Two Catalytic Domains Are Required for Protein Deacetylation*

Histone deacetylase (HDAC)-6 was recently identified as a dual substrate, possibly multisubstrate, deacetylase that can act both on acetylated histone tails and on α-tubulin acetylated on Lys40. HDAC-6 is unique among deacetylases in having two hdac domains, and we have used this enzyme as a useful model to dissect the structural requirements for the deacetylation reaction. In this report, we show that both hdac domains are required for the intact deacetylase activity of HDAC-6 in vitro and in vivo. The spatial arrangement of these two domains in HDAC-6 is essential and alteration of the linker region between the two domains severely affects the catalytic activity. Artificial chimeric HDACs, made by replacing the hdac domains in HDAC-6 with corresponding domains from other class II HDACs, show de novo deacetylase activity. Taken together, our results demonstrate for the first time that the spatial arrangement of hdac domains is critical for in vivo deacetylation reaction and may provide a useful model for the development of novel HDAC inhibitors.

Protein acetylation, especially histone acetylation, is one of the most important posttranslational modifications. It is involved in the regulation of protein structure and functions and therefore has potentially important roles in most of cellular processes. In particular, the impact of histone N-terminal acetylation on chromatin organization and gene expression has been well documented. Acetylation and deacetylation of histone tails or of other proteins are essential posttranslational modifications. It is involved in the regulation of protein function in many processes, such as transcriptional regulation, DNA repair, and cell cycle progression.

Materials and Methods

Plasmids and Mutagenesis—Mutations and deletions were generated by QuickChange kit (Strategene). For EGFP insertions, part of the EGFP was PCR-amplified from pEGFP (Clontech) and subsequently cloned into the XbaI site in the linker region of HDAC-6 cDNA. To clone the chimeric HDAC, the hdac domains from either HDAC-4 or -5 were PCR-amplified and used to replace the first or second hdac domain in HDAC-6.

3T3 Cells and Rescue by HDAC-6 Wild Type and Mutants—Mouse embryonic fibroblasts were isolated from E13.5 mouse embryos and subsequently 3T3 cell lines were established following a standard protocol. 3T3 cells were infected with pMSCV-EGFP plasmids containing wild type or mutant mouse HDAC-6 cDNAs. Individual clones were expanded and checked for HDAC-6 expression by Western blot.

Co-immunoprecipitation and HDAC/Tubulin Deacetylation (TDAC) Assays—500 μg of extracts from HEK 293T cells transfected with FuGENE (Roche Applied Science) were immunoprecipitated with the primary antibody or mouse IgG. HDAC/TDAC assays were performed as described (5).

Purification of Recombinant Mouse HDAC63—A His6 tag was added to the C-terminal end of mouse HDAC-6 DNA in pDEST8 vector by PCR. Bacmids for insect cell transformation were generated using the Bac-To-Bac Baculovirus Expression System (Invitrogen). The recombinant enzymes were purified with a nickel-nitriatoic acid superflow (Qiagen) and HiTrap Q FF columns (Amersham Biosciences).

Immuno fluorescence and Immunoblotting—Cells were fixed and stained with anti-HA polyclonal antibody (Santa Cruz Biotechnology) and Tu6–11 for acetylated tubulin (Sigma). The antibodies used were: Tu6–11, DM1A, FLAG2 M2 (Sigma), anti-HA (Santa Cruz Biotechnology), Glu-tubulin and Tyr-tubulin (Synaptic Systems), and mHDAC-6 (6).

Results

Two hdac Domains Are Required for Deacetylation by HDAC-6—To investigate whether the two hdac domains in HDAC-6 might have different roles in the deacetylation reaction, we prepared several mutant constructs, with mutations in the catalytic cores or in the presumed substrate recognition regions (so-called ER motif; Ref. 7) (Fig. 1A). The different proteins were prepared from transiently transfected 293T cells by immunoprecipitation with an anti-HA antibody and were used for in vitro activity assays with chemically acetylated histone H4 or α-tubulin peptides (5). The expression levels of each mutant in transiently transfected cells were similar as demonstrated by Western blot analysis (Fig. 1B, upper panel). As shown in Fig. 1B, lower panel, point mutations in the catalytic core of both hdac domains (HD1/2m), completely abolished the HDAC and the TDAC activities of HDAC-6. Surprisingly, mutating either of the hdac catalytic cores (HD1m or HD2m) also destroyed the whole activity on both substrates. This suggests that the cooperation between the two hdac catalytic cores is critical for the deacetylation reaction mediated by HDAC-6. Interestingly, the mutations in the presumed substrate recognition region (7) led to somewhat different effects on enzymatic activities. The mutation in the second substrate recognition site (L798A) completely inactivated the catalytic activity on both peptides, whereas the mutation of the corresponding region in the first hdac domain (L402A) retained partial activity. Interestingly, the latter mutation had a stronger effect on TDAC activity than on HDAC activity. This result suggests that in the deacetylation reaction the two different peptide substrates might interact differently with the N-terminal catalytic domain of HDAC-6.

To rule out the possible interference of co-immunoprecipitated proteins with HDAC-6, we purified recombinant wild type or mutant HDAC-6 from a baculovirus expression system. After nickel-nitriatoic acid and QFF columns, His tagged HDAC-6 proteins could be purified as single protein and equal amount of wild type and mutant proteins were used for activity assays (Fig. 1C, left panel). As shown in Fig. 1C, right panel, the HDAC and TDAC activity of HDAC-6 is intrinsic and requires both intact catalytic cores.

To confirm these in vitro results, tubulin deacetylation was also tested in vivo. For this, HDAC-6 wild type and mutant constructs were transfected into NIH3T3 cells, and the cells were subsequently immunostained for acetylated tubulin and expression of the HA epitope, which marks transfected cells. As shown in Fig. 2A, the results of these experiments agree well with the above in vitro assays; endogenous tubulin acetylation was dramatically reduced by over-
expression of wild type HDAC-6 but not by the different HDAC-6 catalytic core mutants.

To rule out any possible effect from endogenous HDAC-6 on these assays, we also made use of HDAC-6-deficient 3T3 cell lines. In the complete absence of HDAC-6, 3T3 cells showed dramatically increased tubulin acetylation (lane 4 versus lane 1 in Fig. 2B, upper panel), in agreement with the notion that tubulin is the physiological substrate of HDAC-6. Stable re-introduction of HDAC-6 into the knock-out cells at an expression level comparable with the wild type efficiently reduced tubulin acetylation (Fig. 2B, lane 5). Clones expressing lower levels of HDAC-6 also showed a decrease in tubulin acetylation, albeit less pronounced (lane 6). Examination of the degree of tubulin acetylation in the different cell lines (lanes 2–4) revealed that in the second cell lines expressing mutant HDAC-6 tubulin acetylation was not reduced compared with control-transfected cells expressing GFP (lane 1). This result indicates that these two HDAC-6 mutants are inactive when tested in cells lacking endogenous HDAC-6.

The Spatial Arrangement of the hdac Domains in HDAC-6 Is Important for the Selective Activities on Different Substrates—To examine whether the spatial arrangement of the two catalytic domains is important for the activity of HDAC-6, we prepared a series of constructs in which the distance between the two domains was modulated by insertions or deletions. Fragments derived from the EGFP protein, ranging from 5 amino acids to full-length of EGFP (239 amino acids), were inserted between the two hdac domains (Fig. 3A). To shorten the distance between the two hdac domains, the linker region was deleted by 5, 25, or 68 amino acids, respectively. As shown in Fig. 3B, all constructs were equally expressed in transiently transfected 293T cells and subsequently used for immunoprecipitation and activity assays. Surprisingly, even slight modulation of the linker length, by addition or removal of only 5 amino acids, dramatically affected the catalytic activity (Fig. 3C). Generally, both HDAC and TDAC activities decreased along with increasing length of the insertions (Fig. 3C). The most dramatic loss of activity was observed when the linker length was increased by 68 amino acids. The impairment of the activity clearly showed substrate preference and TDAC activity was found to be more sensitive to spatial changes than HDAC activity.

Generation of Active Artificial Chimeric HDACs from Inactive HDAC Fragments—Finally, we tested whether artificial HDACs, made from combinations of different class II HDACs, might be selectively active. To create chimeric HDACs, we replaced the first or the second hdac domain of HDAC-6 by the hdac domains from either HDAC-4 or HDAC-5 (Fig. 4A). Since the distance between two hdac domains is important for activity (Fig. 3), in the

FIGURE 1. Two intact HDAC domains are required for deacetylation by HDAC-6 in vitro. A, schematic representation of the HDAC-6 protein and the mutations made. The conserved hdac domains are shown as gray boxes with the catalytic cores highlighted in red. The ER motif is shown in yellow. The HDAC-6 mutants have the following structure: HD1m, Asp426 and Asp427 are replaced by Asn, and His524 and His525 are replaced by Val; HD2m, Asp408 is replaced by Asn and His550 and His551 are replaced by Val. The mutants in the ER motif have either Leu402 replaced by Ala (L402A) or Leu798 replaced by Ala (L798A). B, in vitro HDAC or TDAC activity assays with wild type and mutant HDAC-6s. 293T cells were transfected with appropriate expression vectors and cell extracts were immunoprecipitated with an anti-HA antibody. Upper panel, equal protein input was confirmed by Western blotting with HA antibody. Lower panel, for the assays, acetylated tubulin peptide or histone H4 tail peptide were used as substrates. The results presented are averaged from three independent experiments. C, recombinant HDAC-6 needs two intact hdac domains to be active. Left panel, purified wild type and mutant HDAC-6 proteins (5 pl) were analyzed by SDS-PAGE. Right panels, acetylated tubulin peptide or histone H4 tail peptide were used as substrates for deacetylation assays performed with equal amounts of purified proteins. The results presented are averaged from three independent experiments.

Y. Zhang, unpublished data.
chimeric HDACs we used the linker region from HDAC-6 to keep the distance between two catalytic cores as it is in the wild type HDAC-6 protein. After transfection into 293T cells, the extracts were subsequently used for immunoprecipitation and activity assays. The specific activities were normalized to the protein expression levels determined by Western blot. As shown in Fig. 4B, replacement of the second hdac domain of HDAC-6 by domains from either HDAC-4 or HDAC-5 resulted in a chimeric protein with almost no activity on either tubulin or histone substrates. On their own, full-length HDAC-4 and -5 show no deacetylase activity (Refs. 5 and 12 and results not shown). On the other hand, chimeric proteins with the first hdac domain derived from either HDAC-4 or HDAC-5 and the second domain from HDAC-6 showed activity on both histone and tubulin substrates. Here again activity was greater on the histone peptide than on the tubulin substrate, which might be due to selective recognition and/or enzymatic activity of HDAC-4 or -5 on the histone but not on the tubulin peptide. These experiments showed that artificial combination of the hdac domains from HDAC-4 or -5 and the second HDAC-6 domain, either of which are inactive by themselves, led to de novo activity.

**DISCUSSION**

HDAC-6 contains two intact hdac catalytic domains which might mimic native HDAC-containing complexes. Since the two hdac domains in HDAC-6 are well conserved, the first question was whether they are both important and/or functionally different. Here we demonstrate that mutating a single hdac core is sufficient to inactivate HDAC-6 on both histone and tubulin substrates, both in vitro or in vivo. In addition, changing the spatial arrangement between these two domains by insertions or deletions has a significant impact on the activity. This confirms that both hdac domains are necessary for the activity and also suggests that their precise arrangement relative to another is important. We have shown previously that each hdac domain in HDAC-6 is sufficient to bind on its own β-tubulin, and this interaction is maintained even when the catalytic core is mutated (5). Within the hdac domain, in addition to the conserved catalytic core, a region of homology between HATs (such as Esa1) and HDACs (such as Rpd3) has been identified. This motif, termed ER (Esa1-Rpd3) motif (7), is located near the active center in the tertiary structure of Esa1. Recent structure analysis of the IGCNS/CoA/H3 complex (9) showed that this motif might be involved in the interaction and recognition with histone tails. Mutation analysis revealed that the ER motif regions of Esa1 or Rpd3 are required for HAT activity of Esa1 and HDAC activity of Rpd3, respectively (7). By mutating these putative substrate recognition motifs in HDAC-6, we find that the second ER motif might be more important for interaction with the substrate(s). This is the first evidence to show a functional difference between the two hdac domains in HDAC-6. The results obtained with chimeric HDACs further support this hypothesis (Fig. 4). Moreover, we observed that the mutation in the first ER motif had different effects on deacetylation of the tubulin or histone peptide: TDAC activity is more sensitive to this mutation than HDAC activity. This suggests that the two hdac domains selectively interact with and recognize different substrates. Interestingly, modulation of the distance between the two hdac domains in HDAC-6 also has a stronger effect on tubulin peptide deacetylation than on histone peptide deacetylation. We think that this might be also partially due to selective substrate recognition. While the tubulin substrate only has one acetylated lysine (Lys40), histone tails usually have several acetylated lysine residues. In vitro experiments have demonstrated that class I and II HDACs could deacetylate all acetylated lysines on core histone substrates, albeit with slightly different efficiencies (2). This suggests that there might be a dynamic sliding between HDACs and histone tails to allow deacetylation of all residues. Because of this the recognition of the histone substrates might be inherently more flexible than that of tubulin. In the deletion and insertion constructs of HDAC-6, the fact that the effect was weaker on histone than on tubulin substrates also suggests that tubulin deacetylation needs a more tightly controlled conformation of HDAC-6.

It is generally assumed that most of the in vivo deacetylation activity for histones, and possibly other proteins, is found in HDAC-containing multiprotein complexes. Interestingly, in all known HDAC-containing complexes, there are normally two HDACs (10). For example, HDAC-1 is commonly found to work together with HDAC-2. Moreover, HDAC-1 itself can homo-oligomerize through its N-terminal domain; the same domain is necessary for interaction in vitro with HDAC-2 or -3 and also for catalytic activity (11). This raises the question whether the in vivo deacetylation reactions also need two HDAC molecules together. Previous results demonstrated that class II HDACs regulate transcription by bridging the enzymatically active SMRT/N-CoR-HDAC-3 complex and select transcription factors, independently of any intrinsic class II HDAC activity (12). While HDAC-4 and other class II HDACs
The results presented are the average from three independent experiments. The spatial arrangement of two hdac domains in HDAC-6 is important for the selective activities on different substrates. A, schematic representation of insertion and deletion mutants of HDAC-6. Fragments from EGFP, varying from 5 amino acids to full-length (shown by green), were inserted between the two hdac domains in wild type (W.T.) HDAC-6. In the deletion mutants, various lengths were deleted from the linker region (depicted by the dotted boxes). B, 293T cells were transfected with appropriate expression vectors and cell extracts were immunoprecipitated with an anti-HA antibody. Western blotting (WB) with HA antibody was used to check the protein input used for the activity assays, as in Fig. 1B. C, extracts from B were used HDAC or TDAC activity assays. The results presented are the average from three independent experiments.

are inactive in the context of the SMRT/N-CoR-HDAC-3 complex, binding between the catalytic domain of HDAC-4 and HDAC-3 via N-CoR/SMRT is crucial for the activity of the complex. In vivo analysis of HDAC-1 function in Drosophila found that flies have different phenotypes when they are either completely deficient for HDAC-1 or only have a single point mutation, which may toxify HDAC-containing complexes (13). This evidence also indirectly suggested that the mutation in one of the hdac domains in the HDAC-containing complexes could inactivate the whole complex. So far, HDAC-6 is the only HDAC that has been shown to have catalytic activity independently from other HDACs or dimerization. Our results showed that the catalytic activity of HDAC-6 is dependent on both intact hdac domains. Moreover, artificially tethering parts of HDAC-6 and HDAC-4 or -5 were found to result in de novo catalytic activity; this mimics the result from N-CoR/SMRT complex, where HDAC-4 is made active by being tethered to HDAC-3. Based on these observations, we propose a possible general model for the deacetylation reaction, in which two hdac domains are required. As in the case for HDAC-6, HDAC-containing complexes might have a specific spatial arrangement of hdac domains, originating from two different HDAC molecules. These two hdac domains cooperate to confer the catalytic activity of the whole complex. The components of the different complexes determine the spatial arrangement of the two core hdac domains and therefore the specific activity of the complexes on different potential substrates. Solving the crystal structure of native whole HDAC-containing complexes should help to verify this hypothesis.

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