A Chromatin Binding Site in the Tail Domain of Nuclear Lamins That Interacts with Core Histones

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Abstract. Interaction of chromatin with the nuclear envelope and lamina is thought to help determine higher order chromosome organization in the interphase nucleus. Previous studies have shown that nuclear lamins bind chromatin directly. Here we have localized a chromatin binding site to the carboxyl-terminal tail domains of both A- and B-type mammalian lamins, and have characterized the biochemical properties of this binding in detail. Recombinant glutathione-S-transferase fusion proteins containing the tail domains of mammalian lamins C, B1, and B2 were analyzed for their ability to associate with rat liver chromatin fragments immobilized on microtiter plate wells. We found that all three lamin tails specifically bind to chromatin with apparent Kds of 120–300 nM. By examining a series of deletion mutants, we have mapped the chromatin binding region of the lamin C tail to amino acids 396–430, a segment immediately adjacent to the rod domain. Furthermore, by analysis of chromatin subfractions, we found that core histones constitute the principal chromatin binding component for the lamin C tail. Through cooperativity, this lamin–histone interaction could be involved in specifying the high avidity attachment of chromatin to the nuclear envelope in vivo.

The nuclear lamina is a filamentous protein meshwork that lines the nucleoplasmic surface of the nuclear envelope (NE)1 (reviewed by Gerace and Burke, 1988; McKeon, 1991; Nigg, 1992; Georgatos et al., 1994). The lamina is thought to provide a structural framework for the NE and an anchoring site at the nuclear periphery for interphase chromosomes, and therefore could play a major role in interphase nuclear organization. The lamina consists of a polymeric assembly of nuclear lamins, members of the intermediate filament (IF) protein superfamily (see McKeon, 1991; Nigg, 1992), as well as a number of less abundant lamina-associated polypeptides (discussed by Gerace and Foisner, 1994). Vertebrate lamins are classified as A- or B-subtypes based on their sequence and biochemical properties. B-type lamins (lamins B1 and B2) are present in somatic cells throughout development, while A-type lamins (lamins A and C) are expressed only during or after terminal differentiation in most cells. Mammalian lamins A and C appear to be alternative splice products of the lamin A gene. They are identical for the first 566 amino acids, and contain unique carboxyl termini of 98 residues and 6 residues, respectively. By contrast, the two mammalian B-type lamins of somatic cells are the products of separate genes (Hoger et al., 1990). Additional alternative splice variants of the lamin A and lamin B2 genes have been characterized in mammalian germ cells (Furukawa and Hotta, 1993; Furukawa et al., 1994).

Like other IF proteins, lamins consist of a central α-helical rod domain flanked by an NH2-terminal “head” domain and a COOH-terminal “tail” domain (see McKeon, 1991; Nigg, 1992; Heins and Aebi, 1994). Vertebrate lamins are classified as A- or B-subtypes based on their sequence and biochemical properties. B-type lamins (lamins B1 and B2) are present in somatic cells throughout development, while A-type lamins (lamins A and C) are expressed only during or after terminal differentiation in most cells. Mammalian lamins A and C appear to be alternative splice products of the lamin A gene. They are identical for the first 566 amino acids, and contain unique carboxyl termini of 98 residues and 6 residues, respectively. By contrast, the two mammalian B-type lamins of somatic cells are the products of separate genes (Hoger et al., 1990). Additional alternative splice variants of the lamin A and lamin B2 genes have been characterized in mammalian germ cells (Furukawa and Hotta, 1993; Furukawa et al., 1994).

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Like other IF proteins, lamins consist of a central α-helical rod domain flanked by an NH2-terminal “head” domain and a COOH-terminal “tail” domain (see McKeon, 1991; Nigg, 1992; Heins and Aebi, 1994). The head domain of vertebrate lamins is usually ~30 amino acids, while the tail domain is typically ~180–275 residues. The basic lamin protomer is a homotypic dimer formed by parallel, unstaggered association of the rod domain to form a two-stranded coiled-coil α-helix. This subunit, which forms a rod-like structure with a length of ~50 nm, engages in both head-to-tail and lateral interactions to form lamin filaments and related structures with an axial periodicity of ~25 nm (Aebi et al., 1986; Gieffers and Krohne, 1991; Heitlinger et al., 1991; Moir et al., 1991). Thus, discrete regions of the lamin molecules (e.g., tail domains) are displayed at repeating intervals along lamin filaments. In vitro assembly studies with mutant lamins have shown that both the rod domain and head and tail domains are involved in filament formation (Gieffers and Krohne, 1991; Moir et al., 1991; Heitlinger et al., 1992).

The major functions of the lamina are likely to involve

1. Abbreviations used in this paper: GST, glutathione-S-transferase; IF, intermediate filament; NE, nuclear envelope; NLS, nuclear localization sequence.
expressions of fusion proteins and recombinant lamin

Materials and Methods

Expression of Fusion Proteins and Recombinant Lamin Fragments in Escherichia coli

cDNA clones for human lamins A and C were provided by the laboratory of Dr. G. Blobel (Rockefeller University, NY), and cDNA clones for mouse lamins B1 and B2 were obtained from Dr. G. Krohne (University of Würzburg, Germany). Lamin fragment sequences were amplified by PCR, using synthetic oligonucleotide primers flanked by sequences for restriction enzymes sites for cloning into the expression plasmid pGEX-4T (Pharmacia LKB Biotechnology, Piscataway, NJ).

Polypeptides were expressed in the E. coli strain BL21 (Novagen, Inc., Madison, WI). Single colonies from transformed bacteria were grown to an A600 of 0.5-0.7 at which point expression was induced by addition of 2 mM IPTG. Bacterial growth was continued another 2 h. Purification of recombinant polypeptides was performed by a modified procedure used to attach the DNA to microtiter wells, which involved adsorption of lightly biotinylated DNA to streptavidin-coated plates. This is because purified DNA did not significantly bind to microtiter wells under the conditions where purified proteins and protein–DNA complexes were efficiently adsorbed (see above).

Individual binding experiments shown in this paper were carried out at 34°C.
Other Procedures

Protein concentrations were determined with a Bio-Rad protein assay kit. SDS-PAGE was performed by the method of Laemmli (1970).

Results

Analysis of Binding of the Lamin Tail Domain to Chromatin with a Solid Phase Assay

We developed a quantitative binding assay to investigate a possible interaction between the tail domains of nuclear lamins and chromatin. Previous studies of the lamin-chromatin interaction have involved intact lamins and lamin fragments containing the α-helical rod domain (Burke, 1990; Glass and Gerace, 1990; Hoger et al., 1991; Yuan et al., 1991; Glass et al., 1993). Since these proteins are insoluble under conditions of physiological salt and pH due to the strong tendency of the rod to self-associate, they are difficult to use for quantitative binding studies. Moreover, they generally require the use of buffers containing denaturants (e.g. urea) for isolation, and their capacity for complete in vitro renaturation after these treatments is unknown. By contrast, we found that the lamin tail domains can be expressed as soluble fusion proteins in E. coli and purified under non-denaturing conditions. Since the tail domains do not strongly self associate, it was feasible to use recombinant fusion proteins containing the lamin tail domains for saturation binding analysis with isolated chromatin fragments. We immobilized the chromatin fragments on the surfaces of microtiter wells to analyze binding using a solid phase assay, because the strong tendency of chromatin to aggregate in physiological buffers (van Holde, 1989) made it difficult to carry out reproducible binding assays in solution. By contrast, the solid phase assay was highly reproducible (see Materials and Methods) and permitted the rapid analysis of a large number of samples.

Interphase chromatin used for these binding studies was prepared by micrococcal nuclease digestion of isolated rat liver nuclei followed by sucrose gradient centrifugation of the nuclease-released material (Fig. 1 A). The peak gradient fractions that were pooled and used for the binding studies (fractions 8–10) contained ~6–10-kb fragments of DNA, corresponding to 30-50 nucleosomes (Fig. 1 B). The overwhelmingly major proteins in these fractions were histone H1 and core histones (Fig. 1 C). Tail domains of lamins were expressed in E. coli as glutathione-S-transferase (GST) fusion proteins, which were purified from soluble bacterial extracts using glutathione affinity columns. The recombinant proteins that we analyzed were

![Image](A) Preparation of interphase chromatin and recombinant fusion proteins containing the lamin tail domains. (A) Sucrose gradient sedimentation of chromatin fragments released from rat liver nuclei by micrococcal nuclease digestion. Chromatin was sedimented on a 10–50% sucrose gradient, and DNA was measured by absorbance at 260 nm. (B) Agarose gel electrophoresis of DNA present in different chromatin fractions. DNA from the peak region of the sucrose gradient (fractions 6–13) was analyzed by electrophoresis on a 0.3% agarose gel. (C) SDS–gel electrophoresis of proteins present in different chromatin fractions. Aliquots of sucrose gradient fractions 6–13 were analyzed on a 15% SDS–polyacrylamide gel, and proteins were visualized by Coomassie blue staining. (D) SDS–gel electrophoresis of purified recombinant GST–lamin tail fusions and GST. About 3 μg of each protein was analyzed on a 12% SDS–polyacrylamide gel. Lane 1, GST–lamin C tail (389–572); lane 2, GST–lamin B1 tail (391–588); lane 3, GST–lamin B2 tail (382–596); lane 4, GST.
GYT–lamin C tail (residues 389–572), GST–lamin B1 tail (residues 391–588), GST–lamin B2 tail (residues 382–596) and GST alone. The GST and GST–lamin C tail obtained in this fashion were mainly intact and migrated as single major bands at the expected mobilities, while the GST–lamin B1 tail and GST–lamin B2 tail preparations contained intact fusion protein and some faster migrating degradation products (Fig. 1 D).

In initial studies where immobilized chromatin was incubated with 2 μg/ml 125I-labeled GST–lamin C tail, GST–lamin B1 tail, or GST–lamin B2 tail, each of the three proteins bound to the chromatin at significant levels (Fig. 2 A). By contrast, very little radiolabeled GST by itself (<10% of the amount of the lamin tail constructs) associated with chromatin (data not shown). A substantial fraction of the GST–lamin tail binding appeared to be specific, since association of the radiolabeled ligand was competed by ~50% with a 50-fold excess of added nonradiolabeled GST–lamin tail constructs, but was not significantly competed with a 50-fold excess of nonradiolabeled GST (Fig. 2 A). The residual binding obtained with 2 μg/ml radiolabeled ligand and a ~50-fold excess of unlabeled ligand was used as nonspecific background for the calculations in this study (see Materials and Methods).

The binding of the radiolabeled GST–lamin C tail construct to chromatin in the presence or absence of a 50-fold excess of nonradiolabeled competitor was examined under a variety of solution and washing conditions to further characterize this interaction (Fig. 2 B). Binding was similar in solutions containing either 5 mM MgCl₂, 5 mM EDTA, or 5 mM EGTA, indicating that binding of the lamin tail to chromatin does not require divalent cations. Inclusion of 1% Triton X-100 in the standard assay decreased the specific binding about threefold. By contrast, most binding persisted when wells were washed with 0.25–1.0 M NaCl, and about 70% of the specific binding remained after washing in buffer containing 1.0 M NaCl. Analysis of a time course of the GST–lamin tail binding to chromatin showed that the maximal levels of binding were obtained at ~90–120 min (Fig. 2 C).

We then analyzed in detail the binding of GST–lamin tail constructs to immobilized chromatin by examining the displacement of radiolabeled constructs with increasing concentrations of the corresponding unlabeled polypeptides (Fig. 3). For all three lamin constructs, half maximal displacement of the labeled polypeptide in the concentration range tested (up to ~117 μg/ml) was achieved at ~7–12 μg/ml unlabeled competitor. Data from these displacement experiments was expressed as linearizing plots for single site competitive interactions (Hulme and Birdsell, 1992). This analysis indicated that the GST–lamin C tail, GST–lamin B1 tail and GST–lamin B2 tail interacted with single classes of sites in chromatin with apparent Kₘ values of 300, 120, and 230 nM, respectively. Since the percentage of native protein in these preparations is unknown, and since the preparations of GST–lamin B1 tail and GST–lamin B2 tail contained significant amounts of degradation products as well as intact proteins, these values should be regarded

Figure 2. Characterization of lamin tail–chromatin binding. (A) Chromatin binding of 125I-labeled GST–lamin C tail, GST–lamin B1 tail and GST–lamin B2 tail. 125I-labeled fusion proteins (2 μg/ml) in binding buffer were incubated in microtiter wells containing immobilized chromatin fragments for 120 min (standard binding assay; see Materials and Methods) in the absence (open bars) or presence (solid bars) of a 50-fold excess of corresponding unlabeled polypeptides, or in the presence of a 50-fold excess of GST (hatched bars). (B) Binding to chromatin of 125I-labeled lamin C tail under different solution and wash conditions. 2 μg/ml of 125I-labeled GST–lamin C tail was incubated in microtiter wells containing immobilized chromatin fragments for 120 min in the absence (open bars) or presence (solid bars) of a 50-fold excess of the unlabeled GST–lamin C tail under the following conditions: standard binding buffer (Mg, 0.15 M NaCl); solutions containing 5 mM EDTA (EDTA, 0.15 M NaCl) or 5 mM EGTA (EGTA, 0.15 M NaCl) instead of 5 mM Mg²⁺; standard buffer containing 1% Triton X-100 (Triton X-100, 0.15 M NaCl); or standard buffer followed by postincubation washes in 0.25–1.0 M NaCl (Mg, 0.25, 0.5, or Mg, 1.0 M NaCl). (C) Time course of GST–lamin tail binding to chromatin. 2 μg/ml of 125I-labeled GST–lamin C, B1, and B2 tail was incubated in the standard binding assay for various times. All points were corrected for nonspecific binding by subtraction of values obtained with a 50-fold excess of corresponding unlabeled polypeptides.
Figure 3. Displacement of 125I-labeled GST–lamin C, B1, and B2 tails from chromatin by the corresponding unlabeled polypeptides, and calculation of dissociation constants. 2 μg/ml of 125I-labeled GST–lamin C tail, GST–lamin B1 tail or GST–lamin B2 tail (A–C, respectively) were incubated in the standard binding assay in the presence of various concentrations of the corresponding unlabeled GST-polypeptides. Binding at each point was corrected for nonspecific background by subtraction of values obtained with 117 μg/ml unlabeled competitor (see Fig. 2). Insets: Data for specific binding was analyzed by plotting (1-RL/RLo)/A vs. 1-RL/RLo, where RL is the amount of radioactive fusion protein bound to chromatin at cold competitor concentration A, and RLo is the amount of radioactive fusion protein bound in the absence of unlabeled competitor. The slope given by this plot equals -1/Kd (Hulme and Birdsall, 1992).

as approximate. It is not possible to calculate the amount of lamin bound to chromatin at saturation with this solid phase assay, because the fraction of sites within the immobilized chromatin fragments that was active for binding is unknown.

We tried to express the lamin A (389–664) tail as a GST fusion protein in E. coli, but found that it was extensively proteolyzed under all conditions tested, especially within the A-specific region. However, we successfully expressed largely undegraded lamin A tail without a fusion partner in insect cells using the baculovirus expression system, and also expressed undegraded lamin C tail without a fusion partner in E. coli using a pET vector. These lamin fragments were purified by ion exchange chromatography in the presence of 8 M urea, and were used for binding studies after removal of the urea. In binding displacement experiments, the curves for the lamin A tail and the lamin C tail were very similar to each other. When the data was expressed in linearizing plots for single site competitive interactions (see Fig. 3 legend), Kd of ∼400 nM were calculated for both the lamin A tail and lamin C tail (data not shown). The higher apparent Kd for the chromatin binding of the lamin C tail isolated in urea, compared with that for the GST–lamin C construct isolated under nondenaturing conditions, could be explained by incomplete renaturation of the lamin C tail after urea treatment. If the lamin A tail and lamin C tail refold to an active chromatin binding conformation to the same extent, this would indicate that the unique 98 and 6 residue extensions present on lamin A and lamin C, respectively, do not differentially influence chromatin binding.

Mapping the Chromatin-binding Region of the Lamin C Tail
To define the specific region of the lamin C tail involved in chromatin binding, we expressed as GST fusion proteins a series of deletion mutants of the lamin C tail lacking portions of either the amino- or carboxyl-terminal ends (Fig. 4 A). These were purified as largely intact fusion proteins (Fig. 4 B) and were evaluated for their ability to displace a radiolabeled GST fusion protein containing the full-length lamin C tail (389–572) from chromatin, in comparison to the displacement by the unlabeled GST–lamin C tail itself (Fig. 4, C and D). The carboxyl-terminal deletions lamin C (389–480) and lamin C (389–430) had full displacement activity, whereas lamin C (389–416) was almost completely inactive (Fig. 4 B). The amino-terminal deletion lamin C (396–572) resulted in complete displacement, while the amino-terminal deletions lamin C (401–572) and lamin C (415–572) exhibited only partial displacement of binding. A final deletion, lamin C (431–572), had no displacement activity (Fig. 4 C). Together, the results with these amino- and carboxyl-terminal deletion mutants suggest that at least two regions between residues 396–430 of the lamin C tail are important for chromatin binding.

The nuclear localization sequence (NLS) of lamins A/C is present in the tail domain at amino acids 417–422 (KKRKLE). To determine whether the NLS is important for the chromatin binding activity, we prepared several lamin C tail constructs, including amino-terminal tail deletions, from which residues 417–422 were deleted (ΔNLS). These were GST–lamin C (389–572 ΔNLS), GST–lamin C (396–572 ΔNLS), and GST–lamin C (401–572 ΔNLS) (Fig. 5, A and B). Lamin C (389–572 ΔNLS) and lamin C (396–572 ΔNLS) both exhibited only partial displacement of the binding (Fig. 5 C). Combining the amino-terminal deletion of lamin C (401–572), which by itself had lost some displacement activity, with the ΔNLS mutant, which also was partially inactive, yielded the construct lamin C (401–572 ΔNLS) that lost almost all ability to displace the intact lamin C tail from chromatin (Fig. 5 C). These results together indicate that residues 396–401 and 417–422 (the NLS) both have important roles in the chromatin binding activity of the lamin C tail, and that the combined effects of these regions are additive.
We further prepared several bidirectional (NH₂- and COOH-terminal) deletions to test in the binding displacement assay (Figs. 5, A and B). Lamin C (425–480), lamin C (415–480), and lamin C (411–480) were inactive in displacing the lamin C tail from chromatin (Fig. 5 D). By contrast, lamin C (396–480) and even lamin C (396–430) were sufficient for complete displacement of binding (Fig. 5 D). These data are consistent with the results of the amino- and carboxyl-terminal deletions (above), and further demonstrate that the minimal region required for complete displacement of chromatin binding by the lamin C tail in the context of these fusion proteins is residues 396–430.

To complement the results of the binding displacement experiments discussed above, we directly investigated the chromatin binding of several of the deletion mutants (Fig. 6). We radiolabeled GST fusion proteins containing lamin C (389–572), lamin C (389–430), lamin C (415–572), and lamin C (389–572 ΔNLS), and examined association of these proteins with chromatin in the absence and presence of an excess of each unlabeled polypeptide to correct for nonspecific background (see Fig. 6 legend). The construct containing lamin C (389–430) showed a very similar level of specific chromatin binding compared to the full-length lamin C tail (389–572). By contrast, lamin C (415–572) and lamin C (389–572 ΔNLS), which were only partially active in competing for chromatin binding by the lamin C tail, were significantly reduced in their specific chromatin-binding activity. These results extend the binding competition studies presented above (Figs. 4 and 5) and verify that a short segment near the amino terminus of the lamin C tail contains the chromatin binding site of this lamin domain.

Identification of Core Histones as the Chromatin Binding Site for Lamin C

To identify the specific chromatin component that pro-
Figure 5. Displacement of $^{125}$I-labeled GST–lamin C tail from chromatin by GST fusion proteins containing bidirectional and internal deletions of lamin C tail. (A) Schematic diagram of the deletions analyzed. Terminal amino acids are numbered, and their displacement activity is summarized (competition). (B) Electrophoresis of purified recombinant GST fusion proteins on a 12% SDS gel. Proteins were visualized by staining with Coomassie blue. Lane numbers correspond to the number of each construct designated in A. (C–D) Binding of $^{125}$I-labeled GST–lamin C tail (2 μg/ml) to chromatin was measured in the presence of various concentrations of each unlabeled recombinant polypeptide. Binding at each point was corrected for nonspecific background by subtraction of the value obtained with 122 μg/ml unlabeled GST–lamin C tail (see Fig. 2). (C) Displacement of the binding with NLS and amino-terminal combined deletions. (D) Displacement of the binding by various bidirectional deletions.

vides the binding site for the lamin C tail (Fig. 7), we prepared several chromatin subfractions. A histone H1-enriched fraction (which also contained nonhistone chromosomal proteins) and a second fraction consisting of core histones bound to DNA were obtained by treatment of chromatin fragments with 0.6 M salt and sucrose gradient sedimentation (Fig. 7 A, lanes 1 and 2, respectively). A third fraction consisting of purified core histones was obtained by binding chromatin fragments to a hydroxylapatite column followed by salt elution (Fig. 7 A, lane 3; see Materials and Methods). These fractions were separately adsorbed to microtiter wells and analyzed in a binding displacement assay with the radiolabeled GST–lamin C tail (389–572), where the unlabeled competitors were GST fusions containing lamin C (389–572), lamin C (389–430), and lamin C (431–572). It should be noted that no attempts were made to normalize the amount of protein bound to the microtiter wells with the three histone fractions, so the amount of ligand bound to the three fractions cannot be directly compared. Also, raw binding data corrected for nonspecific background is presented for all of the fractions analyzed (Figs. 7, B–D), since a priori we did not know which fraction displayed specific binding.

The radiolabeled lamin C tail construct bound to all three of the histone subfractions (Figs. 7, B and D). Most of the binding to the histone H1-enriched fraction (Fig. 7 B) appeared to be nonspecific, as it was only weakly displaced by lamin C (389–572) and lamin C (389–430). However, since even weak binding displacement was not obtained with lamin C (431–572), which lacks the chromatin binding site, it is possible that the histone H1-enriched fraction contains a specific chromatin binding component (possibly low amounts of contaminating core histones; see below). The high nonspecific background in this case precludes clear-cut conclusions. By contrast, binding of the radiolabeled lamin C tail to the core histone/DNA fraction (Fig. 7 C) and the purified core histone fraction (Fig. 7 D) was strongly displaced by lamin C (389–572) and lamin C (389–430). The degree of binding displacement in these cases was similar to that obtained when binding to intact
chromatin fragments was analyzed (compare to Fig. 2). Moreover, no displacement was obtained with lamin C (431–572), which also does not displace binding of the lamin C tail to intact chromatin (Fig. 4). The binding of GST-lamin C (389–430) to purified core histones was corrected for nonspecific background, and these data were expressed in a linearizing plot for single site competitive interaction (Hulme and Birdsall, 1992) to calculate a dissociation constant (Fig. 7E). This analysis revealed a single class of binding sites with an apparent $K_d$ of 320 nM. Thus, the binding specificity and affinity of the lamin C tail for purified core histones is very similar to that for chromatin fragments.

In other experiments, we extracted the DNA from the chromatin fragments used for these binding studies, biotinylated it, adsorbed it to the surface of streptavidin-coated microtiter wells, and then evaluated its ability to bind the radiolabeled lamin C tail (see Materials and Methods). No specific binding of the lamin tail was observed (data not shown), indicating that bulk sequence DNA does not contain detectable binding sites for the lamin C tail. These results, together with the histone fraction binding results discussed above, indicate that core histones are the predominant binding site for the lamin C tail in isolated chromatin. However, it should be noted that our analysis might not detect binding sites in chromatin for the lamin tail that are either low abundance or low affinity.

Discussion

Specific Chromatin Binding of Lamin Tail Domains

Previous work has established that vertebrate nuclear lamins specifically interact with several different chromatin substrates (Burke, 1990; Glass and Gerace, 1990; Hoge et al., 1991; Yuan et al. 1991). In this study we have defined and characterized an interaction between the tail domains of mammalian lamins and rat liver chromatin fragments. Our analysis involved the use of recombinant tail domains expressed as soluble GST fusion proteins. Unlike intact lamins and lamin fragments containing the rod domain, which are insoluble under conditions of physiological salt and pH, the tail domains do not strongly self-associate and therefore could be used for quantitative binding analysis. Our use of soluble fusion proteins also avoided possible complications of protein refolding after solubilization in chemical denaturants such as urea (see below).

Using a solid phase binding assay, we found that the tail domains of lamins C, B1, and B2 specifically interact with chromatin, with apparent $K_d$s of 120–300 nM. Furthermore, by using binding displacement and direct binding analyses with a series of deletion constructs, we mapped the chromatin binding region of the lamin C tail to a 35–amino acid region distal to the rod domain, corresponding to residues 396–430 (Fig. 8). Our studies showed that two amino acid stretches in this segment (residues 396–401 and residues 417–422, the latter comprising the NLS), which both are enriched in basic amino acid residues, are particularly important for the ability of recombinant fusion proteins to compete for the chromatin binding of the intact lamin C tail domain (Fig. 8, bold sequences). It is unclear whether these amino acid stretches directly interact with chromatin, or whether they are important for the proper folding of the region containing residues 396–430 into a chromatin-binding structure. The finding that the NLS is important for the chromatin binding of the lamin tail supports the possibility that many NLSs may be multifunctional (discussed in Gerace, 1992). Interestingly, the chromatin binding site in the lamin C tail does not involve the highly charged region at its COOH terminus (residues 551–572), which contains a cluster of eight acidic residues followed by a second cluster of six basic residues.

We have not analyzed the regions of the lamin B tails that are responsible for their chromatin binding, and do not know whether they coincide with the chromatin binding domain of the lamin A/C tail. A comparison of the sequences of human, mouse and chicken lamins A, B1, and B2 in the region corresponding to residues 396–430 of human lamins A/C is shown in Fig. 8. The only highly conserved sequence in this region is the NLS (residues 417–422 of human lamins A/C). The region corresponding to residues 396–401 of human lamins A/C contains at least two basic residues in all lamins but varies in their spacing and surrounding residues, while the areas between these sequences and distal to the NLS are enriched in serine/threonine residues but differ considerably in exact sequence.

Using specific histone and DNA fractions isolated from rat liver chromatin, we determined that the specificity and $K_d$ for the binding of the lamin C tail to purified core histones was very similar to that for chromatin fragments. Since the lamin tail did not bind to isolated DNA, we infer that core histones represent the predominant chromatin binding site for the lamin C tail in isolated chromatin. While our analysis showed no specific binding of the lamin...
Figure 7. Displacement of 125I-labeled GST-lamin C tail from various chromatin subfractions by GST fusion proteins containing various lamin C tail regions. (A) Protein composition of chromatin subfractions. The histone H1-enriched fraction, core histone–DNA fraction and purified core histones were isolated as described in Materials and Methods. Proteins were analyzed by electrophoresis on a 15% SDS-gel and staining with Coomassie blue. Lane 1, histone H1-enriched fraction; lane 2, core histone–DNA fraction; lane 3, purified core histones. (B–D) Chromatin subfractions were immobilized on microtiter wells in coating buffer, and incubated with 125I-labeled GST–lamin C residues 389–572, 389–430, or 431–572. Shown are uncorrected binding data. (B) Displacement of 125I-labeled GST–lamin C tail from the histone H1-enriched fraction by unlabeled fusion proteins. (C) Displacement of 125I-labeled GST–lamin C tail from the core histone–DNA fraction by unlabeled fusion proteins. (D) Displacement of 125I-labeled GST–lamin C tail from purified core histones by unlabeled fusion proteins. (E) Determination of a dissociation constant for the binding of 125I-labeled GST–lamin C tail to purified core histones. The data for each point obtained with 125I-labeled GST–lamin C tail in D was corrected for nonspecific background by subtracting the binding obtained in the presence of 125 μg/ml unlabeled GST–lamin C tail. These data were used to plot (1-RL/RLo)/A vs. 1-RL/RLo to determine the Kd (see Fig. 3).

Relationship to Other Investigations of the Lamin–Chromatin Interaction

In a previous study where chromatin association was assayed by dialysis of solubilized recombinant lamin constructs into a solution of physiological pH and salt in the presence of mitotic chromosomes, we showed that the rod domain of nuclear lamins A/C by itself specifically interacts with chromatin (Glass et al., 1993). However, since association of the rod domain with chromatin occurred with significantly lower efficiency than seen for constructs containing both rod and tail domains (Glass et al., 1993), it was possible that the lamin tail also contributed to chromatin binding. This notion was consistent with studies showing that certain deletions in the tail domains of Xenopus lamin A and L11 compromised their ability to associate

C tail to bulk double-stranded DNA, we cannot exclude an interaction with a specific DNA sequence class that is not sufficiently enriched in bulk sequence DNA to be detectable with our assay. We note that lamins and other proteins containing coiled-coiled α-helices, including cytoplasmic intermediate filament proteins, have been found to interact in vitro with single stranded DNA (Shoeman and Traub, 1990; Luderus et al., 1994), as well as with A/T-rich SAR/MAR DNA sequences (Luderus et al., 1992), which have a propensity to form single-stranded regions (Kohwi-Shigematsu and Kohwi, 1990). Whether single-stranded SAR/MAR sequences occur in vivo is unknown. However, an interaction of SAR/MAR sequences with the nuclear lamina was not observed in studies involving an approximately physiological buffer with divalent cations (Izaurralde et al., 1988).
with minichromosomes assembled in vitro (Hoger et al., 1991).

The results of the present study directly establish the existence of a chromatin binding site in the lamin tail. Interestingly, at least in the case of lamin C, the chromatin binding site of the lamin tail is immediately adjacent to the rod domain. This raises the possibility that the rod and tail domains interact with the same chromatin structure (i.e., core histones), possibly as two components of a larger composite binding site. Unfortunately, it is not possible to compare the affinity of the rod vs. tail domain binding to chromatin, because the rod domain binding can be measured only in an association assay involving both lamin-chromatin and lamin-lamin associations.

Studies with turkey erythrocyte lamins isolated in the presence of urea showed a specific association of avian lamin A with chromatin fragments, in a fashion that was consistent with a $K_d$ of ~1 nM (Yuan et al., 1991). This contrasts with the results of the present study, which show a significantly lower apparent affinity (300 nM) of lamin tails with chromatin fragments. While the basis for this discrepancy is unknown, it is possible that the former assay measured a cooperative association of lamin A with chromatin rather than simple binding of a lamin protomer. This would suggest an affinity that is substantially higher than the actual chromatin binding affinity of a lamin protomer that does not self assemble during chromatin binding. Consistent with this interpretation, other studies have shown that intact lamins self-associate when they interact with chromatin in vitro (Glass and Gerace, 1990; Hoger et al., 1991) and that chromatin lowers the critical concentration for self-assembly (Glass and Gerace, 1990).

The inability of turkey erythrocyte lamin B isolated in the presence of urea to interact with chromatin (Yuan et al., 1991) contrasts with our results, which showed chromatin binding for both A- and B-type lamin tails when the latter were expressed as soluble GST fusions. This difference may be explained by differences in the self-association capacity of the different avian lamin isotypes (see above), or the possibility that A- and B-type lamins have different abilities to refold into a native structure during dialysis from urea solutions. We have found that pretreatment of the GST--lamin C tail fusion protein with 8 M urea does not influence its capacity for chromatin binding, while pretreatment of the GST--lamin B tail fusion protein with urea results in loss of all detectable chromatin binding activity (our unpublished observations).

**Role of Lamin-Chromatin Binding in Interphase Chromosome Structure**

We believe that the in vitro interaction of lamin tail domains with chromatin measured in this study is likely to be physiologically significant, as our studies involved a native chromatin substrate analyzed under approximately physiological solution conditions. Moreover, the interaction was found to be salt-stable, and specific by multiple criteria (see above). Considering the abundance of nuclear lamins at the inner nuclear membrane, the interaction we have characterized is expected to be of major importance for anchorage of chromatin at the NE during interphase.

A priori, it is likely that chromatin has a high avidity, stable interaction with the nuclear lamina in vivo (see Gerace and Burke, 1988). Moreover, light microscope studies have shown that monomeric lamin tails bind to chromatin with intermediate rather than high avidity, and that the interaction (at least for lamin C) involves core histones, which are ubiquitous chromosomal components. A simple model can accommodate both these in vivo and in vitro features. This speculative model (Fig. 9) proposes that higher order chromatin architecture is involved in determining the chromosomal regions that interact with the lamina in vivo, and can convert the intermediate affinity interactions of monomeric binding units into a high-avidity association. Specific chromosomal regions that are packaged in a higher order structure capable of cooperatively associating with the repeating array of binding sites on lamin fila-
Figure 9. Speculative model for specification of the lamin-chromosome interaction by higher order chromatin structure. The lamina, depicted as a polynm eric array of nuclear laminas with a regular longitudinal repeat, is shown to be attached to the inner nuclear membrane by integral membrane proteins. According to this model, chromatin packaged into higher order structures that can cooperatively bind to the lamina (large hatched spheres) can become stably associated with the latter. Chromatin packaged into structures that are unable to cooperatively bind to the lamina (small hatched spheres) do not become stably associated with the latter.

interphase cells can be relatively low. For example, the Drosophila polytene chromosome contains 15–20 sites closely associated with the NE with high frequency (Hochstrasser et al., 1986; Hochstrasser and Sedat, 1987). Thus it is unlikely that the lamina-chromosome association is involved defining the 10–100-kb “loops” that are thought to comprise units of chromosome folding and function (van Holde, 1989). Understanding the functions of the lamina-chromosome interaction more precisely will require in vivo studies in which it is specifically disrupted.

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