 10 min. For reduced gels, samples were mixed with 10x reducing agent (Invitrogen) prior to heating.

**Western Blot**

The gels were electro-blotted onto poly vinyldene fluoride (PVDF) membranes using a BioRad Transblot SemiDry Transfer Cell (Richmond, CA) for 30 min at 25 volts. For total F9, including all F9 species, blots were probed by rabbit polyclonal antibody (Pab) anti-F9 (F0652, Sigma-Aldrich St. Louis, MO); The furin was detected by using rabbit
Pab anti-furin (476-490) (F8806, Sigma-Aldrich St. Louis, MO); The mouse monoclonal antibody (Mab), PROFIX 3D2.6H12 (Green Mountain Antibody, Burlington, VT), was used in probing pro-peptide of F9. The secondary antibody (HRP-conjugated) anti-rabbit (A9169) and mouse (A4416) IgG (Sigma-Aldrich St. Louis, MO) was used to detect the primary antibody respectively. The chromogenic DAB substrate (Thermo, Rockford, IL) was used in color developing.

**Quantification of Recombinant Human Factor IX (rF9) and Recombinant Human Pro-peptide attached Factor IX (pro-rF9) in Transgenic Milk**

Western blot was performed as described before. Mononine or purified pro-rF9, as calibrator, was loaded along with the transgenic milk samples (triplicated). The concentration mononine or pro-rF9 was determined by measuring the optical density at 280 nm in a 1 cm quartz cuvette and using an extinction coefficient, $\varepsilon^{1\%} = 13.4$. The pictures of the blots were analyzed by using the Image J(43,44). The amount of rF9 and pro-rF9 was then calculated by using the standard curve created by the calibrators.

**Scaled-up Processing Pro-rF9 in Transgenic Milk by Incubating with Rfurin Co-expressed Transgenic Milk before Purification**

Whole transgenic milk with rfurin co-expressed sample was first added to heparin sepharose fast flow (FF) (GE Healthcare Bio-Sciences AB, Sweden) resin at 1:1 (v/v) ratio and incubated for 30 min at 4°C. The supernatant was collected (F9 depleted) and was then incubated with the whole transgenic milk with only rF9 expressed at 1:4 (v/v) ratio for 2 hour. All above milk samples were not treated with EDTA and any protease inhibitors.
Scaled-up Purification of High Acidic Recombinant Human Factor IX from Transgenic Swine Milk

High acidic rF9 was purified using the procedures adapted from previous study (23). The clarified transgenic milk samples was first diluted with the loading buffer (20 mM Tris, 50 mM NaCl, pH 7.4) at 1:3 ratio then loaded onto a heparin hyper D column, 26 cm ID X 20 cm L (GE Healthcare Bio-Sciences AB, Sweden). The impurities were washed out by increasing [NaCl] to 200 mM, then the whole rF9 was eluted by increasing [NaCl] to 500 mM. The flow rate of the chromatography was 4 ml/min. The enriched rF9 sample was further loaded on the phenyl 650C column, 26 cm ID X 20cm L (Tosoh Bioscience, LLC) in the loading buffer (500 mM NaCl), the rF9 was collected in the flow through with flow rate at 4 ml/min. The rF9 sample was loaded on Q sepharose fast flow column (GE Healthcare Bio-Sciences AB, Sweden), 26 cm ID X 20cm L. The low acidic F9 population was washed out by increased [Ammonium acetate] to 537 mM, and the high acidic F9 was eluted at [Ammonium acetate] at 800 mM with the flow rate at 4 ml/min. All buffer exchanges of rF9 samples were performed by using the tangential flow filter (TFF) system (10 kDa MWKO, Pall Corporation, Port Washington, NY). All steps were performed at 4 °C.

Separate Active rF9 from High Acidic rF9 population by High Pressure Liquid Chromatography-Size Exclusion Chromatography (HPLC-SEC)

The high acidic rF9 was exchanged into SEC running buffer (20 mM Tris, 200 mM NaCl, 10 mM CaCl₂, pH 7.4) by using the Minimate tangential flow filtration systems with 10 kDa molecular weight cut off (MWCO) membrane (Pall Corporation, Port Washington, NY) or Amicon tube (10 kDa MWCO) (EMD Millipore, Billerica, MA). F9 sample was
loaded on a TSK gel G3000SW\textsubscript{XL}, 7.8 mm ID x 30 cm, 5 µm (particle size), equipped with a guard column, 6 mm ID x 4 cm, 7 µm (particle size), (Tosoh Bioscience, LLC). The flow rate was 0.5 ml per min and duration of the run was 45 min with all major peaks eluting before 35 min. The chromatography were performed by using Knauer Smartline chromatography apparatus, including Manger 5000, Pump 1000 and UV Detector 2600 (Berlin, Germany), equipped with a Gilson FC 204 fraction collector (Middleton, WI). Both columns were equilibrated and run with 20 mM Tris base, 200 mM NaCl, 10 mM CaCl\textsubscript{2}, pH 7.0. The fractions of each peak were pooled together for further analysis.

**Purification of Pro-rF9 and rF9 from Transgenic Milk**

Transgenic milk, no rfurin co-expressed with rF9 (K96 lactation day 24), was used to purify both rF9 and pro-rF9 subpopulation. The whole rF9 population (including both rF9 and pro-rF9 subpopulation) was purified by using the heparin hyper D column as described above. Then it was loaded on the immunoaffinity column, mouse monoclonal antibody (Mab) anti-propeptide of pro-rF9(Green Mountain Antibody, Burlington, VT) immobilized Protein G Sepharose FF(GE Healthcare Bio-Sciences AB, Sweden) at 1 mg Mab/ml resin , 10 mm ID X 127 mm L (10 mL). The loading buffer was 20 Mm Tris, 50 mM NaCl, pH 7.4; the wash buffer was the loading buffer with 500 mM NaCl with the flow rate at 150 cm/hr. The rF9 subpopulation was achieved in the flow through. The pro-rF9 was eluted by using 0.1 M Glycine, pH 2.8 and then neutralized by 1:10 (v/v) 1 M Tris, pH 8.5 to the eluate.

**Quantitation of total factor IX activity**

Total F9 activity was determined using the activated partial thromboplastin time (aPTT) assay (45). Briefly, 50µl each of PTT Automate 5 reagent (Diagnostica Stago, Inc.,
Parsippany, NJ, USA), factor IX deficient plasma (George King Bio-Medical, Overland Park, Kansas, USA), and a sample of interest were added to a cuvette and incubated at 37 °C for 3 min. 50 µL of 25mM CaCl2 (Sigma) was then added and the clotting time was measured using the STart Hemostasis Analyzer (Diagnostica Stago, Inc., Parsippany, NJ). The normal human plasma (Diagnostica Stago, Inc., Parsippany, NJ) was used as the standard, assigning 1 unit of F9 clotting activity per milliliter of plasma. The concentration of purified rF9 was determined by measuring the optical density at 280 nm in a 1 cm quartz cuvette and using an extinction coefficient, ε\text{1%} =13.4.

**NH2-terminal sequencing of the plasmin cleavage products of F9**

Amino acid sequencing was performed at the University of Nebraska Medical Center, Protein Structure Core Facility. Protein samples were subjected to SDS-PAGE and transferred to PVDF as described above. The membrane was stained with Colloidal Blue and bands excised and subjected to Edman degradation using Applied Biosystems Procise protein sequencer, a Hitachi 8800 Amino Acid Analyzer and a Michrom MAGIC HPLC equipped with a Diode Array Detector.

**Purification of Recombinant Truncated Human Furin (rfurin) from Transgenic Milk with Rfurin Co-expressed**

Transgenic milk sample (R1014, lactation day 5-22 pool), having rfurin co-expressed, was first diluted with DEAE loading buffer, 20 mM HEPES, 50 mM NaCl, 2 mM CaCl2, 0.1% (w/v) Brij-35, pH 7.5, at 1:4 (v/v) ratio and centrifuged at 12000 rpm, 4 °C for 20 min. The supernatant (clarified milk) was loaded on the DEAE fast flow column (GE Healthcare Bio-Sciences AB, Sweden), 10 mm ID X 127 mm L (10 ml) with the flow rate at 150 cm/hr; and the furin fraction was eluted by increasing [NaCl] to 140 mM. The
DEAE eluate was exchanged to the CHT binding buffer (20 mM HEPES, 2 mM Na2HPO4, 0.1% (w/v) Brij-35, pH 7.5) and loaded on the Ceramic Hydroxyapatite, CHT (Bio-Rad, Hercules, CA) column, 10 mm ID X 127 mm L (10 ml) at 150 cm/hr. The flow through, which had rfurin, was collected. Rfurin fractions were exchanged to the Q Sepharose binding buffer (20 mM HEPES, 50 mM NaCl, 2 mM CaCl2, 0.1% (w/v) Brij-35, pH 7.2) and loaded onto the Q Sepharose FF (GE Healthcare, Bio-Sciences AB, Sweden) column, 10 mm ID X 127 mm L (10 ml) with the flow rate at 150 cm/hr; the furin fraction was eluted at 140 mM NaCl. Final sample was exchanged to 20 mM HEPES, 2 mM CaCl2, 0.1% (w/v) Brij-35, pH 7.5.

**Quantification of Activity of Furin**

Activity of Furin in Milk—Fluorometric assays were carried out essentially as described (46). Whole milk sample was diluted 1:50 to 1:200 with assay buffer (20 mM HEPES, 2 mM CaCl2, 0.1% (w/v) Brij-35, pH 7.5). Calibrator is the 7-amino, 4-Methyl Coumarin (AMC), concentration is from 0.39 uM to 25 uM in assay buffer. 50 uL 100 uM substrate, L-PyroGlu-Arg-Thr-Lys-Arg-AMC (pERTKR-AMC) (R&D systems, Minneapolis, MN, USA) was incubated with the 50 uL diluted sample at room temperature. Fluorescence was measured by Cary Eclipse Fluorescence Spectrophotometer (Agilent Technologies, USA) at λex 342 nm; λem 440 nm with kinetic mode for up to 20 mins. The control consisted of substrate and assay buffer. 1 Unit of furin is equal to 1 pmol AMC/min in the above conditions.
Cleavage of Pro-peptide of Pro-rF9 by Partial Purified Recombinant Truncated Human furin (rfurin) *in vitro*

Add 346 µL rfurin sample (43.35 U/mL), total activity was 15 U (cleaved 15 pmol prpeptides/min), to 200 µg (0.2 mg/ml, total 3500 pmol pro-rF9) purified pro-rF9 described above in furin activity assay buffer (20 mM HEPES, 2 mM CaCl2, 0.1% (w/v) Brij-35, pH 7.5). At each time point (0, 30min, 1, 2, 4, 8 and 24 hr), reaction was quenched by taking 20 µL sample and mixed with 4 X SDS-PAGE sample buffer (with or without 10 X reduced agent) for non-reduced, reduced SDS-PAGE respectively. Additional 50 µL sample was quenched by 50 µL 20 mM sodium citrate, pH 7.4 for the F9 activity (aPTT) assay. The reaction was in room temperature (25°C)

RESULTS

Generation F9 and Furin Co-expressed Pigs

Thirteen live female *F9* transgenic piglets were born from 5 litters. Six of 13 pigs were positive for *F9* and *FURIN* transgenes. Fifteen male *F9* transgenic piglets were born from 3 litters and all of them were positive for F9 and furin transgenes (Table 2).

Production of Female Transgenic Offspring for Milk Collection and Mendelian Inheritance of the Transgenes

Male transgenic founder lines, Line A (78-2, 78-4), Line B (79-2) and Line C (80-4) were mated with wild type Landrace sows to produce the female offspring for milk production to test the foreign protein expression. Sixty-four offspring were produced from 5 litters. Of those 64 offspring, 26 were positive for *F9* and *FURIN* (Table 3, Figure 2). The
percentage of transgenic positive offspring is 41% which is closed to the expected ratio of 50% for Mendelian inheritance of the transgenic loci. Transgenic males were mated to a wild-type boar and allowed to farrow. Milk samples were collected from all three integration sites (Line A, B and C).

<table>
<thead>
<tr>
<th>Litter</th>
<th>Litter size</th>
<th>Sex</th>
<th>Transgenic</th>
<th>Wild type</th>
</tr>
</thead>
<tbody>
<tr>
<td>65</td>
<td>1</td>
<td>Female</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>66</td>
<td>1</td>
<td>Female</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>67</td>
<td>6</td>
<td>Female</td>
<td>4</td>
<td>2</td>
</tr>
<tr>
<td>68</td>
<td>4</td>
<td>Female</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>69</td>
<td>1</td>
<td>Female</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>78</td>
<td>6</td>
<td>Male</td>
<td>6</td>
<td>0</td>
</tr>
<tr>
<td>79</td>
<td>5</td>
<td>Male</td>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td>80</td>
<td>4</td>
<td>Male</td>
<td>4</td>
<td>0</td>
</tr>
</tbody>
</table>

Table 2. Summary of production of rF9 transgenic founder pigs

<table>
<thead>
<tr>
<th>Founder</th>
<th>Litter number</th>
<th>offspring</th>
<th>F9 and Furin</th>
<th>Wild type</th>
</tr>
</thead>
<tbody>
<tr>
<td>78-2</td>
<td>122</td>
<td>16</td>
<td>6</td>
<td>10</td>
</tr>
<tr>
<td>78-4</td>
<td>123</td>
<td>15</td>
<td>1</td>
<td>14</td>
</tr>
<tr>
<td>79-2</td>
<td>125</td>
<td>10</td>
<td>4</td>
<td>6</td>
</tr>
<tr>
<td>80-4</td>
<td>23, 129</td>
<td>23</td>
<td>15</td>
<td>8</td>
</tr>
<tr>
<td>Total</td>
<td>5</td>
<td>64</td>
<td>26(41%)</td>
<td>38 (59%)</td>
</tr>
</tbody>
</table>

Table 3. Male founders mated to the wild type sows for production of female transgenic offspring
The total rF9 expression rate was high in the transgenic milk, from 1.50 ± 0.02 g/L (Avg.±SD, n=3) to 2.30 ± 0.05 g/L (Avg.±SD, n=3) (Table 4). Western blot developed by antibody anti pro-peptide of human factor IX confirmed the existing of pro-rF9, which was not fully processed by endogenous porcine furin, in the transgenic milk (Fig. 3); and there was 9% to 27% pro-rF9 of total rF9 in the transgenic milk sample (Fig. 3, Table 4). The molecular weight of purified pro-rF9 was 57 kDa, 2 kDa more than the rF9 (Fig. 5A, lane 1). N-terminal amino acid sequencing showed the result, Thr-Val-Phe-Leu-Asp, matching the sequence of the pro-peptide of pro-rF9.
Fig. 3. Western blot of milk samples. Milk samples included rF9 only expressed transgenic milk (K75 lactation day 11-23 pool and K101, lactation day 12-29 pool) and the rfurin co-expressed transgenic milk (R175 & 179 lactation day 5-35 pool, R180 lactation day 5-35 pool and R1014 lactation day 5-22 pool). All milk samples were diluted with 200 mM EDTA 1:1 and skimmed as described in methods. Lane 1: K75 lactation day 11-23 pool; Lane 2: K101, lactation day 12-29 pool; Lane 3: R175 & 179 lactation day 5-35 pool; Lane 4: R180 lactation day 5-35 pool; and lane 5: R1014 lactation day 5-22 pool. 2 µL of each milk sample was loaded on each lane. The 55 kDa bands indicated the rF9 (including the rF9 zymogen and the pro-rF9); the 65 kDa bands indicated the rfurin; and the 57 kDa bands indicated the pro-rF9 (the 47 kDa bands were unspecific binding).

No F9 activity was detected for the pro-rF9 (Table 4). No furin antigen was detected by the Western blot developed using antibody anti-human furin; neither furin activity was detected in the milk sample.

<table>
<thead>
<tr>
<th>PIG ID</th>
<th>Lactation Pool</th>
<th>[Total rF9] (mg/ml)</th>
<th>[Pro-rF9] (mg/ml) (Percentage of Pro-rF9 %)</th>
<th>Furin Activity (U/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td>R175 &amp; 179</td>
<td>Day 5-35</td>
<td>2.23 ± 0.07</td>
<td></td>
<td>1402 ± 40</td>
</tr>
<tr>
<td>R180</td>
<td>Day 5-35</td>
<td>1.60 ± 0.35</td>
<td>Not Detected</td>
<td>539 ± 217</td>
</tr>
<tr>
<td>R1014</td>
<td>Day 5-22</td>
<td>2.22 ± 0.06</td>
<td></td>
<td>2214 ± 33</td>
</tr>
<tr>
<td>K75</td>
<td>Day 11-23</td>
<td>2.30 ± 0.05</td>
<td>0.21 ± 0.05 (9%)</td>
<td>Not Detected</td>
</tr>
<tr>
<td>K96</td>
<td>Day 10-25</td>
<td>1.63 ± 0.36</td>
<td>0.25 ± 0.04 (15%)</td>
<td></td>
</tr>
<tr>
<td>K101</td>
<td>Day 12-29</td>
<td>1.50 ± 0.02</td>
<td>0.40 ± 0.10 (27%)</td>
<td></td>
</tr>
</tbody>
</table>

Table 4. Amount of total rF9, pro-F9 and rfurin in transgenic milk samples (n=3).
Rfurin Expressing and Processing Pro-peptide of rF9 in vivo

Not like the endogenous human furin, this truncated rfurin is eliminated transmembrane domain, cytoplasmic domain and trans-Golgi network (TGN) signal domain (Fig. 1B). This rfurin secretes into the milk, remaining its furin activity, while endogenous furin cycled in the TGN of epithelium. The Western blot developed by antibody anti-furin showed the rfurin signal, whose molecular weight is about 65 kDa (Fig. 5, lane F). And the furin activity reached up to 2214 ±33 U/mL (Avg.±SD, n=3) in transgenic milk (R1014, lactation day 5-22 Pool). The expression of rfurin was stable during the lactation, and the more furin activity was detected during the late lactation (Fig. 4).

![Furin Activity in Transgenic Milk Samples](image)

**Fig. 4. Furin activity in transgenic milk.** The furin activity of R180 transgenic milk samples (each lactation day) was measured. 1 Unit of furin is equal to 1 pmol AMC/min in the above conditions. The error bars is the standard deviation (n=3)
The co-expression of rfurin did not interfere the producing rF9 in transgenic milk, which reached $2.23 \pm 0.07$ g/L (Avg.±SD, n=3) (Table 4). No more pro-rF9 was detected (Fig. 3, Table 4).

**Rfurin Processing Pro-rF9 in vitro**

Rfurin was enriched (partially purified) from the transgenic milk sample. ~40% furin activity was recovered after 4 purification steps (Table 5). N-terminal amino acid sequencing of the 65kDa band (on the non-reduced SDS-PAGE) (Fig. 5A, lane F), Asp-Val-Try-Gln-Glu, matched the mature form of human furin (47). Purified pro-rF9 was incubated with partially purified rfurin at room temperature for up to 24 hours. We noticed the molecular weight of pro-rF9 shifted about 2 kDa after incubated with rfurin on both SDS-PAGE and western (Fig. 5A). Pro-rF9 signal was decreasing, while signal on total rF9 (including both pro-rF9 and rF9) remained same on the non-reduced western blots (Fig. 4B). Also, we noticed that the F9 specific activity of the sample increased after incubated with rfurin (Fig.5C).

<table>
<thead>
<tr>
<th>Sample</th>
<th>Volume (ml)</th>
<th>Activity (U/ml)</th>
<th>Total Activity (U)</th>
<th>Activity Recovery %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Whole Milk</td>
<td>10</td>
<td>1925</td>
<td>19247</td>
<td>100</td>
</tr>
<tr>
<td>Clarified Milk</td>
<td>45</td>
<td>323</td>
<td>14527</td>
<td>75</td>
</tr>
<tr>
<td>DEAE Elution</td>
<td>85</td>
<td>142</td>
<td>12040</td>
<td>63</td>
</tr>
<tr>
<td>CHT Flow Through</td>
<td>175</td>
<td>50</td>
<td>8666</td>
<td>45</td>
</tr>
<tr>
<td>Q Elution</td>
<td>135</td>
<td>53</td>
<td>7209</td>
<td>37</td>
</tr>
</tbody>
</table>

Table 5. Purification table of isolation rfurin from transgenic milk (R1014 lactation day 5-22 pool)
Fig. 5. RFurin cleave pro-peptide of pro-rF9 in vitro. A. Non-reduced and Reduced SDS-PAGE. B. Non-reduced western blot anti-FIX and proFIX. On non-reduced gel, lane F is partially purified rfurin sample and arrow pointing rfurin (65 kDa); On reduced gle, lane F is partially purified rfurin sample which loaded as same amount as in the reaction. The 65 kDa band is the band (~55 kDa) on non-reduced gel, not the rfurin. Lane 1: Purified pro-rF9 (57 kDa), same amount as the reaction loaded on the following lanes. Lane 2-8: Furin processing pro-rF9 in vitro reaction time= 0, 30 min, 1, 2, 4, 8 and 24 hr. C. Specific activity of pro-rF9; pro-rF9 and total rF9 content in the rfurin processing pro-rF9 reaction sample.

Scaled-up Purification of Active rF9 from Transgenic Milk

Both transgenic without rfurin co-expressed (K82, K89, K92 and K102 Pool) and with rfurin co-expressed (R185 Pool) were used to purify active rF9. The pro-rF9 in the transgenic milk was processed by incubated with rF9 depleted transgenic milk with rfurin co-expressed. The yield of active rF9 from the non- and rfurin co-expressed transgenic milk were 31.6 mg (active rF9) out of 1479 mg (total rF9) and 22.9 mg out of 1409 mg respectively; And there was no significant difference between the F9 specific activity of both active rF9 (Table 6).

<table>
<thead>
<tr>
<th>Transgenic Milk</th>
<th>Heparin Eluate (mg)</th>
<th>Acidic Eluate (mg) / Recovery %</th>
<th>Active rF9 (mg) / Recovery %</th>
<th>Specific Activity (U/mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>No rfurin co-expressed</td>
<td>1479</td>
<td>119 / 8 %</td>
<td>31.6 / 2 %</td>
<td>226 ± 42</td>
</tr>
<tr>
<td>Rfurin co-expressed</td>
<td>1409</td>
<td>90 / 6 %</td>
<td>22.9 / 2 %</td>
<td>216 ± 14</td>
</tr>
</tbody>
</table>

Table 6. Comparison of rF9 from both transgenic without rfurin co-expressed (K82, K89, K92 and K102 Pool) and with rfurin co-expressed (R185 Pool) milk by scaled-up purification.

Discussion

The demand of producing F9 proteins in a safe and highly efficient manner has increased.

Based on the data from the World Federation of Hemophilia (Montreal, Canada), the consumption of F9 was approximately 250,100,000 U in the United States and
1,005,358,368 U worldwide in 2012(1). And we also need to consider the about 80% patients in developing and undeveloped area could not afford the high cost of the F9 concentrates. So the need for F9 concentrates is way more than the current consumption (3,48). Besides the high cost of hemophilia treatment, proteins derived from human plasma carry with them the risk of transmission of blood-borne diseases and infections(3). Considering bio-safety reasons, the application of recombinant human F9 products is widely recommended(49). A transgenic animal bioreactor is an attractive system for meeting the need for therapeutic recombinant proteins. Compared with other recombinant protein expression systems, transgenic animals have the ability to produce the biological active proteins approximately a 10-fold higher concentration of the target protein(6). In addition, a transgenic farm with a single purification facility should not cost more than US$80 million(50). However, building a large-scale (10,000 liter bioreactor) manufacturing facility for a mammalian cell expression system is time consuming and costs US$ 250–500 million(50). One successful example is ATryn, an anticoagulant, the first ever biologic product produced by a genetically engineered (GE) animal – a goat(51), which was approved by FDA to be used for the prevention of blood clots in patients in 2009.

The recombinant human F9 was expressed in several mammary gland of transgenic animals by using the SCNT technology. Very low amounts of inactive F9 have been detected in the transgenic sheep milk (52). Zhang et al reported that the highest production of F9 in goat milk was 13.7 ng/mL 3 days after transfection plasmid DNA directly into the mammary gland lobule of a lactating goat and > 90% rF9 protein in milk appeared to be a gamma-glycosylated and biologically active (53). In mice, up to 60
mg/L at 50% of biologically active F9 have been reported (54). In contrast to the species listed above, Van Cott et al reported that full specific activity rF9 produced by porcine mammary gland cells of F9 was only 200 mg/L in the milk (55). Lindsay et al made pigs capable of producing rF9 at 2-3 g/L (23). However, with the 10-fold increasing in expression rate, the active rF9 decreased to only 10-20%, in addition, we noticed about 10-30% rF9 had pro-peptide attached, which was no pro-coagulation activity. The low percentage of active rF9 in total over-expressed rF9 is because of the rate limited enzymatic PTMs after nascent rF9 synthesis in mammary epithelia. To increase the yield of active rF9 by converting no-active pro-rF9 into active rF9 zymogen, we bioengineered the pig mammary gland by introducing truncated human furin gene to process the excessive propeptide. Three male founder lines, Line A (78-2, 78-4), Line B (79-2) and Line C (80-4) were mated with wild type landrace sows to produce the female offspring for milk production. Sixty four offspring were obtained in 5 litters (Table 3). Among these piglets, 26/64 (41%) expressed both rF9 and rfurin. Offspring of were either carrying two genes or totally wild type (Table 3) which implies linkage, and that the multiple genes might be integrated as clusters. The highest expression level of rF9 was 2.2 mg/mL milk in pig (R1014), 76-fold higher than production cell line which was 30 µg/mL (56); and the furin activity in the same milk was more than 2000 U/mL. No significant difference in rF9 level compared to the pig (K75) without rfurin co-expressed. This indicates that the co-expressing rfurin did not suppress the rF9 expression. In contrast to the milk without rfurin co-expressed, no pro-rF9 was detected in the milk with rfurin co-expressed (Table 3). Unlike the endogenous furin, the co-expressed truncated rfurin was no transmembrane and following domain (Fig. 1B), so this rfurin secreted out
the cell rather than the endogenous furin cycled in the trans-Golgi network (TGN). This secreted rfurin not only processing nascent rF9 in cell but cleaving pro-peptide in the milk as well (Fig. 5). Because the rfurin does not have the transmembrane, which anchors the furin on the TGN membrane, we worried the over expressed rfurin moved back into the ER removing propeptide, which required by the carboxylase, before or during the γ-carboxylglutamic acids synthesis, which is required for F9 activity. The active rF9 was purified from both milk samples, with and without rfurin co-expressed, by using the same purification procedures (except the pro-peptide processing). The overall yield of active rF9 was similar, which indicated the co-expressed rfurin not interfering the carboxylation of glutamic acids. We also noticed in the 10-20% active rF9 subpopulation, almost half was activated rF9 or degraded rF9, which was active as rF9 zymogen before activation and/or degradation. This was partially caused by protease in milk activating and degraded rF9 during processing pro-rF9 in vitro. With the co-expressed the rfurin, the in vitro processing pro-rF9 was eliminated, and milk could be treated with protease inhibitors (i.e. ε-aminocarporic acid and benzamidine). The yield of active rF9 could further increase by decreasing the activation and degradation of rF9 during the processing.

In summary, we increased the quality of rF9 by co-expressed rfurin removing the pro-peptide of pro-rF9. rF9 was expressed at a level of 2.2 g/L of milk, and no pro-rF9 was detected in the milk. The consumption of rF9 in the U.S. can be estimated at 1.25 kg/year (250,100,000 U); and world consumption, at 5 kg/year(1). At 2 g/L rF9 expression rate and 400 L milk year⁻¹ pig⁻¹, and the yield of purified active rF9 zymogen, about 70 transgenic pigs could meet US’s market and about 270 transgenic pigs can produce enough rF9 for the entire world.
Acknowledgement

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CHAPTER 4

SCALED-UP PURIFICATION OF RECOMBINANT HUMAN COAGULATION FACTOR IX FROM MILK PRODUCED IN MAMMARY GLAND OF TRANSGENIC PIG

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ABSTRACT

Hemophilia B is a congenital bleeding disorder caused by the deficiency of functional coagulation factor IX (FIX). The current treatment is restricted to the protein replacement, including the on-demand or prophylaxis. In 2012, approximately 1 billion FIX concentrates were consumed by 28,008 hemophilia B patients worldwide. However, still about 80% patients, mostly in developing countries, receive inadequate or no treatment because of unavailable or unaffordable FIX concentrates. Consider the plasma derived FIX transmitting blood-borne pathogen, recombinant human FIX is recommended. More than 99% of consumed FIX concentrates was recombinant in United States. Our lab reported expressing recombinant human FIX (tg-FIX), 2-3 g/L with 10-20% active FIX, in milk by mammary gland of transgenic pig with lab scale purification developed. In this study, large scale purification protocol was established. The brand new camelid IgG based immunoaffinity chromatography efficiently in capture the whole tg-FIX population in the milk and the high pressure liquid chromatography effectively separate the active tg-FIX from non-active tg-FIX and activated tg-FIX subpopulation. 4 chromatography isolated active tg-FIX with similar specific activity as plasma derived FIX.

INTRODUCTION

Hemophilia type B (Christian disease) is a congenital bleeding disorder caused by the deficiency of coagulation factor IX (FIX). 28,008 patients has been diagnosed with hemophilia B in 2012 worldwide(1). The ideal treatments for hemophilia B patients are prophylactically, which significantly reduces complications and improves the quality of life (2), or the on-demand replacement of blood FIX when bleeding episodes occur (3). In 2012, about 1 billion IU of FIX concentrates was consumed worldwide(1). However,
actual need of the FIX supply could be much more than the reported number, since 70-80% patients received inadequate or no treatment because of the high price of the FIX concentrates (4). Up-to-date, 14 plasma derived (pd-) and 1 recombinant human FIX concentrates are licensed and commercially available on the market (3). Consider the transmission of blood-borne diseases and infections, the recombinant human therapeutic protein was recommended(5). So, producing the safe recombinant human FIX in an economically is required.

The FIX gene is located on the X-chromosome at q27 and expressed in hepatocytes in a highly tissue-specific manner (6,7). The nascent FIX is expressed in a pre-pro form and conducted multiple post-translational modifications (PTMs). These PTMs include the removal signal peptide, vitamin-K dependent gamma-carboxylation of first 12 glutamic acid(8,9), pro-peptide removal(10,11), glycosylation(12-15), beta-hydroxylation of Asp-64(16), sulfation of Tyr-155(17) and phosphorylation of Ser-158(18-20). The complexity of theses PTMs could be performed by certain type of mammalian cells. Chinese hamster ovary (CHO) cell, for example, was used for expression the only one recombinant human FIX (BeneFIX) on the market approved by FDA. It was characterized having limitations on performing those PTMs. Unlike the plasma-derived human FIX, BeneFIX contains a mixture of subpopulations with 10, 11 and 12 γ-carboxyglutamatic acids, no phosphorylation at Ser158, and only 15% sulfation of Tyr155(21).

Currently, mammary gland of transgenic livestock is a promising bioreactor for producing recombinant human proteins economically. Considering the high cell density (about 10^9 cell mL^-1) of the gland tissue, at the production of recombinant proteins could be 2-3 orders of magnitude greater than density of mammalian cells in steel bioreactors
Additionally, the milk production is high, for example, a pig produces about 200-400 L per year (23,24). However, not all of them are suitable for producing active FIX efficiently. No active FIX had been detected in the transgenic sheep milk (25). Zhang et al reported that > 90% recombinant protein in milk appeared to be a gamma-glycosylated and biologically active but the expression level was only 13.7 ng/mL (26). In contrast, the transgenic pig, was reported expressing 2-3 g/L recombinant human FIX (tg-FIX) in the milk and 10-20% population with bio-activity (27). Pig is not sensitive to prions; while the bovine PRNP gene required for the development of prion diseases (28). In addition, cost of establishing a transgenic commercial production herd could be approximately a sixth of building a commercial cell-culture facility (29). So mammary gland of transgenic pig could produce the safe recombinant FIX, economically, to meet the need for the hemophilia B patient worldwide. In addition, with the drop of the cost of FIX concentrates, oral administration of FIX concentration will be an option to replace the traditional discomfort, potential for opportunistic infection intravenous.

After active tg-FIX successfully expressed in the pig milk, the downstream processing is important for achieving pure active FIX. However, milk is a challenging feedstock for purification because of the large amount native proteins, including the casein (~ 30g/L), whey proteins (lactoferrin, α/β-lactalbumin), and serum-passover proteins (serum albumin, immunoglobulins, transferrin) and its natures as a multiple-phase mixture, including fat, solid and aqueous phases [paper in draft]. Our lab previously made progress in developing purification steps by using the heparin-affinity chromatography combined with ion-exchange chromatography to isolate the active tg-FIX subpopulation from the transgenic pig milk (27). In this study, the more efficient camelid IgG (30)
based immunoaffinity chromatography was applied to capture the whole tg-FIX population, and the high pressure liquid chromatography size exclusion chromatography (HPLC-SEC) was applied to separate active tg-FIX from the low active and activated tg-FIX subpopulation. In addition, the scaled up protocol was established to meet the large quantity of tg-FIX.

**MATERIALS AND METHODS**

All buffer components were purchased from VWR International LLC (Radnor, PA), Thermo Fisher scientific (Waltham, MA), or Sigma (St. Louis, MO) unless otherwise stated. Reference pd-FIX (Mononine, CSL Behring, USA) was a kind gifts from James Brown (Lincoln, NE). These stocks of were expired for clinical use but when used in experiments exhibited full procoagulant activity by one stage clotting assay. It was reconstituted in 20 mM calcium TBS (20 mM Tris, 0.15 M NaCl) pH 7.4 or 10 mM EDTA TBS pH 7.4 and then characterized by one stage clotting assay and SDS-PAGE to assure homogeneity and biological activity before using in the plasmin degradation studies made here.

**Transgenic Milk Collection and Storage**

Transgenic pigs were generated as described previous [paper in draft]. In this study, transgenic milk with recombinant human FIX expressed (tg-FIX milk) and transgenic milk with recombinant human furin co-expressed with recombinant human FIX (tg-furin-FIX milk) were both investigated. The transgenic swine milk was collected as described with modification whole milk samples were directly stored at -80°C without treatment of EDTA or any other protease inhibitors before storage.
Cleavage of Pro-peptide of Pro-FIX by Tg-furin in vitro

Whole tg-furin-FIX milk sample was first added to heparin Sepharose FF (GE Healthcare Bio-Sciences AB, Sweden) resin at 1:1 (v/v) ratio and incubated for 30 min. The supernatant was collected (FIX depleted) and was then incubated with the whole tg-FIX milk at 1:2 or 1:4 (v/v) ratio for 1.5 hour at 4°C. For the scaled up preparation, the whole tg-furin-FIX milk was directly incubated with whole tg-FIX milk at 1:4 (v/v) ratio for 2 hour at room temperature. All above milk samples were not treated with EDTA and any protease inhibitors.

Clarification of Transgenic Milk

Milk samples, pro-peptide was processed, were mixed with 0.43 M Citrate, pH 6.2 at 1:1 (v/v) ratio (No PIs treated) or 0.43 M Citrate, 200 mM EDTA, 80 mM ε-aminocaporic acid (EACA), 40 mM Benzamidine, pH 6.2 at 1:1 (v/v) ratio (with PIs treated), then centrifuged for 2 hours at 9000 rpm at 4°C (Sorvall Evolution RC centrifuge with SLC-4000 rotor, Thermo). The top fat layer and the bottom casein pellet were removed and the middle supernatant was further filtered with cheesecloth.

Capture of Whole FIX Population in Transgenic Milk by FIX Select

The milk samples were loaded on the FIX select, camelid Monoclonal antibody anti-human FIX coupled to Sepharose fast flow (GE), XK26/20 column (GE healthcare, Sweden). The flow rate is 6mL/min. And whole FIX population was eluted by elution buffer (2M MgCl₂). The chromatography was performed at room temperature.
Isolation of High Acidic FIX from FIX Select Eluate

This methods was adapted from previous (27). The total FIX population (FIX select elution product) was exchanged into the equilibrium buffer (20mM imidazole, 0.1M Ammonium acetate, pH 7.0). The FIX sample was loaded onto Q Sepharose fast flow, XK26/20 column (GE healthcare, Sweden). The flow rate is 4 ml/min. The low acidic FIX population was washed out by increased [Ammonium acetate] to 537 mM, and the high acidic FIX was eluted at [Ammonium acetate] at 800 mM. The Q eluate (EL) was further exchanged into the ceramic hydroxyapatite (CHT) equilibrium buffer (20mM potassium phosphate, pH 7.2) and loaded on the CHT Type I 40um (BioRad, Richmond, CA) XK16/25 column (GE healthcare, Sweden). The flow rate is 3mL/min. The low acidic FIX was removed in the wash step by at 65 mM potassium phosphate. Then high acidic FIX population was eluted at 200 mM potassium phosphate. Latter portion (about 80%) of EL (CHT EL 2) was collected. All buffer exchanges of tg-FIX samples were performed by using the tangential flow filter (TFF)10 kDa MWKO (Pall Corporation, Port Washington, NY).

Separate Active FIX from High Acidic FIX population by High Performance/Pressure Liquid Chromatography-Size Exclusion Chromatography (HPLC-SEC)

The high acidic tg-FIX was exchanged into SEC running buffer (20 mM Tris, 200 mM NaCl, 10 mM CaCl₂, pH 7.4) by using the Minimate tangential flow filtration systems with 10 kDa molecular weight cut off (MWCO) membrane (Pall Corporation, Port Washington, NY) or Amicon tube (10 kDa MWCO) (EMD Millipore, Billerica, MA). For analytical run (≤ 1 mg FIX), FIX sample was loaded on a TSK gel G3000SWXL, 7.8
mm ID x 30 cm, 5 µm (particle size), equipped with a guard column, 6 mm ID x 4 cm, 7 µm (particle size), (Tosoh Bioscience, LLC). The flow rate was 0.5 ml per min and duration of the run was 45 min with all major peaks eluting before 35 min. For large preparations (up to 10 mg FIX), FIX sample was loaded on a TSK gel G3000SW with 21.5 mm ID x 60 cm, 13 µm (particle size), equipped with a guard column, 8 mm ID x 4 cm, 10 µm (particle size), (Tosoh Bioscience, LLC). The flow rate was set at 3 ml/min and duration of the run was 90 min with all major peaks eluting before 60 min. The chromatography were performed by using Knauer Smartline chromatography apparatus, including Manger 5000, Pump 1000 and UV Detector 2600 (Berlin, Germany), equipped with a Gilson FC 204 fraction collector (Middleton, WI). Both columns were equilibrated and run with 20 mM Tris base, 200 mM NaCl, 10 mM CaCl2, pH 7.0. The fractions of each peak were pooled together for further analysis.

**Sodium Dodecylsulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE)**

Samples were analyzed by SDS-PAGE stained with colloidal Blue gel stain (Invitrogen, Carlsbad, CA, USA) using Invitrogen 12% Bis-Tris Novex acrylamide precast gels and the Invitrogen Surelock XL apparatus (200 Volts for 1 hour). Briefly, samples were mixed with 4x LDS sample buffer (Invitrogen) and deionized water followed by heating at 74 °C for 10 min. For reduced gels, samples were mixed with 10x reducing agent (Invitrogen) prior to heating.

**Western Blot**

The gels were electro-blotted onto poly vinylidene fluoride (PVDF) membranes using a BioRad Transblot SemiDry Transfer Cell (Richmond, CA) for 30 min at 25 volts. For total FIX, including all FIX species, blots were probed by rabbit polyclonal antibody (Pab)
anti-F9 (F0652, Sigma-Aldrich St. Louis, MO); The furin was detected by using rabbit Pab anti-furin (476–490) (F8806, Sigma-Aldrich St. Louis, MO); The mouse monoclonal antibody (Mab), PROFIX 3D2.6H12 (Green Mountain Antibody, Burlington, VT), was used in probing pro-peptide of FIX. The secondary antibody (HRP-conjugated) anti-rabbit (A9169) and mouse (A4416) IgG (Sigma-Aldrich St. Louis, MO) was used to detect the primary antibody respectively. The chromogenic DAB substrate (Thermo, Rockford, IL) was used in color developing.

Quantification of Recombinant Human Factor IX (rF9) and Recombinant Human Pro-peptide attached Factor IX (pro-rF9) in Transgenic Milk

Western blot was performed as described before. Mononine, as calibrator, was loaded along with the transgenic milk samples (triplicated). The concentration mononine was determined by measuring the optical density at 280 nm in a 1 cm quartz cuvette and using an extinction coefficient, \( \epsilon_{1\%} = 13.4 \). The amount of tg-FIX was then calculated by using the standard curve created by the calibrators. The pictures of the blots were analyzed by using the Image J(31,32).

Quantification of FIX by ELISA

The procedure was modified from previous literature (33). Enzyme immunosorbent assay plates (Greiner Bio-One, Monroe, NC) were coated overnight at 4°C with 100 µL at 2 µg/ml mouse anti-human factor IX IgG (Haematologic Technologies, Inc., Essex Junction, VT) per well in carbonate buffer. Factor IX samples at 100 µL/well including those for the standard curve (0.98–200 ng/mL) were incubated for 2 hours at 25°C. Then sheep anti-human factor IX IgG conjugated with horseradish peroxidase (HRP; Affinity Biologicals, Hamilton, Canada) (100 µL/well at 1 µg/ml in blocking buffer) was added
and incubated for 1 hour at 25 °C. After washing, 150 µL/well 1-step ABTS (Thermo, Rockford, IL) was added and color was allowed to develop up to 45 minutes and measuring absorbance at 405 nm.

**Quantitation of Total Factor IX Activity**

Total FIX activity was determined using the activated partial thromboplastin time (aPTT) assay (34). Briefly, 50µl each of PTT Automate 5 reagent (Diagnostica Stago, Inc., Parsippany, NJ, USA), factor IX deficient plasma (George King Bio-Medical, Overland Park, Kansas, USA), and a sample of interest were added to a cuvette and incubated at 37 °C for 3 min. 50 µL of 25mM CaCl2 (Sigma) was then added and the clotting time was measured using the STart Hemostasis Analyzer (Diagnostica Stago, Inc., Parsippany, NJ). The normal human plasma (Diagnostica Stago, Inc., Parsippany, NJ) was used as the standard, assigning 1 unit of FIX clotting activity per milliliter of plasma. The concentration of purified tg-FIX was determined by measuring the optical density at 280 nm in a 1 cm quartz cuvette and using an extinction coefficient, ε\(^{1%}\) =13.4.

**NH2-terminal Sequencing of the Plasmin Cleavage Products of FIX**

Amino acid sequencing was performed at the University of Nebraska Medical Center, Protein Structure Core Facility. Protein samples were subjected to SDS-PAGE and transferred to PVDF as described above. The membrane was stained with Colloidal Blue and bands excised and subjected to Edman degradation using Applied Biosystems Procise protein sequencer, a Hitachi 8800 Amino Acid Analyzer and a Michrom MAGIC HPLC equipped with a Diode Array Detector.
RESULTS

Capture Total TG-FIX Population in Transgenic Milk by FIX Select

The camelid IgG anti-FIX based immunoaffinity column was used in capture whole tg-FIX population in the transgenic milk. A sharp peak in the elution step followed the huge amount unbound flow through (FL) and tiny amount of wash (Fig. 1A); the recovery of tg-FIX by using FIX select column was ~ 85% (Table 3). The heparin affinity chromatography, widely used in purifying FIX from both plasma, mammalian cell culture and transgenic milk, required additional wash step to removed caseins and other impurities in milk; the quantity of these heparin binding impurities was larger than the tg-FIX population and taking large amount of binding capacity of the column (Fig. 1B). By comparing the BCA results (total protein in sample) and FIX specific ELISA (tg-FIX in sample), FIX select eluate (EL) (batch112213) was about 95% tg-FIX (data not shown). The non-reduced SDS-PAGE showed FIX select EL was much purer (Fig. 1C, lane 2) than EL from heparin affinity chromatography (Fig. 1C). Large quantity of porcine plasmin was detected in the milk sample. No plasmin signal could be detected in the EL sample after the chromatography (Fig. 1E), which indicate the efficiency of FIX select in removing protease in the milk sample. The FIX select EL was then analyzed by the HPLC-SEC, it had only peak 1 compared to 3 peaks (larger peak 2 and 3) of high acidic tg-FIX (batch040813) (Fig. 1D). The FIX specific activity of the FIX select EL was 174 ± 10 U/mg (Avg. ± SD, n=3), looks “normal” compared to the 200 U/mg of pd-FIX. However, this activity was contributed mostly by the activated tg-FIX population (SEC pool 3, 2288 ± 204 U/mg) (Avg. ± SD, n=3) (Table 1)
**Isolation of High Acidic Tg-FIX from FIX Select Eluate**

Q sepharose fast flow column was used in isolating high acidic, active, tg-FIX population and the methods were adapted from gradient (27) to step wash (Fig. 2A). The Q EL (batch 091713) had 4 times more FIX specific activity than the FIX select EL (batch112213), and an additional lower band (45 kDa) than the wash fraction (Fig. 2D, lane 3-4). We noticed the increasing in activity was from both the fraction of active tg-FIX, SEC pool 2, and activated tg-FIX (tg-FIXa), SEC pool 3 (Table 1).

The Ceramic Hydroxyapatite (CHT) chromatography was performed after Q to further enrich the high acidic tg-FIX. The high acidic tg-FIX subpopulation was enriched in latter 80% EL (EL 2), whose peak 1 on the HPLC-SEC was less than CHT EL 1 (Fig. 2B, 2C). Like the Q EL, CHT EL 2 had more 45 kDa band on the non-reduced gel (as shown...
in the Q EL) (Fig. 2D, lane 5 and 6). SEC pools of CHT ELs loaded on reduced SDS-PAGE was analyzed by N-terminal amino acids sequencing, majority of the pool 3, which only shown in EL 2, was tg-FIXa (the 28 kDa band showed a.a. sequence of VVGGE, indicating the heavy chain of tg-FIXa), while no tg-FIXa was detected in CHT EL 1 (Fig. 2E), This was also confirmed by the activity assay (Table 1 and 2).

<table>
<thead>
<tr>
<th>Batch</th>
<th>Samples</th>
<th>Mass Percentage</th>
<th>Specific Activity (U/mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>112213</td>
<td>FIX Select Eluate</td>
<td>100</td>
<td>174 ± 10</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 1</td>
<td>55</td>
<td>1 ± 0</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 2</td>
<td>43</td>
<td>9 ± 1</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 3</td>
<td>1</td>
<td>2288 ± 204</td>
</tr>
<tr>
<td></td>
<td>Q Eluate</td>
<td>100</td>
<td>714 ± 7</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 1</td>
<td>21</td>
<td>9 ± 1</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 2</td>
<td>43</td>
<td>107 ± 7</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 3</td>
<td>36</td>
<td>2755 ± 182</td>
</tr>
<tr>
<td>91713</td>
<td>CHT Eluate</td>
<td>100</td>
<td>2351 ± 335</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 1</td>
<td>16</td>
<td>No Activity</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 2</td>
<td>41</td>
<td>165 ± 9</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 3</td>
<td>43</td>
<td>4284 ± 728</td>
</tr>
<tr>
<td></td>
<td>CHT Eluate</td>
<td>100</td>
<td>1471 ± 147</td>
</tr>
<tr>
<td>40813</td>
<td>SEC Pool 1</td>
<td>18</td>
<td>No Activity</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 2</td>
<td>48</td>
<td>138 ± 8</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 3</td>
<td>34</td>
<td>3753 ± 278</td>
</tr>
<tr>
<td>42313</td>
<td>CHT Eluate</td>
<td>100</td>
<td>1471 ± 147</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 1</td>
<td>18</td>
<td>No Activity</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 2</td>
<td>48</td>
<td>138 ± 8</td>
</tr>
<tr>
<td></td>
<td>SEC Pool 3</td>
<td>34</td>
<td>3753 ± 278</td>
</tr>
</tbody>
</table>

**Table 1.** Comparison of FIX Purification Samples by using Analytical HPLC-SEC. About 700 µg FIX eluate sample of each batch (purified by using different procedures) was loaded on HPLC-SEC and the fractions were pooled (SEC pool 1, 18-19.5 min; SEC pool 2, 20-22 min; and SEC pool 3, 22.5-27 min) and calculated FIX specific activity. All above batches were purified from the transgenic milk (K108). The mass percentage was calculated based on amount of FIX in each fraction. The specific activity of control plasma derived FIX was 211 ± 9 U/mg (Avg. ± SD, n=3).
Fig. 2. Isolation of High Acidic FIX by Using Ion-exchange Chromatography. 

A. Q sepharose FF run. B. CHT run. Flow through (FT), wash (W) and eluate (EL) were labeled. The blue line indicate the protein (OD$_{280}$), the green line indicate the conductivity (mS).

C. Comparison of SEC profile of CHT EL 1 and 2 (batch031313). D. Non-reduced SDS-PAGE of FIX purified from Q and CHT (batch040813). Lane 1: FIX select EL; Lane 2: Q FT; Lane 3: Q wash; Lane 4: Q EL; Lane 5: CHT EL 1; Lane 6: CHT EL 2. E. Reduced SDS-PAGE of FIX samples (Batch031313). Lane 1: CHT EL 1; Lane 2: CHT EL 1 SEC pool 1; Lane 3: CHT EL 1 SEC pool 2; Lane 4: CHT EL 2; Lane 5: CHT EL 2 SEC pool 2; Lane 6: CHT EL 2 SEC pool 3. The 28 kDa band of each lane was sequenced and the N-terminal first 5 amino acid sequence listed.

Separate Active Tg-FIX from High Acidic Tg-FIX population by High Pressure Liquid Chromatography-Size Exclusion Chromatography (HPLC-SEC)

Although the FIX had been purified into a highly acidic tg-FIX subpopulation, the FIX material only contained ~40% active tg-FIX analyzed by HPLC-SEC. The CHT EL 2 (batch040813) had about 10% non-active tg-FIX species and the other ~40% was mixture of tg-FIXa and degraded tg-FIX (mostly tg-FIXɤ) (Table 1). To scale up the separation of active tg-FIX from no-active and tg-FIXa/degraded tg-FIX, TSK gel G3000SW with 21.5 mm ID x 60 cm L, 13 µm (particle size) at higher throughputs was applied in purification procedure. We noticed resolution in separation of peak 2 and 3 was better in using the
processing HPLC-SEC (Fig. 3). However, with 10-folds higher load on the HPLC-SEC, approximately 30% of total loaded tg-FIX came out before the regular 3 peaks, which was not present in analytical runs and was considered as the aggregation of tg-FIX sample.

<table>
<thead>
<tr>
<th>CHT Eluate (Mass Percentage)</th>
<th>SEC Pool Specific Activity (U/mg) (Mass Percentage)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (8%)</td>
<td>11 ±1 (31.6%)</td>
</tr>
<tr>
<td></td>
<td>122 ±7 (68.4 %)</td>
</tr>
<tr>
<td></td>
<td>N/A</td>
</tr>
<tr>
<td>2 (73%)</td>
<td>25 ±3 (18 %)</td>
</tr>
<tr>
<td></td>
<td>155 ±13 (46 %)</td>
</tr>
<tr>
<td></td>
<td>3203 ±890 (37 %)</td>
</tr>
</tbody>
</table>

**Table 2.** Comparison of CHT eluate 1 and 2 SEC pools (Batch031313) (Avg. ± SD, n=3).

**Fig. 3. Processing HPLC-SEC Profile of CHT EL 2 (batch031313).** 10 mg FIX CHT EL 2 (~ 2mg/ml) was loaded on the TSK gel G3000SW (21.5 mm ID x 60 cm L) with running buffer (20 mM Tris, 200 mM NaCl, 10 mM CaCl2, pH 7.0). The Flow rate was 3 ml/min. The run was 90 min. All peaks came out before 60 min. Fractions were pooled as indicated on the figure.
Inefficiency in Separating Tg-proFIX from Active Tg-FIX

We previously reported the inefficiency in processing of pro-peptide of tg-proFIX (pro-peptide attached tg-FIX) by endogenous porcine furin in mammary gland [paper in draft].

Fig. 4. Reduced SDS-PAGE and Western blots of FIX purified by HPLC-SEC. A. Reduced SDS-PAGE; B. Reduced Western blot developed by using antibody anti-total FIX; C. Reduced Western blot developed by using antibody anti-proFIX. Lane 1: High acid FIX (4 µg, Q Sepharose eluate, batch091713); Lane 2: SEC pool 1 of high acid FIX (2 µg, non-active FIX); Lane 3: SEC pool 2 of high acid FIX (2 µg, active FIX); Lane 4: SEC pool 3 of high acid FIX (1 µg, activated FIX or FIXɤ) (SEC pool 1, 18-19.5 min; SEC pool 2, 20-22 min; and SEC pool 3, 22.5-27 min). The concentration of each FIX sample was measured by optical density with wavelength = 280 nm, $\varepsilon = 13.4$. D. Western blot of removal of propeptide of FIX by furin co-expressed in the transgenic milk. Lane 1: Furin co-expressed FIX milk (0.8 µL, R175); Lane 2: FIX depleted furin co-expressed FIX milk (0.8 µL); Lane 3: FIX milk (0.8 µL, K96); Lane 4: Sample of furin co-expressed FIX milk incubated with FIX milk, 1:2 (v/v) at 4°C for 1.5 hour; Lane 5: Sample of furin co-expressed FIX milk incubated with FIX milk, 1:4 (v/v) at 4°C for 1.5 hour. All samples were whole milk without EDTA or protease inhibitor treatment.
We noticed the ion-exchange chromatography could not separate the non-active tg-proFIX from the active tg-FIX. The high acidic tg-FIX (batch 091713, without pro-peptide cleavage) contained a large portion of tg-proFIX (Fig. 4, lane 1). HPLC-SEC failed in separating tg-proFIX, 2 kDa difference, from FIX zymogen. All three SEC pools contained tg-proFIX (Fig. 4, lane 2-4), which decreased the activity of final FIX samples (batch 091713) (Table 1). To eliminate tg-proFIX and recover the activity by converting inactive tg-proFIX to active zymogen, the pro-peptide needs to be processed before all purification steps. Tg-proFIX was converted into tg-FIX after incubated with tg-furin in a lab scale expriment (Fig. 4D, lane 4 and 5). For large preparation, the FIX milk (K108) was treated with the tg-furin-FIX milk (R185) at 1:4 ratio at room temperature for 2 hours before the FIX select step. No tg-proFIX was detected in the final produce (data not shown), and the FIX specific activity of tg-FIX sample (batch04081 SEC pool 2) was increased (Table 1).

**Minimize the tg-FIX Degradation during the Purification**

We previous reported that the major protease in transgenic swine milk, plasmin, degrades the tg-FIX [paper in draft]. In addition, some other protease, such as trypsin, might be also involved in the proteolysis of tg-FIX in transgenic milk (35). The ε-aminocaporic acid (EACA), which is the specific inhibitor of plasmin, and benzamidine, inhibiting trypsin, was used to prevent the degradation of tg-FIX in milk. SEC profile of batch 040813, which was not treated PIs, has larger peak 3 (43%), than the batch 042313 (34%), which was treated PIs (Fig. 5, Table 1), although both batches were used the same transgenic milk sample. The activity assay showed batch 040813 has more tg-FIXα
(Table 1). So, introducing PIs helped decreasing the activation/degradation of tg-FIX in the milk sample.

**CONCLUSION**

The mammary gland of transgenic swine has the advantages, including the high cell density in the gland tissue, the high volume of milk produced per swine, the high recombinant protein yield and its capability to perform certain PTMs for recombinant human coagulation proteins, making it a promising bioreactor for producing FIX economically. Biologically active recombinant human coagulation factors have been successfully produced in pig milk and reported by several studies, such as human F8 (36),

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**Fig. 5. Comparison the SEC profile of Purified FIX Sample with or without treated by protease inhibitors.** The upper one was not treated by PIs (batch 040813). The lower one was treated by PIs (batch 042313). Both batches were from same milk and using the same purification procedures.
protein C (37), VWF (38) and F9 (27, 39). Additionally, the capital investment is substantially less than the traditional steel bioreactor for both mammalian cells and bacteria. However, the complexity of the milk, such as the large quantity of the native proteins and multiple phase nature, make it more of a challenge for downstream processing than current mammalian and bacteria system.

<table>
<thead>
<tr>
<th>Purification Step</th>
<th>Batch031313 FIX in Eluate (mg) (Overall Yield %)</th>
<th>Batch040813 FIX in Eluate (mg) (Overall Yield %)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clarified Milk</td>
<td>1400 (100)</td>
<td>1400 (100)</td>
</tr>
<tr>
<td>FIX Select</td>
<td>1171 (84)</td>
<td>1180 (84)</td>
</tr>
<tr>
<td>Q Sepharose</td>
<td>136 (10)</td>
<td>169 (12)</td>
</tr>
<tr>
<td>CHT</td>
<td>88 (6)</td>
<td>92 (7)</td>
</tr>
<tr>
<td>SEC</td>
<td>32 (2)</td>
<td>38 (3)</td>
</tr>
</tbody>
</table>

Table 3. Purification Table of Active FIX from Transgenic milk. Both batches were purified from the same pig milk, batch 031313 was using the lactation day 16-19 pool, and batch040813 was used the lactation day 5-14 pool.

The new camelid IgG anti-FIX immuno-affinity chromatography, more efficient than the traditional heparin affinity column, captured whole FIX population with about 84% yield and close to 100% purity (Table 3). The efficiency in purifying tg-FIX from impurities is also important in decreasing the proteolysis of tg-FIX by proteases, e.g. porcine plasmin, in the milk. In addition, no acidic pH was needed in elution steps that are required by traditional immunoaffinity chromatography. The ion-exchange chromatography, Q sepharose and Ceramic Hydroxyapatite columns were used to isolated high acidic (activity) tg-FIX. These two chromatography enriched active tg-FIX subpopulation, resulting in a specific activity increased more than 10 fold (Table 1). Finally, the property of γ-carboxylglutamic acid residue conducting a size compaction in the presence of
calcium ions was utilized to further separated active tg-FIX subpopulation from the non-active tg-FIX subpopulations by HPLC-SEC; and the activated/degraded tg-FIX subpopulation was also eliminated caused by the molecular weight difference.

We noticed the amount of activated and degraded tg-FIX decreased about 9% (mass) by adding the protease inhibitors. By co-expressing tg-furin, which processes excessive propeptide in transgenic milk [paper in draft], no extra cleavage step needed and EDTA and PIs can be added right after milking. This will further improve the yield of active tg-FIX by decreasing activation and degradation of tg-FIX.

The overall yield of active tg-FIX was approximated 3% of whole tg-FIX population in the transgenic swine milk by using the purification protocol (Table 3). The final product, active tg-FIX, had about 200 U/mg FIX specific activity without any detected activated tg-FIX (tg-FIXa). Assuming average tg-FIX expression rate in pig was 2.5 mg/ml, and milk production was 400 liters per pig and per year, approximately 40 pigs could produce enough FIX concentrates for US consumption (250 million units) and 160 pigs was enough for the worldwide (1 billion units). We are now working on the project of introducing the vitamin K 2,3-epoxide reductase enzyme (VORK), which produces the cofactor for γ-carboxylase, gene and co-expressing with tg-FIX to accelerate the formation of γ-carboxylglutamate (Gla) that is relative pro-coagulant activity(40). The active tg-FIX subpopulation could be further increased.
REFERENCES

oligosaccharides O-glycosidically linked to threonine residues at 159 and 169. *Biochemistry* **33**, 5167-5171


CHAPTER 5

SUMMARY AND FUTURE WORK

SUMMARY

The success in expressing recombinant human FIX (tg-FIX) with approximately 2-3 g/L and 10-20% bio-active in the milk (1) makes this mammary gland of transgenic pig a promising bioreactor in producing recombinant human FIX with full pro-coagulate activity. The goal of this project was to increase the yield of the bio-active tg-FIX, and this was fulfilled by the following specific aims:

Specific Aim#1: Characterize the tg-FIX and its degraded species in the milk sample. And investigate the predominant milk-borne protease, plasmin, in degrading the tg-FIX.

Specific Aim#2: Bioengineer pig mammary gland by introducing truncated human furin gene co-expressing with tg-FIX. Characterize the recombinant truncated human furin (r-furin) in processing the excessive pro-peptide and convert non-active tg-proFIX to active tg-FIX both in vivo and in vitro.

Specific Aim#3: Establish scaled-up purification protocol, using the more efficient, immune-affinity chromatography FIX select column to capture whole tg-FIX population from transgenic milk; then enrich high acidic tg-FIX by anion exchange chromatography; finally separate the active tg-FIX subpopulation from the inactive and activated tg-FIX subpopulation.

We noticed about 50% of the high extent γ-carboxylated tg-FIX was activated or degraded in the purified high acidic tg-FIX. By investigating the degraded species, plasmin, which is the predominant protease in milk, was involved the degrading and
facilitate activating the tg-FIX in the milk. The extent of degradation/activation of tg-FIX could be decreased by introducing the protease inhibitors, by introducing the ε-aminocapric acid (EACA), which is the specific inhibitor of plasmin, and benzamidine during the storage of milk. The percentage of degraded/activated tg-FIX dropped from 43% to 34%. However the degradation and activation before collecting milk could not be reversed. We noticed the tg-FIX having high extent Gla, which conducted the conformation change in Gla domain in presence of calcium ion, was prevented light chain being cleaved by plasmin. However, cleaved at C-terminal of catalytic domain and deactivated the tg-FIX happened not dependent on its Gla content and in presence of calcium ion or in chelated environment. The plasmin also performed cleavage at Arg^{145}, making FIXα (intermediate of activated FIX), facilitated the activation of tg-FIX, which only needed one more cleavage at Arg^{180}. In order to increase the yield of active tg-FIX, the action of the protease in the milk need to minimize.

In the tg-FIX expressed only transgenic pig, we noticed approximately 10-30% pro-peptide attached tg-FIX, which was not processed by endogenous porcine furin in the mammary epithelium during the tg-FIX synthesis. And this unprocessed pro-tgFIX, which interferes conformational changes in Gla domain causing no pro-coagulation activity, could not be separated by current purification methods. This causes the decreasing in FIX specific activity of the purified tg-FIX sample; in addition, the pro-tgFIX, which has high extent Gla, could be waste if we left it unprocessed. By introducing the truncated human furin cDNA and co-expressing with the tg-FIX, this tg-furin, with furin specific activity, helped the endogenous porcine furin in processing over-expressed nascent tg-FIX. In addition, without the transmembrane domain, this tg-
furin secreted into the milk, and approved to process pro-peptide in vitro also. No pro-tgFIX was detected with co-expressing this tg-furin. More important, no evidence showed this co-expressed tg-furin decreasing the percentage of the active tg-FIX, which indicated the over-expressed tg-furin did not interfere the formation of gamma-carboxylation in tg-FIX in ER.

The scaled-up purification protocol was established with modifying the previous lab-scale one. By introducing the new camelid IgG based immunoaffinity chromatography, the capture of whole tg-FIX population is more efficient than the current heparin based affinity chromatography. The anion exchange chromatography further enriched the high acidic tg-FIX subpopulation, which is highly related to its extent of Gla. And the HPLC-SEC not only separated the active tg-FIX from non-active (low extent of Gla) tg-FIX, and also the activated, also high extent Gla, tg-FIX by their size difference in presence of calcium ion. The final tg-FIX showed similar specific activity to the plasma-derived and recombinant (CHO) FIX.

**FUTURE WORK**

Approximately half of the high acidic tg-FIX subpopulation were degraded or activated in the milk sample and during the processing. The degradation and activation after tg-FIX secreting into the milk could not be reversed. The plasmin specific inhibitor, α2-antiplasmin (A2AP), could be the candidate in inhibiting the plasmin activity in the milk(2). The efficiency of co-expressing this serine protease inhibitor with the tg-FIX needs to be investigated. Also, the precaution needs to be taken, since both tg-FIX and furin are serine protease, the co-expressed A2AP might inhibit their activity. In addition,
since the A2AP involves in inhibiting plasmin activity in blood, the current purification protocol and the final purified tg-FIX need to be investigated to remove all A2AP.

The current expression level of recombinant human FIX in milk of transgenic pig is about 2-3 g/L, however, only 10-20% high acidic/carboxylated FIX population could be enhanced. It is believed that incomplete-carboxylation occurs when an excess of newly synthesized precursors of vitamin K-dependent proteins appears in the ER and exceeds the capacity of the cell’s-carboxylation system to fully modify all of the precursors (3,4). The under-carboxylated FIX is less active, prone to be degraded, and cleared more rapidly from the bloodstream than fully carboxylated FIX (5). The reduced form of vitamin K, vitamin K hydroquinone (KH2), is the cofactor as carboxylase in the reaction of γ-carboxylation(6). This KH2 is recycle between its oxidized form by the enzyme, vitamin K epoxide reductase (VKOR)(6). So, this VKOR maintains the level of the KH2 and also accelerate the reaction of carboxylase(7,8), and the truncated recombinant human VKOR, an 18-kDa ER membrane protein VKORC1(9), was expressed and proven in increasing production of functional FIX in the CHO cells(10). With the success in bioengineering of the mammary gland of pig in processing excessive pro-peptide of FIX by co-expressing the truncated recombinant human furin, introducing this VKORC1 could increase the yield of fully carboxylated FIX.

At the meanwhile, the in vivo effects of our recombinant human FIX, expressed and purified as in the previous study, should be investigated in pharmacokinetics by using animal models. The wild type mice (as control), hemophilia mice, including R333Q mice(11) and FIX knockout (FIXKO) mice (12), and hemophilia dog(13) will be administrated intravenously using purified active tg-FIX in multiple doses and the FIX
antigen and activity level will be monitored by the ELISA and aPTT, respectively, at multiple time points after administration. Oral administration of coagulation therapy will obviate the invasiveness, discomfort, potential for opportunistic infection, and complications of storage and supplies that accompany with current intravenous administration. With the progress in producing recombinant human FIX economically in mammary gland of transgenic pig, the cost of the FIX concentrates would drop and make this oral administration affordable. The safety and efficiency of oral administration of this recombinant human FIX should also be investigated by using the animal models that were used in intravenous administration.

REFERENCES


