

A Transfected L-*myc* Gene Can Substitute for c-*myc* in Blocking Murine Erythroleukemia Differentiation

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We investigated the ability of the proto-oncogene L-*myc* to substitute for c-*myc* in blocking murine erythroleukemia differentiation. Murine erythroleukemia cells (line C19) were transfected with recombinant plasmids containing genomic and cDNA fragments of the L-*myc* gene driven by a Moloney murine leukemia virus long terminal repeat. Clones expressing constitutive high levels of L-*myc* failed to differentiate in response to the chemical inducer *N,N'*-hexamethylene bisacetamide (HMBA). The block to differentiation correlated with the level of L-*myc* expression. Furthermore, transfected clones grown in the presence of inducer for an extended period of time showed an increased level of L-*myc* expression. These results suggest that functional domains of the c-*myc* gene involved in differentiation are located in the discrete regions of homology between the c- and L-*myc* genes.

The Friend virus-derived murine erythroleukemia (MEL) cell line C19 is a transformed cell line that still retains the ability to terminally differentiate into erythrocytes under the influence of a number of inducers (8, 17). This differentiation program has been characterized well on both biologic and molecular levels (13, 15). Of particular interest are the proto-oncogene (c-*myc* and c-*myb*) expression patterns during differentiation. Several groups have reported an inverse relationship between c-*myc* and c-*myb* expression levels and the degree of erythroid differentiation (13, 15). Additional evidence for the need to down-regulate these genes to permit differentiation comes from studies in which these genes were transfected into MEL cells under the control of powerful promoters. The results of these experiments showed that a highly expressed c-*myc* gene can block MEL differentiation (5, 7, 18). Likewise, recent data with c-*myb* suggest that constitutive expression will also block differentiation (4, 13a).

We hoped to identify regions in the *myc* gene that are responsible for the apparently critical role of this gene in MEL differentiation. As one approach, we chose to study the effect of constitutive expression of L-*myc* (another member of the *myc* family) on differentiation. The L-*myc* gene has a genomic structure similar to that of c-*myc* and codes for a protein with an overall amino acid sequence 30% homologous with the c-*myc* protein sequence (6, 10). However, this homology is located in several discrete areas of highly conserved amino acid sequence (homology boxes; >90% homology), with major insertions and deletions interspersed between these homology boxes (6, 10). Studies with deletion mutants of c-*myc* have demonstrated that although several of these conserved regions are indispensable for transforming activity, other homology regions are not, which suggests other important functions associated with these areas of the gene (20, 22). Since MEL cells do not express L-*myc*, by examining the effect on differentiation of a transfected L-*myc* gene, we were able to determine whether regions conserved between c- and L-*myc* are important for blocking differentiation.

MEL cells were transfected with the Moloney murine

leukemia virus long-terminal-repeat expression vector pVcos-7, containing (i) 1.6 kilobases (kb) of L-*myc* cDNA corresponding to a truncated version of the long-form mRNA (3.9 kb) or (ii) a 10-kb genomic fragment containing the entire L-*myc* gene (10). These plasmid constructs have been shown to be biologically active in two different transfection assays (1; M. Birrer, unpublished data). Transfections were done by CaPO₄ precipitation, and G418-resistant clones were isolated and characterized as previously described (7, 21). Analysis of 50 MEL clones expressing L-*myc* mRNA demonstrated inhibition of differentiation, as measured by the decreased formation of a red pellet and benzidine staining after 5 days of induction with *N,N'*-hexamethylene bisacrylamide (HMBA). The degree of inhibition of differentiation varied widely among the transfectants. Seven clones transfected with pVcos-7 alone were analyzed, all of which differentiated normally.

Several independent clones representing MEL transfectants with either the L-*myc* cDNA or genomic constructs were subcloned and used for evaluation. L-*myc* expression in these clones was determined by Northern (RNA) blots and RNase protection assay (Fig. 1), using a probe spanning exon 2 and the 5' portion of intron 2 of L-*myc*. The results revealed a wide range of expression levels. No endogenous L-*myc* mRNA was detected in the parental MEL cell line C19. In the transfectants receiving the cDNA construct, L-*myc* expression varied between the low levels seen in clone CL3 and the much higher levels seen in clones BL-1 and EB12/S6 (Fig. 1). Clone FB10/S2, transfected with the genomic fragment, expressed high levels of normal L-*myc* mRNAs (3.9, 3.6, and 2.2 kb) comparable to those seen in the small-cell lung cancer (SCLC) cell line 510 amplified for the L-*myc* gene (6, 10). The four clones (CL3, BL-1, EB12/S6, and FB10/S2) and the parental cell line (C19) were subjected to log-phase inductions (three times) with 3 mM HMBA as previously described (7, 21) (Fig. 2). The parental cell line C19 and a pVcos-7 control transfectant (data not shown) accumulated benzidine-positive cells rapidly, with 90% of the culture becoming positive by day 3. In contrast, clone CL3, which expressed low levels of L-*myc* mRNA, was partially delayed in its differentiation profile, whereas

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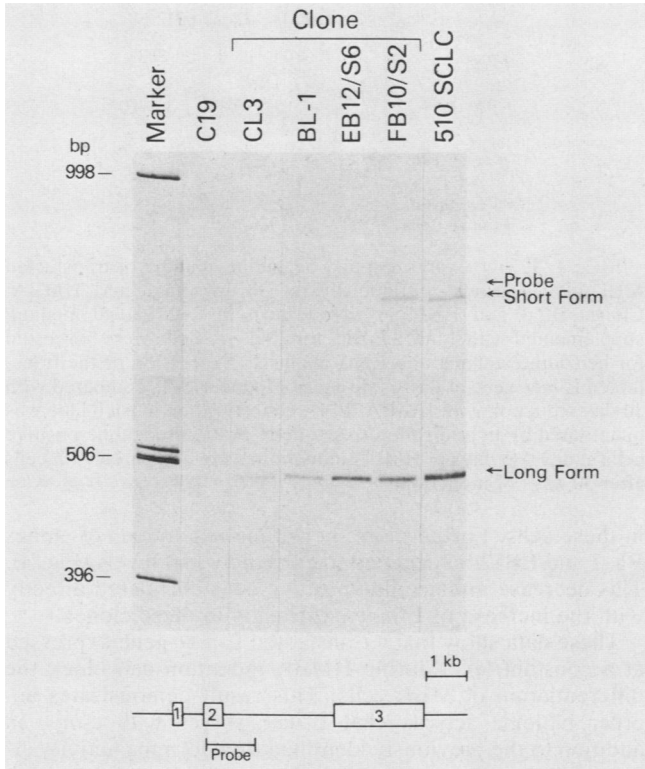


FIG. 1. L-myc expression levels in transfected MEL clones as detected by RNase protection assay. The single-stranded ³²P-labeled riboprobe was obtained from T7 polymerase transcription of a plasmid containing a 700-base-pair (bp) L-myc cDNA fragment spanning exon 2 and the 5' portion of intron 2 and hybridized to 10 μg of total RNA from MEL transfectants, the parental line C19, and the SCLC cell line 510 overnight at 50°C in 50% formamide. After digestion with RNase, the protected fragments were fractionated on an 8 M urea-5% polyacrylamide gel. Clones CL3, BL-1, and EB12/S6 are L-myc cDNA transfectants expressing mRNA corresponding to exons 2 and 3 of the gene and therefore display a protected species of approximately 400 bp (long form) corresponding to the exon 2 coding sequence. Clone FB10/S2 is an L-myc genomic transfectant expressing native L-myc long-form (3.9 and 3.6 kb) and short-form (2.2 kb) mRNAs. The RNA of this clone gives rise to two protected species: a 400-bp fragment corresponding to exon 2 sequences and a 700-bp fragment corresponding to exon 2 and intron 2 sequences. This pattern is identical to that of the SCLC cell line 510. Arrows indicate positions of the undigested probe and the long-form (exon 2) and short-form (exon 2 and 5' region of intron 2) protected species. Markers were made by digesting pBR322 with *Eco*RI and *Hinf*I and end labeling with [³⁵S]dATP. 1, 2, and 3 represent L-myc exons.

BL-1 and EB12/S6, which expressed higher levels of L-myc mRNA (2.5 and 5 times, respectively, the level in CL3, as determined by densitometric analysis) demonstrated a more complete block to differentiation. Therefore, the degree of differentiation seemed to correlate with the level of L-myc expression in these clones. On the other hand, clone FB10/S2, although expressing high levels of L-myc mRNA (five times the level expressed by CL3), was only partially blocked. This clone was transfected with a genomic fragment of L-myc in which transcription of the gene is more complex and the number of mRNA species differs from those seen in L-myc cDNA transfectants (Fig. 1).

Steady-state mRNA levels of L-myc, c-myc, β-globin, and c-myb with or without HMBA induction were established for

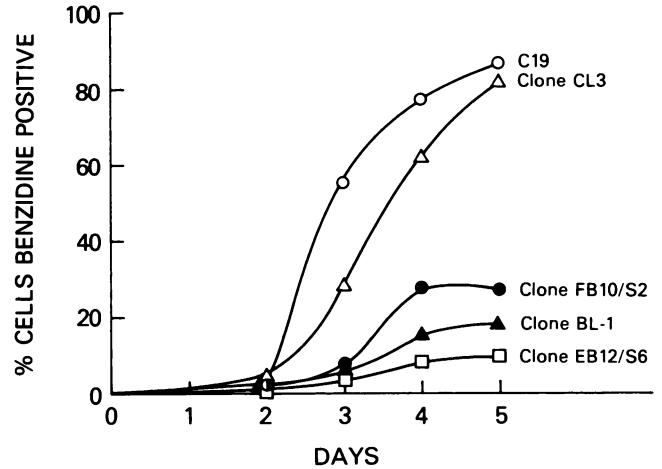


FIG. 2. Benzidine staining of transfected clones and the parental cell line during HMBA induction. Uninduced and logarithmic-phase induced cultures of the parental cell line C19 and clones CL3, BL-1, EB12/S6, and FB10/S2 were assayed for accumulation of benzidine-stained cells (expressed as percentage of total cells in culture). Logarithmic-phase inductions were performed as follows. Logarithmic-phase growing cells were plated at 10⁵ cells per ml in growth medium. The next day, 50% of the culture was replaced with fresh growth medium containing 6 mM HMBA (final concentration, 3mM; Sigma Chemical Co., St. Louis, Mo.). This process was repeated each day, and the removed cells were analyzed for the presence of hemoglobin by the color of the pellet or staining of individual cells with benzidine as previously described (7). For both uninduced and induced cultures, 200 cells were scored daily for benzidine reactivity; percentages of positive cells are shown for the indicated time points.

clones EB12/S6, CL3, and C19 (Fig. 3). L-myc was expressed with no evidence of down-regulation throughout the induction period in clones EB12/S6 and CL3, whereas no detectable expression was found in the parental cell line C19. Surprisingly, at 1 to 6 h postinduction, we detected a small increase in expression of the L-myc gene in all L-myc-expressing clones analyzed.

Although there was no evidence for down-regulation of L-myc expression during the induction period in the clones, we detected major changes in expression of the endogenous c-myc and c-myb genes. During the process of differentiation of MEL cells, expression of c-myc and c-myb displayed a biphasic pattern. The steady-state levels of these two genes dropped dramatically during the first 6 h of induction, which was followed by a transient reexpression during the next 18 h. A second drop occurred after 24 h of induction, which resulted in a two- to three-fold drop in c-myc expression, whereas expression of c-myb declined more substantially. This pattern was seen for the parental cell line C19 and clone CL3 (Fig. 3). However, whereas clone EB12/S6 did demonstrate the initial drop and recovery in expression of these two genes, it did not display the second drop in expression of the c-myb gene. These findings are similar to the previously reported results for MEL cells blocked in differentiation by a constitutively expressed c-myc gene (7). This finding is of particular importance given recent data suggesting that the late decline of c-myc is required for commitment to terminal differentiation (14, 24).

Analysis of β-globin mRNA levels during HMBA induction revealed that whereas C19 and the low-L-myc-expressing clone CL3 were induced to differentiate and produced high levels of globin mRNA, clone EB12/S6 was

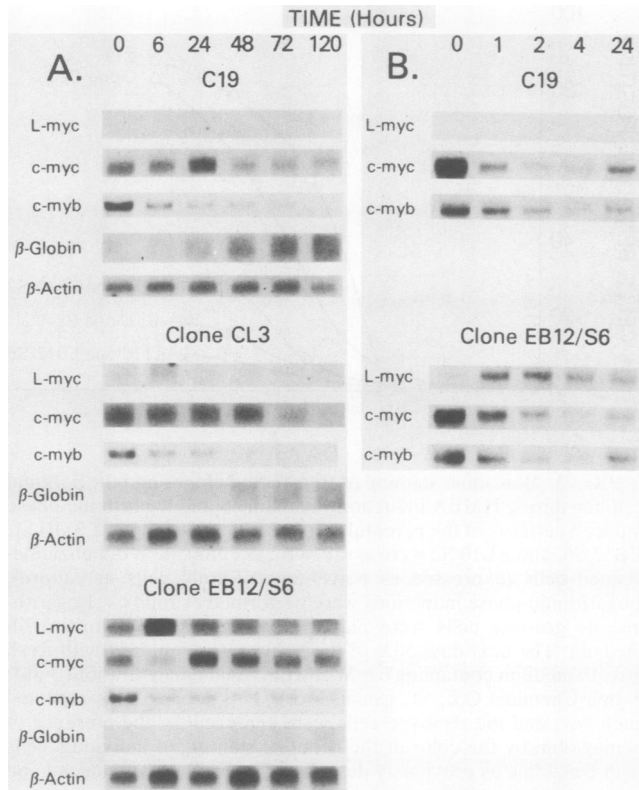


FIG. 3. (A) Data on 120-h time course expression of *L-myc*, *c-myc*, *c-myb*, β -actin, and β -globin in transfected clones and the parental cell line during logarithmic-phase induction with HMBA. Transfected clones CL3 and EB12/S6 and the parental cell line C19 were grown logarithmically. *L-myc*, *c-myc*, *c-myb*, and β -globin mRNA expression levels were analyzed by electrophoretically separating 10 μ g of total RNA from each clone on 1% agarose gels by the technique of Lehrach et al. (16) and blotting by transfer to nitrocellulose filters. The nitrocellulose filters were then hybridized to the following 32 P-labeled nick-translated probes (19): for *L-myc*, a 700-bp cDNA fragment; for *c-myc*, a 1.5-kb murine cDNA fragment containing exons 2 and 3; for β -globin, a 4.4-kb *Pst*I fragment of the human gene; and for *c-myb*, a 2.4-kb cDNA fragment of the mouse gene. The blots were sequentially hybridized to these probes without stripping. Hybridization with β -actin (2.0-kb *Bam*HI fragment) was performed last to ensure and quantitate the presence of intact RNA in each lane. Filters were exposed to XAR-5 or XRP film at -70°C with intensifying screens for variable times. (B) Data on 24-h time course expression of *L-myc*, *c-myc*, and *c-myb* during HMBA induction. Total RNA (10 μ g each) from clone EB12/S6 and parental cell line C19 was electrophoresed on 1% agarose gels and blotted. The Northern blots were hybridized to different probes as described above. For these early time points, no hybridization to β -globin was done, since minimal levels are transcribed. The amounts of RNA in all lanes were equal, as determined by ethidium bromide staining.

significantly suppressed in expression of globin RNA message (Fig. 3A), which reflected its block to differentiation.

To further explore the function of *L-myc* in MEL clones BL-1 and EB12/S6, we grew these clones in the presence of HMBA for 30 days and then examined *L-myc* expression by Northern blot analysis (Fig. 4). Survival of the clones under these conditions depended on their inability to differentiate. It is clear that a significant increase in *L-myc* expression occurred during growth in the presence of inducer, consistent with a critical *L-myc*-dependent block to differentiation

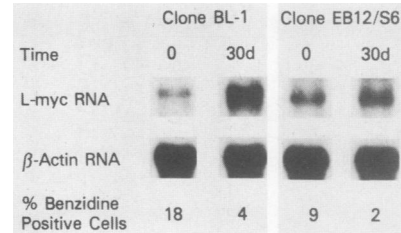


FIG. 4. *L-myc* expression and benzidine staining of transfected MEL clones grown continuously for 30 days in 3 mM HMBA. Clones BL-1 and EB12/S6 were grown in RPMI 1640 medium supplemented with 3 mM HMBA for 30 days. Cells were harvested for benzidine staining and RNA analysis. Expression of the transfected *L-myc* gene at day 0 (absence of inducer) was compared with 30-day induction with HMBA. RNA concentration in each lane was quantitated by hybridization to a β -actin probe. Benzidine-positive cells at day 0 (5 days of HMBA induction) were compared with cells after 30 days of induction.

in these cells. Furthermore, benzidine reactivities of clones BL-1 and EB12/S6 declined to extremely low levels (Fig. 4). This decrease in benzidine-positive cells correlated directly with the increase of *L-myc* expression in these clones.

These data show that a transfected *L-myc* gene expressed at a constant level during HMBA induction can block the differentiation of MEL cells. This result demonstrates another biologic activity that *L-myc* shares with *c-myc* in addition to the previously identified transforming activity (1, 6). Of interest, *L-myc* has been reported to have weak transforming activity in comparison with *c-myc*, but, as seen in the data presented here, it seems to function efficiently in blocking the differentiation of MEL cells (1). *L-myc* is frequently amplified and overexpressed in SCLC cell lines (10). It is interesting to hypothesize whether one of its functions in these cells is to maintain them in a partially undifferentiated state.

Multiple lines of evidence suggest that *c-myc* plays a critical role in the balance between cell growth and differentiation. High or constitutive levels of *c-myc* expression are often associated with some form of growth deregulation (11, 12). Conversely, during terminal differentiation, *c-myc* mRNA decrease in a number of cell lines (2, 15, 23). In addition, constitutive expression of a transfected *c-myc* gene inhibits or blocks differentiation in several of these systems (5, 7, 18, 21). Our findings for the structurally related *L-myc* gene support the important role of *c-myc* in the differentiation of MEL cells. Furthermore, since *L-myc* is not normally expressed in these cells, its effectiveness in blocking differentiation presumably stems from structurally similar domains shared by these two genes. These domains, known as homology boxes, are discrete regions of 70 to 90% predicted amino acid sequence homology located in exons 2 and 3 (6, 10). Interestingly, while some of these regions are indispensable for rat embryo cell transformation activity, two regions (*c-myc* amino acids 1 to 104 and 144 to 320) have been shown to tolerate some or even extensive mutations, with little effect on transformation. Since sequence conservation suggests functional selection, these areas of the gene may serve as targets for functions other than transformation. It is possible that these regions are more critical to *c-myc* in its physiologic role during differentiation than during transformation. Further dissection of the *myc* gene will be required to test this hypothesis.

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