Immortalization of pituitary cells at discrete stages of development by directed oncogenesis in transgenic mice

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SUMMARY

Targeted expression of oncogenes in transgenic mice can immortalize specific cell types to serve as valuable cultured model systems. Utilizing promoter regions from a set of genes expressed at specific stages of differentiation in a given cell lineage, we demonstrate that targeted oncogenesis can produce cell lines representing sequential stages of development, in essence allowing both spatial and temporal immortalization. Our strategy was based on our production of a committed but immature pituitary gonadotrope cell line by directing expression of the oncogene SV40 T antigen using a gonadotrope-specific region of the human glycoprotein hormone α-subunit gene in transgenic mice. These cells synthesize α-subunit and gonadotropin-releasing hormone (GnRH) receptor, yet are not fully differentiated in that they do not synthesize the β-subunits of luteinizing hormone (LH) or follicle-stimulating hormone (FSH). This observation lead to the hypothesis that targeting oncogenesis with promoters that are activated earlier or later in development might immortalize cells that were more primitive or more differentiated, respectively.

To test this hypothesis, we used an LHβ promoter to immortalize a cell that represents a subsequent stage of gonadotrope differentiation (expression of α-subunit, GnRH receptor, and LH β-subunit but not FSH β-subunit). Conversely, targeting oncogenesis with a longer fragment of the human α-subunit gene (which is activated earlier in development) resulted in the immortalization of a progenitor cell that is more primitive, expressing only the α-subunit gene. Interestingly, this transgene also immortalized cells of the thyrotrope lineage that express both α- and β-subunits of thyroid-stimulating hormone and the transcription factor GHF-1 (Pit-1). Thus, targeted tumorigenesis immortalizes mammalian cells at specific stages of differentiation and allows the production of a series of cultured cell lines representing sequential stages of differentiation in a given cell lineage.

Key words: transgenic mice, targeted oncogenesis, gonadotropins, thyroid-stimulating hormone, pituitary, mouse

INTRODUCTION

Organogenesis in mammals is a highly complex process that has been difficult to study experimentally. The anterior pituitary gland is an excellent model system for the study of cellular differentiation during organogenesis since the appearance of its five constituent endocrine cell types occurs in a well-defined order based on the expression of specific hormone genes. Thus, defining the regulation of hormone gene expression at various stages of anterior pituitary development will also enable us to elucidate the mechanisms of regulation of cytodifferentiation in this multifunctional organ. To this end, we have focused on creating cultured models that reflect distinct steps in anterior pituitary development.

The anterior pituitary is derived from a single epithelial layer referred to as Rathke’s pouch (Simmons et al., 1990). The earliest marker of anterior lobe differentiation is the glycoprotein hormone α-subunit gene which is expressed at approximately embryonic day 11.5 (E11.5) of gestation in the mouse (Japon et al., 1994). Beginning on E13.5, there is a clear progression of cell differentiation initiated by the commitment of the corticotrope lineage marked by the expression of the pro-opiomelanocortin (POMC) gene. Differentiation of the thyrotrope lineage occurs on E14.5 with the expression of thyroid-stimulating hormone (TSH) β-subunit. The somatotrope and lactotrope cells arise on E15.5, with the expression of growth hormone (GH) and prolactin (Prl) genes, respectively. The last lineage to emerge is the gonadotrope. Its differentiation pathway can be subdivided into two stages marked by the expression of the individual β-subunits of luteinizing hormone (LH) on E16.5 and follicle stimulating hormone (FSH) on E17.5. The individual β-subunits bind noncovalently to the common α-subunit to form the mature glycoprotein hormones, TSH, LH and FSH, and, appropriately, the expression of the...
α-subunit is restricted to the gonadotrope and thyrotrope lineages in adult pituitary.

Directed oncogenesis in transgenic mice allows the production of differentiated immortal cell lines for the study of tumorigenesis, gene expression, and the molecular and cellular biology of specific tissue types (Camper, 1987; Hanahan, 1989). Previously, we demonstrated that a transgene with 1.8 kb of the 5′ regulatory region of the human α-subunit gene linked to the coding region for the oncogene SV40 T antigen immortalized immature gonadotrope cells (the αT3-1 cell line) that expressed the α-subunit gene and responded to the gonadotrope-specific hypothalamic-releasing factor, gonadotropin-releasing hormone (GnRH), but did not express gonadotrope-specific hypothalamic-releasing factor, which the molecular mechanism of pituitary cellular differentiation at various stages of differentiation with hybrid oncogenic transgenes utilizing the regulatory regions of genes expressed at distinct stages of development. To test this hypothesis, we have used hybrid genes consisting of either the human or rat LH β-subunit promoter linked to T antigen to immortalize a cell that succeeds the αT3-1 cell in the gonadotrope lineage. Conversely, to capture a more primitive α-subunit-expressing cell that represents an earlier stage of anterior pituitary development than the αT3-1 cell, we introduced the oncogene T antigen under the control of a longer portion (5.5 kb) of the 5′ flanking region of the human α-subunit gene into transgenic mice. Using this approach, we have produced cell lines that express either the α-subunit alone, TSH (α and TSHβ), or LH (α and LHβ) genes. These cell lines maintain the phenotypic markers of their developmental stages and represent a progression of differentiation within the glycoprotein hormone-producing cell lineages. They provide novel model systems in which the molecular mechanism of pituitary cellular differentiation can be dissected. This study demonstrates that directed tumorigenesis controlled by regulatory regions that specify cell-type and temporal expression can result in the immortalization of cells at distinct stages of differentiation in a given developmental cell lineage.

MATERIALS AND METHODS

Plasmid construction

The α-Taq plasmid is as described (Windle et al., 1990). Digesting a parent Bluescript vector (p5.5TbSSK+) with BamHI followed by a partial digest with EcoRI released the α-subunit promoter spanning from approximately −5.5 kb to +49 (Fiddes and Goodman, 1981). This fragment was subsequently cloned into the EcoRI and BamHI sites upstream of the SV40 early region coding sequence for both large and small T antigens in the identical vector used to generate the 1.8 kb 5′ α-subunit/T antigen plasmid (Windle et al., 1990). The human gene for LHβ contains only 10 bases between the mRNA start site and the ATG initiation codon. Styl restriction enzyme cleaves this region at +5. Styl partial digest was treated with E. coli large fragment polymerase to repair the four base overhang, leaving a blunt end at +9. This was joined to the T antigen coding sequence with a XhoI linker at the BgII site of SV40. Similarly, a 1.8 kb fragment of the 5′ flanking region of the rat LH gene was isolated by digestion with HindIII and XhoI of a pUC19 plasmid (kindly provided by J. L. Roberts) which has an XhoI linker inserted at +5 of the rat LHβ gene. This fragment was cloned with the same SV40 T antigen DNA as described above. The structures of the human α-subunit/T antigen, and rat and human LHβ/T antigen transgenes are diagrammed in Fig. 1.

Transgenic animals

The transgene fragments were isolated with the appropriate restriction enzymes and purified after gel electrophoresis by binding to glass beads (BIO101, Inc., La Jolla, CA: GeneClean). The fragments were quantitated and diluted to a concentration of 2 μg/ml in injection buffer consisting of 10 mM Tris, pH 7.4 and 0.25 mM EDTA. The DNA was injected into the pronuclei of fertilized one cell mouse embryos derived from matings of CB6F1/J mice (C57Bl/6J × BALB/c; Jackson Laboratory, Bar Harbor, ME or Harlan Sprague Dawley, Indianapolis, IN). The injected embryos were implanted into CD-1 or ICR pseudopregnant hosts (Hogan et al., 1986). Genomic DNA was isolated from a small portion of the tail and analyzed for the presence of the transgene by Southern blot (Maniatis et al., 1982). For those transgenic lines that could be established from a fertile founder animal, transgene transmission was observed at approximately 50%.

Derivation of cell lines

Tumors were dissected from the sella turcica and gross autopsies were performed to identify any ectopic tumor formation. A small portion of each pituitary tumor was retained for RNA analysis and the remainder was minced and dispersed in Hanks Balanced Salt solution containing 10 mg/ml collagenase (Cooper Biomedical, Malvern, PA), and 10 μg/ml DNase I (Sigma, St Louis, MO) at 37°C for 30 minutes. The cells were washed in PBS and subsequently plated in Dulbecco’s Modified Eagles Medium (Gibco Laboratories, Grand Island, NY) containing 10% fetal calf serum (Hyclone Laboratories, Logan, UT), 4.5 mg/ml glucose, 100 U/ml penicillin, and 0.1 mg/ml streptomycin (Sigma, St. Louis, MO). The floating and weakly adherent cells were transferred to fresh plates every 2 days until the cells were freed of fibroblast contamination. After approximately 2-6 months, the endocrine cells became more adherent and began to grow on plastic. In the case of the TuxT1 line, the cells were seeded on Matrigel-coated plates (Collaborative Biomedical Products, Bedford, MA) which facilitated adhesion. Matrigel was diluted 30-fold prior to coating the plates. Subclones of each cell line were subsequently identified following clonal dilution or colony isolation. The cells are maintained in the above-mentioned medium in an environment of 5% CO2.

Northern analysis

Total RNA was isolated by the method of Chomczynski and Sacchi (Chomczynski and Sacchi, 1987) and 10 μg of each sample was electrophoresed in a 1% agarose gel containing formaldehyde. Equivalent loading was further verified by ethidium bromide staining (data not shown). Following transfer onto nylon membrane (Genescreen, NEN Research Products, Boston, MA), the RNA was fixed by UV-crosslinking using a Bio-Rad UV chamber (Bio-Rad Laboratories, Richmond, CA). Membranes were hybridized with a 32P-labeled cDNA probe overnight at 55°C in a 25% formamide solution. DNA probes to the hormones designated in the figure legends were radioactively labeled by random priming (Feinberg and Vogelstein, 1983, 1984). Excess probe was removed by washing at 65°C with 0.2× SSPE (36 mM NaCl, 2 mM sodium phosphate, 0.2 mM EDTA) and 0.1% sodium dodecyl sulphate. Blots were stripped by boiling in 1% glycerol, 0.5% sodium dodecyl sulfate and 2 mM EDTA before rehybridization with subsequent probes.

Electrophoretic mobility shift assay (EMSA)

Nuclear extracts were prepared as previously described by Eraly and Mellon (1995), and stored at −80°C. Protein concentrations were determined using Bio-Rad protein assay reagent (Bio-Rad, Richmond, CA). In a total volume of 20 μl, 5 μg of nuclear extract was mixed with 1 μg poly(dl-dc) as nonspecific competitor and 1% Ficoll 400 in a buffer containing 75 mM NaCl, 15 mM Tris, pH 7.4, 1.5 mM EDTA, 4% glycerol, 20 μg/ml bovine serum albumin and 1.5 mM DTT. Following preincubation at 4°C for 20 minutes, 1 ng of radiolabeled oligonucleotide was added to each reaction mix and incubated

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RESULTS

Tissue-specific tumorigenesis in transgenic mice
To test the hypothesis that cells representative of different stages of a given cell lineage could be immortalized by targeting expression of an oncogene using regulatory regions of genes expressed sequentially during development, we generated transgenic mice using various glycoprotein gene 5' regulatory regions linked to the early coding region of SV40. This portion of the virus produces both the large and small T antigens by differential splicing (herein referred to as T antigen). Fig. 1 illustrates the structure of the transgenes that were injected into fertilized eggs. The resultant founder mice derived from these tumors only expressed the partner glycoprotein hormone subunits of TSH, LH and FSH were not detectable, demonstrating that the tumors were composed predominantly of cells that only expressed α-subunit but not β-subunit genes. As expected, GH and POMC mRNAs were not detectable with the exception of a weak signal for POMC in the αT12-2 tumor. This may be due to inclusion of some tissue from the intermediate lobe of the pituitary in the tumor sample. It is likely that some portion of the tumors contained normal pituitary tissue that was unidentifiable and unavoidable upon initial dissection.

Surprisingly, the majority of the tumors did express Prl RNA. This implies that either the tumor cells expressed both α-subunit and Prl genes, or that normal pituitary cells are intermingled with transformed cells. Since the lactotrope (the cell that expresses Prl) is the only anterior pituitary cell type that is under negative growth regulation by the hypothalamus (through dopamine), high Prl expression may be due to physical disruption of hypothalamic regulation of normal lactotrope cells by the tumor followed by expansion of the lactotrope population due to derepression of mitosis. High levels of Prl mRNA would be due to a lack of hypothalamic dopaminergic inhibition of Prl expression and a lack of inhibition of mitosis (Weiner et al., 1988) in nontransformed lactotropes due to compression of the hypothalamic stalk by the tumor and consequent lack of dopamine. In support of this, the cell lines derived from these tumors only expressed α-subunit and did not express Prl (Windle et al., 1990).

To generate tumors that contain cells that are more differentiated than the cells in the αT tumors, i.e. that express the tumor fragments from four αT transgenic lines (αT-1 was a single animal which did not breed to allow creation of a mouse line). Hybridization with cDNA probes of the seven pituitary hormone markers demonstrated that these tumors expressed varying levels of the endogenous α-subunit mRNA (Fig. 2). The partner glycoprotein hormone β-subunits of TSH, LH and FSH were not detectable, demonstrating that the tumors were composed predominantly of cells that only expressed α-subunit but not β-subunit genes. As expected, GH and POMC mRNAs were not detectable with the exception of a weak signal for POMC in the αT12-2 tumor. This may be due to inclusion of some tissue from the intermediate lobe of the pituitary in the tumor sample. It is likely that some portion of the tumors contained normal pituitary tissue that was unidentifiable and unavoidable upon initial dissection.

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expression in the hLT mice was similar to the αT mice in that α-subunit was expressed in all tumors (Fig. 3A). However, in contrast to the αT tumors, hLT tumors also expressed the glycoprotein hormone β-subunits. The tumor dissected from animal hLT15-10 expressed both TSHβ and LHβ, and that of animal hLT15-10 expressed high levels of LHβ and FSHβ.

In contrast to the hLT mice, those animals generated using the rat LHβ 5′-flanking sequence lacked pituitary-specific T antigen expression, developing tumors more frequently in the brain and the pancreas (rLT mice, Table 3). Ectopic tumor formation in the brain and pancreas are common in T antigen transgenic mice due to ‘leaky’ T antigen expression in these tissues (Brinster et al., 1984). One transgenic mouse line, rLT4, occasionally developed pituitary tumors which were manifested at an early age of 100-200 days, but this phenotype was not uniformly inherited. Tumors derived from the rLT4 mouse line expressed high levels of three gonadotropin subunits but not TSHβ (Fig. 3B). (The lower band seen in the blot hybridized with an FSHβ probe is residual α-subunit probe which was inadequately stripped.) As was the case for the αT tumors, GH and POMC mRNA were not expressed but Prl mRNA was expressed to varying degrees in the tumors from the hLT animals (data not shown).

Since the human LHβ 5′ region targeted the pituitary with fidelity, while a longer fragment of the rat LHβ 5′ DNA failed to demonstrate specificity, it is clear that the species derivation of the promoter used to drive T antigen expression can be an important variable in the determination of the type of tumors formed. Furthermore, the appearance of FSHβ mRNA in some of the hLT and rLT tumors may signal the presence of fully differentiated gonadotropes within the tumor cell population.

To target T antigen-mediated immortalization to the α-subunit-expressing bipotential progenitor cells that exist prior to the branching of the thyrotrope and gonadotrope lineages in the pituitary anlage, we used a transgene that contained 5.5 kb of the promoter used to drive T antigen expression can be an important variable in the determination of the type of tumors formed. Furthermore, the appearance of FSHβ mRNA in some of the hLT and rLT tumors may signal the presence of fully differentiated gonadotropes within the tumor cell population.

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thryotrope lineage. Four transgenic mouse lines were generated using 5.5 kb of the human α-subunit gene linked to T antigen. Mice from three of these transgenic lines develop pituitary tumors at various ages (5aT mice, Table 4). Pituitary tumors in the 5aT12 line are the most aggressive resulting in female infertility and fatality by 67 days of age. Both sexes of lines 5aT40 and 5aT45 are fertile and were bred to homozygosity to accelerate tumor formation. Northern blot analysis of pituitary tumor RNA shows that the α-subunit gene is expressed to varying degrees in the pituitary tumors from the three transgenic mouse lines (Fig. 4). Unlike the αT tumors created with the 1.8 kb fragment of the human gene, some of the 5aT tumors expressed the β-subunits of the gonadotropin hormones. Interestingly, however, the expression of the β-subunits was inconsistent between tumors even from the same transgenic mouse line. For example, Fig. 4 illustrates that, while some tumors analyzed from line 5aT45 expressed the β-subunit of LH and/or FSH (5aT45-3), other tumors taken from animals of the same line did not (5aT45-6). This inconsistency points out that not all tumors generated from a single transgenic mouse line are identical and that they may arise from multiple independent clonal events within each tumor. Though this transgene might have been expected to target both the thyrotrope and gonadotrope lineages, none of these tumors expressed detectable levels of the β-subunit of TSH.

**Cell lines derived from the pituitary tumors reflect various stages of pituitary cell differentiation**

Tumors isolated from many of the transgenic lines were dispersed and maintained in culture for several months to free the immortalized cells (those that express T antigen) from supportive connective tissue, blood cells, endothelial cells, and nontransformed pituitary cells. Three novel cell lines were derived from tumors of the rLT and 5aT transgenic mouse lines. Cell lines could not be derived from the hLT mice since the tumors grow slowly and are not manifested until the animals are over 1 year old. In several attempts, we have not been successful at generating cell lines from tumors taken from animals older than 10 months of age (see Table 2). Once subclones were isolated, the expression pattern of pituitary hormones in the individual cells lines was analyzed and compared to the primitive gonadotrope cell line, αT3-1, to identify the lineages and developmental stages targeted by the respective promoters (Fig. 5). None of the cell lines generated express markers of the corticotrope, somatotrope or lactotrope lineages (Fig. 5).

The LβT4 cell line was generated from pituitary tumors that developed in transgenic animals of the rLT4 line in which T antigen is under the control of the rat LHβ-subunit promoter. As predicted from the expression pattern in the tumor, the LβT4 cells express the β-subunit of LH in addition to α-subunit and GnRH receptor (GnRH-R), the gonadotrope genes expressed by the αT3-1 cell line (Fig. 5). LβT4 and a second cell line derived from a tumor in another mouse from the same transgenic line (LβT2; data not shown) are the only cell lines that express the more differentiated gonadotrope marker, the LHβ-subunit gene. They do not express the β-subunit of FSH (Fig. 5), and therefore are most likely to represent a narrow window in pituitary gonadotrope development between the onset of LHβ-subunit (E16.5) and FSHβ-subunit (17.5) gene expression.

In accordance with our original hypothesis that the 5.5 kb fragment of the human α-subunit gene might target expression to an earlier stage of pituitary development, we isolated a primitive cell, the αT1-1 cell line, that expresses the α-subunit gene but does not express any further differentiated markers of the anterior pituitary lineages (Fig. 5). The αT1-1 cell line was isolated from a tumor from the 5aT12 mouse line. Several cell lines generated from the 5aT45 transgenic mouse line were of the gonadotrope lineage and were similar to the αT3-1 cell line.

### Table 4. Transgenic mice carrying the 5.5 kb human α-subunit promoter linked to T antigen

<table>
<thead>
<tr>
<th>Mouse line</th>
<th>Pituitary tumors*</th>
<th>Ectopic tumors†</th>
<th>Reproductive status‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>5aT12</td>
<td>67 d brain</td>
<td>M fertile; F infertile</td>
<td></td>
</tr>
<tr>
<td>5aT17</td>
<td>none choroid plexus, 67 d</td>
<td>infertile</td>
<td></td>
</tr>
<tr>
<td>5aT40</td>
<td>homogoyte, 197 d bladder, liver, 253 d</td>
<td>kidney, stomach fertile</td>
<td></td>
</tr>
<tr>
<td>5aT45</td>
<td>165 d</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Animals were killed or died due to pituitary or other tumors at the age indicated.
†Tumors in addition to pituitary tumors which were identified upon autopsy.
‡Indicates the fertility profile of the founder and transgenic lines. (M) male, (F) female.
line, while others resembled the αT1-1 cell line (data not shown).

Though we did not detect TSHβ gene expression in the 5αT pituitary tumor fragments that we analyzed, we were able to isolate a single TSHβ-expressing cell line, the ToT1 cell line (Fig. 5), from a tumor of the 5αT12 transgenic line. One possible explanation for the presence of thyrotropes is that two independent clonal transformation events may have taken place in the same pituitary giving rise to two cell types present at different levels or locales within the same tumor. Alternatively, since TSHβ-subunit initiates 3 days after α-subunit expression, one might predict that a population of immortalized primitive α-subunit expressing cells was present prior to the immortalization of a differentiated thyrotrope. If this were the case, the majority of the tumor would be composed of the primitive cell type that gave rise to the αT1-1 cell line and the thyrotrope cells that gave rise to the ToT1 cell line would be in the minority and below the sensitivity of the assay. However, more sensitive detection methods, such as RT-PCR and immunocytochemistry, would likely confuse the interpretation of tumor data because of possible contamination with normal pituitary cells.

**Immortalized cell lines express pituitary transcription factors**

The individual endocrine cell types and lineages of the anterior pituitary are marked by the expression of specific transcription factors as well as hormone subunits and receptors. Recent studies have identified two factors from the lim homeodomain family, mLIM-2 and mLIM-3 (also termed LH-2 and P-lim, respectively) that are expressed in the fetal and adult anterior pituitary (Bach et al., 1995; Roberson et al., 1994; Seidah et al., 1994). These two factors are expressed during active differentiation in the fetal pituitary and may be important in transcriptional activation of gene expression in several anterior pituitary cell types. Therefore, we tested for their expression in the precursor (αT1-1), thyrotrope (ToT1) and two gonadotrope cell lines (αT3-1 and LβT4) (Fig. 6). Both mLIM-3 and mLIM-2 were expressed in all four cell lines indicating that expression of these factors does not correlate with the transitions during thyrotrope and gonadotrope differentiation.

**Fig. 3.** Glycoprotein hormone subunit mRNA expression in tumors created by the LHβ promoter/T antigen transgenes. 10 μg of total RNA from pituitary tumors from (A) hLT and (B) rLT transgenic mice were analyzed for the expression of glycoprotein hormone subunit mRNAs relative to a normal pituitary control. Northern blots were sequentially hybridized with the following cDNA probes: mouse α-subunit, rat LHβ, rat FSHβ, mouse TSHβ (as in Fig. 2).

**Fig. 4.** Analysis of pituitary hormone mRNA expression in 5αT transgenic mouse tumors. 10 μg of total RNA from pituitary tumors from 5αT mice were analyzed by northern blot for the expression of anterior pituitary hormones relative to a normal control pituitary. Northern blots were sequentially hybridized with the following cDNA probes: mouse α-subunit, mouse LHβ, rat FSHβ, mouse TSHβ, rat GH, mouse PRL and rat POMC (as in Fig. 2).
represented by these cell lines and that they are likely to be active prior to the activation of the α-subunit gene.

Another murine homeobox gene localized to Rathke’s pouch, Rpx, is the earliest known transcriptional regulator detected in this embryonic tissue (Hermesz et al., 1996). Rpx expression is observed as early as E9 in the layer of ectodermal cells that will give rise to Rathke’s pouch and is progressively lost from E12.5 to E15.5, correlated with the emergence of the differentiated endocrine cell types. Northern blots using an Rpx cDNA probe (kindly provided by K. Mahon) have thus far failed to detect Rpx expression in the RNA from these cell lines, perhaps indicating that Rpx expression is lost prior to commitment to differentiated cell fate in the gonadotrope and thyrotrope lineages.

**Pituitary cell lines produce cell type-specific transcription factors**

Baehrecke and Mellon (1994) demonstrated that the transcription factor, steroidogenic factor (SF-1), regulates the α-subunit gene in the αT3-1 cell line through a gonadotrope specific element (αGSE) and that its expression is restricted to gonadotrope cell lines. Moreover, Ingraham et al. (1994) determined that expression of SF-1 colocalizes with LHβ and FSHβ expression in the pituitary, initiating at E13.5, subsequent to α-subunit expression. To test whether SF-1 expression precedes the expression of other differentiated markers of the gonadotrope lineage (i.e. GnRH receptor), the cell lines were assayed for SF-1 expression with particular interest in the αT1-1 cell line. Appropriately, SF-1 is expressed in both of the αT3-1 and LβT4 gonadotropic cell lines but was not detectable in either the TSH-expressing TαT1 thyrotropic cells or the early αT1-1 early progenitor cells (Fig. 7A). Upon screening multiple α-subunit-expressing cell lines, we have yet to find one that expresses SF-1 in the absence of GnRH receptor or vice versa, suggesting that these genes may share common regulatory components.

To demonstrate the gonadotrope specificity of the SF-1 protein, we utilized the αGSE as a probe in electrophoretic mobility shift assays (EMSAs) with nuclear proteins (Fig. 7B). Specific protein complexes bind to this element in nuclear extracts from all cell lines as determined by competitions with unlabeled probe and a mutant αGSE (mGSE) probe. However, an SF-1 competitor oligonucleotide derived from −50 to −36 of the human cholesterol side-chain cleavage enzyme gene (Rice et al., 1990) is only capable of displacing the specific complex in the αT3-1 and LβT4 gonadotrope cells, demonstrating that this major complex is SF-1.

The POU-homeodomain protein GHF-1 (Pit-1) is crucial for the maintenance of mature somatotropes, lactotropes and thyrotropes in vivo (Li et al., 1990). Yet the onset of TSHβ expression precedes GHF-1 by at least one day (Simmons et al., 1990) and may be present in two populations of cells, an early transient population present in the developing pars tuberalis of the anterior pituitary that does not express GHF-1 and a later population arising in the pars distalis that is dependent on GHF-1 for survival and persists through adulthood (Lin et al., 1994). Therefore, to further delineate the identity and developmental stage of the thyrotropic TαT1 cells, northern blots were performed using a radiolabeled GHF-1 cDNA probe and EMSAs were performed with a probe corresponding to a consensus GHF-1 DNA-binding site (Fig. 8). The TαT1 cells expressed two transcripts of the approximate size of 2.6 kb and 1.9 kb that comigrate with transcripts in the normal mouse pituitary (Fig. 8A). However, evidence exists that the onset of GHF-1 transcription may precede the appearance of GHF-1 protein (Dollé et al., 1990). Furthermore, it has been suggested that GHF-1 is translationally controlled in the αTSH cell line (Gordon et al., 1993), a thyrotropic cell line that expresses α subunit but not TSH β-subunit (Akerblom et al., 1990). EMSA demonstrates that nuclear extracts from the TαT1 cells contain a protein that binds a consensus GHF-1-binding site with an identical pattern to extracts from the GHFT-1 cell line that expresses GHF-1 (Lew et al., 1993). This specific complex was displaced from the binding site by 100-fold excess of unlabeled GHF-1 oligonucleotide but not unlabeled SF-1 oligonucleotide (Fig. 8B). GHF-1 binding was not observed in an EMSA performed with αT1-1, αT3-1 or LβT4 nuclear protein extracts (data not shown). These data indicate that the thyrotropic TαT1 cell line is most likely derived from the surviving pars distalis...
thyrotrope cell population that is dependent on GHF-1 and persists in adult pituitary.

Fig. 6. Expression of lim homeodomain transcription factors. The indicated cell lines were analyzed for the expression of two lim-homeodomain transcription factor family members, mLIM-3 and mLIM-2 by northern blot analysis. The cDNA probe for mLIM 2 was generously provided by Dr Tom Jessell and Dr Fred Alt (Xu et al., 1993). The cDNA used for the mLIM-3 probe is a PCR-derived sequence cloned from mouse anterior pituitary cDNA using primers encompassing the entire coding sequence (Seidah et al., 1994). Though expression was detected in all four cell lines, mLIM-2 could not be detected in total RNA from the adult pituitary and may be present below the level of detection.

DISCUSSION

Targeted tumorigenesis in transgenic mice has been a powerful tool for the study of oncogenesis and gene expression, and for the production of differentiated immortal cell lines from particular tissues (Camper, 1987; Hanahan, 1989). Here we demonstrate that immortalization can be targeted not only spatially but temporally as well. This approach allows the generation of cell lines representative of discrete stages of development within cell lineages that occur transiently within complex tissues and would otherwise be inaccessible. In this study, we utilized 5’ flanking regions of genes expressed at definitive stages of commitment along the differentiation pathway of the gonadotrope and thyrotrope cell lineages to direct oncogene expression. In each case, this initiated a transformation process that immortalized cells at the stage when the regulatory regions contained within the respective upstream sequences become active (Fig. 9). The resulting cells maintain expression of the set of differentiated markers of the cell lineages characteristic of the stage of differentiation at which the targeting gene is first activated during development.

Based on our previous results in which immature gonadotrope cell lines were generated using 1.8 kb of the human α-subunit promoter to direct Tag expression (Windle et al., 1990), we hypothesized that it might be possible to immortalize cells that represented intermediate steps in the differentiation pathway of a given cell lineage by directing T antigen expression with upstream regulatory sequences of markers that are activated at sequential stages of development. The glyco-
The specificity of the shifted complexes. An excess of cold probes of the GHF-1- and SF-1-binding sites verifying a positive control. Competitions were performed using 100-fold line, GHFT-1 (Lew et al., 1993), were analyzed in the same assay as consensus binding site. Extracts from the GHF-1 overexpressing cell line, GHFT-1 (Bodner et al., 1988). (B) Extracts from the T cell line are a differentiated thyrotrope cell that produces GHF-1 (Pit-1). (A) 10 μg of total RNA isolated from the various cell lines were analyzed for the expression of GHF-1. The cDNA probe used was a fragment of the rat GHF-1 coding sequence (Bodner et al., 1988). (B) Extracts from the TαT1 were assayed by EMSAs for the ability to form specific complexes with a GHF-1 consensus binding site. Extracts from the GHF-1 overexpressing cell line, GHFT-1 (Lew et al., 1993), were analyzed in the same assay as a positive control. Competitions were performed using 100-fold excess of cold probes of the GHF-1- and SF-1-binding sites verifying the specificity of the shifted complexes.

Fig. 8. The TαT1 cell line is a differentiated thyrotrope cell that produces GHF-1 (Pit-1). (A) 10 μg of total RNA isolated from the various cell lines were analyzed for the expression of GHF-1. The cDNA probe used was a fragment of the rat GHF-1 coding sequence (Bodner et al., 1988). (B) Extracts from the TαT1 were assayed by EMSAs for the ability to form specific complexes with a GHF-1 consensus binding site. Extracts from the GHF-1 overexpressing cell line, GHFT-1 (Lew et al., 1993), were analyzed in the same assay as a positive control. Competitions were performed using 100-fold excess of cold probes of the GHF-1- and SF-1-binding sites verifying the specificity of the shifted complexes.

Thyrotropes

Gonadotropes

Fig. 9. The TαT1 cell line is a differentiated thyrotrope cell that produces GHF-1 (Pit-1). (A) 10 μg of total RNA isolated from the various cell lines were analyzed for the expression of GHF-1. The cDNA probe used was a fragment of the rat GHF-1 coding sequence (Bodner et al., 1988). (B) Extracts from the TαT1 were assayed by EMSAs for the ability to form specific complexes with a GHF-1 consensus binding site. Extracts from the GHF-1 overexpressing cell line, GHFT-1 (Lew et al., 1993), were analyzed in the same assay as a positive control. Competitions were performed using 100-fold excess of cold probes of the GHF-1- and SF-1-binding sites verifying the specificity of the shifted complexes.

protein lineage of the anterior pituitary proved to be an excellent model in which to test this hypothesis since multiple stages of its differentiation pathway are distinguished by the expression of individual subunit genes allowing us to target expression to intermediate stages in development and to identify characteristic marker genes expressed in the resultant cell lines.

The initiation of anterior pituitary differentiation is marked by the expression of the glycoprotein hormone α-subunit gene. Subsequently, α-subunit-expressing cells commit to either the thyrotrope or gonadotrope lineage. The mature thyrotropes arise first on E14.5 with the expression of TSHβ-subunit, while the emergence of mature gonadotropes occurs in two stages – with the expression of LHβ-subunit gene and FSHβ-subunit gene on E16.5 and E17.5, respectively. Based on this temporal pattern of expression of individual subunit genes, 5′ flanking sequences were chosen that when linked to T antigen were likely to immortalize cells that developmentally flank the original αT3-1 pregonadotrope cell line. Using 1.8 kb of the rat LHβ promoter and 5.5 kb of the human α-subunit promoter, we successfully immortalized cells that represent multiple steps of the above defined differentiation pathway.

As predicted, targeting oncogenesis with the 5′ flanking region of the LHβ gene produced cell lines that exhibit many of the highly specific characteristics of a mature gonadotrope, with the exception of the expression of FSHβ gene. In addition to expressing both the LHα and LHβ subunits, the GnRH receptor and the transcription factor SF-1, the LβT4 and LβT2 cell lines secrete intact, biologically active LH (Turgeon et al., 1996). This response is strongly augmented by estrogen, dexamethasone and pulsatile administration of GnRH (Turgeon et al., 1996). Furthermore these cells demonstrate intracellular calcium fluxes in response to GnRH indicating fidelity of gonadotrope physiological behavior (Thomas et al., 1996). The 5.5 kb α-subunit regulatory region linked to T antigen caused immortalization of cell lines representative of α-subunit-expressing cells that are present prior to the commitment to either glycoprotein lineage or are present subsequent to the branching of the gonadotrope and thyrotrope lineages. This suggests that elements necessary for thyrotrope-specific targeting and for early expression of α-subunit in a bipotential progenitor reside between –5.5 kb and –1.8 kb of the human gene, upstream of gonadotrope-specific elements. This presumptive enhancer likely contains both cell-specific as well as temporal regulatory sequences. These results emphasized that, while 1.8 kb of the 5′ flanking region is sufficient to direct oncogene expression to the gonadotrope lineage, it does not contain the regulatory elements necessary for α-subunit expression in the anterior pituitary anlage or in the thyrotrope lineage (see also Hamernik et al., 1992). These observations are in agreement with Kendall et al. (1994), who, using varying lengths of 5′ flanking region of the mouse α-subunit linked to the reporter gene, β-galactosidase, demonstrated that while 0.48 kb was sufficient to direct minimal expression to both the gonadotrope and thyrotrope cells in transgenic mice, sequences between –4.6 and –2.7 conferred high levels of reporter gene expression in the thyrotrope lineage. This enhancer in the
mouse gene was not detectable using in vitro assays. Future studies will attempt to delineate enhancer elements upstream of ~1.8 kb in the human α-subunit gene.

Surprisingly, in addition to the progenitor cell expressing only the α-subunit gene, a thyrotrope cell was derived from tumors in which TSHβ-subunit could not be detected by northern blot. This cell expresses the transcription factor GHF-1 and responds to thyroid hormones (B. Yusta, personal communication) and thus represents a mature thyrotrope. Similar attempts to direct transgene expression to the thyrotrope lineage were unsuccessful using the mouse TSHβ promoter (David Gordon, personal communication). The only successful targeting with a TSHβ promoter generated pituitary tumors that were completely undifferentiated (Maki et al., 1994). Thus, in this case, using sequences upstream of ~1.8 kb of the human α-subunit gene (which drive expression in both thyrotropes and gonadotropes) proved to be more successful than using the cell type-specific TSHβ promoter to immortalize mature thyrotrope cells.

The question remains as to whether the immortalization event occurs during development, freezing the cells in a discrete stage of differentiation, or whether the transformation event occurs in more differentiated cells, which then dedifferentiate during tumor formation. The dedifferentiation process would be limited by the fact that expression of the oncogene is controlled by regulatory region from genes expressed only in differentiated cells. Thus, dedifferentiation beyond the point at which the regulatory region is active would result in cessation of cell division and loss from the tumor or cell culture. It is unlikely that dedifferentiation occurs only during culturing, since the pattern of expression in the cultured cells correlates with that of the original tumors. Most likely, the final phenotype of the cell lines derived results from a combination of these events. Regardless, it is clear that directed oncogene expression as well as the molecular events that confer cell identity during differentiation and that control cell fate decisions. Our results demonstrate the potential for immortalization of a series of developmental progenitor cells using the regulatory regions from cell-type-specific genes, an approach that may prove to be uniquely suited to the study of mammalian organogenesis.

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