Title
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Permalink
https://escholarship.org/uc/item/9cp7w56m

Journal
Nucleic acids research, 41(1)

ISSN
0305-1048

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Publication Date
2013

DOI
10.1093/nar/gks1051

Peer reviewed
Mammalian cells acquire epigenetic hallmarks of human cancer during immortalization

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Received June 7, 2012; Revised October 1, 2012; Accepted October 10, 2012

ABSTRACT
Progression to malignancy requires that cells overcome senescence and switch to an immortal phenotype. Thus, exploring the genetic and epigenetic changes that occur during senescence/immortalization may help elucidate crucial events that lead to cell transformation. In the present study, we have globally profiled DNA methylation in relation to gene expression in primary, senescent and immortalized mouse embryonic fibroblasts. Using a high-resolution genome-wide mapping technique, followed by extensive locus-specific validation assays, we have identified 24 CpG islands that display significantly higher levels of CpG methylation in immortalized cell lines as compared to primary murine fibroblasts. Several of these hypermethylated CpG islands are associated with genes involved in the MEK–ERK pathway, one of the most frequently disrupted pathways in cancer. Approximately half of the hypermethylated targets are developmental regulators, and bind to the repressive Polycomb group (PcG) proteins, often in the context of bivalent chromatin in mouse embryonic stem cells. Because PcG-associated aberrant DNA methylation is a hallmark of several human malignancies, our methylation data suggest that epigenetic reprogramming of pluripotency genes may initiate cell immortalization. Consistent with methylome alterations, global gene expression analysis reveals that the vast majority of genes dysregulated during cell immortalization belongs to gene families that converge into the MEK–ERK pathway. Additionally, several dysregulated members of the MAP kinase network show concomitant hypermethylation of CpG islands. Unlocking alternative epigenetic routes for cell immortalization will be paramount for understanding crucial events leading to cell transformation. Unlike genetic alterations, epigenetic changes are reversible events, and as such, can be amenable to pharmacological interventions, which makes them appealing targets for cancer therapy when genetic approaches prove inadequate.

INTRODUCTION
Cellular senescence is characterized by irreversible loss of cell proliferation, and is considered a powerful tumor suppressor mechanism to eliminate damaged cells prone to transformation (1,2). Cellular senescence has been shown to function as a barrier to somatic cell reprogramming (3), and to play a role in organismal aging (4). Features of senescence are often detected in pre-malignant lesions of mice and humans, but not in their respective invasive/malignant tumors. This suggests a role for senescent cells in the initiation and progression of tumorigenesis (2,5,6). For example, senescent cells are known to give rise to neighboring cancer cells through paracrine signaling with their microenvironment (7–9). Alternatively, cells may bypass or escape senescence and re-enter the cell cycle to become transformed following the inactivation of key components of the senescence-promoting pathways (2,4,10). Thus, investigating the underlying mechanisms of senescence bypass and immortalization may help elucidate tumor initiation and progression.

Despite obvious differences between human and mouse, key aspects of cellular senescence in the two species are well-conserved during evolution (11,12). Mouse models

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have been shown to provide mechanistic insights into the chain of events that leads to senescence bypass and immortalization of relevance to human carcinogenesis (2,13–15). Mouse embryonic fibroblasts (MEFs) are a validated model system to study senescence bypass and spontaneous immortalization (16,17). Primary MEFs have a limited growth capacity and undergo stress-induced senescence, presumably due to oxidative damage caused by standard cell culture conditions (10,18,19). Upon prolonged culturing and passaging, however, MEFs can override the senescence block and become spontaneously immortalized, partly due to mutation/deletion of the p53/p19Arf pathway (16,18,20).

The phenotypically normal 
Hupki (human p53 knock-in) mouse strain, harboring the humanized p53 gene (15), has extensively been used as a model system to study the underlying mechanisms of senescence bypass and immortalization (13,15,21,22). Using a library of several hundred immortalized cell lines, Whibley et al. (17) have demonstrated that MEFs derived from Hupki mice undergo senescence and become immortalized in the same way as their wild-type counterparts, i.e., embryonic fibroblasts from standard laboratory mice with a murine Trp53 gene. In both cases, immortalized cells typically harbor either a missense point mutation in the p53 gene leading to loss of p53 transactivation, or a biallelic deletion at the p19Arf locus. Surprisingly, however, more than half of the immortalized cell lines examined had neither a p53 mutation nor loss of the p19Arf activity (17). In some of these cell lines, genetic defects in tumor suppressor pathways, other than those affecting the p53/p19Arf axis, may contribute to escape or release from the senescence block into an immortal phenotype (17,23). Furthermore, active acquisition of epigenetic modifications, such as DNA methylation at regulatory CpG sites may interfere with the expression of key senescence genes, and pave the way to immortalization and cell transformation (23,24). To explore novel epigenetic/genetic routes that may modulate senescence bypass and immortalization, we have globally profiled DNA methylation in relation to gene expression in primary, senescent and immortalized fibroblasts derived from both the Hupki and wild-type mice. Using microarray-based approaches together with locus/gene-specific validation assays, we have constructed the whole methylome and transcriptome of MEFs at three distinct proliferation stages, including primary, senescent and immortalized cell lines.

MATERIALS AND METHODS

Isolation and immortalization of primary MEFs

Primary MEFs were obtained from embryos derived from either Hupki (Sets 1, 2 and 3) or wild-type (Sets 5 and 7) mice according to standard procedures (15). Briefly, mouse embryos were harvested in utero at 13.5 days of gestation. Following the removal of the head and internal organs, embryo carcasses were roughly minced and digested for five times, 5 min each, with 0.25% trypsin at 37°C. Remaining tissue clumps were disaggregated by passage through a syringe equipped with an 18-gauge needle, and vigorous pipetting. Homogenous cell suspensions were then transferred to tissue culture flasks, and cultured in standard Dulbecco Modified Eagle’s Medium (DMEM, Irvine Scientific, Santa Ana, CA), supplemented with 10% fetal calf serum (FCS), non-essential amino acids and 0.1 mM β-mercaptoethanol. Following 1–3 days of incubation at 37°C, confluent cultures were trypsinized and frozen, at 2–3 × 10^6 cells per vial. To establish cell lines, thawed and seeded onto T75 flasks containing DMEM supplemented with 10% FCS. At 80% confluence, the cells were trypsinized and re-seeded onto 6-well culture dishes or small flasks (12.5 cm²) at a density of ~1 × 10^5 cells per well/flask in DMEM plus 10% FCS. Cultures were maintained under standard conditions (37°C, 5% CO₂ in a humidified atmosphere), and passaged serially when reaching confluence [pass to: 1:3 or 1:4, as described previously (17)]. During crisis, which typically occurs by passage 5-6 and lasts up to 3 weeks, culture medium was changed twice a week. Upon the crisis, over 95% of all cultures became spontaneously immortalized. For all experiments, cells were harvested at different passages before-, during- and after crisis, as outlined in Figure 1A, and genomic DNA/RNA was isolated according to standard procedures (17).

Genome-wide DNA methylation profiling by MIRA-microarray analysis

We used the methylated CpG (mCG) island recovery assay (MIRA) in combination with microarray analysis (25,26) to globally profile DNA methylation in primary, senescent and immortalized MEFs. As a pull-down assay for enrichment of mCG islands, the MIRA is based on the ability of the methyl-CpG binding 2b (MBD2b) protein to bind methylated-CpG dinucleotides, while this reaction is enhanced in the presence of MBD3L1 protein (27). The MIRA-enriched- and input (non-enriched) DNA fractions were amplified by polymerase chain reaction (PCR), and subsequently labeled and hybridized to the Roche NimbleGen mouse methylation microarrays (Roche NimbleGen Inc., Indianapolis, IN) to interrogate the entire CpG-island battery of the mouse genome (see Supplementary Data) (25,26). The accession number for DNA methylation microarray data is GSE39034.

Single gene/locus DNA methylation analysis by COBRA and bisulfite sequencing

We verified the methylation status of individual target loci/genes identified by MIRA-microarray analysis using the conventional combined bisulfite restriction analysis (COBRA) (28), and sodium bisulfite sequencing (29). The primer sets used for PCR amplification of all the analysed targets are listed in Supplementary Table S1 (see Supplementary Data).

DNA methylation analysis of repetitive DNA elements

We have specifically determined the methylation status of major repetitive DNA elements, including long interspersed nuclear elements (LINE L1), intracisternal A particle long terminal repeat retrotransposons.
(IAP-LTR), and short interspersed nuclear elements (SINE B1) (30–32), in the genome of primary, senescent or immortalized MEFs using a bisulfite-based sequencing analysis (see Supplementary Data) (33).

Genome-wide gene expression profiling by Affymetrix-microarray analysis

We used the GeneChip® Mouse Genome 430 2.0 Array (Affymetrix Inc., Santa Clara, CA) to establish the global gene expression profile of MEFs at three different stages (before crisis, crisis, after crisis). Currently, this microarray platform is the most comprehensive mouse genome expression array, which enables interrogation of over 39,000 transcripts and variants from over 34,000 well-characterized mouse genes (see Supplementary Data). The accession number for gene expression microarray data is GSE39034.

Quantitative real-time PCR

Standard quantitative real-time-PCR (qRT-PCR) was used to confirm the transcriptional status of individual target genes identified by microarray analysis (34). The primer sets used for qRT-PCR are listed in Supplementary Table S1 (see Supplementary Data).

RESULTS

Genome-wide detection of aberrant DNA methylation following senescence bypass and immortalization

We have used the MIRA in combination with microarray analysis (25,26) to detect changes in the global methylation pattern of murine cells undergoing immortalization. MEFs were cultured in vitro as described in ‘Materials and Methods’ section (outlined in Figure 1A), and harvested at...
different passages (i.e., before crisis (bc): primary, during crisis (c): senescent and after crisis (ac): immortalized). Following pull-down of mCG islands by MIRA, the enriched- and input (non-enriched) DNA fractions were labeled, mixed and hybridized to the mouse CpG island plus promoter tiling arrays (Roche NimbleGen Inc.). Using standard algorithms for peak calling (see Supplementary Data), we have identified 24 CpG islands that were aberrantly methylated in three independent sets of immortalized MEF cell lines, but were methylation-free in the correspondent low-passage primary cells (Table 1). The identified CpG islands mapped to intergenic regions (21%), within gene bodies (38%), at promoter regions (29%) and near the 3′-end of genes (12%). Using a combination of the Ingenuity Pathway Analysis® (IPA®; v 9.0) and the Database for Annotation, Visualization and Integrated Discovery (DAVID: v 6.7) (35), we obtained gene ontology (GO) information for the annotated genes and the Database for Annotation, Visualization and Integrated Discovery (DAVID: v 6.7) (35), we obtained gene ontology (GO) information for the annotated genes identified as hypermethylated targets in immortalized MEFs. Functional annotation analysis revealed that gene targets involved in intracellular signaling cascade (Rem 2, Rasd1, Wnk4, Adra1d, Mapk11, Plec3; P < 0.007), small GTPase-mediated signal transduction (Rem2, Rasd1, Mapk11; P < 0.04), as well as neuropeptide signaling pathway (Eltd1, Lphn3; P < 0.09) were particularly enriched. Of significance, several genes involved in the MEK–ERK pathway, one of the most frequently disrupted pathways in cancer (36–39), showed progressive DNA hypermethylation as the cells bypassed senescence and became immortalized. Using reverse criteria for data analysis, we detected no significant loss of CpG island methylation across the three independently established immortalized cell lines relative to counterpart primary cells.

### Verification of aberrantly methylated targets by COBRA and bisulfite sequencing

To validate the DNA methylation microarray results, we have randomly selected and analysed several of the targets identified by MIRA-microarray analysis using both the COBRA and bisulfite DNA sequencing analysis (28,29). Representative results of the COBRA assay are shown in Figures 2C and 3C and Supplementary Figures S1–S4. Here, we have inspected the methylation status of CpG islands associated with the Pld3 gene (target #2), Phox2a (target #6), Mapk11 (target #9), Cldh5 (target #11) and Rasd1 (target #18) genes. As shown in Table 1, these CpG-rich loci displayed enrichment ratios, by MIRA-microarray analysis, ranging from 5.99 to 3.48, respectively (on a linear scale, immortalized versus low-passage fibroblasts). COBRA analysis of the above-specified targets confirms the microarray results, indicating that novel epigenetic marks, i.e., CpG methylation, are established during cell immortalization (Figures 2A and 3A and Supplementary Figures S1A–S3A). Of note, these methylation changes were consistent in both the Hupki and wild-type immortalized MEFs (Supplementary Figures S3 and S4).

To obtain a detailed methylation map for each CpG within the CpG islands, we also performed bisulfite sequencing on the targets analysed by COBRA. The sequencing results of the Phox2a-, Mapk11-, Rasd1- and

### Table 1. Hypermethylated targets detected in immortalized versus primary fibroblasts

| Target no. | Gene symbol | Description | CGI location | Position relative to gene | Strand | Enrichment ratio |
|------------|-------------|-------------|--------------|---------------------------|--------|-----------------|
| 1          | Plec3       | phospholipase C, delta 3 | chr19:5953322-5953496 | Intragenic | + | 6.40 |
| 2          | Wnk4        | WNK lysine deficient protein kinase 4 | chr11:102941383-102942047 | Intragenic | + | 5.99 |
| 3          | Adra1d      | adrenergic receptor, alpha 1d | chr2:131371751-131372295 | Downstream | | 5.01 |
| 4          | Phox2a      | paired-like homeobox 2a | chr7:109096905-10909729 | Intragenic | + | 4.80 |
| 5          | Rem2        | Rad- and gem-related GTP-binding protein 2 | chr14:5598125-5598574 | Downstream | + | 4.78 |
| 6          | Mapk11      | mitogen-activated protein kinase 11 | chr7:77514032-77515167 | Intragenic | | 4.71 |
| 7          | Sh2d5       | SH2 domain containing 5 | chr15:8897696-8897946 | Intragenic | + | 4.67 |
| 8          | Cldn5       | claudin 5 | chr4:13780496-13780960 | Upstream | + | 4.25 |
| 9          | Hoxc9       | homeobox C9 | chr16:18777229-18778053 | Intragenic | + | 4.20 |
| 10         | Ntn3        | netrin 3 | chr15:24345612-24346041 | Upstream | – | 4.19 |
| 11         | Fhox11      | dendir | chr5:110815430-110815859 | Intragenic | – | 4.16 |
| 12         | Ddn         | dendir | chr15:98637075-98637154 | Intragenic | – | 3.85 |
| 13         | Amh         | anti-Mullerian hormone | chr10:8029688-8027092 | Downstream | + | 3.67 |
| 14         | Eltd1       | EGF, latrophilin seven transmembrane domain containing 1 | chr3:151100756-151110200 | Upstream | + | 3.57 |
| 15         | Rasd1       | RAS, dexamethasone-induced 1 | chr11:5977219-59777763 | Intragenic | + | 3.48 |
| 16         | Adra1d      | adrenergic receptor, alpha 1d | chr2:13136864-131387318 | Upstream | + | 3.46 |
| 17         | Lphn3       | latrophilin 3 | chr5:18175778-18179233 | Intragenic | + | 3.38 |
| 18         | Akap5       | A kinase (PRKA) anchor protein 5 | chr12:7742570-77426441 | Upstream | + | 3.19 |
| 19         | Ccedc14     | coiled-coil domain containing 114 | chr7:53179579-53180028 | Upstream | + | 3.06 |
| 20         |             |             |             |             |        |     |

*Downstream of Med9 gene.*
Cldn5-associated CpG islands are shown in Figures 2D and 3D, and Supplementary Figures S1D and S2D. In all cases, we confirmed DNA methylation differences (up to 6-fold) between immortalized and primary MEFs, mirroring the differences observed in the microarray and COBRA analyses (Table 1). As shown in Figures 2D and 3D and Supplementary Figures S1D and S2D, aberrant methylation at the CpG islands is established mostly during the crisis stage, suggesting that DNA methylation of crucial genes involved in the maintenance of senescence may drive cells to the immortal phenotype.

We did not detect any gene-specific CpG island that was hypomethylated across all the three immortalized cell lines. However, when less stringent criteria were used in the analysis (a methylation peak present in all primary cells but absent in two out of the three immortalized cell lines), we found several hypomethylated CpG islands common to two immortalized cell lines. Representative examples of hypomethylated targets are shown in Figure 4, which combines bisulfite sequencing results for the Neat1 gene (Figure 4A) and COBRA data for an unknown RIKEN cDNA 4833420G17 gene (Figure 4B).
and the Hoxa3 gene (Figure 4C, bottom). As illustrated in Figure 4C, loss of methylation may occur at entire gene clusters, e.g., the Hoxa homeobox gene cluster that is known to be aberrantly methylated in a variety of human cancers (25,40,41).

Using a sodium bisulfite-based sequencing analysis (33), we have also investigated the methylation status of major repetitive DNA elements, including LINE L1, IAP-LTR and SINE B1, which constitute 18.78, 3.13 and 2.66% of the mouse genome (30–32). As shown in Figure 5, DNA methylation at these repeat elements, in particular IAP-LTR and SINE B1 elements, was reduced in immortalized cell lines relative to primary MEFs, which indicates that genome-wide DNA methylation decreases with in vitro passaging.

**Gene expression profiling of primary, senescent and immortalized MEFs**

To identify novel genes that are differentially expressed during immortalization, we have profiled the whole transcriptome of primary, senescent and immortalized MEFs using an Affymetrix-microarray platform (Affymetrix Inc.). Following standard bioinformatics analysis, we identified a large number of dysregulated genes across three independently established immortalized cell lines (Figure 6A). When we compared the expression profile of senescent versus primary fibroblasts (based on a log2 ratio of one = 2-fold difference), we detected 95 differentially expressed targets/probes, of which 34 were overexpressed (up to a log2 ratio of +5.54) and 61 were down-regulated (with a log2 ratio as low as −3.51) in all the three datasets. A much higher number of differentially expressed targets/probes (n = 313) was detected when immortalized cells were compared to low-passage primary fibroblasts (Figure 6B and Supplementary Table S2). Of the 313 identified targets, 80 were up-regulated (up to a log2 ratio of +6.07) and 233 were down-regulated (with a log2 ratio as low as −3.66). Interestingly, 50 of these probes/targets were common in the senescent and immortalized phenotype, suggesting a crucial role for
these genes in circumventing senescence and initiating uncontrolled cell proliferation (Figure 6B).

We have also investigated the functional relationships between genes that were differentially regulated in immortalized versus primary fibroblasts. Based on the IPA®, we found that these genes were mostly involved in cell signaling networks, cell cycle and cell morphology, embryonic and tissue development (Figure 6D) and were overrepresented compared to the senescent phenotype (Figure 6C). In agreement with the methylation data, we found that several pathways implicated in human cancer, such as the MEK–ERK, PI3K/Akt, NfkB and Vegf pathway (36–39) were mostly affected upon immortalization (Figures 7A and 8). These findings are in agreement with those of a recent report in which major pathways involved in controlling senescence/immortalization were identified (42).

**Correlation between DNA methylation and gene expression during senescence bypass and immortalization**

To investigate the impact of DNA methylation on gene expression during senescence bypass and cell immortalization, we have individually quantified the transcription level of several of the hypermethylated genes identified by our DNA methylation analysis using standard qRT-PCR. The analysed targets are known to interact with key components of the MAP kinase pathways (Figure 7A), and are potentially relevant for the establishment of a malignant phenotype. Figure 7B shows the mean normalized expression levels of the *Clhn5, Hoxc9, Wnk4, Mapk11, Rasd1, Adra1d* and *Akap5* genes in three independently immortalized cell lines (1ac, 2ac, 3ac) relative to primary cells (1bc, 2bc, 3bc). With the exception of the *Akap5* gene, which is down-regulated, all the other targets show steady increase in transcription levels upon immortalization.

We have also selected several of the up-regulated and down-regulated genes detected by Affymetrix-chip analysis, and validated their relative expression by standard qRT-PCR. Representative qRT-PCR results are shown in Figure 7C. In line with microarray data (Supplementary Figure S5 and Supplementary Table S2), we confirmed that the *Pfl1* and *Foxg1* genes were up-regulated, whereas the *Hoxd10, Hoxd13* and *Igf2*
genes were down-regulated in immortalized MEFs (Figure 7C). Of significance, some of these genes encode proteins, which are relevant for MAPK cascades (Figures 7A and 8).

DISCUSSION

Bypass from senescence is widely recognized as the first step toward immortalization, which, in turn, may drive cells to malignancy (43). To gain insights into the epigenetic and genetic mechanisms involved in the senescence/imortalization switch, we have analysed the whole methylome and transcriptome of primary, senescent and immortalized MEFs, a well-established in vitro model of cell immortalization (16,17). Using a high-resolution genome-wide mapping technique (MIRA-chip) (25,26), followed by extensive single gene/locus-specific validation assays (COBRA and bisulfite sequencing) (28,29), we have identified 24 CpG islands that display aberrant DNA methylation in three independently established immortalized MEF cell lines as compared to counterpart low-passage primary cells (Table 1). Furthermore, we observed significant loss of CpG methylation at major repetitive DNA elements (Figure 5), a genome-wide epigenetic event often associated with genetic instability and cancer (44–46).

In immortalized murine fibroblasts, de novo DNA methylation marks preferentially genes that are involved in the development and function of the nervous system (Phox2a, target #6; Rem2, target #7; Cldn5, target #11; Ntn3, target #13; Amh, target #16; Adra1d, target #19; Akap5, target #21; IPA®, P = 9.75E-04 – 4.30E-02; Table 1). These and other developmental regulators (47% of the identified genes) are targets of the Polycomb repressive complexes, and often associate with bivalent modifications (H3K4me3 active marks and H3K27me3 inactive
marks) in murine embryonic stem (ES) cells, as deduced by comparison of our data to published databases (47–49). Polycomb group (PcG) proteins are critical for the maintenance of stem cell identity and cell differentiation (47,50,51), and PcG-associated genes in ES cells are often the target of aberrant CpG methylation in cancer, thus, supporting the ‘stem cell origin’ model of transformation (52–54). The DNA methylation/PcG connection has been consistently observed in the epigenome of several human malignancies (55,56), and our findings suggest that epigenetic reprogramming of pluripotency genes may take place at early pre-neoplastic stages, once the cells acquire an infinite life span. Interestingly, GO analysis of the annotated hypermethylated targets (n = 19), identified in immortalized MEFs, confirmed a trend of enrichment for genes involved in intracellular signaling cascades, such as the MEK–ERK pathway, one of the most frequently altered genetic pathways in human cancer (Figures 7A and 8) (36–39). This finding reinforces the notion that alternative epigenetic mechanisms may contribute to the disruption of genetic pathways that are crucial for cell immortalization and growth, and tumor development (2,3,17,18,42).

To examine the potential impact of DNA methylation on gene expression during senescence bypass and immortalization, we have also constructed the whole transcriptome of primary, senescent and immortalized murine fibroblasts. A large number of differentially expressed targets/probes (n = 313) was identified in independently established immortalized MEF cell lines when compared to low-passage primary fibroblasts (Figure 6B and Supplementary Table S2). Apart from few known
Figure 7. Gene network analysis and relative quantification of gene expression by standard qRT-PCR. (A) Upon immortalization, genetic and epigenetic events may contribute to dysregulation of MAP kinase pathways. Upstream and downstream components of the p38-MAPK and MEK–ERK cascade are shown in pink. Network interactions were deduced from IPA analysis and are illustrated in detail in Figure 8. Continuous line, direct interaction; broken line, indirect interaction. Red and green molecules represent up-regulated and down-regulated targets, respectively. Yellow node color is indicative of hypermethylation. Up-white-arrows represent up-regulation and down-white-arrows represent down-regulation. (B) Transcription levels of the Cldn5, Hoxc9, Wnk4, Mapk11, Rad1d, Adra1d and Akap5 genes following immortalization. Bars represent the mean normalized expression (±SD) of three independent immortalized cell lines (ac: 1ac & 2ac & 3ac; each in triplicate) relative to primary cells (bc: 1bc & 2bc & 3bc; each in triplicate). Data analysis was performed using the 2−ΔΔCt method (34) with Gapdh as reference gene. (C) The expression status of individual target genes identified by Affymetrix-microarray analysis was confirmed by standard qRT-PCR. Two up-regulated (Plf1 and Foxg1) and three down-regulated genes (Igf2, Hoxd10 and Hoxd13) were analysed in senescent (1c, 2c, 3c) and immortalized (1ac, 2ac, 3ac) samples according to the 2−ΔΔCt method (34). Expression data were normalized using an endogenous housekeeping gene as reference (Gapdh), and samples 1bc, 2bc, 3bc (RNA of primary fibroblasts) as calibrators within the respective group (fold ratio = 1). Data are expressed as mean ± SD of three replicates.
markers of senescence [i.e., Igfbp6, Ahr, Colla1, Aldh1a2; reviewed in (42)], several of our identified transcripts are novel, and represent starting points for future research on transcriptional pathways that may regulate the acquisition of an infinite life span in somatic cells. We have further classified the function of the differentially expressed genes (crisis and after crisis versus before crisis phenotypes) by GO analysis. According to DAVID, a larger number of dysfunctional gene clusters was identified in the immortal phenotype, including genes involved in signaling, development, morphogenesis and neurogenesis (Figure 6C and D). The vast majority of these dysregulated genes converge into specific pathways, such as MEK/ERK, PI3K/Akt, NFkB and Vegf that are often impaired during tumorigenesis (Figure 8) (36–39). In addition, out of the 244 annotated DAVID IDs (from the 313 transcripts differentially expressed in immortalized MEFs), 41% (n = 101) are normally expressed in the brain, and play a role in neural development.

We have also confirmed gene expression changes in several of the hypermethylated targets identified by our DNA methylation analysis using standard qRT-PCR. Apart from Akap5 and Hoxc9, which are aberrantly methylated at their promoter regions, the majority of the analysed targets contain intragenic CpG islands that become hypermethylated upon immortalization. These latter genes are all up-regulated in immortalized versus low-passage primary cells (Figure 7B). Our findings are in agreement with several reports indicating that intragenic methylation often correlates with gene up-regulation [reviewed in (57–61)]. Along with Cldn5, Wnk4, Mapk11 and Rasd1, several other targets are methylated within gene bodies (38%) rather than at canonical 5′-end promoters (29%) (Table 1), a trend
consistently reported for different human epigenomes (62,63). Although the exact functional role of these intragenic CpG-rich elements remains to be determined, the general consensus is that these elements constitute short independent transcriptional units and/or regulate alternative isoforms (62,63). A recent study has demonstrated a crucial role for the DNA-binding protein, CTCF (CTCF), in regulating alternative exon splicing by inhibiting PolII elongation dynamics (64). CTCF binding to the DNA occurs mostly intragenically (40–45%), and is inhibited by CpG methylation (64). In the present study, we have observed that about 70% of the methylated intragenic CpG islands are located at or adjacent to (within 1 kb) potential consensus elements for CTCF, when compared to published databases (Figures 2B and 3B, and Supplementary Figures S1 and S3) (http://genome.ucsc.edu/ENCODE/downloadsMouse.html). It is plausible that de novo methylation established during cell immortalization may impede the binding of the CTCF protein at these intragenic sites, thereby, resuming RNA polymerase extension and/or splicing. Alternatively, methylation-dependent CTCF release within gene bodies can predispose the DNA to an open chromatin configuration, which may lead to unusual gene activation, uncontrolled cell proliferation (i.e., immortalization), and cancer development (65,66).

A large body of evidence exists indicating that the Ras/Raf/ERK and the p38 MAP kinase pathways are two of the most relevant pathways involved in the activation of senescence as a fail-safe mechanism against oncogenic transformation and other damage in primary cells (42,67–69). By marked contrast, deregulated activation of the MEK/MAPK cascade can result in forced mitogenesis and transformation in immortal cells (67). These two totally opposite outcomes, cell cycle arrest and induction of proliferation, imposed by identical signal-transduction pathways are mostly cell context-dependent and dictated by the strength of the stimuli and the integration of proliferation, imposed by identical signal-transduction pathways are mostly cell context-dependent and dictated by the strength of the stimuli and the integrity of the senescence program (67). Interestingly, high-passage MEFs (PD 13), cultured according to the 3T3 protocol (as in this study), displayed elevated levels of activated p38\(^{MAPK}\) (p38-P), compared to early passage MEF cells (PD 3), although apparently immortalized MEFs (PD 35) proliferate independently of the status of p38\(^{MAPK}\) (70). In our study, although we did not directly analyse the activity (i.e. phosphorylation) of the kinases involved in the MAPK signaling cascades, all the indications are that these cascades are indeed activated during immortalization. Of note, we have shown that proliferin 1 (Plf1) a well-known component of the MAPK pathway is greatly up-regulated in senescent and immortal fibroblasts (up to 67-fold on linear scale; Supplementary Table S2). Plf1 modulates the activation of the MEK/ERK pathway and is transcriptionally regulated by β-catenin, which accumulates following activation of p38\(^{MAPK}\), via repression of GSK3β (Figure 7A) (71,72).

In conclusion, our global profiling of the methylome and transcriptome of primary, senescent and immortalized murine fibroblast cells shows abrogations of epigenetic and genetic pathways during cell immortalization, which closely resemble those found in human cancer (36,37,39,57–59). Despite species differences between human and mouse, identification of novel biomarkers of senescence bypass and immortalization in mouse models may help elucidate the underlying mechanisms of human carcinogenesis. If validated in vivo in humans, these biological markers can be used to predict cancer risk in early stage lesions, and help devise future strategies for cancer therapies, e.g., re-activation of key signaling effectors of senescence in tumor cells.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online: Supplementary Tables 1–3, Supplementary Figures 1–5 and Supplementary Materials and Methods.

FUNDING

Funding for open access charge: American Cancer Society [RSG-11-083-01-CNE]; University of California Tobacco Related Disease Research Program [18KT-0040 and 20XT-0116 to A.B.].

Conflict of interest statement. None declared.

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