# The interaction of boar sperm proacrosin with its natural substrate, the zona pellucida, and with polysulfated polysaccharides

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# Summary

Boar sperm acrosin is an acrosomal protease with trypsin-like specificity, and it functions in fertilization by assisting sperm passage through the zona pellucida by limited hydrolysis of this extracellular matrix. In addition to a proteolytic active site domain, acrosin binds the zona pellucida at a separate binding domain that is lost during proacrosin autolysis. In this study, we quantitate the binding of proacrosin to the physiological substrate for acrosin, the zona pellucida, and to a nonsubstrate, the polysulfated polysaccharide fucoidan. Binding was analogous to sea urchin sperm bindin that binds egg jelly fucan and the vitelline envelope of sea urchin eggs. Proacrosin was found to bind to fucoidan and to the zona pellucida with binding affinities similar to bindin interaction with egg jelly fucan. These interactions were competitively inhibited by similar

# Introduction

Sperm-egg interaction is a species-specific cell recognition and binding event and a necessary prerequisite for fertilization. This interaction involves proteincarbohydrate interactions and is inhibited by carbohydrates in a wide variety of species (Ahuji, 1982; Shalgi et al. 1986). The extracellular matrix of the mammalian egg, the zona pellucida (ZP), is composed of sulfated glycoproteins (Bliel and Wassarman, 1980; Shimizu et al. 1983; Hedrick and Wardrip, 1987), and it contains the ligands that interact with sperm receptors. In the mouse, an O-linked oligosaccharide from the unfertilized egg ZP3 component of the ZP interacts with mouse sperm (Florman and Wassarman, 1985), whereas both the  $55 M_r$  glycoprotein families (designated  $\alpha$  and  $\beta$ ) and the 90  $M_r$  glycoprotein family of porcine ZP contain ligands for porcine sperm (Berger et al. 1989). Several mammalian sperm receptors have been described with either a specific recognition function or a less specific or secondary binding function. Examples of these include macromolecules that bind protease inhibitors, sperm autoantigens with lectin-like

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relative molecular mass polysulfated polymers. Since bindin and proacrosin have distinctly different amino acid sequences, their interaction with acidic sulfate esters demonstrates an example of convergent evolution wherein different macromolecules localized in analogous sperm compartments have the same biological function. From cDNA sequence analysis of proacrosin, this binding may be mediated through a consensus sequence for binding sulfated glycoconjugates. Proacrosin binding to the zona pellucida may serve as both a recognition or primary sperm receptor, as well as maintaining the sperm on the zona pellucida once the acrosome reaction has occurred.

Key words: cell adhesion molecules, fertilization, acrosin, fucoidan.

activity, and galactosyl transferase (Poirier *et al.* 1986; Benau and Storey, 1987; O'Rand *et al.* 1988; Hathaway and Shur, 1988). In sea urchin sperm, an acrosomal protein called bindin binds specifically and tightly to the egg jelly fucan and to the vitelline envelope. Bindin was first characterized as a lectin, but it has recently been redescribed as a binder of polysulfated macromolecules (DeAngelis and Glabe, 1990).

The sperm enzyme acrosin assists sperm penetration of the ZP by specific limited hydrolysis of ZP glycoproteins (reviews: Urch, 1991; Hedrick *et al.* 1988). An additional function for acrosin in fertilization has been described as ZP binding, possibly at a domain other than the proteolytic active site (Brown and Jones, 1987). Support for this latter function comes from western blot analyses, where sperm extract macromolecules that bound ZP had similar mobilities to macromolecules with epitopes recognized by proacrosin antibodies (Urch *et al.* personal communication; Jones and Brown, 1987; Töpfer-Petersen and Henschen, 1987). This approach has recently implicated proacrosin/acrosin as part of the several ZP binding molecules in the guinea pig, where the acrosome-

reacted sperm makes initial contact with the ZP. This study characterized the interaction of those sperm extracts with fucoidan, through the use of polysulfated polysaccharide inhibition, as a sea urchin bindin-like phenomenon (Jones and Williams, 1990). In the pig, western blots of purified proacrosin bound <sup>125</sup>I-ZP with the same  $M_r$  as the fucose-binding protein of boar sperm (Jones, 1989), and the sperm receptor for ZP that bound HRP-fucose has the same amino acid N-terminal sequence as proacrosin (Töpfer-Petersen and Henschen, 1988). These observations taken together suggest that proacrosin is a primary recognition receptor for porcine ZP on the surface of boar sperm. This interpretation conflicts with the recent description of a boar sperm receptor with the same  $M_r$  as proacrosin, but which was antigenically dissimilar to it (Peterson and Hunt, 1989). However, placed on the sperm, the interaction of two acrosin domains with the ZP allows for an elegant mechanism of binding and hydrolysis that would assist sperm penetration of the ZP (Urch, 1991; Hedrick et al. 1988).

This novel binding function of a proteolytic proenzyme is thought to be modulated through a fucosebinding domain in proacrosin, distinct from the proteolytically active site, with this functional binding domain exposed on the sperm surface to interact with the ZP (Töpfer-Petersen and Henschen, 1988). There are other examples of enzymes binding non-substrates with high affinities, some of which also inhibit enzymatic activity. One of the most studied systems is the binding and inhibition of glutathione transferase by the non-substrate bile acids (Hayes and Mantle, 1986; Boyer and Vessey, 1987; Young and Briedis, 1990), although the physiological importance of this interaction has not yet been determined. In the case of proacrosin-binding polysulfated polysaccharides, these polymers inhibit sperm-ZP binding in the pig (Peterson et al. 1984), as well as inhibiting the amidase and protease activities of active boar acrosins (Urch and Hedrick, 1988). Therefore, proacrosin binding to, and modulation of acrosin activity by, the ZP would have significant physiological importance in fertilization.

In this investigation, we qualitatively and quantitatively describe the binding of purified proacrosin to polysulfated polysaccharides and to the ZP by using analogous binding experiments to those described for sea urchin bindin (DeAngelis and Glabe, 1987). This binding represents a novel mechanism for recognition between mammalian gamete molecules and for the utilization of a proteolytic enzyme for more than a single function. A similar investigation, with similar findings, has been reported in a study by Jones (1991).

## Materials and methods

### Materials

Fucoidan from *Fucus vesiculosus* (Sigma, St Louis, MO) was treated with pronase to remove contaminating protein in the following fashion: 50 mg of fucoidan was treated with 0.5 mg of pronase (Sigma) at 37°C for 24 h on a shaker, with a few drops of toluene added as a bacteriostatic agent. A second

0.5 mg pronase was then added for an additional 12 h. The solution was lyophilized and dissolved in water. *Xenopus laevis* jelly coat (the kind gift of Dr Jerry Hedrick, University of California, Davis) was also treated in a similar manner.

Fucoidan was partially acid hydrolyzed and desulfated after the methods of DeAngelis and Glabe (1987). Briefly, mild acid hydrolysis was performed in  $0.1 \,\text{m}$  hydrochloric acid at  $100 \,^{\circ}\text{C}$  for 2 min. After hydrolysis, the samples were plunged into a dry ice/ethanol bath and lyophilized prior to gel filtration on Sephadex G-100 in  $1 \,\text{mm} 3$ -[*N*-morpholino] propanesulfonic acid (Mops), pH 8.0. For desulfation, samples were mixed, after Dowex 50 column equilibration in  $0.1 \,\text{m}$  pyridine, with dimethyl sulfoxide/pyridine (50:1) and kept in an air-free environment for 9 h. The pyridine was removed with N<sub>2</sub> and then the samples were dialyzed extensively with water and lyophilized.

Dextran sulphate ( $M_rs$  5000 and 500000), mannose-6phosphate, chondroitin sulphate A and C, poly(vinyl alcohol), and poly(vinyl sulfate) were obtained from Sigma (St Louis MO). Dextran (500 000  $M_r$ ) was obtained from Pharmacia (Piscataway, NJ). Poly(vinyl phosphate), poly(vinyl styrene sulfonic acid), polyacrylic acid, and the ammonium salt of polyacrylic acid were obtained from Polysciences (Warrington, PA). The poly(vinyl sulfate) was dissolved in water, separated from undissolved materials by centrifugation and filtration, and lyophilized. Metachromatic shift assays using toluidine blue were performed as outlined in DeAngelis and Glabe (1987). Only polyanions demonstrating metachromasia were utilized. The other chemicals were used as supplied.

Sea urchin egg jelly fucan was the kind gift of Dr Charles Glabe, University of California, Irvine. Yeast polyphosphate mannan was the kind gift of Dr Steven Rosen, University of California, San Francisco. Both polymers were used as supplied.

All other reagents and chemicals used in this study were of the highest quality commercially available.

### Zona pellucida isolation

Porcine ovaries were obtained from slaughter houses, and ZP and ZP families were prepared after the method of Hedrick and Wardrip (1986). Heat-solubilized ZP were prepared by heating ZP for 30 min at 70°C in 5 mM ammonium bicarbonate. SDS-dissociated ZP were prepared by heating ZP in 0.5% SDS at a 100°C for 2 min.

## Radiolabelling of fucoidan and zona pellucida

Pronase-treated fucoidan was activated with cyanogen bromide after the method of Glabe *et al.* (1982). The sample was then desalted on Sephadex G-50, and fractions containing carbohydrate were pooled, lyophilized and resuspended in  $0.2 \,\text{m}$  sodium borate, pH8.0. The activated fucoidan was added to 5.0 mg of tyrosine and allowed to react overnight at 4°C. The resulting complex was re-chromatographed on Sephadex G-50, and fractions containing carbohydrate were pooled and concentrated. The resulting tyrosine-fucoidan complex was radioiodinated using Iodogen as a catalyst, and desalted prior to use with Sephadex G-50 in 1 mm Mops, pH8.0. The ZP, either heat solubilized or SDS dissociated, was radiolabelled in a similar manner using Iodogen, and similarly desalted prior to use.

## Proacrosin purification and immobilization

Boar proacrosin was purified following the method of Parrish and Polakoski (1978) with only minor modifications. Contaminating protein at  $M_r 28\,000$  (possibly a proacrosin-binding protein) was removed using gel filtration in the presence of  $8\,M$  urea or 6 M guanidine. Proacrosin was immobilized onto agarose beads using Actigel-ALD (Sterogene Biochemicals, San Gabriel, CA) in 0.1 M sodium acetate at pH 3.0. After blocking the unreacted aldehyde groups with ethanolamine, the proacrosin-Actigel was washed and kept in 1 mM Mops, 50 mM benzamidine HCl, pH 8.0.

#### Proacrosin activation and blotting

Proacrosin was activated by adding 0.1 vol of 1.1 m Tris buffer, pH 8.0, following the appearance of active acrosins enzymatically (Urch and Hedrick, 1988). The reaction was stopped by the addition of HCl to pH 3.0. The resultant autoactivation time points were separated on SDS-PAGE and western blotted onto nitrocellulose overnight at 25 volts. The nitrocellulose sheets were blocked in 5 % skimmed milk in Tris-buffered saline, and 50000 cts min<sup>-1</sup> of <sup>125</sup>I-fucoidan or <sup>125</sup>I-ZP (preadsorbed with skimmed milk-blocked nitrocellulose sheets) was added. The sheets were incubated overnight, rinsed in 0.05 % NP-40 in Tris-buffered saline for 30 min (4× changes), air dried and autoradiography of the bound label performed. The autoradiograms were photographed and reflective densitometry with the Visage 60 BioAnalyzer was performed.

#### Filter binding assay

The filter assay is a modification of the procedure of DeAngelis and Glabe for sea urchin bindin interaction with fucoidan (1987). Agarose-immobilized proacrosin  $(3.5 \,\mu g)$  was added to <sup>125</sup>I-tyrosine-fucoidan  $(0.5-6.0 \,\mu g)$  in a total volume of 1.0 ml with 1 mM Mops, pH 8.0. The initial concentration of fucoidan was determined by radioactivity. After incubation for 15 min, the reaction mixture was filtered through glass fiber filters (Whatman GF/C) with 2×4.0 ml washes of 1 mM Mops, pH 8.0. The filters were counted in a gamma counter for 2 min to determine the amount of fucoidan bound to the proacrosin beads. For the binding of ZP, 1.65  $\mu g$  of proacrosin bound to Actigel-ALD was added to <sup>125</sup>I-ZP (4.5-55  $\mu g$ ) and incubated for 150 min at the same pH and ionic strength as above.

Scatchard plot analysis of the saturation curves was performed by plotting bound/free *versus* bound amounts of the radiolabelled components. For the determination of relative binding affinities, saturating levels of fucoidan or ZP were added to the assay along with varying amounts of the test chemical. The results are graphed as the percentage of maximal binding, or the amount of binding obtained at saturating levels of fucoidan or ZP.

# Results

Agarose-insolubilized beads of proacrosin could be saturated by radiolabelled ZP and fucoidan, and binding affinities were determined from Scatchard analysis of these saturation curves. Assuming  $M_r$ s of  $2 \times 10^6$  for heat-solubilized ZP and  $1 \times 10^5$  for fucoidan, binding affinities of  $2 \times 10^{-8}$  m for ZP and  $6 \times 10^{-8}$  m for fucoidan were obtained. The fucoidan binding affinity was similar to that reported for bindin [ $K_d = 5.5 \times 10^{-8}$  m (Glabe *et al.* 1982)].

The ability of sulfated and nonsulfated polysaccharides and polymers to compete with fucoidan- or ZP-proacrosin binding was measured with the filter assay. The binding of both radiolabelled materials to proacrosin was more sensitive to ionic strength than the

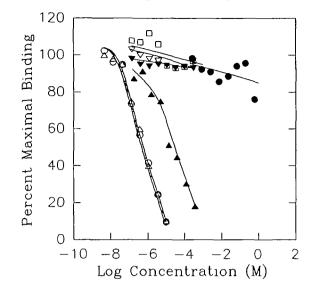


Fig. 1. The effect of added carbohydrates on the fucoidanproacrosin binding assay measured as the percentage of maximal binding at saturating levels of <sup>125</sup>I-fucoidan. The carbohydrates are: unlabeled fucoidan ( $\bigcirc$ ); dextran sulphate ( $M_r$  5000) ( $\blacktriangle$ ); dextran sulphate ( $M_r$  500 000) ( $\triangle$ ); chondroitin sulphate A or C ( $\nabla$ ); hyaluronic acid ( $\Psi$ ); dextran ( $M_r$  500 000) ( $\square$ ); fucose ( $\Phi$ ).

binding of fucan or fucoidan to sea urchin bindin; also proacrosin binding was totally inhibited at the ionic strength maximum for bindin interaction [0.1-0.6м (DeAngelis and Glabe, 1988)]. However, there were several similarities between proacrosin and bindin. Dextran sulphate (both  $M_1$ s) and 'cold' fucoidan competed effectively with <sup>125</sup>I-fucoidan for proacrosin, whereas, neither the nonsulfated carbohydrates hyaluronic acid, dextran and fucose, nor the sulfated carbohydrates, chondroitin sulphates A or C inhibit the interaction (Fig. 1). The lack of competition with fucose is contradictory to the interpretation of proacrosin as a fucose-lectin (Töpfer-Petersen and Henschen, 1988). Inorganic sulfate at constant ionic strength wasalso without effect. Similar inhibition of <sup>125</sup>I-ZPproacrosin interaction was obtained with the sulfated polysaccharides (data not shown) and the unlabeled components competed effectively in both the homologous and heterologous assays. When ZP was added to the fucoidan-proacrosin assay, the degree of inhibition was greater than with the same molar equivalent of fucoidan, assuming a  $M_r$  for ZP of  $2 \times 10^6$ . However, in an attempt to determine which ZP component is the ligand for proacrosin, the SDS-PAGE isolated and electroeluted components did not compete effectively for intact ZP or fucoidan. This was not a direct effect of SDS, since SDS-dissociated ZP was as effective a competitor as heat-solubilized ZP. When intact ZP was western blotted, both proacrosin and biotinylated DIPacrosin bound to the acidic end of the 55  $M_r$  family (data not shown). This glycoprotein family is not hydrolyzed by acrosin in intact ZP (Urch, 1991; Hedrick et al. 1988). These data suggest that proacrosin/acrosin binding to the non-substrate portion of the ZP is similar

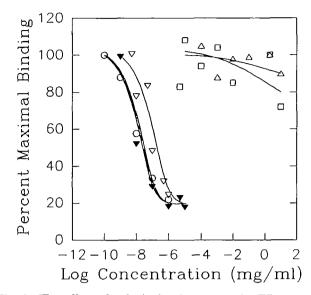


Fig. 2. The effect of polyvinyl polymers on the ZPproacrosin binding assay measured as the percentage of maximal binding at saturating levels of <sup>125</sup>I-ZP. The polymers are: poly(vinyl sulfate) ( $\bigcirc$ ); poly(vinyl styrene sulfonic acid) ( $\mathbf{\nabla}$ ); polyacrylic acid ( $\nabla$ ); poly(vinyl phosphate) ( $\Box$ ); poly(vinyl alcohol) ( $\triangle$ ).

to its binding to fucoidan. Sea urchin jelly fucan inhibited the interaction of both radiolabelled materials with the same affinity as fucoidan, a result similar to bindin. Interestingly, *Xenopus laevis* egg jelly inhibited fucoidan-, but not ZP-, proacrosin interaction.

The role of the polymeric back bone in proacrosin binding to the ZP was investigated by the addition of polyanions to the ZP binding assay (Fig. 2). Poly(vinyl sulfate) was able to compete with <sup>125</sup>I-ZP for proacrosin, while both poly(vinyl phosphate) and poly(vinyl alcohol) did not inhibit binding, and at high concentrations they increased apparent binding 2- to 3-fold. <sup>125</sup>I-ZPsulfonic acid) inhibited Poly(styrene proacrosin binding, indicating polymeric sulfonic acid groups are important in addition to the sulfate esters. Polyacrylic acid, but not the ammonium salt of polyacrylic acid, inhibited binding, even though they both exhibited dye metachromasia consistent with the carboxylic acid residues being on the polymer. This effect may be due to a generalized ionic strength phenomenon; however, neither polymeric uronic acid groups [hyaluronic acid above (Fig. 1)], nor mannose-6phosphate or polyphosphated mannan from yeast competed effectively in either assay (data not shown). The same inhibition results were obtained with fucoidan binding to proacrosin. The polymeric backbone does not seem to be of importance in the binding assays with either ZP or fucoidan, a finding similar to that of sea urchin bindin.

Since the competition for fucoidan appeared to be dependent on the  $M_r$  of the competing agent [the lower  $M_r$  dextran sulfate was tenfold less effective a competitor (Fig. 1)], fucoidan was acid hydrolyzed and the resultant products separated on gel filtration. The smaller  $M_r$  fractions were not as effective as intact

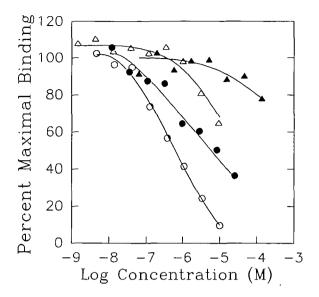


Fig. 3. The effect of partially acid hydrolyzed fucoidan on the fucoidan-proacrosin binding assay measured as the percentage of maximal binding at saturating levels of <sup>125</sup>Ifucoidan. The molecular sizes of the fucoidan pieces from gel filtration analysis are: intact fucoidan  $(M_r > 100000)$ ( $\bigcirc$ );  $M_r$  approx. 30000 fucoidan ( $\bigcirc$ );  $M_r$  approx. 10000 fucoidan ( $\triangle$ );  $M_r$  approx. 4000 fucoidan ( $\blacktriangle$ ).

fucoidan (Fig. 3). Similar data were obtained with pronase-digested ZP. The larger glycopeptides were found to interact with a proacrosin affinity column, whereas smaller glycopeptides did not (data not shown). The partial removal of sulfate ester groups from fucoidan by solvolytic desulfation resulted in 10fold less inhibition of proacrosin-fucoidan binding (Fig. 4). All these data are quite similar to those described for sea urchin bindin, and indicate that sulfate (or sulfonic acid) esters on a macromolecular backbone are the important ligand features for binding.

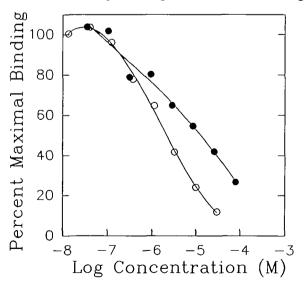


Fig. 4. The effect of partial desulfation of fucoidan on the fucoidan-proacrosin binding assay measured as the percentage of maximal binding at saturating levels of <sup>125</sup>I-fucoidan. Intact fucoidan ( $\bigcirc$ ); partially desulfated ( $\spadesuit$ ).

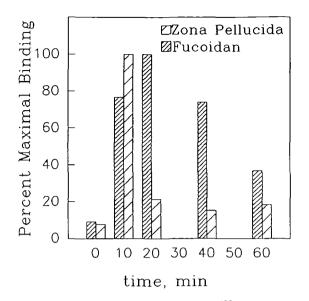


Fig. 5. Percentage of maximal binding of <sup>125</sup>I-fucoidan and <sup>125</sup>I-ZP to  $m_{\alpha}$ -acrosin ( $M_r$  49 000) on nitrocellulose blots as a function of proacrosin autolysis time.

Proacrosin was autoactivated to active acrosins by incubation at pH8.0. The resultant autolysis products were blotted onto nitrocellulose after SDS-PAGE, and these western blots were probed with both <sup>125</sup>I-ZP and <sup>125</sup>I-fucoidan. Both forms of proacrosin ( $M_r$  55000 and 53000) and the first active acrosin  $m_{\alpha}$ -acrosin ( $M_r$ 49000) bind the radiolabelled components avidly. With continued C-terminal processing of  $m_{\alpha}$ -acrosin, and the appearance of  $m_{\beta}$ -acrosin ( $M_r$  38000), there is a loss of fucoidan binding. However, the ability to bind ZP is lost sooner than fucoidan binding (Fig. 5).  $m_{\beta}$ -acrosin binds fucoidan and ZP, but not as avidly as the  $m_{\alpha}$ acrosin. This would indicate either that the binding domain for the two components is not the same size or that a specific recognition sequence for ZP is lost before the recognition sequence for fucoidan. These data are consistent with those for polysulfated polysaccharide inhibition of amidase and protease activities of acrosin, since inhibition is lost with autolysis of acrosin (Urch and Hedrick, 1988). In addition to the  $m_{\theta}$ -acrosin, there are low relative molecular mass components that bind to the labeled materials as avidly as  $m_{\alpha}$ -acrosin, indicating that acrosin autolysis releases a competent binding domain, which is also consistent with previous studies (Töpfer-Petersen and Henschen, 1988).

# Discussion

Cell-cell recognition and adhesion involve specific interactions between proteins and/or carbohydrates on the cell surface. Several of these macromolecular factors have been isolated and described. Cell adhesion molecules (CAMS) have been isolated and characterized from differentiating neural crest cell surface [N-CAM (Brackenbury *et al.* 1981)], from liver cells [L-CAM (Sorkin *et al.* 1988)] and from the adherens junction [A-CAM (Geiger *et al.* 1987)]. Proteincarbohydrate interactions are important for recognition and attachment of cell homing factors [e.g. leucocyte (Stoolman *et al.* 1984)], stem cell proliferation factors (Vohmeyer *et al.* 1988) and for the species-specific aggregation of sponge cells (Coombe *et al.* 1987). The molecules involved in recognition and binding are typically multidomain molecules that are either members of the IgG superfamily or lectins (Brackenbury, 1988) Yednock *et al.* 1987). In addition to these interactions, carbohydrate–carbohydrate cell surface interactions have been described recently (Eggens *et al.* 1989).

Fertilization requires the successful recognition and binding of gametes. In a variety of species, gamete binding is inhibited by carbohydrates (Ahuji, 1982; Shalgi et al. 1986), although other mechanisms may also be involved, such as the fibronectin amino acid adhesion sequence arg-gly-asp-ser which inhibits binding of mouse gametes (Bunch and Saling, 1988). In the pig, polysulfated polysaccharides inhibit sperm-egg interaction (Peterson et al. 1984), and these same polysaccharides inhibit the amidase and protease activities of boar acrosin (Urch and Hedrick, 1988). With sea urchin gametes, the necessary elements for attachment are polysulfated egg jelly fucan and sperm bindin (DeAngelis and Glabe, 1988). This chargecharge interaction retains species-specific agglutination properties through the novel use of a sulfate docking site on bindin, modulated with species-specific recognition factors (DeAngelis and Glabe, 1990). In this present study, we describe a recognition mechanism between mammalian gamete molecules, based on a charge-charge interaction of ZP nonsubstrate components for a separate and distinct binding domain on the proteolytic enzyme acrosin. This mechanism may play a role in maintaining the penetrating sperm on the ZP, and allow for cycles of hydrolysis and binding that facilitate sperm penetration of the ZP (Urch, 1991; Hedrick et al. 1988).

Using analogous experimentation to sea urchin bindin and its interaction to fucoidan and egg jelly fucan (Glabe et al. 1982), proacrosin was found to bind to its natural substrate, the ZP, and to fucoidan with high avidity similar to the sea urchin bindin-fucoidan or bindin–egg jelly fucan interaction ( $K_{ds} > 10^{-8} \text{ M}$ ). Like bindin, proacrosin-fucoidan binding was competitively inhibited with macromolecular polysulfated polysaccharides and polymers, whereas nonsulfated carbohydrates had no effect on binding (Figs 1, 3, and 4). Because there is very little structural similarity in amino acid sequence between bindin (Gao et al. 1986) and boar proacrosin (Baba et al. 1989a; Adham et al. 1989), these data represent an example of convergent evolution: sperm molecules stored in analogous granules behaving in an analogous fashion by binding to similar polysulfated polysaccharides with similar affinities. These data also represent an example of similar binding function with very different primary structures, consistent with a growing body of information that suggests primary sequence information does not alone predict specific secondary structural considerations in several

classes of molecules (Bowie et al. 1990; Bowie and Sauer, 1989; O'Neill and DeGrado, 1990).

Even though they have functions, there were several differences between sea urchin bindin and proacrosin in binding to fucoidan, that were not unexpected. Bindin functions in the milieu of sea water and the binding to fucoidan and egg fucan is maximum at 0.1-0.6 м ionic strength. Proacrosin binding to both ZP and fucoidan is inhibited by ionic strengths above 0.066 м. DeAngelis and Glabe argued for specificity of bindin interaction by comparing fucoidan binding to polymers of basic amino acids with fucoidan binding to bindin (DeAngelis and Glabe, 1988). They reported that polylysine– and polyhistidine– $^{125}$ I-fucoidan binding was more sensitive to ionic strength than bindin– $^{125}$ I-fucoidan binding. Also all three polymers tested [polyacrylic acid, poly(vinyl sulfate) and poly(vinyl phosphate)] inhibited <sup>125</sup>I-fucoidan binding to polylysine, polyarginine and polyhistidine (DeAngelis and Glabe, 1988), whereas bindin-fucoidan interaction was only inhibited by polyvinyl sulfate. Proacrosin binding to either ZP or fucoidan is more sensitive to ionic strength than the interaction of fucoidan with any of the polyamino acids reported. However, there is retention of binding specificity, since poly(vinyl sulfate), but not poly(vinyl phosphate), inhibits ZP- and fucoidan-binding assays.

Proacrosin-fucoidan interaction was competed for effectively by polyacrylic acid, whereas bindinfucoidan interaction was not. The ammonium salt of polyacrylic acid did not compete, and it is not clear why the salt was not effective, since both acid and salt exhibited dye metachromasia. Fucoidan contains other charged carbohydrates, e.g. 7-25% uronic acids, depending on the species of Fucus that it was extracted from (Medcalf and Larsen, 1977). These acid groups may be involved in proacrosin binding, from the result that fucoidan desulfation decreases, but does not eliminate competition (Fig. 4). Since macromolecular size is very important for effective competition (Fig. 3), macromolecular ZP has sufficient charge density of acidic groups (both sulfate and carboxylic acidic groups) for effective proacrosin binding.

High concentrations of nonsulfated carbohydrates did not compete with fucoidan (or ZP) for proacrosin binding (Fig. 1). Neoglycoprotein probes of fucose attached to either horse-radish peroxidase or to bovine serum albumin have been used to label intact sperm (Töpfer-Petersen et al. 1988). They have also been used to identify bands on western blot analyses of sperm extracts with the same  $M_r$ s as proacrosin, active acrosin and breakdown products of acrosin (Jones, 1989). The data presented in this study suggest that the molecular size of the binding molecule is important. It may be that macromolecular fucose (either in the form of fucoidan or fucose neoglycoprotein) may be recognized by proacrosin, whereas the monosaccharide is not. Previous inhibition data also indicated that fucose was not an inhibitor of acrosin amidase or protease activity (Urch and Hedrick, 1988).

The autolytic processing of proacrosin to active acrosins takes place at both the N and C termini of the

molecule (Zelezna et al. 1989; Baba et al. 1989b). The C-terminal end of the molecule is not as homologous among acrosins as the rest of the sequence. These data led Adham et al. (1989) to suggest that the C terminus is the species-specific region of proacrosin. In support of this hypothesis, our study demonstrated the loss of ZP binding by  $m_{\alpha}$ -acrosin through autolysis before the loss of binding to the non-specific fucoidan (Fig. 5). This is intriguing since the ZP ligand for proacrosin/acrosin appears to be the acidic end of the 55  $M_r$  families: ZP families that are not hydrolyzed by acrosin (Urch, 1991; Hedrick et al. 1988). Since the interaction of proacrosin with ZP is so closely mimicked by polysulfated polysaccharides, these polymers should prove invaluable for determining and understanding the ligand structure of the ZP. Also since the ZP ligand is a nonsubstrate for the protease domain of acrosin, the 55  $M_r$ families should act in a similar fashion to fucoidan and inhibit the protease and amidase activities of acrosin. Their function physiologically then would be not only as ligands, but also as inhibitors of acrosin to limit the random and total proteolysis of the ZP. Non-substrate inhibition of acrosin would be similar to the action of other non-substrates, e.g. bile acid inhibition of glutathione transferases (Hayes and Mantle, 1986; Boyer and Vessey, 1987; Young and Briedis, 1990). The data presented in Fig. 5 suggest that the differences seen with the proacrosin binding domains for ZP and fucoidan may be due to specific recognition sequences for both. The importance of the C-terminal end of proacrosin in recognition and binding can now be properly tested with the assay described in this study, by investigating the binding affinities of different proacrosins for the same ZP, or the same proacrosin for different ZPs.

Recently, Holt et al. (1989) described the amino acid sequence cys-ser/thr-val-ser/thr-cys-gly-X-gly-X-X-Xarg/lys-X-arg/lys as a consensus sequence for the binding of sulfated glycoconjugates (Table 1). Acrosin has at least one, and perhaps as many as four, sequences that are similar to this reported sequence. These might function as potential binding sites for the sulfated glycoconjugates, fucoidan and ZP. One of these sequences spans the active site serine and may account for the observed competitive inhibition with polysulfated polysaccharides (Urch and Hedrick, 1988). Surprisingly, these sequences are all located in the interior or N-terminal end of the molecule, and not on the C-terminal end. Even though active acrosins still retain this internal sequence, there is less avid binding with time, consistent with the loss of important recognition sequences through the C-terminal processing of proacrosin to active acrosins. Also the replacement of arginine by lysine in the most conserved acrosin binding sequence would result in binding more sensitive to ionic strength, based on the data collected by DeAngelis and Glabe (1988). Recently, Jones (1990) determined that trypsinogen and chymotrypsinogen bound polysulfated polysaccharides. However, the binding constants determined were considerably lower than proacrosin, indicating that the unique binding

		cys	ser	val	ser	cys	gly	x	gly	х	x	X	arg	Х	arg		
			or		or								or		or		
			thr		thr								lys		lys		
														l			
Acrosin and related pig protease sequences, sequence 137-148																	
	Acrosin	cys	trp	val	thr	-	gly	$\operatorname{trp}$	gly	$\mathbf{tyr}$	leu	-	lys	glu	lys†		
	Trypsin	-	-					-		-			-	-	ser‡		
	Chymotyr							-	-						•		
	0119 110 09 1	035	uiu	0111			8-1	στp	8-3	190	UIII		195	0 J I	uon+		
Boar acrosin, other possible binding sequences																	
							cys										
	196-209	cys	gln	gly	asp	$\operatorname{ser}$	gly	-	gly	pro	leu	${\tt met}$	arg	asp	arg		
	169-180	cys	asn	ser	thr	arg	$\operatorname{trp}$	asn	gly	-	-	-	arg	ile	arg		
	287-302	phe	gln	arg	pro	pro	gly	pro	ser	gln	gln	$\operatorname{ser}$	arg	pro	arg		
		-	-	0	-	-		-		5	-	gly j		-	Ģ		
											· ·		••••				
-, missing; X, any amino acid.																	
* Holt, G. D. et al. (1989) J. biol. Chem. 264, 12 138–12 140.																	
†Baba,	T. et al. (1989a)	) J. bio	l. Che	m. 264	4, 119	20-11	927.										
					-												

 Table 1. Consensus sequence for binding sulfated glycoconjugates\*

‡Dayhoff, M. O., (1976) Atlas of Protein Sequence and Structure, Vol. 5, National Biomedical Research Foundation, Washington, D.C.

character of proacrosin results from changes in the sequence of these related molecules. When potential binding sequences in acrosin are compared to trypsin and chymotrypsin (Table 1), both these proteases lack the basic amino acid pair at the end of the consensus sequence. We assert therefore that acrosin was selected through evolution by modification to this basic pair of amino acids. This hypothesis is testable utilizing sitedirected mutagenesis, where a basic pair of amino acids could be inserted into porcine trypsin. We would predict that this modified trypsin would then bind the non-substrate polysulfated polysaccharides in a manner similar to acrosin. Also similar site-directed mutagenesis of proacrosin to remove that basic pair should produce enzymatically active, but binding deficient, acrosins. Possible recognition sequences in the C-terminal portion of acrosin for binding ZP and fucoidan could also be established through such a study.

The striking similarities of cellular location and biological function of sea urchin bindin and proacrosin through convergent evolution, give the following quotation made by Lajos Piko (1969) an interesting new perspective: 'It is tempting to speculate that the outer acid layer of the zona may be analogous to the gelatinous coat of the sea urchin egg....' It would appear that evolution has utilized a similar motif of charge-charge interaction between gamete molecules in both the sea urchin and mammals.

The authors are indebted to Jocelyn Villalobos and Barbara Nitta for their excellent technical assistance. The work in this manuscript was supported by USDA grant 88-37240-3969.

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(Accepted 28 January 1991)