Abstract. Ectopic expression of various members of the human carcinoembryonic antigen (CEA) family of intercellular adhesion molecules in murine myoblasts either blocks (CEA, CEACAM6) or allows (CEACAM1) myogenic differentiation. These surface glycoproteins form a subset of the immunoglobulin (Ig) superfamily and are very closely related, but differ in the precise sequence of their external domains and in their mode of anchorage to the cell membrane. CEA and CEACAM6 are glycophaspatidyl-inositol (GPI) anchored, whereas CEACAM1 is transmembrane (TM) anchored. Overexpression of GPI-linked neural cell adhesion molecule (NCAM) p125, also an adhesion molecule of the Ig superfamily, accelerates myogenic differentiation. The molecular requirements for the myogenic differentiation block were investigated using chimeric constructs in which the COOH-terminal hydrophobic domains of CEA, CEACAM1, and NCAM were exchanged. The presence of the GPI signal sequence specifically from CEA in the chimeras was sufficient to convert both CEACAM1 and NCAM into differentiation-blocking proteins. Conversely, CEA could be converted into a neutral protein by exchanging its GPI anchor for the TM anchor of CEACAM1. Since the external domains of CEA, CEACAM1, and NCAM can all undergo homophilic interactions, and mutations in the self-adhesive domains of CEA abrogate its differentiation-blocking activity, the structural requirements for differentiation-inhibition are any self-adhesive domains attached to the specific GPI anchor derived from CEA. We therefore suggest that biologically significant functional information resides in the processed extreme COOH terminus of CEA and in the GPI anchor that it determines.

Key words: CEA • GPI anchors • inhibition of differentiation • Ig superfamily • NCAM

Introduction

Carcinoembryonic antigen (CEA) is overexpressed in many human cancers, including those of colorectal, breast, and lung origins, and for 30 yr has been one of the most prevalent tumor markers (Averbach and Sugarbaker, 1995; Boucher et al., 1989; Ilantzis et al., 1997). CEA is the prototypic member of a large gene subfamily (Öbrink, 1997) of the Ig superfamily that includes CEACAM1 (formerly BGP) and CEACAM6 (formerly NCAM). CEACAM6, like CEA, is upregulated in human malignancies (Boucher et al., 1989; Hinoza et al., 1991; Ilantzis et al., 1997; Kim et al., 1992), whereas CEACAM1 is usually downregulated, suggesting that CEACAM1 could act as a tumor suppressor, as has been shown for the mouse and rat homologues of human CEACAM1 (Hsieh et al., 1995; Kleinerman et al., 1995; Kunath et al., 1995; Neuhaus et al., 1993). CEA, CEACAM1, and CEACAM6 all possess homotypic intercellular adhesion activity in vitro (Benchimol et al., 1989; Okawa et al., 1989; Rojas et al., 1990; Zhou et al., 1990). CEA and CEACAM6 are glycophaspatidyl-inositol (GPI)-linked to the cell surface (Helft et al., 1988, 1990; Takami et al., 1988), whereas CEACAM1 has transmembrane (TM) and cytoplasmic domains, features that correlate with observed differences in function to date (Rojas et al., 1996).

Myogenic fusion requires the functional integrity of...
cell–cell adhesion systems, such as the cadherins (N-cadherin, M-cadherin) and Ig superfamily adhesion molecules (N-CAM, vascular [V]CAM), and cell–ECM-binding interactions mediated by the integrin family, which includes VLA-4/α4β1 and αvβ3 (Kudsen, 1990). Overexpression of various splice variants of human NCA M accelerates myogenesis in mouse C2 myoblasts (Peck and Walsh, 1993; Dickson et al., 1990) and in transgenic mice (Fazeli et al., 1996). These include the p125 isoform, which possesses five Ig C2-like repeats, two partial non-RGD fibronectin type III–like domains, a 5-kD skeletal muscle-specific domain (Dickson et al., 1987), and a GPI anchor (Barton et al., 1988). We have demonstrated that ectopic expression of CEA and CEA CAM 6 disrupts the differentiation program of rat L6 myoblasts, whereas CEA CAM 1 and an adhesion-defective deletion mutant of CEA (ΔNCEA) were unable to inhibit differentiation (Eidelman et al., 1993; Rojas et al., 1996). These results are consistent with the observed upregulation of CEA and CEA CAM 6 and downregulation of CEA CAM 1 in human tumors. Moreover, CEA significantly reduces the latency required to form tumors in nude mice, and cooperates with M yc and B cl-2 in transformation; we have proposed that CEA’s differential gene blocking activity represents a novel contribution to oncogenesis (Screaton et al., 1997).

GPI proteins are specifically targeted to apical membranes and excluded from the basolateral membranes of polarized epithelial cells (Rodriguez-Boulan and Nelson, 1989). Conversely, proteins with a bona fide TM domain are generally transported to basolateral surfaces, by virtue of signals in their cytoplasmic domains. The lateral compartmentalization of GPI proteins within the lipid bilayer is initiated during membrane biosynthesis, and results not from protein–protein interactions, but from the preferential miscibility of the glycolipid moiety of the GPI anchor with sphingolipids and cholesterol, perhaps together with the hydrophobic COOH-terminal domain of CEA. C1–C was produced by ligation of nucleotides (nt) 1–1314 of CEA CAM 1-4L (the longest splice variant of CEA CAM 1, denoted C1-4L in Fig. 9 and with the basic structure shown therein) to nt 2106–3037 of CEA at HindIII sites introduced into both cDNAs at the specified positions. The C–C15 chimera consists of the external domains of CEA linked to the TM and short cytoplasmic domains of the CEA CAM 1 splice variant, CEA CAM 1-15; this chimera was generated by PCR overlap extension modeled after Sippel et al. (1996), as follows: a first round of PCR was performed using: (i) the CEA cDNA and 5’ outside primer 5’ T A G G G A T T C T C A T A T G C T G C A 3’ (nt 975–996, containing the underlined natural BamHI site) and internal antisense primer 5’ T G A G G G C A T T T T C G A C T G T A G G C T C T G C A T C A 3’ (corresponds to nt 992–1006 of CEA CAM 1-15 at the 5’ end and nt 2099–2018 of CEA at the 3’ end) to produce a 1.1-kb product, and (ii) the CEA CAM 1-15 cDNA and 3’ outside primer 5’ A G A A G A G C T C A G T C G A A A T G C C C T C T G C A T C A 3’ (antisense of the internal primer used in i, minus 5 nt at 5’ end) to produce a 0.3-kb product. A second round of PCR using the 1.1- and 0.3-kb round 1 products and the two outside primers listed above produced a 1.4-kb product, which was digested with BamHI (5’ end) and EcoRI (3’ end) and ligated to the 5’ end of the BamHI-digested CEA cDNA to produce C–C15.

N–C and C–N were generated using overlap extension as follows: at the ω-site in NCA M is unknown, we assigned it to be the last amino acid (A736) encoded by exon 14; thus the TM domain in NCA M begins at Thr737. Exon 14 is spliced onto the GPI-specific exon 16 in the p125 splice variant (Barton et al., 1988). Sequence alignment supports this as a possible ω-site (Udenfriend and Kodukula, 1995; Moran et al., 1991; Nuoffer et al., 1993). Other possible sites (Gly739, Gly740, Asn741, and Ser742) were excluded on the basis of nonconservation between chickens and humans in chemical cross-linking techniques, respectively (Friederichsen and Kurzchalia, 1998; Varma and Mayor, 1998). We have addressed the role of the external domains and the GPI anchor in the CEA-mediated myogenic differentiation block using chimeras between CEA, CEA CAM 1, and GPI-linked NCA M p125. We confirm that overexpression of NCA M accelerates myogenesis (Peck and Walsh, 1993), and report that the CEA, CEA CAM 1, or NCA M extracellular domains are sufficient to inhibit differentiation when attached specifically to a CEA GPI anchor. Conversely, replacing the GPI linkage of CEA with the TM domain of CEA CAM 1 cancels the differentiation block. These results lead to the following hypothesis: the differentiation inhibition activity of CEA requires the combination of CEA GPI linkage with any functional external self-adhesion domain. Since the COOH-terminal domain of CEA and not that of NCA M is necessary for the block, the GPI anchors that replace these domains harbor specific biological information.

Materials and Methods

Cell Culture and Differentiation Assay

CHO-derived LR-73 fibroblasts (Pollard and Stanners, 1979) were grown in monolayer in α–MEM plus 10% FBS in a humidified atmosphere of 5% CO2 at 37°C. Rat L6 (yaffe, 1968) myoblasts were grown as monolayer cultures in DME containing 10% FBS (growth medium) as previously described (Screaton et al., 1997). A II myoblast cultures were passaged while subconfluent to avoid selection of nonfusing variants. The differentiation/fusion assay was performed in DME plus 2% horse serum (differentiation medium) as previously described (Screaton et al., 1997); cultures were assessed for fusion after 4 d in differentiation medium.

Constructs

The CEA CAM 1–CEA (C1–C) chimera (Drăber, P., and C.P. Stanners, unpublished data) possesses the leader, N, A1B1, and A2 domains of CEA CAM 1 and six extracellular residues plus the hydrophobic COOH-terminal domain of CEA. C1–C was produced by ligation of nucleotides (nt) 1–1314 of CEA CAM 1-4L (the longest splice variant of CEA CAM 1, denoted C1-4L in Fig. 9 and with the basic structure shown therein) to nt 2106–3037 of CEA at HindIII sites introduced into both cDNAs at the specified positions. The C–C15 chimera consists of the external domains of CEA linked to the TM and short cytoplasmic domains of the CEA CAM 1 splice variant, CEA CAM 1-15; this chimera was generated by PCR overlap extension modeled after Sippel et al. (1996), as follows: a first round of PCR was performed using: (i) the CEA cDNA and 5’ outside primer 5’ T A G G G A T T C T C A T A T G C T G C A 3’ (nt 975–996, containing the underlined natural BamHI site) and internal antisense primer 5’ T G A G G G C A T T T T C G A C T G T A G G C T C T G C A T C A 3’ (corresponds to nt 992–1006 of CEA CAM 1-15 at the 5’ end and nt 2099–2018 of CEA at the 3’ end) to produce a 1.1-kb product, and (ii) the CEA CAM 1-15 cDNA and 3’ outside primer 5’ A G A A G A G C T C A G T C G A A A T G C C C T C T G C A T C A 3’ (antisense of the internal primer used in i, minus 5 nt at 5’ end) to produce a 0.3-kb product. A second round of PCR using the 1.1- and 0.3-kb round 1 products and the two outside primers listed above produced a 1.4-kb product, which was digested with BamHI (5’ end) and EcoRI (3’ end) and ligated to the 5’ end of the BamHI-digested CEA cDNA to produce C–C15.

N–C and C–N were generated using overlap extension as follows: at the ω-site in NCA M is unknown, we assigned it to be the last amino acid (A736) encoded by exon 14; thus the TM domain in NCA M begins at Thr737. Exon 14 is spliced onto the GPI-specific exon 16 in the p125 splice variant (Barton et al., 1988). Sequence alignment supports this as a possible ω-site (Udenfriend and Kodukula, 1995; Moran et al., 1991; Nuoffer et al., 1993). Other possible sites (Gly739, Gly740, Asn741, and Ser742) were excluded on the basis of nonconservation between chickens and humans.
chicken NCAM, Gal740, Aαn741, and Ser742 are Ser740, Pro741, and Ser742 (see Fig. 1). The presence of a proline residue at position 742 in chicken makes GPI substitution at these positions unlikely, if not impossible. The junction site between NCAM and CEA was selected to be six residues from the beginning of the TM domain, as for C1–C. For N–C, PCR was performed with the 5' primer GCA GTG ACA CGT CATG C3 (nt 2214–2231 of NCAM, containing a natural AspI site, underlined), and 3' primer 5' GAAG CTGGAGCTGGCAGG 3' (nt 2327–2339 NCAM 125), with an added HindIII site (underlined). After digestion with AspI and HindIII, this 0.13-kb fragment was ligated together with 2.2-kb SalI–AspI NCAM and 0.9-kb HindIII-EcoRI CEA fragments in one reaction into pBluescript (Stratagene). For N–C blunt, a first round of two PCR reactions was performed using CEA or NCAM template cDNA. For the NCAM template, the 5' outside primer was 5' GCA GTG ACA CGT CATG C3 (nt 2214–2231 of NCAM containing a natural AspI site, underlined), and for CEA the 3' anti-sense outside primer was 5' ATA GAA CTG AGG ATG C3 (sequence from pBluescript MCS containing a BamHI site, underlined). The inside primers were 5' AAGG AAGA AATTCCAGATGTGGAGATGCTG 3' (nt 2327–2339 of NCAM and 2014–2047 of CEA in both the anti-sense and sense directions, respectively). The second round of PCR used the two first round products, as described above for C–C–S. The final PCR product was digested with AspI and BamHI, and was cloned into pBluescript (N–C) at the corresponding AspI and BamHI sites, thus removing the fragment containing the HindIII site junction. All constructs were subcloned into the pRIO23B expression vector (courtesy of R. Kaufman, Genetics Institute, Boston, MA) for transfection.

Transfections

L6 myoblasts and LR-73 fibroblasts were seeded at 1.8 × 10^5, or 4 and 6 × 10^5 cells/100-mm dish, respectively, and cotransfected 24 h later by calcium phosphate coprecipitation with 5 μg of pRIO23B expression vector containing appropriate cDNA chimeras. L6 cells were transfected with AspI and HindIII, this 0.13-kb fragment was ligated together with 2.2-kb SalI–AspI NCAM and 0.9-kb HindIII-EcoRI CEA fragments in one reaction into pBluescript (Stratagene). For N–C blunt, a first round of two PCR reactions was performed using CEA or NCAM template cDNA. For the NCAM template, the 5' outside primer was 5' GCA GTG ACA CGT CATG C3 (nt 2214–2231 of NCAM, containing a natural AspI site, underlined), and for CEA the 3' anti-sense outside primer was 5' ATA GAA CTG AGG ATG C3 (sequence from pBluescript MCS containing a BamHI site, underlined). The inside primers were 5' AAGG AAGA AATTCCAGATGTGGAGATGCTG 3' (nt 2327–2339 of NCAM and 2014–2047 of CEA in both the anti-sense and sense directions, respectively). The second round of PCR used the two first round products, as described above for C–C–S. The final PCR product was digested with AspI and BamHI, and was cloned into pBluescript (N–C) at the corresponding AspI and BamHI sites, thus removing the fragment containing the HindIII site junction. All constructs were subcloned into the pRIO23B expression vector (courtesy of R. Kaufman, Genetics Institute, Boston, MA) for transfection.

FACS Analysis

Exponentially growing cultures were trypsinized (CEA family transfec-
tants) or incubated with PBS-citrate plus 4 mM EDTA (PBS-C-E) (NCAM p125 transfants) for 3–4 min at 37°C. NCAM is sensitive to trypsin, which removes a major 50-kD NCAM fragment (estimated from SDSPAGE mobility), reducing overall NCAM surface levels two to threefold (data not shown). 1.25 × 10^5 cells were resuspended in 0.25 ml ice cold PBS plus 2% FBS (PBSF) containing mAb bs J2 or ERIC-1 at a dilution of 1:50 to 1:100 for 30 min on ice. Cells were centrifuged, rinsed with 2 ml PBSF, and resuspended in 0.25 ml PBSF containing goat anti-
mouse FITC- or phycoerythrin-conjugated antibody (BIOCAN Scientific) diluted 1:100. A fter 30 min of incubation, cells were resuspended in 0.3 ml PBSF for cyttofluorometric analysis using a FACSscan® instrument (Becton Dickinson).

Triton X-100 Solubility Assay and Immunoblotting

Exponentially growing cultures were rinsed with PBS and rendered single cell suspensions by incubating with PBS-C-E for 4 min at 37°C, followed by passage once through a 27-gauge needle. Cell concentrations were determined using a particle counter (Coultuer Electronics, Inc.). Cell populations were resuspended at 10^6 cells/ml in ice cold isxy buffer (20 mM Tris, pH 8.0, 150 mM NaCl, and 2.5 mM EDTA plus protease inhibitors) containing 1% Triton X-100 (Sigma-Aldrich). Cells were sonicated with 10 and down strokes using a 27-gauge needle, and left at 0°C for 15 min. Solu-
table fractions were collected after 20 min of centrifugation at 13,500 g at 4°C. The pellets were resuspended in 0.9-vol isxy buffer without Triton X-100 and syringed 5 times at 0°C with a 23-gauge needle. 0.1 vol 10% SDS was added (equivalent cell concentration: 10^6/ml) before syringing 5 times with a 23-gauge needle, then 10 times with a 27-gauge needle (pellet fraction). Lysates of soluble and pellet fractions were normalized to surface expression level (from 10^6 [NCAM] to 2 × 10^7 [C1–4L] cell equivalents), resolved by SDS-PAGE, and transferred electrophoretically to a 0.45-μm PVDF membrane (Millipore) for immunoblotting. The following monoclonal antibodies were used: j22 for CEA, CEACAM6, C–C, C–N, and C–N; TEC-11 (Dráberova et al., 1997) for C1–4L and C1–C; and ERIC-1 for NCAM, N–C, and N–C blunt at a dilution of 1:1,000 for 1 h at 25°C in TBS-Tween 20M, and processed as previously described (Sreaton et al., 1997). For solubility determinations, increasing volumes of lysates were separated by SDS-PAGE and transferred to PVDF for immunoblotting. Mfilti tuple ECL exposures of each immunoblot were scanned and an-
alyzed with a DoBe Photoshop and NIH image 1.61 software. Solubility was determined using only values in the linear exposure range.

Adherent Cell PI-PLC Assay

Cells were seeded at 7 × 10^5/cm² in 24-well plates in αMEM on day 0 on day 2, exponentially growing cultures were rinsed twice with PBS, and incubated with 0.03–0.09 U bacterial phosphatidylinositol phospholipase C (PI-PLC; Boehringer M annheim) in 1:1 DME/PBS plus 0.2% BSA for 40 min at 37°C. The PI-PLC was removed, cultures were rinsed with PBS and rendered single cell suspensions by trituration after incubation with PBS-C-E at 37°C for 4 min. The cells were then processed for FACS analysis as above.

Adhesion Assays

A says were performed essentially as previously described (Zhou et al., 1993). In brief, 10 cells of LR 73 transfant cultures were seeded in 80-
cm² culture flasks (Nunc) on day 0. On day 2, cells (CEA family transfec-
tants) were harvested with BACOTO-Trynpsin (GIBCO BRL) for 3 min at 37°C or with PBS-C-E (N–C blunt). The cell suspensions were syringed up and down once through a 27-gauge needle before cell counting. 3 × 10^5 cells were resuspended in 3 ml of α-MEM plus 0.8 FBS plus 10 μg/ml Na2e s, and allowed to aggregate at 37°C with stirring at 100 rpm. A li-
quots were taken at the indicated time points and the percentage of single cells was determined visually in a hemocytometer.

Colocalization Assay

7 × 10^5 cells were seeded in 8-well chamber slides (Nunc) on day 0. On day 2, cells were rinsed with PBS and fixed with 4% paraformaldehyde for 20 min at room temperature before placing on ice, or else rinsed and placed on ice immediately to inhibit cellular metabolism and GPI protein mobility. Nonspecific antibody interactions were blocked with DME plus 5% goat serum (D GS) for 20 min before antibody addition. All antibody incubations were carried out for 30 min on ice, followed by 3 × 5 min rinsing with ice-cold D GS. Antibodies and dilutions were as follows: rabbit polyclonal anti-CEA (1:50), goat anti-rabbit-Cy2 conjugate (1:800), ERIC-1 (1:10), and goat anti-mouse-rodhamine conjugate (1:200). For patching, unfixed cells were incubated stepwise with the appropriate pri-
mary and secondary antibody combination to stain the first antigen, rinsed with D GS, and incubated at 37°C for 60 min to induce patch formation.
After patching, the cells were returned to ice for staining of the second antigen, as described above. Cells were fixed with 4% paraformaldehyde for 20 min at room temperature after staining, mounted, and viewed with a fluorescence microscope (Nikon).

Results

Synthesis and Characterization of COOH-terminal Domain Exchange Constructs

To determine the domains involved in the inhibition of myogenesis by CEA, chimeric constructs were constructed using CEA and CEACAM1 cDNAs in which the mode of membrane attachment was exchanged. We replaced the TM and cytoplasmic domains of CEACAM1–4L (C1–4L) with the 32 COOH-terminal residues of CEA, which possesses the CEA ω-site for GPI attachment, Ala677, to produce C1–C (Fig. 1). The reciprocal chimera, C–C1S, possesses the complete extracellular domains of CEA attached to the TM and short cytoplasmic domains (43 amino acids total) of the CEACAM1 1–1S splice variant (Barnett et al., 1993). The COOH-terminal sequence of the CEACAM 1–1S (C1-1S) splice variant with its short cytoplasmic domain of about eight residues was selected for use in the construction of C–C1S to most closely mimic a GPI anchor, i.e., a membrane attachment with no intracellular sequence information. Stable pooled transfectant populations or individual clones of L6 myoblasts (see Materials and Methods) expressing the chimeras at their surface were isolated, and the FACS profiles for these and all L6 transfectants used in this study are shown in Fig. 2.

Cell surface proteins that possess a TM domain are soluble in nonionic detergents such as Triton X-100 at 4 °C; insolubility under these conditions indicates that the protein may possess a GPI membrane anchor (Brown and Rose, 1992; Hooper and Bashir, 1991; Hooper and Turner, 1988). To determine if the membrane attachment modes were faithfully exchanged in the chimeras, we investigated the solubility of the CEA family members and C1–C and C–C1S in cold Triton X-100 (Fig. 3 A). CEA, CEACAM6, and C1–C detected by immunoblotting and quantitated by densitometric analysis were ≈10–20% soluble, supporting their GPI linkage, whereas C1–4L and C–C1S were >90% soluble, indicating that they both possess a TM anchor. All proteins were >90% soluble in octylglucoside (data not shown), which extracts GPI-linked proteins from Triton X-100-insoluble membrane domains (Brown and Rose, 1992). It was possible that, by overexpressing these GPI-linked proteins, they were saturating the glycosphingolipid rafts in which they are normally localized. However, we observed no change in solubility, for CEA at least, over the range of surface expression found in these transfectants (data not shown). To confirm the presence of a GPI anchor on the various constructs, we also investigated the sensitivity of each protein to bacterial PI-PLC, an enzyme...
that digests the phosphate-glycerol ester linkage of GPI anchors. Sensitivity of a cell surface molecule to PI-PLC treatment can be measured as a reduction in its cell surface level by cytofluorometry (Lisanti et al., 1990). We observed that the GPI proteins under investigation had different sensitivities to PI-PLC when treated in monolayer culture or in suspension after EDTA or trypsin treatment (data not shown). We therefore chose to treat cells with PI-PLC in monolayer culture to test their sensitivity in a physiologically normal state during their growth phase. L6 transfectants were treated with PI-PLC, labeled with appropriate monoclonal antibodies, and analyzed by FACS (Fig. 3 B). PI-PLC partially removed surface-bound CEA, C1–C, and C–C1S to PI-PLC (+) or no treatment (−), including vector only controls (neo), as assessed by FA CS analysis.

**Chimeric Constructs Retain Homotypic Adhesion Function**

Previous results demonstrated a requirement for intact CEA extracellular adhesion domains to block differentiation (Eidelman et al., 1993). We thus examined the aggregation properties of total transfectant populations of the nonaggregating CHO fibroblast cell line, LR-73, expressing C1–C and C–C1S at their cell surface (Fig. 4 A). Single cell suspensions of all transfectants, including the LR(CEA) and LR(C1–4L) positive controls, aggregated readily at 37°C (Fig. 4 C). Transfectants with the neo vector alone did not aggregate appreciably. The extent of aggregation was greater for C1–C than C–C1S (14 vs. 27% single cells at 2 h), which was probably due to differences in levels of surface expression (FACS mean fluorescence values of 600 vs. 200, respectively). Thus, both C1–C and C–C1S chimeras retained homotypic adhesion function, indicating self-binding of their extracellular domains, and could be used to test for the role of the mode of membrane attachment in inhibiting myogenic differentiation.

**Effect of Mode of Membrane Attachment on L6 Differentiation**

L6 myoblast transfectants were grown to confluence in growth medium and tested for their ability to differentiate by incubation in low growth factor–containing differentiation medium. Fig. 5 shows photomicrographs of the cultures after 4 d in differentiation medium, at which time both the neo control and L6(C1–4L) cultures showed extensive cell fusion and myotube formation. L6(CEA) cultures, however, consisted of single cells, indicating blocked cell fusion. Interestingly, L6(C1–C1S) cultures formed myotubes, whereas cultures of L6 cells expressing the GPI-linked C1–C, even at lower cell surface levels than C–C1S or CEA (Fig. 2), like L6(CEA) remained completely as single cells (Fig. 5 and Table I). This indicates a direct correlation between GPI anchorage of CEA and differentiation-blocking ability.

**Effect of Type of GPI Anchor on Adhesion and Differentiation**

To confirm the specificity requirements of the extracellular adhesive domains and to test for the necessity of the CEA GPI anchor, chimeric constructs between CEA and the p125 GPI anchored isoform of the more distantly related Ig family member, NCAM, were generated. The COOH-terminal hydrophobic domains and six extracellular amino acids of CEA (as in C1–C) and NCAM were exchanged, to produce N–C and C–N. A construct, N–C blunt, with no extracellular residues from CEA, was also prepared (Fig. 1). Stable pooled transfectant populations

| Cell                | % Fusion* |
|---------------------|-----------|
| L6(neo)             | 70        |
| L6(CEA)             | 0         |
| L6(C1–4L)           | 84        |
| L6(C–C1S)           | 60        |
| L6(C1–C)            | 0         |
| L6(NCAM)            | 100       |
| L6(NC)              | 0         |
| L6(NC blunt)        | 0         |

*Fusion indices provide a measure of myogenic differentiation and were measured as the % of total cells having three or more nuclei, as described previously (Eidelman et al., 1993).
of L6 myoblasts expressing cell surface NCAM and N–C (Fig. 2) and of L6 and LR-73 cells expressing N–C blunt (Figs. 2 and 6) were isolated. No clones showing cell surface expression transfected with the C–N cDNA could be isolated; Western blot analysis and immunofluorescence data demonstrated that the C–N protein was synthesized but accumulated in the ER compartment (data not shown). NCAM, N–C, and N–C blunt were mainly insoluble in cold Triton X-100 (Fig. 6, upper left, ~25% soluble), and sensitive to PI-PLC (Fig. 6), indicating a GPI membrane attachment. Therefore, cold Triton X-100 solubility and PI-PLC treatment do not distinguish biochemically between the GPI membrane anchors of CEA and NCAM.

The adhesion domain of human NCAM has been narrowed to a decapeptide sequence, residues 243–252, present in the third Ig domain, similar to chicken NCAM (Rao et al., 1992; Siu, C.-H., personal communication). We verified that NCAM extracellular sequences retain homotypic adhesion ability when linked to the cell membrane with a CEA GPI anchor by performing an aggregation assay, using LR-73(N–C blunt) cells together with neo (vector alone) and CEA CA M 1–4L as negative and positive controls, respectively. Fig. 4 D shows that N–C blunt mediated aggregation of LR fibroblasts efficiently under these conditions (8% single cells at 2 h), indicating that the presence of NCAM Ig domains are sufficient to mediate homotypic adhesion in the chimera.

L6(NCAM), L6(N–C), and L6(N–C blunt) myoblasts were tested for their ability to differentiate by fusion into myotubes in differentiation medium (Fig. 7 and Table I). L6(neo) and L6(NCAM) cells differentiated readily, with a moderate increase in the rate of L6(NCAM) fusion (data not shown). However, L6(N–C) and L6(N–C blunt), like L6(CEA) cultures, were completely blocked in their ability to differentiate, forming no myotubes whatsoever (Table I). The cell surface expression levels of N–C blunt and N–C bracket those of CEA and both are lower than that of NCAM (Fig. 2), so that the differentiation-inhibitory effects of the CEA GPI anchor cannot be ascribed to higher expression levels of the hybrid constructs. These results

Figure 4. C–C1S and C1–C retain homotypic adhesion function, and NCAM sequences confer homotypic adhesion ability to N–C blunt. (A and B) FACS profiles showing cell surface expression of CEA family members and chimeras in LR73 control cells (neo) and LR73 transfectant cells. (C) Adhesion assay for LR73 control (neo) and transfectant populations by the kinetics of aggregation in suspension. (D) Adhesion assay for LR(N–C blunt) transfectants, harvested with EDTA to avoid proteolysis by trypsin of NCAM sequence, together with neo and C1–4L controls. C–C1S, C1–C, and N–C blunt were pooled transfectant populations, whereas the CEA and C1–4L positive controls were representative clones.
confirm that ectopic expression of GPI-linked p125 can accelerate myoblast fusion (Dickson et al., 1990), and demonstrate that NCAM or C1–4L extracellular domains can substitute for those of CEA, and can block fusion, provided they are linked to a CEA-derived GPI anchor. Thus, the specificity of the differentiation block resides in the extreme COOH terminus of CEA.

**Cell Surface Distribution of GPI-linked NCAM and CEA**

We hypothesized that CEA and NCAM p125, which although both GPI-linked exert opposite phenotypic effects on L6 differentiation, could be distributed differently on the surface of L6 myoblasts as a manifestation of their presumably different GPI anchors. Such a differential distribution might influence their respective molecular interactions, and explain their different biological effects. Therefore, we analyzed the cell surface distribution of CEA and NCAM for overlapping localization in transfected cells expressing both CEA and NCAM, L6 (CEA + NCAM). In cells fixed with paraformaldehyde before labeling with fluorescent antibodies, both CEA and NCAM showed diffuse, finely punctate staining throughout the cell surface (Fig. 8, a and b), in agreement with previous analyses (Fujimoto, 1996; Mayor and Maxfield, 1995; Harder et al., 1998). A reas of segregation of the two antigens were easily discernible, which suggested that the antigens were not colocalized. To clarify this question, we cross-linked CEA and NCAM one at a time in unfixed L6(CEA + NCAM) cells at 37°C with specific antibodies to consolidate their fluorescent signals into patches, and looked for areas of overlap after patching. If there were no association between the two proteins sufficient to result in colocalization, the steady-state distribution of NCAM should be unaffected by the patching of CEA, and vice versa. After using anti-CEA antibody to cross-link CEA, the CEA fluorescence pattern was no longer diffuse, but concentrated in patches (Fig. 8 c). However, the distribution of NCAM was diffuse and different after patching of CEA (Fig. 8 d). Similar results were seen when the reciprocal experiment was performed (NCAM patched, CEA...
unpatched; Fig. 8, e and f). Although patching of one antigen is insufficient to induce copatching of the second, it is possible that both CEA and NCAM are present in the same rafts, but in separate lipid environments within these rafts, which themselves are only weakly associated. This caveat notwithstanding, we conclude that CEA and NCAM are present in different raft domains. This is consistent with their radically different biological effects.

Discussion

Previous work on the structural requirements for the inhibition of myogenic differentiation by CEA showed the necessity of self interaction of the extracellular domains (Eidelman et al., 1993). A GPI-linked adhesion-defective mutant of CEA (ΔNCEA), lacking a large portion of the N domain, did not block differentiation, and the addition of soluble peptides corresponding to the CEA adhesion domains restored myogenic fusion in L6(CEA) cells. Moreover, recent work has shown that single amino acid substitutions in the N domain that affect the adhesion function can abrogate the differentiation blocking activity (Taheri et al., 2000). We subsequently demonstrated that, although both CEA CAM6 and all CEA CAM1 splice variants also mediate cell aggregation, only GPI-linked CEA CAM6, like CEA, could block differentiation, whereas all of the TM-linked CEA CAM1 isoforms could not (Rojas et al., 1996). These observations prompted the current investigation of the specific structural features of CEA required to inhibit myogenic differentiation.

The L6 Myoblast System

The adequacy of the experimentally convenient L6 myoblast differentiation system as a test system having biological relevance deserves comment. The effects of CEA on L6 myoblasts have also been observed in other cellular systems. Thus, CEA disrupts adipogenic differentiation (3T3-L1/2 and 3T3L fibroblasts) and neurogenic differentiation (retinoic acid–treated P19 EC cells), and deregulate overexpression (i.e., before polarization and crypt-like formation) both of CEA and CEA CAM6 inhibits colonocyte polarization and tissue architecture in vitro and in vivo (DeMarte, L., and C.P. Stanners, unpublished results; Ilantzis, C., L. DeMarte, R.A. Screaton, and C.P. Stanners, manuscript submitted for publication; Malette, B., and C.P. Stanners, manuscript submitted for publication); in addition, anoikis, an apoptotic mechanism of maintaining tissue architecture by killing cells not properly bound to their underlying matrix, is also inhibited in L6 myoblasts and in human colonocytes (Ordoñez et al., 2000). These results indicate that the findings in the L6 model system also apply to more biomedically relevant systems. In further support of this suggestion, we have recently shown that the CEA GPI anchor interacts with a molecular system common to all of these pleiotrophic and multiple system effects. Thus, recent evidence indicates perturbation of the function and/or regulation of specific integrin ECM receptors as the underlying cause of the inhibition of both differentiation and anoikis by CEA and CEA CAM6 in L6 myoblasts, P19 EC cells, and human colonocytes (Ordoñez, C., R.A. Screaton, C. Ilantzis, M. Fan, L. DeMarte, and C.P. Stanners, manuscript submitted for publication; Malette, B., and C.P. Stanners, manuscript submitted for publication).

The CEA GPI Anchor Is Required to Inhibit Differentiation

A summary of the results of the domain-exchange experiments between CEA, CEA CAM1, and NCAM is shown.
The GPI-linked CEACAM1 chimera, C1-C, inhibited differentiation, indicating that CEA extracellular sequences can be functionally substituted by those of CEACAM1, provided they have the GPI linkage of CEA. Importantly, the reciprocal construct, a TM-linked CEA, C–C1S, allowed fusion to proceed, confirming that the extracellular domains of CEA alone are insufficient to inhibit differentiation and demonstrating that CEA retains this function only when GPI anchored. C–C1S can mediate homotypic intercellular adhesion (Fig. 4), demonstrating that CEA extracellular domains do not require the GPI anchor for self binding.

The p125 isoform of human NCAM is a GPI-linked Ig superfamily member that mediates homotypic intercellular adhesion through its third IgC domain (Siu, C.-H., personal communication). NCAM p125, unlike CEA and CEACAM6, accelerates fusion in L6 myoblasts (Fig. 7 and Screaton, R.A., and C.P. Stammers, unpublished observations), as in C2 myoblasts (Peck and Walsh, 1993), indicating the specificity of the CEA effect. The high degree of homology between the adhesion domains of CEA and CEACAM1 (>70%) could have accounted for the ability of CEACAM1 extracellular domains to substitute for those of CEA in the C1-C construct. The most highly related amino acid sequences of NCAM and CEA, however, show <30% homology (NCAM 3, 4, and 5, versus CEA B1-A2-B2 IgC domains). Thus, it is intriguing that replacing the COOH-terminal GPI signal sequence of NCAM with that of CEA converts NCAM into a differentiation-inhibiting molecule. NCAM sequences provide a homotypic adhesion function when attached to the CEA GPI signal sequence (Fig. 4), allowing NCAM extracellular domains to substitute for CEA extracellular domains. Given that the extracellular sequences from CEA, CEACAM1, and NCAM can all contribute to the differentiation inhibition phenotype, we conclude that any sequence able to confer homotypic adhesion is required, but that the specificity for the inhibition of differentiation resides in the specific GPI anchor of CEA. By extension, the latter specificity would also reside in the GPI anchor determined by CEACAM6 (Fig. 9).

Figure 7. Inhibition of myogenic differentiation requires the specific GPI-determining COOH-terminal domain of CEA. Photomicrographs of neo, CEA, NCAM p125, and N–C and N–C blunt L6 transfectant cultures incubated for 4 d in differentiation medium. Neo and NCAM cultures differentiate into myotubes in differentiation medium, whereas CEA, N–C, and N–C blunt transfectants remain as single cell populations. Thus, acquisition of the COOH-terminal domain of CEA by NCAM p125 converts NCAM into a differentiation-blocking protein.
GPI Anchors as Gain of Function Structures

Aside from the biological specificity observed here in different GPI anchors derived from different COOH-terminal domains, there is precedent for the fact that the mode of membrane linkage (GPI versus TM) per se can affect protein function. Thus, the cellular isoform of the prion protein requires a GPI signal sequence for conversion to the infectious scrapie isoform; a TM form not targeted to rafts cannot adopt the pathogenic conformation (Kaneko et al., 1997). GPI functional dependency has also been reported for the folate receptor (Wang et al., 1996), murine DAF (Song et al., 1996), and the lymphocyte surface antigens Qa-2 and Ly6 (Robinson et al., 1989; Su et al., 1991). Replacing the GPI anchor of Qa-2 and Ly-6 with a TM sequence abrogates their ability to stimulate T cell activation, whereas replacing the TM domain of the signaling incompetent H-2 protein with a GPI anchor from Qa-2 generates a signaling-competent protein. In some cases, GPI/TM anchor exchange has no measurable effect on function, as shown for CD14 and tissue factor (Lee et al., 1993; Paborsky et al., 1991). Our data provides additional evidence that a GPI membrane attachment can be a gain of function structure.

Membrane Localization May Explain Opposite Effects of TM and GPI CEA Family Members

Extensive evidence suggests that asymmetries in lipid composition in cell surface membranes can affect localization of membrane proteins, exemplified by the mutual affinity of sphingolipids/cholesterol found in raft domains and the highly saturated lipid components of the GPI anchor itself (Simons and Ikonen, 1997). We propose that the ability of the GPI-linked CEA family members to inhibit differentiation stems from changes in the repertoire of membrane elements available for interaction due to altered membrane localization. Neither CEACAM1 nor C-C1S, both TM proteins, inhibit myogenesis, and both are soluble in cold Triton X-100 (Fig. 3), suggesting that the TM domain guides these proteins into an area of the membrane distinct from the GPI-anchored proteins under investigation. Interestingly, the localization of the TM protein influenza virus hemagglutinin in rafts is dependent on specific amino acid residues found in the exoplasmic half of the membrane-spanning region, residues expected to be in contact with DIG lipids (Scheiffele et al., 1997). However, apical targeting of hemagglutinin in epithelial cells requires these same residues as well as residues towards the COOH-terminal end of the TM domain (Lin et al., 1998).

How does CEA, lacking proteinaceous intracellular domains, transmit information leading to biological responses? The colocalization and coimmunopurification of GPI proteins, second messengers, and src-family kinases in membrane rafts, areas which generally exclude TM proteins, has suggested a localization-dependent mechanism whereby GPI proteins may participate in signaling (Brown, 1993; Malek et al., 1994). In hematopoietic systems, cross-linking of GPI proteins results in calcium mobilization, cytokine production/release, and proliferative activity (Rob-
Cross-linking of cell surface CEA in rat basophilic leukemia transfectant cells can elicit protein tyrosine phosphorylation of intracellular targets via src-family kinases, events which require the GPI anchor (Dráber, P., and C.P. Stanners, unpublished results). The requirement for cross-linking suggests that aggregation of GPI proteins into high molecular weight complexes containing their signaling partners is a prerequisite for signaling, as has been demonstrated for exogenous DAF "painted" (by exogenous addition) into U937 cell surface membranes (van den Berg et al., 1995).

Specific Raft Domains?

The above considerations pertain to changes in protein function resulting from TM/GPI exchanges. We show here that there exists specificity conferred by the GPI anchor of CEA that is not present in the GPI anchor of NCAM, even where both are attached to the same external domain. How could two proteins, functionally distinguishable only by their GPI anchors, send specific signals, even those eliciting opposite cellular responses? Evidence presented here that CEA and NCAM p125 could be localized to different rafts in L6 cells could be interpreted to indicate that there are distinct raft domains that are able to selectively concentrate different GPI proteins. (As mentioned in Results, this interpretation depends on the assumption that the clustering forces mediated by the antibodies did not pull truly colocalized CEA and NCAM p125 molecular complexes apart.) A consequence of selective localization would be that CEA, through interactions with signaling components unique to a specific membrane subdomain, could elicit distinct responses from other GPI proteins, e.g., NCAM. Therefore, biological specificity could be determined by differences in the membrane microenvironment in which the GPI anchor is found. The recent demonstration in living cells that GPI proteins exclusively reside in submicron scale domains, ~70 nm in diameter, that contain from 15 to 50 GPI-anchored molecules (Friederichson and Kurzchalia, 1998; Varma and Mayor, 1998), suggests that two different GPI proteins may be found in separate compartments at the cell surface. Contrary to our results with CEA and NCAM, Harder et al. (1998) demonstrated that the GPI proteins PLAP and Thy-1 copatch at the surface of BHK cells when simultaneously cross-linked. However, only variable copatching was seen when one protein was patched alone before staining of the second—a result which was attributed to hindered accessibility of antibody against the second antigen, presumed already to be in the patches. We would otherwise interpret these observations as additional evidence of unique raft domains.

Do Individual GPI Anchors Possess Specific Biological Information?

The ability of the COOH-terminal sequence of CEA to confer the differentiation-blocking activity to CEA CAM1...
and NCA M poses two questions: first, is there information in the structure of GPI anchors themselves which is capable of conferring specific biological function? Second, how could specific information found in GPI anchors be determined by the COOH-terminal hydrophobic sequence? For the latter, it is possible that the signal sequence at the extreme COOH terminus directs the protein to a specific GPI transamidase activity in the ER, which in turn directs selective modification of the anchor, or that the signal sequence determines the timing of such modifications resulting in changes to their extent. Regarding the former question, GPI anchors vary in the number and specific composition of additional glycan side chains which may be appended to the core anchor glycan structure (Lisanti et al., 1990). Different glycoforms of the GPI anchor on two NCA M isoforms in C2 myoblasts have been found (Mukasa et al., 1995), indicating that different anchor constituents can coexist in the same cell. GPI anchors of DAF and acetylcholinesterase are commonly modified by acylation of the inositol ring, which makes them resistant to PI-PLC treatment (R oberts et al., 1988; Walter et al., 1990). Interestingly, whether or not DAF is inositol acylated depends on the cellular context, suggesting that different cells can attach different anchors to the same protein precursor (Walter et al., 1990). Possibly an unknown substitution (mannosylation, ethanolamine, lipid modification) of the CEA anchor itself could confer specific information. Controlled release of GPI proteins by PI-PLC or PI-PLD would produce free membrane-bound GPIs, which are known to act as hormone-induced second messengers in cell signaling processes (Gaulton and Pratt, 1994). Moreover, a free GPI toxin from the malarial parasite Plasmodium initiates a protein tyrosine phosphorylation cascade that induces the upregulation of ICA M1, VCA M1, and E-selectin in endothelial cells (Schofield et al., 1996). The CEA effect on differentiation appears to depend on information provided by the adhesion property of the molecule, however, suggesting that the mechanism of inhibition involves more than a cleavage product of the CEA anchor. A laterally, the adhesion function may serve to increase the local concentration of CEA before a cleavage event, resulting in a greater impact of the released anchor on signaling. GPI proteins that act as cellular receptors are endocytosed through caveolae, microinvaginations of the plasma membrane, which may serve as focal points to effect a higher local concentration of ligand. In conclusion, there is ample precedent for significant secondary modifications in GPI anchors that could determine which membrane microdomains they associate with, thereby determining their biological specificity.

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