

Alteration of oestradiol metabolism in *myc* oncogene-transfected mouse mammary epithelial cells

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Summary Targeted overexpression of the *c-myc* oncogene induces neoplastic transformation in immortalized, non-tumorigenic mouse mammary epithelial cells (MMEC). Experiments in the present study were conducted to examine whether cellular transformation induced by *c-myc* oncogene is associated with altered metabolism of 17 β -oestradiol (E₂). The parental, MMEC and the stable *c-myc* transfectant (MMEC/*myc*₃) cell lines were compared for major oestrogen metabolic pathways, namely E₂ and E₁ interconversion, and C2- and C16 α -hydroxylation by both high-pressure liquid chromatography (HPLC) analysis and the ³H release assay using specifically labelled [C2-³H]E₂ or [C16 α -³H]E₂. The reductive conversion of E₁ to E₂ was about 14-fold and 12-fold higher than the oxidative conversion of E₂ to E₁ in MMEC and MMEC/*myc*₃ cells respectively. However, in MMEC/*myc*₃ cells, both reductive and oxidative reactions were decreased by about 32% and 12% relative to those seen in the parental MMEC cells ($P = 0.0028$). The extent of C16 α -hydroxylation was increased by 164.3% ($P < 0.001$), with a concomitant 48.4% decrease ($P < 0.001$) in C2-hydroxylation in MMEC/*myc*₃ cells; this resulted in a fourfold increase in the C16 α /C2 hydroxylation ratio in this cell line. Thus, a persistent *c-myc* expression, leading to aberrant hyperproliferation in vitro and tumorigenesis in vivo, is associated with an altered oestrogen metabolism. However, it remains unclear whether this represents a result of oncogene expression/activation or is rather a consequence of phenotypic transformation of the cells.

Keywords: *c-myc* expression; oestradiol metabolism; mammary carcinogenesis

It is well recognized that oestrogens exert a profound influence on mammary epithelial cell growth, differentiation and neoplastic transformation (Fishman et al, 1980; Prudhomme et al, 1984; Mauvais-Jarvis et al, 1986; Siiteri et al, 1986). The molecular and biochemical mechanisms important for oestrogen responsiveness and the influence of altered oestrogen responsiveness on mammary cell carcinogenesis, however, are not fully understood. Our earlier studies on immortalized, non-tumorigenic mouse mammary epithelial cell lines have shown that transfection of the cell line with *myc* or *Ras* oncogenes results in neoplastic transformation. Before tumorigenesis in vivo, *myc* as well as *Ras* transfectants exhibit aberrant hyperproliferation in vitro (Telang et al, 1990, 1991; Suto et al, 1992). Thus, persistent oncogene expression and aberrant hyperproliferation may represent molecular and cellular biomarkers for neoplastic transformation.

The conventionally recognized markers for oestrogen responsiveness include (1) functional activity of oestrogen receptor as determined by receptor–ligand binding; (2) modulation of transcriptional activity, growth and induction of progesterone receptor (Prudhomme et al, 1984; Mauvais-Jarvis et al, 1986; Siiteri et al, 1986; Dubik and Shiu, 1992); (3) reversible suppression of growth by hormone antagonists (Clark et al, 1977; Mauvais-Jarvis et al,

1986; Siiteri et al, 1986; Dubik and Shiu, 1992). Our recent studies on *Ras*-initiated MMEC/pH06T cells as well as on *Ras*-transformed T1/Prl cells have shown that the oncogene-initiated and tumorigenically transformed cells are responsive to E₂, as also shown by their ability to metabolize the hormone and by reversible growth inhibition upon treatment with the non-steroidal anti-oestrogen tamoxifen (Telang et al, 1991; Suto et al, 1992).

Mammary epithelial cells initiated independently with chemical carcinogen 7,12-dimethylbenz(a) anthracene (DMBA) and *Ras* oncogene exhibit elevated oestrogen metabolism via the formation of C16 α -hydroxylated metabolites (Telang et al, 1991, 1992; Suto et al, 1993). In addition, it has been proposed that the oestrogen-mediated stimulation of growth of breast tumour-derived MCF7 cells may involve transactivation in the *c-myc* promoter region (Dubik and Shiu, 1992). It is not clear whether these molecular and metabolic alterations characterize the initiated phenotype or represent a late-occurring, post-initiation event in a rapidly growing tumour cell phenotype.

The experiments in the present study were designed to (1) establish the validity of oestrogen metabolism as an endocrine biomarker for tumorigenic transformation in *myc* oncogene-transfected mammary epithelial cells; and (2) elucidate the relationship between *myc* expression, the extent of cellular metabolism of E₂ and tumorigenic transformation. To this end, we have compared the extent of E₂ metabolism in the spontaneously immortalized, non-tumorigenic mammary epithelial cell line MMEC and the stable transfectant MMEC/*myc*₃ that expresses activated *c-myc* proto-oncogene and is highly tumorigenic.

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MATERIALS AND METHODS

Cell lines

The non-tumorigenic mammary epithelial cell line MMEC was established from the mammary tissue of a 6- to 8-week-old virgin female BALB/c mouse. The stable *myc* transfectant MMEC/*myc*₃ was obtained by transfection of a recombinant *myc* construct comprising the second and third coding exons expressed from a MLV-LTR promoter in a NEO-derived vector. DM-*myc*, and expansion of a stable G-418-resistant clone in the presence of 400 µg ml⁻¹ G-418, which is cytotoxic to the parental MMEC (Telang et al, 1990). Routinely, MMEC and MMEC/*myc*₃ cells were maintained in DME/F12 medium supplemented with heat-inactivated 10% fetal bovine serum, 4 mM L-glutamine and 5 µg ml⁻¹ insulin. The stock MMEC/*myc*₃ cells were maintained in the presence of 400 µg ml⁻¹ G-418 to eliminate the accumulation of spontaneous revertants. For the experiments measuring the cellular metabolism of E₂, the parental MMEC and the *myc* transfectant MMEC/*myc*₃ cells were cultured in the absence of G-418 for 72 h to exclude the possibility of interference of the antibiotic with E₂ metabolism.

Growth characteristics

The growth pattern of MMEC and MMEC/*myc*₃ cells was determined by a trypan blue exclusion test and haemocytometer counts for viability and growth. In addition, population doubling time (PDT), anchorage-independent growth (AIG) and mammary fat pad tumorigenicity assays were performed according to the published procedures (Ganguly et al, 1982; Telang et al, 1979, 1990, 1991). PDT was determined from the linear portions of the growth curves generated for at least 4 days after plating 5 × 10³ cells cm⁻². AIG was evaluated by determining the number of anchorage-independent, tridimensional colonies formed in 0.33% agar after an initial seeding of 1.0 × 10³ cells, and the data were expressed as colony-forming efficiency (CFE, %) at day 14. Tumorigenicity was determined by counting the number of palpable tumours in mammary fat pads after the injection of 1.0 × 10⁵ cells as a single 20-µl bolus into parenchyma-free mammary fat pads of syngeneic recipients.

c-myc expression and oestrogen receptor content

The relative expression of transfected (exogenous) *c-myc* oncogene was determined by the Northern blot analysis of RNA from

Table 1 Biomarker status of MMEC and MMEC/*myc*₃ cells

Type of biomarker	Cell line	
	MMEC	MMEC/ <i>myc</i> ₃
G418 resistance ^a	–	+
C-myc expression ^b	–	15.0 ± 2.6
Oestrogen receptor ^c	12.5 ± 3.9	5.0 ± 1.7
Population doubling	24.3 ± 0.5	18.3 ± 0.1
Anchorage independence ^d	0.01 ± 0.005	1.33 ± 0.075
Tumorigenicity ^e	–	+

^aGrowth in 400 µg ml⁻¹ G418. ^bArbitrary scanning units for 2.8 kb (exogenous) transcript hybridizing to [³²P]-labelled *c-myc* probe. ^cFmol ER protein per 10 µg DNA. ^dpercentage colony forming efficiency in 0.33% agar. ^eTumour formation after mammary fat pad transplantation.

Table 2 Effect of *c-myc* oncogene expression in 17β-hydroxy steroid dehydrogenase (17β-HSD) activity in mammary epithelial cells

Cell line	17β-HSD activity ^a	
	E ₂ formed	E ₁ formed
MMEC	(n = 12) 22.14 ± 2.72	(n = 11) 1.47 ± 0.13
MMEC/ <i>myc</i> ₃	15.14 ± 3.39	1.30 ± 0.13
	d.f. 11 t 4.16 P = 0.0028 ^b	d.f. 10 t 3.40 P = 0.05 ^b

^aDetermined after 24 h incubation with [6,7-³H(N)]E₁ or [6,7-³H(N)]E₂ and HPLC analysis of conversion products. ^bTwo-tailed Student *t*-test. Values represent mean ± s.d. pmol 10 µg⁻¹ DNA

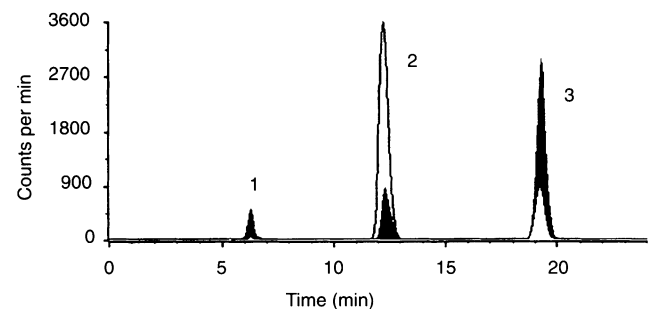


Figure 1 Typical high-pressure liquid chromatography (HPLC) profiles of 1 nM [6,7-³H(N)]E₁ metabolites formed after 72 h incubation of 5 × 10⁵ MMEC (white peaks) and MMEC/*myc*₃ (dark peaks) cells. (1) 16αOHE₁; (2) E₂; (3) E₁

the parental MMEC and the stable transfectant MMEC/*myc*₃ cell lines essentially according to the method published previously (Telang et al, 1990, 1991). A [³²P]-labelled, nick-translated 1.8 kb *Sac*I fragment of human *c-myc* spanning the second exon was used as the probe. The blots were scanned and the hybridization signal was quantified by arbitrary scanning units (ASU) normalized to 20 µg of RNA loaded. The oestrogen receptor content of MMEC and MMEC/*myc*₃ cells was determined by the ligand binding assay (Castagnetta et al, 1992) and was expressed as fmol of oestrogen receptor protein (ERP) per 10 µg of DNA.

HPLC analysis of 17β-HSD activity

The relative extent of 17β-HSD activity was determined by measuring the interconversion of E₂ and E₁ in the two cell lines. T-25 flasks containing approximately 1.0 × 10⁶ MMEC and MMEC/*myc*₃ cells were incubated for 24 h in serum-free, phenol red-free and G-418-free medium in the presence of 2 µCi ml⁻¹ [6,7-³H(N)]E₂ (specific activity 42.3 Ci mmol⁻¹, final concentration 4.6 × 10⁻⁸ M) or 2 µCi ml⁻¹ [6,7-³H(N)]E₁ (specific activity 41.9 Ci mmol⁻¹, final concentration 4.8 × 10⁻⁸ M). The incubation medium was collected, and 1-ml aliquots were extracted with 9:1 ethyl-ether:acetone. The extracts were analysed by reverse-phase HPLC (C18 column, 4.6 i.d. × 250 mm) under isocratic conditions (acetonitrile: 0.05 M citric acid, 40:60) at a flow rate of 1 ml min⁻¹ using a computer-aided optimized mobile phase (D'Agostino et al, 1985; Castagnetta et al, 1986). The detection of E₂ metabolites was carried out using a UV detector and a three-channel radiometric detector, both on-line to HPLC as described previously

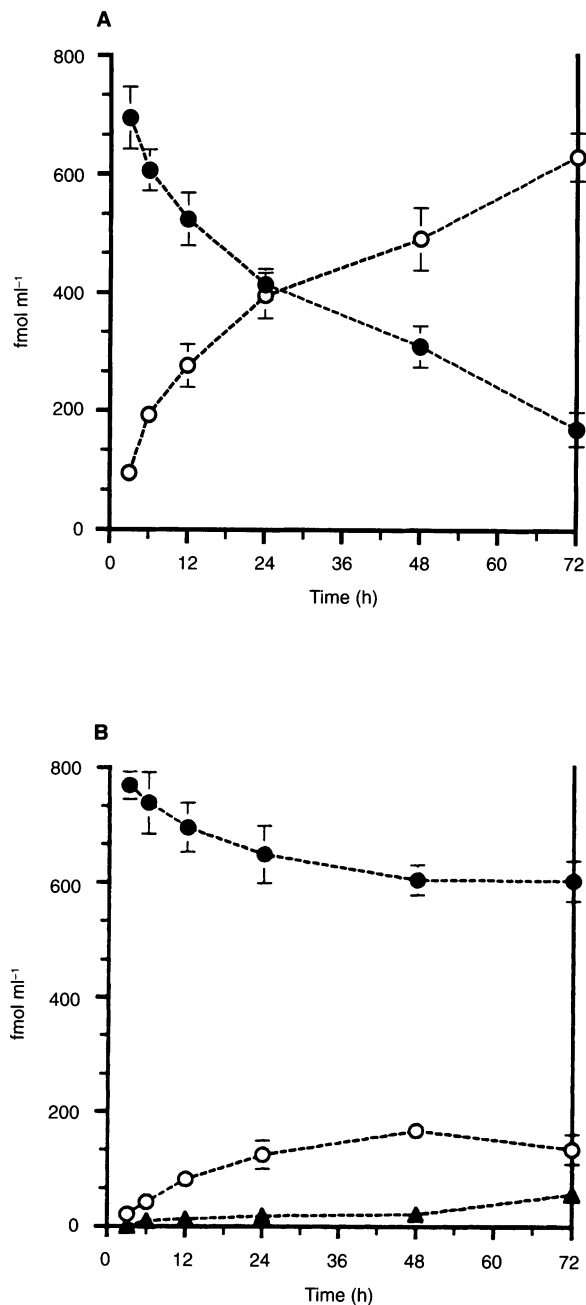


Figure 2 Time course of E_1 metabolism in MMEC (A) and MMEC/*myc*₃ (B) cells. Cells (5×10^5) were incubated in the presence of 1 nM [6,7- $^3H(N)$] E_1 for 3, 6, 12, 24, 48 and 72 h. Each data point represents the mean \pm s.d. of duplicate experiments, performed in triplicate, after correction for equal cell numbers. (●) E_1 ; (○) E_2 ; (▲) $16\alpha\text{OHE}_1$

(Castagnetta et al, 1986, 1991). The cells were lysed in 0.1% sodium dodecyl sulphate (SDS), and DNA content was determined (Carruba et al, 1994). The resulting data were normalized for total radioactivity and expressed as pmol $10 \mu\text{g}^{-1}$ cellular DNA or fmol ml^{-1} after correction for equal cell numbers.

Separate experiments were carried out to inspect the time and dose dependence of oestrogen metabolism in both MMEC and MMEC/*myc*₃ cells. To this end, 5×10^5 cells were incubated in the presence of 1 nM tritiated E_1 for 3, 6, 12, 24, 48 and 72 h or exposed to increasing concentrations (0.1, 1, 10 and 100 nM) of

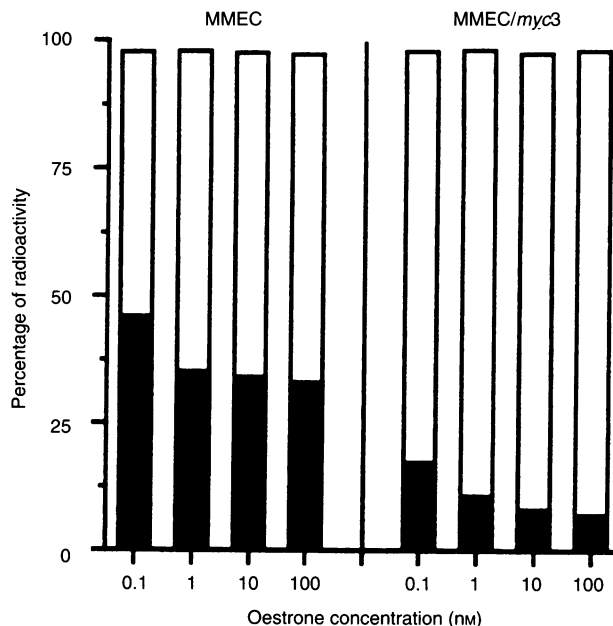


Figure 3 Dose-dependent E_1 conversion to E_2 in MMEC and MMEC/*myc*₃ cells. Cells were incubated for 24 h in the presence of increasing concentrations of [6,7- $^3H(N)$] E_1 . Percentage values represent the mean of triplicate determinations corrected for total radioactivity and cell numbers. (□) unconverted E_1 ; (■) E_2 formed

the same radioactive oestrogen for 24 h, using exactly the same experimental conditions and procedures described above.

Radiometric assay for E_2 metabolism

The relative extent of E_2 metabolism via the C2- and C16 α -hydroxylation pathways was measured by determining 3H_2O formation in cells incubated for 48 h in the presence of [C2- 3H] E_2 or [C16 α - 3H] E_2 (final concentrations 5.6×10^4 d.p.m., 8.0×10^{-10} M) in a medium lacking serum, phenol red and G-418. Aliquots of 500 μl of incubation medium were diluted to 3.5 ml with water, and the lyophilized sublimate was counted for 3H radioactivity in a liquid scintillation counter (Telang et al, 1991, 1992; Suto et al, 1992, 1993). The 3H release from [C2- 3H] E_2 or [C16 α - 3H] E_2 to form 3H_2O provides an indirect measurement of regiospecific hydroxylation of the steroid leading to the stoichiometric formation of 2-hydroxyestrone (2-OHE₁) or 16 α -hydroxyestrone (16 α -OHE₁) (Fishman and Martucci, 1980; Fishman et al, 1980, 1995; Telang et al, 1991, 1992; Suto et al, 1992, 1993; Telang, 1996).

Statistical analysis

The data were analysed for statistical significance of the differences between cell types and treatment groups by unpaired two-tailed Student *t*-test, using the Statview 4.01 statistical software. Probability values of less than 0.05 were considered significant.

RESULTS

Growth characteristics of MMEC and MMEC/*myc*₃ cells

The proliferative status, including AIG and tumorigenic potential, of MMEC and MMEC/*myc*₃ cells, is presented in Table 1. The MMEC cell line exhibited toxicity to the aminoglycoside antibiotic

Table 3 Oncogene-mediated alteration of 17- β -oestradiol (E_2) metabolism in mouse mammary epithelial cells

Cell line	E_2 metabolism ^a		
	2-OHE ₁ formed (n = 12)	16 α -OHE ₁ formed (n = 12)	C16 α /C2 ratio
MMEC	44.29 \pm 5.71	20.00 \pm 2.86	0.45
MMEC/ <i>myc</i> ₃	22.86 \pm 2.86	52.86 \pm 7.14	2.31
	d.f.11 t4.23 P < 0.001 ^b	d.f.11 t5.25 P < 0.001 ^b	

^aDetermined by ³H₂O formed after a 48 h incubation with [C2-³H] E_2 or [C16 α -³H] E_2 . ^bTwo-tailed Student *t*-test; values are mean \pm s.d. fmol 10 μ g⁻¹ DNA.

G-418, lacked the expression of exogenous *myc*-specific 2.8 kb RNA transcript, exhibited a population doubling time of 24.3 \pm 0.5 h, lacked anchorage-independent growth in vitro and lacked the ability to form tumours when transplanted into syngeneic recipients. These cells, however, exhibited a persistent ability for ductal morphogenesis at the transplant site (data not shown). In contrast, the MMEC/*myc*₃ cell line did not exhibit any G-418 cytotoxicity, expressed the exogenous 2.8 kb transcript (15.0 \pm 2.6 ASU 20 μ g⁻¹ RNA) and showed a shorter population doubling time of 18.3 \pm 0.1 h (d.f. 5, *t* = 3.40, *P* = 0.01). Furthermore, MMEC/*myc*₃ cells also showed a 132-fold increase in AIG relative to that observed in MMEC and were highly tumorigenic, exhibiting a 90% tumour incidence at 12 weeks after transplantation (data not shown). These results essentially confirm our earlier report (Telang et al, 1990), suggesting that the expression of activated *c-myc* confers neoplastic transformation to mammary epithelial cells. In addition to overexpression of exogenous *c-myc*, the MMEC/*myc*₃ cells exhibited a substantial reduction in oestrogen receptor levels. Thus, whereas the oestrogen receptor content of parental MMEC was 12.5 \pm 3.9 fmol 10 μ g⁻¹ DNA, it was decreased to 5.7 \pm 1.7 fmol 10 μ g⁻¹ DNA (d.f. 5, *t* = 4.07, *P* = 0.001) in the transfected MMEC/*myc*₃ cells, resulting in about a 60% reduction of ERP levels.

The experiment designed to establish the biological significance of altered E_2 metabolism examined whether treatment of MMEC/*myc*₃ cells with oestrogen metabolites 16 α -OHE₁ or 2-OHE₁ affects aberrant proliferation as shown by anchorage-independent growth. Treatment of MMEC/*myc*₃ cells with 16 α -OHE₁ resulted in about a 152% increase (d.f. 11, *t* = 4.07, *P* = 0.002) in anchorage-independent colony formation. In contrast, treatment with 2-OHE₁ resulted in a 12.6% decrease (d.f. 11, *t* = 3.41, *P* = 0.01) in anchorage-independent colony formation.

17 β -HSD activity in MMEC and MMEC/*myc*₃ cells

The effect of *c-myc* oncogene on intrinsic 17 β -HSD activity was evaluated by comparing the relative extent of interconversion of E_2 and E_1 in MMEC and MMEC/*myc*₃ cells. It is clear from the data presented in Table 2 that the reductive pathway of E_1 to E_2 dominates over the opposing oxidative pathway of E_2 to E_1 conversion, the reductive reaction being about 14-fold and 12-fold greater than the oxidative conversion in MMEC and MMEC/*myc*₃ cells respectively. However, in MMEC/*myc*₃ cells, both reductive and oxidative reactions are found to be significantly reduced, being about

32% (d.f. 11, *t* = 4.16, *P* = 0.0028) and 12% (d.f. 10, *t* = 3.40, *P* = 0.05) lower relative to those observed in MMEC cells.

Typical HPLC profiles of oestrogen metabolism in MMEC and MMEC/*myc*₃ cells are illustrated in Figure 1.

Time course experiments (3–72 h) were specifically designed to compare E_1 conversion to E_2 in parental MMEC and *c-myc*-transfected cells. As shown in Figure 2, the extent of the reductive pathway of 17 β -HSD is significantly reduced (from three- up to 4.5-fold) in MMEC/*myc*₃ cells. It is of interest that maximum E_2 formation in the latter cell line was observed at 24 h (15.3%) or 48 h (20.4%), whereas it was steadily increasing with time in MMEC cells. Consistency in DNA values and cell counts was ensured for reproducibility of data.

Parallel experiments carried out on MMEC and MMEC/*myc*₃ cells using increasing precursor concentrations (from 0.1 up to 100 nM) showed that the proportion of E_2 formed remained relatively unchanged using either 1, 10 or 100 nM E_1 in both MMEC (33–35%) and MMEC/*myc*₃ cells (8–10%), whereas it was remarkably greater (46% in MMEC cells and 17% in MMEC/*myc*₃ cells) at the lowest E_1 concentration (0.1 nM) used (see Figure 3).

Nevertheless, the extent of E_2 formation was again significantly (from 2.6- up to 4.6-fold) lower in MMEC/*myc*₃ cells with respect to the parental MMEC cells.

E_2 hydroxylation in MMEC and MMEC/*myc*₃ cells

The oestrogen metabolism was compared by radiometric determination of the relative extent of E_2 conversion via the C2- and C16 α -hydroxylation pathways (Table 3). The two cell lines exhibited persistent metabolic competence to convert E_2 . In parental MMEC cells, the extent of conversion of [C2-³H] E_2 and of [C16 α -³H] E_2 was 0.32 \pm 0.04% and 0.14 \pm 0.02% (per 10⁴ cells) respectively (mean \pm s.d., *n* = 12). In MMEC/*myc*₃ cells, the extent of conversion of [C2-³H] E_2 was decreased to 0.16 \pm 0.02%, while that of [C16 α -³H] E_2 was increased to 0.37 \pm 0.05%. To maintain consistency with the data from the experiments on interconversion of E_2 and E_1 , the data from E_2 metabolism are expressed as amounts of 2-OHE₁ and 16 α -OHE₁ formed. The data presented in Table 3 demonstrate clearly that MMEC/*myc*₃ cells exhibit about a 164.5% increase (d.f. 11, *t* = 5.25, *P* = 0.001) in 16 α -OHE₁ formation, with a concomitant 48.3% decrease (d.f. 11, *t* = 4.23, *P* = 0.001) in 2-OHE₁ formation. This results in a fourfold increase in the C16 α /C2 hydroxylation ratio.

DISCUSSION

Altered endocrine status of the mammary tissue plays an important role in the expression of tumorigenic phenotype (Telang et al, 1979; Ganguly et al, 1982; McCormick et al, 1982; Mauvais-Jarvis et al, 1986; Siiteri et al, 1986; Welsch, 1987; Castagnetta et al, 1992; Fishman et al, 1995; Telang, 1996). The experiments designed in the present study have used the immortalized, non-tumorigenic MMEC and the tumorigenic *myc*-transfected MMEC/*myc*₃ cells to understand the relationship between oestrogen metabolic pathways and *myc*-mediated tumorigenic transformation better.

The MMEC/*myc*₃ cell line exhibits enhanced expression of the cellular markers for transformation, namely aberrant hyperproliferation in vitro before tumorigenicity in vivo. We have observed previously that (1) non-cancerous mammary tissue exhibits increased C16 α -hydroxylation of E_2 to diverse carcinogenic agents

(Telang et al, 1991, 1997; Suto et al, 1992; Fishman et al, 1995; Telang 1996); (2) exposure to 16α -OHE₁ results in genotoxic DNA damage and aberrant proliferation in non-cancerous mammary epithelial cells (Telang et al, 1992); (3) specific E₂ metabolites modulate proliferation in cells pretreated with chemical carcinogens or those derived from mammary carcinoma (Schneider et al, 1984; Suto et al, 1993); and (4) mechanistically distinct classes of chemopreventive agents inhibit aberrant proliferation and induce C2-hydroxylation of E₂ (Suto et al, 1992, 1993; Telang et al, 1997). These observations taken together support the concept that E₂ metabolism may represent a biochemical/endocrine marker for mammary carcinogenesis and its prevention.

Interconversion of E₂ and E₁ has been reported to be altered in the neoplastic breast tissue owing to a change in intrinsic 17 β -HSD activity (Pollow et al, 1977; Prudhomme et al, 1984; Gompel et al, 1986; Vermeulen et al, 1986; Tait et al, 1989; Poutanen et al, 1992; Pasqualini et al, 1996), which also appears to be different according to the hormone-responsive status of cancer cells (Castagnetta et al, 1995, 1996). This evidence is also relevant for other target cells of steroids (Carruba et al, 1997). The relative extent of 17 β -HSD-mediated interconversion of E₂ and E₁ revealed interesting differences between MMEC and MMEC/*myc*₃ cells. Overall, the reductive conversion of E₁ to E₂ was remarkably greater than the opposing oxidative pathway in both MMEC and MMEC/*myc*₃ cells. However, both reactions were significantly lower in MMEC/*myc*₃ cells with respect to the parental MMEC cells. This could be, only partially, a reflection of the sustained increase of 16α -hydroxylation of E₁ seen in MMEC/*myc*₃ cells in association with the persistent expression of the *myc* oncogene.

Results from time course experiments and those obtained using increasing concentrations of precursor confirmed that the extent of E₁ reduction to E₂ is consistently and significantly lower in MMEC/*myc*₃ cells than that observed in MMEC cells, regardless of incubation time and dose of precursor used.

The alteration in 17 β -HSD activity observed in the present study raises the possibility that deregulated *myc* expression may have preferentially suppressed the reductive isoform of 17 β -HSD enzyme(s), resulting in an altered oestrogen substrate utilization by MMEC/*myc*₃ cells, as has been reported in other systems (Pollow et al, 1977; Strobl and Lippman, 1979; Tait et al, 1989; Poutanen et al, 1993). The oestrogen receptor status is critical for the genesis and/or evolution of a transformed cell phenotype and, as such, modulation of the receptor status may coincide with progression of hormone-dependent tumours to a hormone-independent status (Abul-Hajji, 1979; McCormick et al, 1982; Prudhomme et al, 1984; Welsch, 1985, 1987; Mauvais-Jarvis et al, 1986; Siiteri et al, 1986; Ball et al, 1988; Castagnetta et al, 1995; Nguyen et al, 1995). In this context, it is interesting to note that MMEC/*myc*₃ cells that express exogenous *c-myc* also exhibit about a 60% decrease in oestrogen receptor content relative to the parental MMEC cells.

The experiments in the present study (designed to inspect the metabolic pathways subsequent to the formation of E₁) demonstrated clearly that the two cell lines are able to metabolize E₂ via the mutually exclusive C2-hydroxylation and C16 α -hydroxylation in a manner similar to that previously observed in mammary epithelial cells that are initiated with the *Ras* oncogene or with the chemical carcinogen DMBA (Suto et al, 1992; Telang et al, 1991, 1992). Furthermore, HPLC analysis confirmed that the incubation of MMEC/*myc*₃ cells with close to a physiological E₁ concentration also resulted in an appreciable 16α -OHE₁ formation.

Consistent with the observed cellular effects of specific E₂ metabolites in carcinogen/oncogene-initiated or carcinoma-derived cells (Schneider et al, 1984; Suto et al, 1992, 1993; Telang et al, 1992), 16α -OHE₁ and 2-OHE₁ were also effective in modulating growth response of *c-myc* oncogene-transfected cells in the present model.

Overall, MMEC/*myc*₃ cells exhibit strikingly enhanced proliferative activity and persistence of the transformed phenotype that appear to be associated with (1) altered equilibrium of E₁ to E₂ conversion and consequent reduction in E₂ production; and (2) increased ratio of C16 α /C2 hydroxylation with consequent possible overstimulation of cell proliferation induced by both increased 16α OHE₁ level and decreased 2OHE₁. However, concerning the relationship between aberrant hyperproliferation, altered oestrogen metabolism and *c-myc*-deregulated expression, it remains unclear whether this represents a result of oncogene expression/activation or is rather a consequence of phenotypic transformation of the cells.

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