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F-Actin Binds to the Cytoplasmic Surface of Ponticulin, a 17-kD Integral Glycoprotein from Dictyostelium discoideum Plasma Membranes

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Abstract. F-actin affinity chromatography and immunological techniques are used to identify actin-binding proteins in purified Dictyostelium discoideum plasma membranes. A 17-kD integral glycoprotein (gp17) consistently elutes from F-actin columns as the major actin-binding protein under a variety of experimental conditions. The actin-binding activity of gp17 is identical to that of intact plasma membranes: it resists extraction with 0.1 N NaOH, 1 mM dithiothreitol (DTT); it is sensitive to ionic conditions; it is stable over a wide range of pH; and it is eliminated by proteolysis, denaturation with heat, or treatment with DTT and N-ethylmaleimide. gp17 may be responsible for much of the actin-binding activity of plasma membranes since monovalent antibody fragments (Fab) directed primarily against gp17 inhibit actin-membrane binding by 96% in sedimentation assays. In contrast, Fab directed against cell surface determinants inhibit binding by only 0–10%. The actin-binding site of gp17 appears to be located on the cytoplasmic surface of the membrane since Fab against this protein continue to inhibit 96% of actin-membrane binding even after extensive adsorption against cell surfaces.

gp17 is abundant in the plasma membrane, constituting 0.4–1.0% of the total membrane protein. A transmembrane orientation of gp17 is suggested since, in addition to the cytoplasmic localization of the actin-binding site, extracellular determinants of gp17 are identified. gp17 is surface-labeled by sulfo-N-hydroxysuccinimido-biotin, a reagent that cannot penetrate the cell membrane. Also, gp17 is glycosylated since it is specifically bound by the lectin, concanavalin A. We propose that gp17 is a major actin-binding protein that is important for connecting the plasma membrane to the underlying microfilament network. Therefore, we have named this protein "ponticulin" from the Latin word, ponticulus, which means small bridge.
the membranes with chaotropic agents such as 0.1 N NaOH and 1 mM dithiothreitol (DTT), but are destroyed when membranes are proteolyzed, heat-treated, or alkylated with N-ethylmaleimide (NEM) after reduction with DTT (Luna et al., 1981, 1984; Schwartz and Luna, 1986). Although initial studies have identified potential candidates for integral membrane actin-binding proteins (Luna et al., 1984; Stratford and Brown, 1985; Brown and Petzold, 1987), the exact molecules involved are not yet known.

To investigate the molecular basis for the binding of F-actin to purified D. discoideum plasma membranes, we have used two very different but complementary approaches: a biochemical approach and an immunological approach. In the biochemical approach, low-speed sedimentation assays are used to define conditions for actin–membrane binding with respect to salt concentration and pH. F-actin-binding proteins then are isolated by fractionating detergent-solubilized membrane proteins on F-actin affinity columns. In the immunological approach, polyclonal monovalent antigen-binding fragments of IgG (Fab) directed against integral membrane proteins are used to inhibit actin–membrane binding and the proteins recognized by these antibodies are identified by immunoprecipitation.

In this paper, we report that a 17-kD integral membrane glycoprotein (gp17) is responsible for much of the actin-binding activity of plasma membranes. The actin-binding activity of gp17 is identical to that observed for intact plasma membranes: it resists extraction with 0.1 N NaOH, 1 mM DTT; it is sensitive to ionic conditions; it is stable over a wide range of pH; and it is eliminated by proteolysis, denaturation with heat, or treatment with DTT and NEM. gp17 is relatively abundant in the plasma membrane, constituting $\sim 0.4\%$ of the total membrane protein. Further, gp17 appears to be a transmembrane protein with its actin-binding site located on the cytoplasmic surface of the membrane. Therefore, we propose that gp17 is a major actin-binding plasma membrane protein that is important for linking the plasma membrane to the microfilament network during cellular activities such as adhesion, motility, chemotaxis, endocytosis, and the modulation of cell surface receptors.

This work was presented in a preliminary form at the 26th Annual Meeting of the American Society for Cell Biology, Washington, DC, December 7–11, 1986 (Wuestehube and Luna, 1986).

Materials and Methods

Chemicals

Octyl glucoside (OG), ATP, and phallolidin were purchased from Boehringer Mannheim Biochemicals (Indianapolis, IN). DTT, NEM, disopropyltrifluorophosphate, phenylmethylsulfonyl fluoride (PMSF), Triton X-100 (TX-100), and BSA were supplied by Sigma Chemical Co. (St. Louis, MO). Horseradish peroxidase-conjugated goat anti-rabbit IgG was acquired from Jackson Immunoresearch (West Grove, PA). Octyl glucoside was purchased from Sigma Chemical Co., and 15,000 U of horseradish peroxidase type XIV, 5.3 U/mg solid; Sigma Chemical Co. was supplied by Sigma Chemical Co. (St. Louis, MO). Horseperdush peroxidase-conjugated goat anti-rabbit IgG was acquired from Cooper Biomedical, Inc. (Malvern, PA). Acrylamide and SDS were purchased from Bio-Rad Laboratories (Richmond, CA). Twice crystallized ovalbumin was obtained from Millipore Corp. (Bedford, MA) and control canavalin A (Con A) was from Miles-Yeda (Rehovot, Israel). Sephacryl S-1000 was procured from Pharmacia Fine Chemicals, Inc. (Piscataway, NJ). All other reagents were of the highest available grade.

Proteins

Actin was isolated from rabbit skeletal muscle according to the method of Spudich and Watt (1971). For actin–membrane binding assays, actin was further purified by gel filtration (MacLean-Fletcher and Pollard, 1980).

Rabbit plasma gelsolin was prepared following a protocol graciously provided by Dr. Carl Frieden (Frieden, C., unpublished observations). Protein concentrations were determined in the presence of 1% SDS by the procedure of Lowry et al. (1951), using BSA as a standard.

Cell Culture, Fixation, and Surface-Labeling

Cell Culture. D. discoideum amebae (strain A x3, a gift from Dr. Richard Kessin, Columbia University) were grown in HL-5 medium (Cocucci and Sussman, 1970) to $\sim 1 \times 10^7$ cells/ml for membrane preparations or to $\sim 6 \times 10^7$ cells/ml for glutaraldehyde fixation. The cells were harvested at 1,500 rpm for 2 min and were washed twice with 14.6 mM K$_2$PO$_4$, 2.0 mM Na$_2$PO$_4$, pH 6.1 (Sorensen's buffer) at 650 g for 2 min at 20°C.

Glutaraldehyde Fixation of Cells. Washed cells were resuspended to $1.0 \times 10^7$ cells/ml in 2% glutaraldehyde. Sorensen's buffer and incubated for 5 min at room temperature with gentle agitation. Cells were collected and washed twice in Sorensen's buffer. To block reactive sites, cells were incubated for 2 h at 2.0 $\times 10^7$ cells/ml in 100 mM glycine ethyl ester, Sorensen's buffer and washed five times in Sorensen's buffer. Glutaraldehyde-fixed cells appeared intact and no cell fragments were observed under the light microscope.

Cell Surface Labeling. Cell surface amino groups were labeled with sulfo-N-hydroxysuccinimido-biotin (SNHS-biotin) as described (Fingals et al., 1986).

Membrane Preparation and Extraction

Membrane Preparation. Unless otherwise noted, highly purified plasma membranes were prepared from log phase D. discoideum amebae using the Con A stabilization, Triton-extraction method described by Luna et al. (1984). All membranes were stored on ice in 0.02% NaN$_3$, 20 mM sodium phosphate, pH 6.8.

NaOH Extraction. Plasma membranes were extracted with 0.1 N NaOH, 1 mM DTT, pH 12.5, for 30 min at 0°C. The extraction mixture was sonicated with one 5-s burst from a model 200 Branson Sonifier (Branson Sonic Power Co., Danbury, CT) at 20 W. The NaOH-extracted membranes were pelleted at 27,900 g for 20 min at 4°C. The pellet, containing 30% of the initial membrane protein, was immediately resuspended and washed with 20 mM sodium phosphate, pH 6.8.

Periodate Oxidation. Highly antigenic carbohydrate residues were altered or removed from membrane proteins by periodate oxidation (Dyer, 1956). NaOH-extracted membranes at $\sim 0.6$ mg/ml were incubated in the dark with 50 mM Na$_2$O$_4$, 30 mM sodium phosphate, pH 6.0, for 12 h on ice. The reaction was quenched by the addition of ethylene glycol to a final concentration of 1% (vol/vol). After 30 min on ice, membranes were diluted with 4 vol of 20 mM sodium phosphate, pH 6.8, collected at 250,000 g for 40 min, and washed in 20 mM sodium phosphate, pH 6.8. Control membranes were treated identically except that 1% (vol/vol) ethylene glycol was added before incubation with Na$_2$O$_4$. At least 83% of the protein from both periodate-treated and control membranes was recovered in the final pellet.

Protease Treatment. Proteolytically digested membranes were prepared essentially as described (Luna et al., 1984). Briefly, membranes were sonicated (Luna et al., 1984) and then proteolyzed for 2 h at 37°C in a 2.2-ml reaction mixture containing 1.5 mg membrane protein, 1.2 mg pronase (pro tease type XIV, 5.3 U/mg solid; Sigma Chemical Co.), 20 mM sodium phosphate, pH 6.8. After 30 min, 200 $\mu$l of 100 mM EDTA were added. Proteolysis was inhibited by adding 3.0 ml of 0.4 mg/ml PMSF, 1.4% etha role, 9 mM disopropylfluorophosphate, 20 mM sodium phosphate, pH 6.8 (inhibition buffer). After 30 min at 37°C, proteolyzed membranes were collected and washed with inhibition buffer at 134,000 g for 40 min. The pellets, containing $\sim 31\%$ of the initial membrane protein, were resuspended and stored in 20 mM sodium phosphate, pH 6.8.

DTT-NEM Treatment. Plasma membranes were incubated with DTT at 37°C for 30 min in a 1.4-ml reaction mixture containing $\sim 2.5$ mg membrane protein, 50 mM DTT, 100 mM Tris, pH 7.5. Membranes were pelleted
at 25,300 g for 20 min at 4°C and washed twice in 200 mM Tris, pH 7.5. The pellet was resuspended with an equal volume of 100 mM NEM, 200 mM Tris, pH 7.5, using gentle homogenization or vortexing. After 30 min at 37°C, membranes were centrifuged as described above and washed three times in 40 ml of 20 mM sodium phosphate, pH 6.8. The final pellet, containing 71-76% of the initial membrane protein, was resuspended to 700 µl with 20 mM sodium phosphate, pH 6.8.

**Heat Denaturation.** Plasma membranes in a 1.5 ml polypropylene tube were immersed in a water bath at 90°C for 1 h.

**Glutaraldehyde Fixation of Membranes.** Plasma membranes at 2.0 mg/ml were incubated in 2% glutaraldehyde, 20 mM sodium phosphate, pH 6.8, for 5 min at room temperature. Membranes were collected at 25,000 g for 30 min and washed three times in 200 mM sodium phosphate, pH 6.8. Reactive sites were blocked by incubating membranes at 1.0 mg/ml in 100 mM glycine ethyl ester, 20 mM sodium phosphate, pH 6.8, for 2 h. Fixed membranes were centrifuged as described above and washed five times in 17.5 mM potassium phosphate, pH 8.0.

**Radioiodination**

**Radioiodination of Membranes and Molecular Mass Standards.** Sonicated membranes at 2.0 mg/ml were radioiodolated with 125 µCi [125I]-Bolton Hunter reagent (Bolton and Hunter, 1973) in 200 µl 0.2 M sodium phosphate, pH 8.0, and at 2 h at 0°C. Labeled membranes were separated from unreacted reagent by chromatography on a column of Sephadex G-25 (Sigma Chemical Co.) equilibrated with 20 mM sodium phosphate, pH 6.8. Pre-stained molecular mass standards (Bethesda Research Laboratories, Bethesda, MD) were labeled with [125I]-Bolton Hunter reagent using the same procedure.

**Radioiodination of Actin.** Gel-filtered actin was labeled, polymerized, depolymerized, and stored as described by Schwartz and Luna (1986) with two exceptions. First, [125I]-Bolton Hunter reagent in benzene was purchased from New England Nuclear (Boston, MA) and evaporated to dryness before addition of G-actin. Second, radioiodolated F-actin was collected at 150,000 g for 2.5 h at 4°C and radioiodolated G-actin was clarified at 150,000 g for 30 min at 2°C.

**Radioiodination of Con A.** Con A was radioiodolated using carrier-free Na[125I] (Amersham Corp., Arlington Heights, IL) and chloramine T (Eastman Kodak Co., Rochester, NY) as described by Chang and Cuatrecasas (1978) with the modifications described in Luna et al. (1984).

**F-Actin Affinity Chromatography**

**Bead Preparation.** F-actin beads were prepared as described (Luna et al., 1982) with the exception that F-actin was labeled either with 5-iodoacetamido fluorescein (Molecular Probes Inc., Junction City, OR) as described by Wang and Taylor (1987), or with fluorescein-5-maleimide (Molecular Probes, Inc.) as described by Wang and Taylor (1987).

**Affinity Columns.** Columns were constructed of a 1-ml plastic syringe fitted with a plug of porous polystyrene and contained 100-500 µl of packed IgG-Sepharcl Y-500 beads (Pharmacia Fine Chemicals). Control columns contained IgG-Sepharcl Y-5000 beads without bound actin. Nonspecific protein binding sites were blocked with 4% (wt/vol) BSA in column buffer (50 mM KCl, 1 mM MgCl₂, 0.02% NaN₃, 0.5 µM phalloidin, 20 mM Tris-acetate, pH 7.0 at 20°C). Two F-actin affinity chromatographic procedures were developed to identify F-actin-binding proteins. In the first procedure, sonicated [125I]-labeled membranes were bound at room temperature (20°-25°C) to F-actin columns and unbound membranes were washed away with excess column buffer. Membranes were solubilized and unbound proteins were removed by washing with 10 column vol of 3% OG in column buffer. Bound proteins were eluted from the columns either with 1% SDS, which also removes actin filaments from the beads, or with 2 M NaCl, 2 mM EGTA, 1% OG in column buffer followed by 1% SDS. In the second chromatographic procedure, [35S]labeled membranes were presolubilized with 3% OG in column buffer for >10 min at 6°C and clarified by centrifugation at 150,000 g for 1 h at 6°C. The supernatant was then incubated at room temperature with F-actin affinity columns, which were washed and eluted as in the first procedure.

**Actin-Membrane Binding Assays**

Actin-membrane binding assays were performed essentially as described by Schwartz and Luna (1986). Briefly, [35S]labeled gel-filtered actin at 60 µg/ml was polymerized for 30 min at 25°C with gelsolin at a mole ratio of actin to gelsolin of 2:1 in polymerization buffer (50 mM KCl, 2 mM MgCl₂, 50 mM CaCl₂, 1.0 mM DT T, 0.4 mM ATP, 100 µM PMSF, 20 mM Pipes, pH 7.0) containing 1 mM phalloidin and 1 mg/ml ovalbumin. The pre-assembled short actin filaments then were diluted with 2 vol of polymerization buffer. In actin-membrane binding inhibition studies, membranes were preincubated with Fab in 50 mM KCl, 2 mM MgCl₂, 20 mM Pipes, pH 7.0, for 2 h at room temperature. For each incubation, membranes labeled with short actin filaments were incubated with 1.25 µg of NaOH-extracted membranes in a total volume of 50 µl polymerization buffer for 1 h at room temperature. Membrane-bound actin was measured after centrifugation through 10% (wt/vol) sucrose as described (Schwartz and Luna, 1986). For binding assays in which NaCl was present, 24% (wt/vol) sucrose was used. Error bars on binding curves represent high and low values for duplicate points when the range is greater than the size of the symbol.

**PAGE and Protein Blotting**

**Preparation of Antiserum.** Two New Zealand rabbits were injected intradermally with either 600 µg of NaOH-extracted membranes or 100 µg NaIO₄-treated, NaOH-extracted membranes mixed 1:1 with Freund's complete adjuvant (Miles Laboratories Inc.). 4 wk later, a booster injection was given to each rabbit using the same antigens, i.e., 800 µg of NaOH-extracted membranes or 100 µg of NaIO₄-treated, NaOH-extracted membranes, in Freund's incomplete adjuvant (Miles Laboratories Inc.). The rabbits were bled from the marginal ear vein every week after the booster injection.

**IgG and Fab Purification.** IgG was isolated by ammonium sulfate precipitation and chromatography through DEAE-cellulose (Hudson and Hay, 1980). Fab were prepared from IgG by papain digestion and were purified by chromatography through cyanoxylyl cellulose (Hudson and Hay, 1980). The purity of IgG and Fab preparations was verified by SDS-PAGE.

**Adsorption of IgG against Cells.** IgG was adsorbed by five 1-h incubations with glutaraldehyde-fixed cells in 17.5 mM potassium phosphate, pH 8.0, at a ratio of 1 mg IgG per 5 x 10⁷ cells. After each incubation, cells were pelleted at 955 g for 2 min and the IgG supernatant was collected. The adsorption was considered complete since no difference in titer was observed between the IgG supernatants after the fourth and fifth incubations, as measured by ELISA (see below). The final IgG supernatant was clarified at 25,000 g for 30 min and the IgG was re-purified by ammonium sulfate precipitation and chromatography through DEAE-cellulose. As a control, non-adsorbed IgG also was re-purified.

**Adsorption of IgG against Membranes.** IgG was adsorbed by five 1-h incubations with glutaraldehyde-fixed membranes in 17.5 mM potassium phosphate, pH 8.0, at a ratio of 1 mg IgG per mg membrane protein. After each incubation, membranes were pelleted at 10,000 g for 5 min and the IgG supernatant was collected. The final IgG supernatant was clarified at 150,000 g for 1 h at 6°C.

**Antibody Production, Purification, and Adsorption**

**Preparation of Antisera.** Two New Zealand rabbits were injected intradermally with either 600 µg of NaOH-extracted membranes or 100 µg NaIO₄-treated, NaOH-extracted membranes mixed 1:1 with Freund's complete adjuvant (Miles Laboratories Inc.). 4 wk later, a booster injection was given to each rabbit using the same antigens, i.e., 800 µg of NaOH-extracted membranes or 100 µg of NaIO₄-treated, NaOH-extracted membranes, in Freund's incomplete adjuvant (Miles Laboratories Inc.). The rabbits were bled from the marginal ear vein every week after the booster injection.

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**Adsorption of IgG against Membranes.** IgG was adsorbed by five 1-h incubations with glutaraldehyde-fixed membranes in 17.5 mM potassium phosphate, pH 8.0, at a ratio of 1 mg IgG per mg membrane protein. After each incubation, membranes were pelleted at 10,000 g for 5 min and the IgG supernatant was collected. The final IgG supernatant was clarified at 150,000 g for 1 h at 6°C.
**Immunological Methods**

**Immune Precipitation.** $^{125}$I-labeled membranes (1 x 10$^5$ to 2 x 10$^5$ cpm/µg) were solubilized at 10 µg/ml in 0.3 M NaCl, 5 mM EDTA, 25 mM Tris-HCl, pH 8.0, 1% TX-100, 1 mg/ml BSA (solubilization buffer). To minimize background, solubilized membranes were preclarified by incubation with either 2 µl preimmune serum or 10 µg preimmune IgG per 1 µg membrane protein for 1 h at 25°C followed by incubation for 30 min at 25°C with 10 µl of 10% prewashed *Staphylococcus aureus* (Pansorbin; Calbiochem-Behring Corp., La Jolla, CA) per 1 µl serum or 5 µg IgG. The solution then was clarified at 150,000 g for 1 h at 6°C and 10 µg immune IgG or 2 µl preimmune serum was added to each supernatant. After a 2-h incubation at 25°C, the solution was incubated for an additional 30 min with 25 µl of 10% Pansorbin. The immune complexes were collected at 100,000 g for 4 min at 25°C and washed three times with solubilization buffer. The immunoprecipitated membrane proteins were prepared for electrophoresis by heating in sample buffer at 70°C for 10 min after which the Pansorbin was removed by centrifugation at 10,000 g for 4 min.

**ELISA.** The titer$^2$ of Fab or IgG against membranes and against partially purified gp7 was measured in an ELISA (Engvall and Perlman, 1972). Briefly, 1 µg membrane protein or ~20 ng partially purified gp7 in PBS (150 mM NaCl, 10 mM sodium phosphate, pH 7.2) was allowed to attach to wells in Nunc immunoplates (Vanguard International, Inc., Neptune, NJ) for 2 h at 25°C. Nonspecific binding sites were blocked with 2% BSA, PBS at 25°C for 2 h. Serial dilutions of IgG or Fab in 1% BSA, PBS were incubated in each well for 1 h at 25°C. The binding of primary antibody was visualized by incubating wells with 100 µl of horseradish peroxidase-conjugated goat anti-rabbit IgG diluted 1:1,000 or 1:100 in 1% BSA, PBS for 1 h at 25°C followed by a 30-min incubation at 25°C with 150 µl of 0.03% H$_2$O$_2$, 0.5 mg/ml o-phenylenediamine (Sigma Chemical Co.), 50 mM sodium tartrate, pH 4.5. Between each incubation, wells were washed extensively with PBS. The absorbance at 405 nm of each well was measured using a Bio-Rad model 2550 ELA Reader.

Fab titers against plasma membranes and against gp17 were compared using the ratios of the slopes obtained by plotting OD 405 versus Fab concentration (µg/ml). For example, the percentages of Fab directed against the intracellular surface of the membrane (Fab) were determined using the equation $\text{Fab}_b = 100 \times (\text{OD 405})/\text{adsorbed Fab + OD 405}/\text{non-adsorbed Fab}$. Each calculation was based on 6-10 data points from the linear section of the graph. Correlation coefficients were 0.97-1.00.

**Results**

**Biochemical Analysis of Actin–Membrane Binding**

**Conditions of Actin–Membrane Binding.** The molecular nature of the interactions involved in the binding of F-actin to membranes was explored by analyzing the sensitivity of actin–membrane binding to changes in salt concentration and pH. A quantitative sedimentation assay (Schwartz and Luna, 1986) in which $^{125}$I-labeled actin filaments, limited in length by the actin capping protein gelsolin, are bound to large membrane sheets was used for this purpose. Fig. 1 shows that the extent of actin–membrane binding changes as a function of NaCl concentration. Maximal binding is observed between 20 and 100 mM NaCl. At concentrations higher than 100 mM NaCl, binding is observed to decrease steadily. In the presence of 2 M NaCl, binding is reduced 82%. In contrast, the extent of actin–membrane binding does not vary significantly over a wide range of pH. The amount of F-actin bound to membranes remains relatively constant from pH 5.5 to 7.0. Binding decreases gradually above pH 7.0 and is reduced ~25% at pH 9.5 (data not shown).

**Octyl Glucoside Solubilization of Plasma Membranes.** Integral membrane proteins that are anchored in the lipid bilayer by hydrophobic interactions require the use of detergents for solubilization into aqueous solution (Helensi and Simons, 1975). We have used two established criteria to judge the efficiency of OG in solubilizing *D. discoideum* plasma membrane proteins. First, membrane proteins are considered solubilized if retained in the supernatant fraction after centrifugation at 150,000 g for 1 h at 6°C (Hjelmand and Chrambach, 1984). The concentration of OG required for efficient solubilization of both purified plasma membranes and of plasma membranes that were preextracted with 0.1 N NaOH, 1 mM DTI to remove peripheral proteins was examined using a sedimentation assay. In this assay, membranes at 0.2 mg/ml protein are solubilized with concentrations of OG ranging from 0% (wt/vol) to 3.0% (wt/vol) and then pelleted onto sucrose cushions at 150,000 g for 1 h at 6°C.

Sedimentation assays of $^{125}$I-labeled membranes reveal that at a final concentration of 3% OG, 90% of the counts associated with both plasma membranes and NaOH-extracted membranes are recovered in the supernatant fraction. SDS-PAGE analysis shows that the overall protein composition of the supernatant does not change appreciably as the concentration of OG increases (data not shown). This result indicates that, at these concentrations, OG is not selectively extracting membrane proteins, but rather is solubilizing membrane proteins by disrupting the lipid bilayer.

The efficiency of OG in solubilizing *D. discoideum* plasma membrane proteins is confirmed by a second criterion in which membrane proteins are considered to be solubilized if they partition in the included volume of a Sepharose 6B column (Hjelmand and Chrambach, 1984). Since at least 93% of the counts of $^{125}$I-labeled membrane proteins found in the supernatant fraction elute in the included volume of a Sepharose 6B column (data not shown), protein complexes appear to be no larger than 4 x 10$^6$ D, the exclusion limit of Sepharose 6B.

**F-Actin Affinity Chromatography.** F-actin affinity chromatography has been used to identify potential actin-binding proteins in detergent extracts of plasma membranes. Fig. 2

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2. In this paper, the term “titer” refers to the concentration of Fab or IgG required to generate a given absorbance reading at 405 nm in an ELISA, as described in Materials and Methods.
Figure 2. Chromatography of $^{251}$I-labeled plasma membranes on F-actin affinity (A) and control (B) columns. Membranes were solubilized in 3% octyl glucoside and clarified at 150,000 g immediately before loading onto the columns. The arrows indicate when the columns were loaded and successively eluted with 1% octyl glucoside and with 1% SDS. The run-through peak containing unbound membrane proteins was collected in fractions 5 and 6 for both columns. SDS-elution of the actin column released specifically bound proteins which were collected in fractions 19, 20, and 21. Background radioactivity eluted with SDS from the control column was collected in fractions 17, 18, and 19.

shows typical elution profiles of OG presolubilized $^{251}$I-labeled membranes fractionated on F-actin affinity columns and on control columns which lack actin filaments. Whereas most of the counts associated with $^{251}$I-labeled membranes are eluted from the columns with OG, ~4% of the radioactivity remains bound to the actin column and is eluted with SDS. By comparison, the SDS-eluted fraction from the control column contains only 1.3% of the total radioactivity. Therefore, we estimate that 2.5–3.0% of the radioactivity associated with $^{251}$I-labeled membranes specifically binds to F-actin on affinity columns.

SDS-PAGE analysis of the peak fractions from F-actin and control columns shows that only a subset of OG presolubilized $^{251}$I-labeled membranes fractionated on F-actin affinity columns and on control columns which lack actin filaments. Whereas most of the counts associated with $^{251}$I-labeled membranes are eluted from the columns with OG, ~4% of the radioactivity remains bound to the actin column and is eluted with SDS. By comparison, the SDS-eluted fraction from the control column contains only 1.3% of the total radioactivity. Therefore, we estimate that 2.5–3.0% of the radioactivity associated with $^{251}$I-labeled membranes specifically binds to F-actin columns. SDS-PAGE analysis of the peak fractions from F-actin and control columns shows that only a subset of OG presolubilized membrane proteins specifically bind to F-actin on affinity columns (Fig. 3). The major actin-binding protein that is eluted from the F-actin column with SDS has a molecular mass of 17 kD. Smaller amounts of membrane proteins with molecular masses of 32, 40, and 100 kD also bind preferentially to F-actin columns. The 17-kD protein is also the major actin-binding protein in silver-stained gels of SDS-eluted fractions after actin affinity chromatography of unlabeled membranes. This observation indicates that the intensity of the 17-kD protein in autoradiographs is not due to selective labeling with Bolton-Hunter reagent. The appearance of the 17-kD protein in Con A-stabilized, Triton-extracted membranes is not qualitatively dependent on the membrane preparation technique because this protein also is isolated upon F-actin affinity chromatography of membranes prepared without Con A (Das and Henderson, 1983; Spudich, 1974). These less pure plasma membrane preparations contain several membrane proteins, in addition to the 17-kD protein, that bind specifically to F-actin columns. These proteins have molecular masses of 16, 19, 28, 32, 40, 68, and 100 kD (data not shown). It is not clear, however, whether these other actin-binding membrane proteins are localized to the plasma membrane and perhaps are excluded from Con A–stabilized regions of the membrane, or whether these proteins are localized to other membranous organelles that are contaminants in the plasma membrane preparation.

F-actin affinity chromatography was used further to explore the actin-binding activity of the 17-kD protein. Columns were eluted with a step gradient of NaCl to determine the sensitivity of the actin-binding activity of the 17-kD protein to ionic conditions. Although some 17-kD protein elutes from actin columns at NaCl concentrations as low as 200 mM, more efficient elution of the 17-kD protein is obtained with 2 M NaCl (data not shown). The 17-kD protein is virtu-
Figure 4. A silver-stained 10-20% polyacrylamide SDS gel profile of plasma membrane fractions from F-actin affinity and control columns. Lane 1 shows membranes before affinity chromatography. Peak fractions from the F-actin column include the run-through (lane 2), the fraction eluted with 2 M NaCl (lane 3), and the SDS-eluted fraction (lane 4). The run-through, NaCl-eluted fraction, and SDS-eluted fraction from the control column are shown in lanes 5-7, respectively. Each lane was loaded with 10 μl. Numbers on the left refer to the molecular mass of Bethesda Research Laboratories prestained molecular mass standards.

ally the only membrane protein that is eluted from the actin column with 2 M NaCl (Fig. 4). Except for occasional traces of a 19-kD protein, the other membrane proteins remain bound to the actin column unless eluted with SDS. High NaCl concentrations do not irreversibly denature the actin-binding activity of the 17-kD protein since this protein will bind again to F-actin columns when the NaCl concentration is lowered (data not shown). Salt elution of F-actin columns allows partial purification of the 17-kD protein under non-denaturing conditions. We estimate that the 17-kD protein constitutes ~0.4-1.0% of the total membrane protein, based on the relative amount of radioactivity eluting with 2 M NaCl after F-actin affinity chromatography of 125I-labeled membranes.

The binding of the 17-kD protein to F-actin columns appears to be stable over a wide range of pH. The 17-kD protein does not elute from actin columns between pH 4.0 and 8.0. Trace amounts of the 17-kD protein are eluted from F-actin columns at pH 9.0. At pH 10.0, significant amounts of the 17-kD protein are eluted from F-actin columns (data not shown).

The orientation in the membrane of the 17-kD protein was explored using F-actin affinity chromatography of membranes subjected to various pretreatments (Fig. 6). gp17 can be isolated on F-actin columns from NaOH-extracted membranes (Fig. 6, lane 2) and therefore is considered to be an integral component of the membrane. As in the case of actin binding to intact plasma membranes, the actin-binding activity of gp17 is sensitive to denaturation. gp17 is not isolated on F-actin columns from pre-solubilized membranes that have been denatured either with heat (Fig. 6, lane 3) or by treatment with DTT and NEM (Fig. 6, lane 4). Since gp17 also is not recovered from denatured membrane vesicles solubilized after incubation with F-actin beads (data not shown), the absence of gp17 from the NaCl-eluted fraction must be due to loss of its actin-binding activity and not due to changes in its solubility properties upon denaturation. The actin-binding activity of gp17 also is sensitive to protease treatment of the membranes. In contrast to F-actin affinity chromatography of column-solubilized control membranes (Fig. 6, lane 5), chromatography of proteolyzed membrane vesicles yields no detectable gp17 when proteolyzed membranes are solubilized after incubation with F-actin beads (Fig. 6, lane 6). However, when compared with presolubilized control membranes (Fig. 6, lane 7), trace amounts of gp17 are isolated on F-actin columns after incubation with F-actin beads (Fig. 6, lane 8).

Figure 5. 125I-Con A-stained nitrocellulose blots of a 10-20% polyacrylamide SDS gel containing 25 μl of the NaCl-eluted fraction from F-actin affinity columns. 125I-labeled molecular mass standards are shown in lanes 1 and 3. Con A-binding proteins were visualized by incubation of blots with 125I-Con A in the absence (lane 2) and presence (lane 4) of α-methyl-D-mannoside. Film was exposed to the nitrocellulose blots for 2 d. The arrow denotes the position of gp17.

(Ingalls et al., 1986; Goodloe-Holland and Luna, 1987), this result indicates that a domain of the 17-kD protein is exposed to the extracellular surface of the membrane. A second line of evidence supporting the conclusion that a domain of the 17-kD protein is exposed extracellularly comes from protein blots of the NaCl-eluted fraction probed with Con A (Fig. 5). The 17-kD protein binds Con A in the absence (Fig. 5, lane 2), but not in the presence (Fig. 5, lane 4), of the competing sugar α-methyl-D-mannoside. We interpret this result to mean that the 17-kD protein is glycosylated and henceforth will refer to this protein as gp17. Fig. 5 also shows that no other prominent Con A-binding glycoproteins are found in the NaCl-eluted fraction, a further indication of the relative purity of this fraction.

The binding of gp17 to F-actin was characterized using F-actin affinity chromatography of membranes subjected to various pretreatments (Fig. 6). gp17 can be isolated on F-actin columns from NaOH-extracted membranes (Fig. 6, lane 2) and therefore is considered to be an integral component of the membrane. As in the case of actin binding to intact plasma membranes, the actin-binding activity of gp17 is sensitive to denaturation. gp17 is not isolated on F-actin columns from pre-solubilized membranes that have been denatured either with heat (Fig. 6, lane 3) or by treatment with DTT and NEM (Fig. 6, lane 4). Since gp17 also is not recovered from denatured membrane vesicles solubilized after incubation with F-actin beads (data not shown), the absence of gp17 from the NaCl-eluted fraction must be due to loss of its actin-binding activity and not due to changes in its solubility properties upon denaturation. The actin-binding activity of gp17 also is sensitive to protease treatment of the membranes. In contrast to F-actin affinity chromatography of column-solubilized control membranes (Fig. 6, lane 5), chromatography of proteolyzed membrane vesicles yields no detectable gp17 when proteolyzed membranes are solubilized after incubation with F-actin beads (Fig. 6, lane 6). However, when compared with presolubilized control membranes (Fig. 6, lane 7), trace amounts of gp17 are isolated on F-actin columns after incubation with F-actin beads (Fig. 6, lane 8).
Figure 6. The binding of gp17 from pre-treated membranes to F-actin affinity columns. gp17 was visualized on a silver-stained 15-20% polyacrylamide SDS gel containing 40 µl of the NaCl-eluted fraction from F-actin affinity chromatography of: untreated plasma membranes (lane 1), NaOH-extracted membranes (lane 2), presolubilized heat-denatured membranes (lane 3), membranes treated with DTT and NEM and presolubilized (lane 4), column-solubilized proteolysis control (lane 5), column-solubilized proteolyzed membranes (lane 6), presolubilized proteolysis control (lane 7), and presolubilized proteolyzed membranes (lane 8). Bethesda Research Laboratories prestained molecular mass standards are shown in lane S. Numbers on the left refer to the molecular mass of the standards in kilodaltons.

Figure 7. (A) ELISA analysis of the titer against plasma membranes of Fab prepared from the following: anti-NaOH-PM (●), anti-NaIO4-PM (▲), anti-NaIO4-PM after adsorption against glutaraldehyde-fixed cells (▼), anti-NaOH-PM after adsorption against glutaraldehyde-fixed cells (○), and preimmune IgG (●). (B) Inhibition of binding of 125I-labeled actin to membranes by anti-NaOH-PM (●), anti-NaIO4-PM (▲), and preimmune (○) Fab.

from protease-treated membranes that are solubilized before incubation with F-actin beads (Fig. 6, lane 8). This is most likely due to the release of nonproteolyzed gp17 from sealed membrane vesicles upon detergent solubilization.

Immunological Analysis of Actin-Membrane Binding

Characterization of Antigens. Two antigens were used to raise polyclonal antibodies against integral membrane actin-binding proteins: NaOH-extracted membranes and NaOH-extracted membranes that were further treated with NaIO4 to alter or remove highly antigenic carbohydrate residues.

NaOH-extracted membranes bind F-actin and contain relatively few major membrane proteins (Luna et al., 1984). However, since many of these membrane proteins are glycosylated, we anticipated that the majority of the immune response might be directed against the highly immunogenic carbohydrate residues (Knecht et al., 1984). Therefore, periodate oxidation of NaOH-extracted membranes was explored as a means to deglycosylate membrane proteins. Since these antibodies were to be used to inhibit actin-membrane binding, it was important to verify that NaIO4-treated membranes retained actin-binding activity.

The successful removal of carbohydrate residues from membrane proteins by periodate oxidation was assayed by SDS-PAGE and by 125I-Con A staining of nitrocellulose blots (data not shown). Treatment with NaIO4 eliminates the binding of 125I-Con A to membrane proteins, indicating that the carbohydrate residues of these proteins have been cleaved. Periodate oxidation also results in a lowering of the molecular mass of many membrane proteins. This is due, at least in part, to the removal of carbohydrate residues from membrane proteins, but also may be caused by cleavage of the peptide backbone of these proteins at the amino acid residues, serine and threonine (Dyer, 1956). However, periodate oxidation does not destroy the actin-binding activity of membranes since NaIO4-treated membranes competitively inhibit the binding of 125I-labeled membrane vesicles to F-actin beads in low-speed sedimentation assays (data not shown).

Characterization of Antisera. Adsorption experiments suggest that the antiserum raised against NaOH-extracted plasma membranes (anti–NaOH-PM) is directed predominantly against cell surface determinants, whereas the antiserum raised against plasma membranes treated with both
NaOH and NaIO₄ (anti-NaIO₄-PM) recognizes determinants on both the extracellular and the cytoplasmic surfaces of the membrane (Fig. 7A). After adsorption against glutaraldehyde-fixed cells, the titer against plasma membranes of anti-NaOH-PM is reduced by ~92%. From this result, we estimate that only ~8% of the plasma membrane-specific anti-NaOH-PM antibodies recognize determinants on the cytoplasmic surface of the membrane. In contrast, the titer against plasma membranes of anti-NaIO₄-PM is reduced by ~33% after adsorption against glutaraldehyde-fixed cells. Therefore, we estimate that as much as 67% of the plasma membrane-specific anti-NaIO₄-PM antibodies recognize determinants on the cytoplasmic surface of the membrane.

The alternative explanation, that the antisera recognize glutaraldehyde-sensitive sites, is unlikely since adsorption against glutaraldehyde-fixed membranes reduces the titers against plasma membranes of both anti-NaOH-PM and anti-NaIO₄-PM to preimmune levels (data not shown). These results indicate that the determinants recognized by anti-NaIO₄-PM and anti-NaOH-PM are not destroyed by glutaraldehyde fixation.

**Actin-Membrane Binding Inhibition by Fab.** Fab from anti-NaOH-PM and anti-NaIO₄-PM antisera were used to inhibit actin-membrane binding in sedimentation assays. Fig. 7B shows that anti-NaIO₄-PM Fab inhibit actin-membrane binding by 96%, whereas anti-NaOH-PM Fab inhibit binding by only 0-10% at comparable Fab concentrations. This difference is more striking in light of the observation that anti-NaOH-PM has a higher titer against plasma membranes than does anti-NaIO₄-PM, as measured in an ELISA (Fig. 7A). These results indicate that it is not the titer of the antisera against plasma membranes, but rather the specificity of the antisera that is important for the observed inhibition of actin-membrane binding.

**Specificity of Anti-NaOH-PM and Anti-NaIO₄-PM.** The specificity of anti-NaOH-PM and anti-NaIO₄-PM was determined by immunoprecipitating ³²P-labeled plasma membrane proteins (Fig. 8). Anti-NaOH-PM IgG immunoprecipitates many membrane proteins, possibly due to cross-reactive carbohydrate determinants. In contrast, anti-NaIO₄-PM IgG immunoprecipitates predominantly one protein with a molecular mass of 17 kD. This 17-kD protein is almost certainly the same protein first identified using F-actin affinity chromatography since anti-NaIO₄-PM IgG selectively immunoprecipitates gp17 from a mixture of all the membrane proteins eluting from F-actin columns with SDS (Fig. 9).

**Characterization of the Actin-binding Site of gp17.** The titers of anti-NaOH-PM and anti-NaIO₄-PM Fab against partially purified gp17 were measured by ELISA (Fig. 10A). Although both anti-NaOH-PM and anti-NaIO₄-PM Fab exhibit a substantial titer against partially purified gp17, the titer of anti-NaIO₄-PM Fab is approximately sixfold higher than that of anti-NaOH-PM Fab. After exhaustive adsorption against glutaraldehyde-fixed cells, anti-NaIO₄-PM Fab maintains a high titer against partially purified gp17 while the titer of anti-NaOH-PM Fab drops to preimmune levels. In addition, anti-NaIO₄-PM IgG still immunoprecipitates gp17 after extensive adsorption against glutaraldehyde-fixed cells (data not shown). These results suggest that anti-NaOH-PM recognizes mostly extracellular determinants of gp17, whereas anti-NaIO₄-PM also recognizes cytoplasmic determinants of gp17.

When compared on the basis of equivalent titer against partially purified gp17, anti-NaIO₄-PM Fab and anti-NaOH-PM Fab show significant differences in the ability to inhibit actin-membrane binding (Fig. 10B). Although anti-NaOH-PM Fab will inhibit actin-membrane binding, much higher amounts of anti-NaOH-PM Fab are required to achieve levels of inhibition comparable to those observed with anti-NaIO₄-PM Fab. Even after extensive adsorption against glutaraldehyde-fixed cells, relatively low concentrations of anti-NaIO₄-PM Fab can inhibit 96% of actin-membrane binding. These results demonstrate that Fab directed against the cytoplasmic surface of gp17 efficiently inhibit actin-membrane binding and are consistent with the conclusion that the high-affinity actin-binding site of gp17 is cytoplasmically located.
Discussion

In this report, we present evidence that a 17-kD integral glycoprotein (gpl7) is responsible for much of the F-actin binding activity of purified D. discoideum plasma membranes. Our results show that gpl7 is the major F-actin binding protein isolated from OG-solubilized membranes on F-actin affinity columns (Figs. 3 and 4). The actin-binding activity of gpl7 has the same characteristics observed for purified plasma membranes: it resists extraction with 0.1 N NaOH, 1 mM DTT; it is sensitive to ionic conditions; it is stable over a wide range of pH; and it is eliminated by proteolysis, heat-denaturation, or treatment with DTT and NEM (Figs. 1 and 6). Since the actin-binding activity of gpl7 persists in the presence of high concentrations of detergent, the actin-binding site of the protein is not hydrophobic. Rather, the salt-sensitivity of the actin–gpl7 binding strongly suggests an electrostatic interaction.

Gpl7 may be the primary link between actin filaments and the plasma membrane since Fab directed predominantly against gpl7 inhibit ~96% of actin–membrane binding. In contrast, Fab directed primarily against cell surface determinants inhibit binding by only 0–10% (Fig. 7B). The high-affinity actin-binding site of gpl7 appears to be located on the cytoplasmic surface of the membrane since Fab directed against this protein continue to inhibit 96% of actin–membrane binding even after extensive adsorption against glutaraldehyde-fixed cells (Fig. 10B). A transmembrane orientation of gpl7 is suggested since, in addition to the cytoplasmic localization of the actin-binding site, extracellular determinants of gpl7 are identified. gpl7 is glycosylated since it is specifically bound by Con A (Fig. 5), a lectin that binds to α-mannopyranosides and glucopyranosides (Goldstein et al., 1974). Also, gpl7 is surface-labeled by SNHS-biotin, a reagent that is restricted to the extracellular surface of the membrane. These results demonstrate that a domain of gpl7 is extracellularly exposed. Since gpl7 appears to be an important connection between the plasma membrane and the underlying microfilament network, we have named it “ponticulin,” from the Latin word, ponticulus, which means small bridge.

Although the literature describing cytoplasmic and high molecular mass membrane proteins associated with actin is extensive (reviewed by Pollard and Cooper, 1986), only recently have low molecular mass actin-binding membrane proteins been recognized. While ponticulin is the first integral actin-binding protein to be isolated from plasma membranes, other low molecular mass actin-binding proteins in D. discoideum membranes have been identified. Schleicher et al. (1984) have identified a 17-kD protein that binds 125I-G-actin in gel overlays. However, unlike ponticulin, their protein appears to be peripherally associated with the membrane since it is extracted with 1.5 M KCl. Stratford and Brown (1985) have described a 24-kD integral protein that binds glutaraldehyde–cross-linked F-actin on gel overlays. When purified, this protein also binds radiolabeled F- and G-actin in a two-phase binding assay which partitions proteins based on their hydrophobicity. It is not clear, however, whether this protein is localized to the plasma membrane since these investigators were working with a crude membrane preparation that also contains other membranous organelles.

Recently, Brown and Petzold (1987) have used polyclonal antibodies raised against crude D. discoideum membranes to inhibit actin–membrane interactions in viscosity and sedimentation assays. By adsorbing these antibodies against electrophoretically separated membrane proteins transferred to nitrocellulose, these investigators have shown that ~25% of the activity is adsorbed out by proteins with molecular masses between 15.5 and 18.5 kD and that ~40% of the activity is
adsorbed out by proteins with molecular masses between 18.5 and 22.5 KD. Although these investigators have attributed this inhibitory activity to a single protein with a mass of 20 kD, their results do not preclude the existence of several actin-binding proteins in the molecular mass region between 15.5 and 22.5 kD. Supporting the presence of multiple low molecular mass actin-binding proteins in crude membranes, we find that a crude membrane preparation similar to that used by Brown and Petzold contains at least three actin-binding proteins in this molecular mass region. Further investigation is necessary to explore any structural relationship between ponticulin and the protein(s) in the molecular mass region defined by Brown and Petzold.

We do not yet know how ponticulin interacts with other plasma membrane proteins or how the actin-binding activity of ponticulin is controlled. Considering its small size, we feel that ponticulin probably does not act as a complete transmembrane signaling unit. We propose that ponticulin may function as an intermediary protein such as the integral membrane protein, x, postulated by Bourguignon and Singer (1977). By binding to other membrane proteins and by providing a membrane attachment site for actin, ponticulin may act to transduce signals from one or more membrane receptors to the contractile elements of the cytoskeleton. Future studies will focus on further characterizing the actin-binding activity of ponticulin in vitro and in vivo.

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