Transcription-dependent spatial arrangements of CFTR and adjacent genes in human cell nuclei

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We investigated in different human cell types nuclear positioning and transcriptional regulation of the functionally unrelated genes GASZ, CFTR, and CORTBP2, mapping to adjacent loci on human chromosome 7q31. When inactive, GASZ, CFTR, and CORTBP2 preferentially associated with the nuclear periphery and with perinuclear heterochromatin, whereas in their actively transcribed states the gene loci preferentially associated with euchromatin in the nuclear interior. Adjacent genes associated simultaneously with these distinct chromatin fractions localizing at different nuclear regions, in accordance with their individual transcriptional regulation. Although the nuclear localization of CFTR changed after altering its transcription levels, the transcriptional status of CFTR was not changed by driving this gene into a different nuclear environment. This implied that the transcriptional activity affected the nuclear positioning, and not vice versa. Together, the results show that small chromosomal subregions can display highly flexible nuclear organizations that are regulated at the level of individual genes in a transcription-dependent manner.

Introduction

Mammalian gene loci display a nonrandom positioning within cell nuclei, which is related to their functional regulation. In particular, association with the nuclear periphery and pericentric heterochromatin seems to play a role in the regulation of transcription and recombination (Brown et al., 1997, 1999, 2001; Skok et al., 2001; Kosak et al., 2002). Also, the positioning of gene loci at specific regions of the respective chromosome territory appears to play a role in their functional regulation (Cremer et al., 1993, 1995; Volpi et al., 2000; Cremer and Cremer, 2001; Mahy et al., 2002a; Williams et al., 2002). Currently, it is unclear how the association of gene loci with specific nuclear domains relates to their organization within chromosome territories.

An important question is at which level the functional organization of chromosomal loci in the nucleus is regulated. Previous reports suggested that whole chromosomes (Croft et al., 1999; Boyle et al., 2001) or large chromosomal subregions in the size range of several hundred kb pairs up to several Mb pairs (Ferreira et al., 1997; Croft et al., 1999; Sadoni et al., 1999; Volpi et al., 2000; Williams et al., 2002) displayed a specific nuclear positioning. Also, the results of recent FISH analyses implied that region-specific gene density and transcriptional activity, rather than the activity of individual genes, influenced the organization of chromosome territories (Mahy et al., 2002a,b).

Abbreviations used in this paper: 3D, three-dimensional; CFTR, cystic fibrosis transmembrane conductance regulator; CORTBP2, cortactin-binding protein 2; DRB, 5,6-dichlorobenzimidazole riboside; GASZ, germ cell-specific expression, presence of ANK, SAM, and basic leucine zipper domains; H4Ac8, H4 acetylated at lysine 8; LAF2B, lamina-associated polypeptide 2B; TSA, trichostatin A.

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Key words: CFTR; nuclear architecture; gene positioning; chromatin organization; chromosome territory

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Table I. Test gene expression as percentage of α-actin expression

<table>
<thead>
<tr>
<th>Cell type</th>
<th>CORTBP2</th>
<th>CFTR</th>
<th>GASZ</th>
</tr>
</thead>
<tbody>
<tr>
<td>T-lymphocytes</td>
<td>0.33 ± 0.58%</td>
<td>Zero</td>
<td>Zero</td>
</tr>
<tr>
<td>HEK 293</td>
<td>6.9 ± 4.8% (n = 4)</td>
<td>Zero (n = 4)</td>
<td>Zero</td>
</tr>
<tr>
<td>SH-EP N14</td>
<td>Zero (n = 4)</td>
<td>57.6 ± 23.4% (n = 5)</td>
<td>Zero</td>
</tr>
<tr>
<td>Calu-3</td>
<td>0.27 ± 0.29%</td>
<td>Zero</td>
<td>Zero</td>
</tr>
<tr>
<td>HT1080</td>
<td>0.53 ± 0.45%</td>
<td>2.1 ± 0.4% (n = 4)</td>
<td>Detectable</td>
</tr>
<tr>
<td>Testis</td>
<td>2.2 ± 1.7%</td>
<td>1.3 ± 0.3%</td>
<td>Zero</td>
</tr>
<tr>
<td>Nasal epithelium</td>
<td>0.67 ± 0.12%</td>
<td>77.5 ± 13.0%</td>
<td>-</td>
</tr>
<tr>
<td>Calu-3 control</td>
<td>-</td>
<td>34.7 ± 19.2%</td>
<td>-</td>
</tr>
<tr>
<td>Calu-3 plus DRB</td>
<td>-</td>
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<td>-</td>
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</table>

The values are based on average percentages of experimental gene expression while control gene (α-actin) is still in exponential phase of amplification. The values shown are means ± SD for n = 3 replications, unless otherwise shown. “Zero” indicates that the experimental peak was undetectable within log phase of α-actin amplification and within 40 cycles of normal monoplex PCR amplification. For GASZ, expression in testis was only detected after α-actin amplification had entered the plateau phase, and was confirmed by monoplex PCR.

To address the question of whether nuclear positioning is indeed regulated at the level of larger chromosomal sub-regions rather than at the level of individual genes, we investigated the nuclear positioning of three adjacent genes in the cystic fibrosis transmembrane conductance regulator (CFTR) region on human chromosome 7q31. The genes evaluated besides CFTR were the germ cell-specific expression, presence of ANK, SAM, and basic leucine zipper domains (GASZ) gene localized ~50 kb upstream of CFTR (Yan et al., 2002), and the cortactin-binding protein 2 (CORTBP2) gene localized ~45 kb downstream of CFTR (Cheung et al., 2001). The CFTR gene codes for a cyclic AMP-dependent chloride channel that is expressed in a number of epithelial tissues, in particular in the respiratory tract epithelium (Engelhardt et al., 1994; Li et al., 1988). Mutations in this gene cause cystic fibrosis, which is the most common severe autosomal recessive disease amongst the Caucasian population. GASZ displays germ cell–specific expression and may represent a cytoplasmic signal transducer mediating protein–protein interactions during germ cell maturation (Yan et al., 2002). CORTBP2 codes for a cortactin-binding protein of unknown function and is expressed in a variety of human tissues (Cheung et al., 2001). Our results show that the nuclear positioning of GASZ, CFTR, and CORTBP2 and their association with distinct chromatin fractions is regulated at the level of individual genes in a transcription-dependent manner.

Results

Nuclear positioning of GASZ, CFTR, and CORTBP2

First, we investigated nuclear positioning of CFTR in human SH-EP N14 neuroblastoma cells, where this gene is not transcribed (for levels of transcription see Table I; also see Fig. S2, available at http://www.jcb.org/cgi/content/full/jcb.200404107/DC1), and in Calu-3 adenocarcinoma cells, where CFTR is highly expressed. CFTR was detected by FISH using the prokaryotic artificial chromosome CF1 from the 5’ region of the CFTR gene (Fig. 1). This probe was used in all FISH experiments for detection of CFTR unless otherwise indicated. We investigated formaldehyde-fixed nuclei, which were also immunostained with antibodies against the lamina-associated polypeptide 2β (LAP2β) or histone H4 acetylated at lysine 8 (H4Ac8). H4Ac8 is enriched in the early replicating and transcriptionally active euchromatin in the nuclear interior, whereas later replicating and transcriptionally inactive heterochromatin, including perinuclear heterochromatin, is depleted in H4Ac8 (Sadoni et al., 1999). LAP2B is an integral protein of the inner nuclear membrane, which binds to chromatin (Furukawa et al., 1995; Nili et al., 2001). A fraction of cells was also pulse labeled with FITC-dUTP in order to label distinct fractions of heterochromatin and euchromatin displaying a distinct replication timing and localizing at specific nuclear regions (Sadoni et al., 1999; Zink et al., 2003).

After immuno-FISH, nuclei were imaged by confocal microscopy. In SH-EP N14 cells, 87% of the CFTR-specific FISH signals (n = 100; n always refers to the numbers of FISH signals analyzed) were associated with the nuclear periphery, as visualized by the different labeling methods used (Fig. 2). At the nuclear periphery, CFTR was embedded in the perinuclear heterochromatin not enriched in H4Ac8 (Fig. 2 a; Sadoni et al., 1999) and replicating during the second half of S-phase (Fig. 2 c). Immunostaining of LAP2B revealed a very close association of CFTR with the nuclear periphery (Fig. 2 c). Also, FISH signals, appearing to localize to the nuclear interior, were associated with invaginations of the nuclear periphery forming long invaginations into the nuclear interior in this cell type (Fig. 2 c). Counterstaining of DNA with propidium iodide confirmed the perinuclear localization of CFTR and revealed that it...
was not associated with perinucleolar heterochromatin in SH-EP N14 cells (Fig. 2 f).

In Calu-3 cells, 88% of the CFTR-specific FISH signals were embedded in the nuclear interior within the transcriptionally active euchromatin, which is specifically enriched in H4Ac8 (Fig. 2 b, n = 26; Sadoni et al., 1999), and most of the FISH signals (82%) were not associated with high local concentrations of LAP2β (Fig. 2 d; n = 27). Together, these results revealed that CFTR associated in its inactive state in SH-EP N14 cells with the nuclear periphery and here with later replicating perinuclear heterochromatin depleted in H4Ac8. In contrast, in its actively transcribed state in Calu-3 cells, CFTR did not associate with the nuclear periphery, but with euchromatin enriched in H4Ac8 occupying the nuclear interior.

Next, we investigated the association of GASZ, CFTR, and CORTBP2 with perinuclear heterochromatin, highlighted by replicational pulse labeling, in SH-EP N14, Calu-3, and HEK 293 cells. Cells were fixed with formaldehyde and imaged by confocal microscopy. In SH-EP N14 cells, where none of the genes were transcribed (Table I), all three genes preferentially associated with perinuclear heterochromatin (Fig. 3, a, b, and e; ~80–90%). GASZ and CFTR were not transcribed in 293 cells, and also here 80–90% of the corresponding FISH signals associated with perinuclear heterochromatin (Fig. 3, c and e). In contrast, CORTBP2 was transcribed at relatively high levels in this cell type and only ~10% of the corresponding FISH signals associated with the perinuclear heterochromatin (Fig. 3 e). Closer inspection of the data revealed that although CORTBP2 was clearly not associated with the perinuclear heterochromatin in ~90% of the cases, it still occupied relatively peripheral positions and was typically located just behind the border to the adjacent euchromatin (Fig. 3 d).

In Calu-3 cells, only GASZ was not transcribed. Here, a bias toward association with perinuclear heterochromatin could be observed (Fig. 3 e; ~60%), although in Calu-3 cells the preferential association of GASZ with perinuclear heterochromatin was not as pronounced as in the other cell types examined. CORTBP2, which was expressed in Calu-3 cells, did not preferentially associate with perinuclear heterochromatin, but also here the tendency was relatively weak (~40% of the FISH signals still associated with perinuclear heterochromatin). In accordance with the results described above (Fig. 2), CFTR was in the vast majority of cases not associated with perinuclear heterochromatin in Calu-3 cells (Fig. 3 e; ~95%).

In summary, the results did show that GASZ, CFTR, and CORTBP2 preferentially associated with perinuclear heterochromatin in their inactive states, but not when actively transcribed. When preferential association with perinuclear heterochromatin was observed, the genes always fully colocalized with the heterochromatin and were surrounded by it (Fig. 2 e and Fig. 3, a–c). As the layer of perinuclear heterochromatin is relatively thin (<1 μm), this suggests that the distances of the inactive gene loci to the nuclear envelope were <1 μm. A very tight association with the nuclear envelope and direct physical contact was also suggested by the results obtained after additional immunostaining of LAB2β (Fig. 2 c).

Although we did not quantitate whether the alleles present in one nucleus always showed the same behavior, it is obvious that at least in those cases, where a very pronounced preferential localization was observed (all three genes in SH-EP N14 and 293 cells and CFTR in Calu-3 cells), the alleles of a given gene in one nucleus must have shown the same behavior in the vast majority of nuclei. This can be also ob-
To analyze larger sample numbers we performed erosion analyses with regard to GASZ, CFTR, and CORTBP2 in the following cell types: primary nasal epithelial cells and primary T-lymphocytes obtained from healthy donors, 293 cells, HeLa cells, SH-EP N14 cells, HT1080 fibrosarcoma cells, and Calu-3 cells. The results (Fig. 4) revealed that a close association of a gene locus with the nuclear periphery and perinuclear heterochromatin, as observed for GASZ, CFTR, and CORTBP2 in SH-EP N14 cells and GASZ and CFTR in 293 cells (Fig. 2 and Fig. 3), was indicated in the erosion analysis by a peak in the number of FISH signals in the first (outermost) shell, with at least 40% of the FISH signals being located there (note that the “true” fraction of FISH signals associating with the nuclear periphery [80–90%] is largely underestimated by the erosion analysis). A second feature indicating a close association with the nuclear periphery is a constant decline in the numbers of FISH signals toward the nuclear center, giving rise to a typical “staircase-like” arrangement of the bars in the corresponding diagram. In all cases where one of the three genes was not transcribed a corresponding distribution was observed, with the exception of GASZ in Calu-3 cells (Fig. 4). In this case, our previous analyses indicated a less pronounced association with perinuclear heterochromatin (Fig. 3 e).

In all situations where a given gene was expressed, the erosion analysis indicated a more interior positioning (Fig. 4). Also, dissociation from perinuclear heterochromatin of the active CORTBP2 in 293 cells (Fig. 3) was reliably indicated by the erosion analysis by a drop in the numbers of FISH signals in the outermost shell below 40%. Nevertheless, the erosion analysis also indicated a relatively peripheral positioning of CORTBP2 in 293 cells, in accordance with our previous results (Fig. 3). Also, the more interior positioning of CFTR in Calu-3 cells (Figs. 2 and 3; also see Fig. S1) was reliably indicated by the erosion analysis. A comparable interior positioning of CFTR was observed in primary nasal epithelial cells (Fig. 4), where CFTR was also expressed. This showed that interior positioning of the active CFTR gene was not an aberrant feature of Calu-3 adenocarcinoma cells.

Additional controls showed that the relatively interior positioning of all three gene loci in Calu-3 cells was not due to disruption of the peripheral heterochromatin or disruption of the interactions of the chromosome 7 territory with the nuclear periphery (unpublished data). As a further control, we evaluated the nuclear positioning of the unrelated β-globin locus by erosion analysis in 293, SH-EP N14, and Calu-3 cells (Fig. S3, available at http://www.jcb.org/cgi/content/full/jcb.200404107/DC1). The nuclear positioning of the β-globin locus was not significantly different in Calu-3 cells in comparison to 293 or SH-EP N14 cells (unpaired t test; P < 0.05).

In summary, comparison of the results obtained with the erosion analysis to known gene distributions in the 3D nuclear space allowed to interpret the data and showed that the erosion analysis reliably indicated even subtle changes in gene distributions (e.g., CORTBP2 in 293 cells). Together, the data showed that in all cases transcriptionally active loci preferentially associated with the nuclear periphery, whereas the genes resided at more interior positions in their active states. It should also be noted that with regard to the active CORTBP2 gene, no correlation between its levels of transcription (Table I) and its positions in the nuclear interior could be observed. For example, CORTBP2 was transcribed at relatively high levels in 293 cells, although it occupied in this cell type more peripheral posi-

Figure 3. Spatial arrangements of GASZ, CFTR, and CORTBP2. (a–d) Panels show light-optical sections of formaldehyde-fixed nuclei from SH-EP N14 (a and b) and HEK 293 (c and d) cells (bar, 5 μm). CFTR (a and c) and CORTBP2 (b and d) were detected by FISH (red signals). Perinuclear and perinucleolar heterochromatin has been visualized by replication labeling (green). The arrows in a, b, and c, respectively, point to CFTR and CORTBP2 genes embedded within the perinuclear heterochromatin. The arrow in d points to the CORTBP2 locus (doublet signal) localizing within the adjacent euchromatin. The insets in c and d show the corresponding FISH signals and their nuclear environments enlarged. (e) The fractions of FISH signals (violet bars, GASZ; red bars, CFTR; yellow bars, CORTBP2; average ± SD) colocalizing with perinuclear heterochromatin were determined in the cell types indicated. Replication-labeled nuclei as shown in panels a–d were evaluated after FISH. In each case ~50–60 FISH signals were evaluated.

served on several images shown (Fig. 2 c; see Fig. 5 a; also see Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200404107/DC1).

Erosion analyses (Fig. 4) allow a relatively fast evaluation of nuclear gene distributions and are ideally suited for investigating large sample numbers. The results of erosion analyses can not, per se, be interpreted in terms of the nuclear distribution of FISH signals or their associations with specific nuclear regions. However, by relating results from erosion analyses to known distributions of FISH signals in the three-dimensional (3D) nuclear space, it becomes possible to interpret the data.
tions than in T-lymphocytes, where it was transcribed at substantially lower levels (Table I and Fig. 4). Together with the finding that CORTBP2 did not associate with perinuclear heterochromatin but resided just behind the border to the euchromatin in 293 cells (Fig. 3 d), the results suggested that association with euchromatin plays a more important role than the absolute distance to the nuclear periphery. Our finding that CORTBP2 is expressed in 293 cells at relatively high levels just behind the border to the adjacent euchromatin is in accordance with previous findings (Fakan, 1994; Cmarko et al., 1999; Verschure et al., 1999), showing that nascent RNA synthesis takes place at the surfaces of condensed chromatin domains.

**Simultaneous detection of neighboring genes**

To further address the spatial arrangements of CFTR and adjacent genes and the question of whether neighboring genes associated simultaneously with different regions of the same nucleus, we performed dual-color FISH analyses. Two adjacent genes (GASZ and CFTR, or CFTR and CORTBP2, respectively) were simultaneously detected together in the same nucleus with two different fluorochromes (Fig. 5). Next, it was determined with regard to lymphocytes, 293, SH-EP N14, and Calu-3 cells, how frequently one of these two genes was located more peripherally than the other. In addition, it was determined how frequently both genes were juxtaposed to each other, with neither locus locating more peripheral.

The data summarized in Fig. 5 b show that in T-lymphocytes and 293 cells, the majority of GASZ and CFTR signals were juxtaposed to each other, with no locus being more peripheral. In contrast, CFTR preferentially showed a more peripheral position than CORTBP2. These results were in accordance with the previous results (Fig. 3 and Fig. 4), showing GASZ and CFTR closely associated with the nuclear periphery of T-lymphocytes and 293 cells, in contrast to CORTBP2.

In SH-EP N14 cells, GASZ and CFTR, as well as CFTR and CORTBP2, respectively, were preferentially juxtaposed to each other (Fig. 5 b). All three loci closely associated with the nuclear periphery and perinuclear heterochromatin in this cell type (Fig. 3 and Fig. 4). In contrast, in Calu-3 cells CFTR was located more to the interior than GASZ or CORTBP2, respectively (Fig. 5 b). Also, these findings were in accordance with our previous results (Fig. 3 and Fig. 4). Although all results were in accordance with the data ob-
tained by the previous analyses, the dual-color FISH analysis demonstrated that adjacent gene loci simultaneously associated with different nuclear regions.

Next, we addressed the question of which parts of the chromosomal region provided the flexible linker between CFTR and CORTBP2. Therefore, we performed with 293 nuclei dual-color FISH experiments with the CF1 probe specific for the 5′ region of CFTR and another probe specific for the 3′ region of CFTR (Fig. 1). The results (Fig. 5 c) revealed that the 5′ and 3′ regions of CFTR were juxtaposed next to each other in the majority of cases. Together with the finding that CORTBP2 occupied more interior positions than CF1 (Fig. 5 b), the results suggested that mainly the intergenic region between CFTR and CORTBP2 provided the flexible linker. This was also suggested by the fact that FISH signals obtained with the probe specific for the 3′ region of CFTR showed the same distribution in the erosion analysis as signals obtained with the 5′-specific probe (CF1) in cases where the neighboring CORTBP2 gene showed a markedly different distribution (T-lymphocytes and Calu-3 cells; unpublished data).

To further address the spatial organization of the CFTR region, we analyzed the distances of the gene loci (Fig. 6). Again, GASZ/CFTR and CFTR/CORTBP2 pairs were detected simultaneously with two different fluorochromes in the same nucleus. The smallest distances were measured in SH-EP N14 cells, where all three gene loci were juxtaposed next to each other at the nuclear periphery (Figs. 3–5). The slightly larger distances measured in SH-EP N14 cells between CFTR and CORTBP2, as compared with GASZ and CFTR (Fig. 6 a), likely reflected the larger distances of the probes used for FISH (Fig. 1). Although the distances between GASZ and CFTR still did not exceed the 200-nm interval in 293 cells, as in SH-EP N14 cells, larger distances were measured between CFTR and CORTBP2 in 293 cells as compared with SH-EP N14 cells. In 293 cells, CORTBP2 occupied more interior positions (Figs. 3–5), whereas GASZ and CFTR were both associated with the nuclear periphery (Fig. 3 and Fig. 4). Regarding primary T-lymphocytes, in 90% of the cases the distances between GASZ and CFTR did not exceed 200 nm. In 10% of the cases larger distances were measured, but did not exceed 400 nm. However, between CFTR and CORTBP2 a marked shift toward increased distances was observed (up to 1,100 nm). In primary T-lymphocytes CORTBP2 occupied substantially more interior positions than CFTR (Fig. 4 and Fig. 5). As CFTR is closely associated with the nuclear periphery in T-lymphocytes and 293 cells, the distance measurements relative to CFTR also roughly indicate the distance of the active CORTBP2 locus from the nuclear periphery.

The largest distances between GASZ and CFTR, as well as between CFTR and CORTBP2, respectively, were observed in Calu-3 cells. In this cell type CFTR displayed a markedly interior positioning, in contrast to the other two gene loci (Figs. 2–5). However, we wondered whether these increased distances were due to a more decondensed chromatin structure in Calu-3 cells. Therefore, we measured in the different cell types the sizes of the nuclei and the relative nuclear areas occupied by chromosome 7 territories. It was found that Calu-3 cells did have the smallest nuclei of all cell types ana-

Figure 5. Spatial arrangements of loci as revealed by dual-color FISH. (a) CFTR (green) and CORTBP2 (red) were simultaneously detected by dual-color FISH in a 293 nucleus (enlargements shown in the insets). Chromosome 7 territories are shown in blue (293 nuclei harbor three chromosome 7 territories). (b) The nuclear positions of adjacent loci simultaneously detected in the same nucleus by dual-color FISH were determined with respect to each other. The combinations of gene loci evaluated and the cell types analyzed are indicated. It was evaluated in each case whether CFTR was located more peripheral or more interior, respectively, with regard to the other locus, or whether both loci were juxtaposed with no locus being more interior or peripheral. In all cases for CFTR detection, the CF1 probe from the 5′ region of CFTR was used. A second CFTR-specific probe from the 3′ region of CFTR (compare with Fig. 1) was used in 293 cells, and the orientation of the corresponding FISH signal relative to the CF1-specific signal is shown in c. The bars show for each combination the percentages displaying the indicated orientation (average ± SD). n indicates the number of pairs of loci examined.
imaged by confocal microscopy. It should be noted that applying the FISH technique might lead to topological changes compared with the live cell situation, although generally a good preservation of the spatial organization of chromatin domains is observed at the level of light microscopy in formaldehyde-fixed nuclei (Robinett et al., 1996; Verschure et al., 1999; Solovei et al., 2002).

The results from Fig. 6 b revealed that the largest distances between GASZ and CFTR were in the 300-nm range, whereas the largest distances between CFTR and CORTBP2 were in the 500-nm range. Distances were measured between the intensity centers of the FISH signals. Considering that the distances between the middlepoints of the gene sequences covered by the respective probes used for FISH were ̇~85 kb (GASZ/CFTR) and ̇~255 kb (CFTR/ CORTBP2) apart from each other (Fig. 1), the corresponding degrees of compaction would be ̇~100-fold (GASZ/ CFTR) and ̇~175-fold (CFTR/CORTBP2), respectively (assuming a length of 3.4 × 10^6 nm per Mb DNA). This would be a higher degree of compaction as displayed by nucleosomal DNA or the 30-nm fiber. Nucleosomal DNA displays a packaging ratio of 1:7, whereas the 30-nm fiber is assumed to have an additional packaging ratio of 1:6 (Belmont et al., 1989).

**How are nuclear positioning and transcriptional activity of CFTR related to each other?**

To address the question of how transcriptional regulation and nuclear positioning of CFTR were related to each other, we treated cells with the transcriptional inhibitor 5,6-dichloroobenzimidazole riboside (DRB). The nuclear localization of CFTR was determined in 293, SH-EP N14, and Calu-3 cells by erosion analysis (Fig. 7). After DRB treatment, the perinuclear localization of CFTR remained unchanged in SH-EP N14 and 293 cells (Fig. 7). As revealed by RT-PCR analyses, these cell types did not express CFTR at detectable levels, neither before nor after DRB treatment. In contrast, in Calu-3 cells a significant increase in the numbers of FISH signals was observed in the outermost shell after DRB treatment. The erosion analysis revealed that the level of CFTR transcription was reduced to ̇~50% after DRB treatment (Table I).

To rule out that general changes of the chromatin structure due to DRB treatment in Calu-3 cells led to the positional change of CFTR, we analyzed as a control the positioning of the β-globin locus in this cell type with and without DRB treatment. The erosion analysis revealed that the β-globin locus resided in the nuclear interior in Calu-3 cells and that its positioning was not significantly different before and after DRB treatment (Fig. S3; unpaired t test, P < 0.05). RT-PCR analysis revealed that the level of CFTR transcription was reduced to ̇~50% after DRB treatment (Table I).

The relatively extreme distances observed in Calu-3 cells gave rise to the question of how far the neighboring gene loci could move apart. The 2D distance measurements described above were performed in methanol/acetic acid-fixed nuclei and the absolute distances between two loci might be overestimated by using this method. Therefore, we measured the 3D distances in formaldehyde-fixed Calu-3 nuclei.
The finding that CFTR associated with chromatin containing hyperacetylated histone H4 in Calu-3 cells (Fig. 2) suggested that also the histone acetylation levels might be involved in CFTR positioning. Therefore, we treated cells with the drug trichostatin A (TSA), which leads to histone hyperacetylation. In Calu-3 cells, where CFTR was embedded in the chromatin fraction containing hyperacetylated histone H4, no significant change in its positioning was observed after TSA treatment (Fig. 7; unpaired t test, P < 0.05). However, in 293 and SH-EP N14 cells, where CFTR was normally embedded within the hypoacetylated, perinuclear heterochromatin (Fig. 2 and Fig. 3), a dramatic change in CFTR positioning was observed. After TSA treatment, CFTR did not show perinuclear localization anymore, but occupied significantly more interior positions (Fig. 7; unpaired t test, P < 0.05). It should be noted that TSA treatment specifically affected only the positioning of CFTR when it was associated with hypoacetylated chromatin (293 and SH-EP N14 cells). Exactly in this situation CFTR positioning was not affected by DRB treatment. And vice versa, CFTR positioning was not affected by TSA treatment when CFTR was transcriptionally active and associated with hyperacetylated chromatin (Calu-3 cells), whereas this was the only situation when CFTR positioning was affected by DRB treatment. Also, these findings suggested that the positional changes induced by the different drugs were due to their specific effects on transcription and histone acetylation, and not due to general effects on chromatin structure.

Although the results obtained by TSA treatment suggest that the level of histone acetylation at the CFTR locus might provide positional information, additional careful analyses will be necessary to answer this question more clearly. Nevertheless, CFTR in its inactive state was driven from a repressive into an active environment by TSA treatment. Therefore, the question arose whether this might be accompanied by transcriptional activation of CFTR. RT-PCR analyses revealed that CFTR was not detectably transcribed in 293 and SH-EP N14 cells, neither before nor after TSA treatment. This result demonstrated that driving CFTR into a permissive environment was not sufficient for its transcriptional activation. Together, the results obtained by DRB and TSA treatment suggested that the nuclear positioning of CFTR was dependent on its transcriptional activity, whereas the transcriptional activity of CFTR was not primarily influenced by its nuclear localization.

**Localization of CFTR with respect to α-satellite DNA**

It has been described for a number of genes that they specifically associate with pericentromeric heterochromatin in their inactive states (Brown et al., 1997, 1999, 2001; Schübeler et al., 2000). This applied also to the β-globin locus, which was found to associate specifically with pericentromeric satellite DNA in T-lymphocytes (Fig. S4 a, available at http://www.jcb.org/cgi/content/full/jcb.200404107/DC1), in accordance with previous data (Brown et al., 2001). To investigate whether this also applied to CFTR, we performed dual-color FISH experiments with the CF1 probe and a probe specific for α-satellite DNA. The numbers of CF1 signals associated with α-satellite DNA were evaluated (Fig. S4 b and Table S1, available at http://www.jcb.org/cgi/content/full/jcb.200404107/DC1). In all six cell types, more than 80% of the CF1 signals were not associated with α-satellite DNA. In addition, a relatively high degree of association (17%) was observed in Calu-3 cells, where CFTR is highly expressed (Table S1). These results did not reveal a correlation between transcriptional silencing of CFTR and its association with pericentromeric satellite DNA.

**Positioning of GASZ, CFTR, and CORTBP2 with respect to chromosome 7 territories**

Finally, we investigated the relationships between the expression patterns of GASZ, CFTR, and CORTBP2 and their positioning with respect to the chromosome 7 territory in primary T-lymphocytes, 293 cells, and Calu-3 cells (Fig. 8). Regarding the positioning, three different classes were defined: (1) localization of the gene-specific signal within; (2) at the periphery; or (3) outside of the chromosome 7 territory as defined by the FISH signal of the painting probe.
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(Fig. 8 a). The localizations of the three genes (Fig. 8 b) did not show any correlation to their levels of transcription.

Discussion

We investigated nuclear positioning and transcriptional regulation of the three adjacent human genes GASZ, CFTR, and CORTBP2. Our results demonstrated that adjacent genes can associate simultaneously with distinct nuclear regions and chromatin fractions, in accordance with their individual transcriptional activity. These findings, showing that chromosomal subregions display highly flexible nuclear arrangements regulated at the level of individual genes, seem to be in contrast to previous data demonstrating that whole chromosomes or larger chromosomal subregions show a specific nuclear positioning (Ferreira et al., 1997; Croft et al., 1999; Sadoni et al., 1999; Volpi et al., 2000; Boyle et al., 2001; Mahy et al., 2002a,b; Williams et al., 2002). However, the position of a chromosomal subregion or of a whole chromosome reflects the sum of the positions of all individual genes and sequences comprised. Therefore, our data are in accordance with data showing that the bulk of a chromosome/chromosomal subregion containing many expressed genes localizes more to the interior than the bulk of a chromosome/chromosomal subregion comprising low numbers of genes and many nonexpressed genes (Ferreira et al., 1997; Croft et al., 1999; Sadoni et al., 1999; Boyle et al., 2001). Such data are also in accordance with the finding that larger chromosomal regions containing functionally related genes display a concerted positioning (Volpi et al., 2000; Williams et al., 2002). It should be noted that recent reports (Mahy et al., 2002a,b) suggesting rather region-specific than gene-specific positioning investigated nuclear positioning with respect to the chromosome territory. In agreement with these results, we did not find correlations between the transcriptional activity of individual genes and their positioning with respect to the chromosome territory.

Our findings with regard to endogenous loci are in agreement with the results of a previous work investigating transgenic sequences. It was demonstrated that a lac operator containing chromosome locus moved from the periphery to the nuclear interior after targeting of the transcription factor VP16 and transcriptional activation (Tumbar and Belmont, 2001). Interestingly, when a lac operator–containing construct was integrated in an extremely gene-rich region of human chromosome 1, the transgenic sequences constitutively resided in the nuclear interior and did not change their nuclear localization in conjunction with transcriptional activation (Janicki et al., 2004). These findings suggest that transcription units do not always localize in agreement with their transcriptional regulation, and that gene-rich regions might dominate the positioning of comprised inactive sequences. It will be most interesting to compare in future analyses the positioning of adjacent sequences from gene-poor and gene-rich regions in relation to their transcriptional regulation.

Our data suggested that rather than the positioning within the chromosome territory, the association with specific chromatin fractions and the nuclear periphery/lamina seems to be related to transcriptional regulation. When addressing associations with heterochromatin, our results revealed gene...
specific associations with defined subfractions of heterochromatin. For example, the β-globin locus associated specifically with pericentric heterochromatin, but not with the nuclear periphery. This is in accordance with previous reports demonstrating for the human β-globin locus, as well as for other gene loci, specific associations with pericentric heterochromatin (Brown et al., 1997, 1999, 2001; Schübeler et al., 2000). In contrast, genes from the CFTR region associated specifically with perinuclear heterochromatin, but not with pericentric or perinucleolar heterochromatin. This suggests that different fractions of heterochromatin are not equivalent and play a different role in gene regulation. This view is supported by the findings that the chromatin structure of mammalian pericentric heterochromatin appears to differ from the structure of other fractions of heterochromatin (Maison et al., 2002), and that the transcription factor Ikarus, required for the successful development of lymphocytes, is specifically enriched in pericentric heterochromatin, with which lymphoid-specific genes associate in their inactive states (Brown et al., 1997). A recent report did show that targeting of HP1-proteins to a transgene in mouse cells leads to silencing and recruitment to HP-1–rich pericentric heterochromatin (Ayyanathan et al., 2003). Interestingly, repression and changes in chromatin structure remained highly localized, suggesting that also recruitment to pericentric heterochromatin did not affect closely adjacent gene loci (Ayyanathan et al., 2003), although this possibility was not experimentally tested.

It remains to be determined which role associations with different chromatin fractions and the nuclear periphery play in the transcriptional regulation of CFTR. Cystic fibrosis is one of the most important models for gene therapy. The correlations observed between spatial nuclear arrangements and transcriptional regulation indeed imply that nuclear architecture must add an important level of regulation. However, the results of the experiments involving TSA and DRB treatment do not support this view and suggest that nuclear architecture does not play a primary role in transcriptional regulation of CFTR. However, our data do not allow conclusions with regard to the cell types targeted during gene therapy of CF, nor do they allow conclusions regarding long-term effects and the role of nuclear positioning in the stable maintenance of CFTR expression. Therefore, it will be an important task to find out more about the question of how the nuclear organization of CFTR affects its long-term regulation in the lung tissue.

Materials and methods

Cell culture and fixation

For details of cell culture see supplemental data. Cells were treated with 10 ng/ml TSA for 10 h and with 50 µg/ml DRB for 5 h. For the erosion analyses, 2D distance measurements, determining the orientation of loci in dual-color FISH experiments, and the analyses regarding the positioning with respect to chromosome 7 territories and α-satellite DNA, cells were fixed with methanol/acetic acid (3:1) after hypotonic treatment (70 mM KCl for 20 min). For 3D analyses, cells were fixed with formaldehyde (3.7% in PBS) for 10 min at RT.

DNA probes and probe labeling

As probes for FISH we used four different probes from the CFTR region (Fig. 1). In addition, probes specific for the β-globin locus and α-satellite DNA were used, as well as a painting probe for chromosome 7. For further details see supplemental data.

FISH

FISH was essentially performed as described previously (Zink et al., 1998). For further details see supplemental data.

ImmunofISH

Immunostaining was performed with the antibody R232/8 specific for histone H4Ac8 as described previously (Sadoni et al., 1999) or with an antibody specific for LAP2β (BD Biosciences). Primary antibodies were detected with FITC- or Cy5-conjugated goat anti–rabbit or goat anti–mouse antibodies (Dianova). Immunostaining was performed with formaldehyde-fixed cells, which were fixed again with formaldehyde before in situ hybridization.

Replication labeling

Scratch replication labeling (Schermelh et al., 2001) was performed with FITC-dUTP. Cells were fixed 30 min after scratch replication labeling with formaldehyde. After fixation, the usual FISH procedure was performed. BrdU pulse labeling was performed as described previously (Zink et al., 1998).

Imaging

Confocal imaging was performed as described previously (Eils et al., 1996). Epiﬂuorescence imaging was performed with a microscope (Axiovert; Carl Zeiss MicroImaging, Inc.) equipped with a CCD camera. Further details are provided in the supplemental data.

Erosion analyses, calculations, distance measurements, and statistical analyses

Erosion analyses and the arrangements of images were performed with Adobe Photoshop (version 7.0). Calculations and the arrangement of diagrams were performed with Microsoft Excel 2000. For microscopic calibra-

Quantitative RT-PCR

Human adult testis RNA has been obtained from the BioCat GmbH (Heidelberg, Germany). Other RNA was extracted from the various cell lines by the TRIzol method (Invitrogen Life Technologies), and oligo(dT)-primed reverse transcription reaction was performed with 5 µg total RNA using Superscript III reverse transcriptase (Invitrogen). Duplex PCR was performed to amplify each of the three target genes (CORTBP2, GASZ, and CFTR) simultaneously with α-actin as described previously (Amaral et al., 2004). For further details see supplemental data.

Online supplemental material

The supplemental materials describe details of the materials and methods used. The supplemental ﬁgures show a gallery of confocal sections of a replicational pulse-labeled Calu-3 nucleus after detection of CFTR and examples of relative quantitative PCR ampliﬁcations of CFTR and CORTBP2 in Calu-3 and HEK 293 cells, respectively. Furthermore, they show results of the erosion analysis with regard to the β-globin locus. Also, results of dual-color FISH experiments addressing the association of CFTR and the β-globin locus with α-satellite DNA are presented. Online supplemental material available at http://www.jcb.org/cgi/content/full/jcb.200404107/DC1.

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Spatial organization of active and inactive genes and noncoding DNA within chromosome territories. 


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Cell culture
SH-EP N14 neuroblastoma cells, Calu-3 airway adenocarcinoma cells (no. HTB-55; American Type Culture Collection), HeLa cervix carcinoma cells, HT1080 fibrosarcoma cells, and HEk 293 cells were cultivated in DME supplemented with 10% FCS and antibiotics. Primary human T-lymphocytes (obtained from peripheral blood samples of healthy donors) were cultivated in RPMI 1640 medium supplemented with 15% FCS, antibiotics, and phytohemagglutinin or put into extraction buffer immediately after isolation for RNA analysis. For RT-PCR analysis, normal human nasal epithelial (NHNE) cells were obtained as described previously (Beck et al., 1999). Primary cultures of NHNE cells (see below) were used for microscopy.

Primary cultures of normal human nasal epithelial cells
Nasal specimens were obtained during surgery from inferior turbinate mucosa of patients suffering from septal deviation. Epithelial cells were dissociated from the tissue by mechanical dissection of the tissue and washing in PBS, followed by incubation with 1 U/ml dispase II in PBS for 1 h at 37°C. The cell suspension was then filtered through a 100-μm pore size filter (Falcon filter) and centrifuged at 150 g for 5 min at RT. The cell suspension obtained after centrifugation was resuspended in bronchial epithelial cell growth medium kit (Promocell) and RPMI 1640 containing 10% FCS, 100 U/ml penicillin, 100 μg/ml streptomycin, and 100 μg/ml gentamycin, and was plated on tissue culture dishes coated with 20 μg/cm² of calf skin collagen type I (Sigma-Aldrich). Cells were then cultivated at 37°C in 5% CO₂.

Probes and probe labeling
As a probe for the 5′ region of CFTR, we used purified PAC DNA (Schindelhauer and Cooke, 1997) of PAC CF1 containing exons 1–9 of the CFTR gene (RCIP 704F2220; the probes specific for the 3′ end of CFTR, as well as for GASZ and CORTBP2 were generated by PCR using specific primer pairs from PACs CF3 (RCIP 704G2012) and CF7 (RCIP 704C424). Primers were used as follows: CF21F (Zielenski et al., 1991) and a16BR, 5′-TGGCGGCGTGGTAAACATGTCAGTTG-3′ (includes exons 21–24 of the CFTR gene); primers GSR 5′-GTGATCTTTCACTCCATTATGTTG-3′ (exons 2–5 of the GASZ gene); and primers CO117cR 5′-AGAGCCCGACTGCAACTCTTG-3′ and CO95F, 5′-GCCCTAGAAATCTTGTGATGAC-3′ (exons 9–17 of the CORTBP2 gene). For in situ hybridization, gene-specific probes were labeled with biotin by PCR. The painting probe specific for chromosome 7 was a gift from Stefan Muller (Ludwig Maximilians University Munich, Munich, Germany). This probe was labeled with digoxigenin by PCR. Alternatively, this probe was directly labeled by PCR with FITC-dUTP or Cy5-dUTP. The painting probe was included in most FISH experiments to control the specificity of gene-specific signals. For simultaneous detection of two different gene loci by dual-color FISH, probes were labeled with digoxigenin-dUTP (CFTR) and biotin-dUTP (CORTBP2 and GASZ)

The probe for the β-globin locus (BAC 305, 174 kb) was a gift from the laboratory of Mark Groudine (Fred Hutchinson Cancer Research Center, Seattle, WA). As a template to amplify the probe for the α-satellite DNA we used human genomic DNA. For PCR the following primers were used: PAG, 5′-AGAAGCTTTTCTTGTATGCG-3′; and PAGD, 5′-CTAGTGTATGCGTACACATCTCC-3′.

FISH procedure
Biotinylated gene-specific probes were detected with avidin-Cy3 (Linaris). The hybridization signal was enhanced with a biotinylated anti-avidin antibody (Dianova). For direct labeling of probes, Fluorescein-12-dUTP (Roche Diagnostics), Cy3-dUTP, and Cy5-dUTP (Amersham Biosciences) were used. Before microscopy, DNA was stained with DAPI (0.5 μg/ml, epifluorescence imaging) or propidium iodeide (100 ng/ml, confocal imaging).

Image acquisition
The microscopes used for confocal imaging were as follows: LSM 510 Meta (Carl Zeiss MicroImaging, Inc.) and TCS 4D. For imaging we used either a Plan-Apochromat 63× oil objective (NA 1.4; Carl Zeiss MicroImaging, Inc.) or a PL APO 63× oil objective (NA 1.4; Leica). The software used for confocal imaging was the LSM 510 Meta Professional (Carl Zeiss MicroImaging, Inc.) and the TCS software (Leica). For epifluorescence imaging, we used an Axiosvert 135 TV microscope (Zeiss MicroImaging, Inc.) equipped with a Plan-Apochromat 63× objective (NA 1.4) and a MicroMax high resolution CCD camera (Princeton Instruments). Images were acquired taking advantage of the MetaMorph software (4.17). Imaging was performed at RT and cells were mounted in Vectashield (Linaris).

Quantitative RT-PCR
Relative quantitative RT-PCR was performed as described previously (Amaral et al., 2004). The following primers were used: for CFTR (expected product of 391 bp), although a minor product of 208 bp is also expected, corresponding to the described skipping of exon 9); forward: B3R (Fam-labeled), reverse: C16D as described in Ramalho et al. (2002). For CORTBP2 (expected product of 390 bp), forward: G9CF 5′-GGTCAAAATCTTGTAGGCCAC-3′, reverse: CO10CR2 (5′-CTAGCCGTATGGTGATGCG-3′); for GASZ (expected product of 381 bp), forward: G1CF (Fam-labeled); 5′-GCCGACCTGCGCAGT-3′, reverse: G4C (5′-CTGACGAGCTGTCGACAGTCC-3′), for α-actin (expected product of 385 bp), forward: Act-F (Fam-labeled); 5′-GCACCTACTCCAGCCTTCC-3′, reverse: Act-R2 (5′-AGAAGGCTGTAAACGCAACTAG-3′), cDNA samples were heated at 94°C for 4 min and then were subjected to amplification cycles of denaturation at 94°C for 45 s, primer annealing at 59°C for 1 min, and extension at 72°C for 1 min, followed by a final extension at 72°C for 30 min. All PCR reactions were performed under exactly the same conditions. Additionally, aliquots were removed for analysis at different numbers of cycles (generally n, n + 2 and n + 4) to check whether both reactions (test and control) were still in the log phase (see Fig. S1). PCR products were separated by capillary electrophoresis in an automated sequencer (Prism 373A; Applied Biosystems) and quantitative analysis of peaks was performed with GeneScan software, as described previously (Ramalho et al., 2002; Amaral et al., 2004). This allows a direct integration of the peak area corresponding to the number of Fam-labeled molecules synthesized by PCR in order to determine the percentages of mRNA species from test genes (CFTR, CORTBP2, and GASZ) present relative to control mRNA (α-actin). The latter is assumed to be constant in all cell types and equal to 100%. When the peak corresponding to test gene only showed up when the α-actin amplification was entering the plateau phase, the initial value was considered to be the approximate abundance of the former versus actin. For a general confirmation of the relative levels of expression obtained, all positive amplifications were repeated in triplicate with a 2:8 α-actin primer mixture (nonextendable competitive/normal; see Amaral et al., 2004). This delayed the amplification of the α-actin peak, making it easier to calculate abundance of very scarce test genes, and confirmed the expression relationships presented in the main section (Amaral et al., 2004). However, when competitive primers are used in this way, direct comparisons of data can only be made for reactions with the same ratio of competitive/normal primers, so absolute values were not extrapolated from these supplemental data.
References


