Cancer susceptibility and embryonic lethality in Mob1a/1b double-mutant mice

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Introduction

Tissue homeostasis requires a balance of cell proliferation, apoptosis, and differentiation. During tissue development, progenitor cells divide for a limited number of times before exiting the cell cycle and undergoing terminal differentiation (1). When progenitor cells proliferate inappropriately and/or undergo abnormal differentiation, cancer can result (2).

Skin is a tissue that begins as a single-layered epithelium made up of keratinocytes that later stratify and differentiate into hair follicles (HFs) or interfollicular epidermis (IFE). Disruption of signals balancing growth and differentiation in keratinocytes can initiate skin cancers. The most common skin cancer is basal cell carcinoma (BCC), the nodular subtype of which originates from HFs. Trichilemmal carcinomas are also HF-derived skin cancers, but are much more rare and show characteristic abnormalities of outer hair root sheath differentiation (3). Although impairment of the Sonic Hedgehog (SHH) intracellular signaling pathway is now well established as the cause of BCC (4, 5), the molecular mechanism underlying the development of trichilemmal carcinomas is unknown.

The evolutionarily conserved Hippo signaling pathway was first identified as regulating the cell proliferation and apoptosis-controlling organ size in Drosophila (6, 7). In mammals, the canonical Hippo pathway includes the following: Neurofibromin 2 (NF2) (8), the Mammalian STE20-like protein (MST) kinases (9), large tumor suppressor homolog (LAT5) and Nuclear Dbf2-related (NDR) kinases (10), the adaptor proteins SAV1 (WW45) (11) and MOB1 (12), and their downstream transcriptional coactivators YAP1 and its paralog transcriptional coactivator with PDZ-binding motif (TAZ, WWTR1) (13). All of these molecules (except YAP1 and TAZ) have been implicated as tumor suppressors. For example, mice deficient in Lats1 or Mst1/2 develop various cancers (14, 15), SAV1 and MOB1 are mutated in human cancer cell lines (16, 17), and Hippo components are reduced in human cancer samples (18). Homozygous-null mutant mice lacking Nf2, Mst1/2, SAV1, Lats2, or Yap1 are all embryonic lethal (15, 19–22), precluding study of these mediators in tumorigenesis. To complicate matters, multiple homologs of each mammalian Hippo element exist, and the precise physiological functions of Hippo elements in mammals remain obscure.

Mps one binder 1a (MOB1A) and MOB1B are key components of the Hippo signaling pathway and are mutated or inactivated in many human cancers. Here we show that intact Mob1a or Mob1b is essential for murine embryogenesis and that loss of the remaining WT Mob1 allele in Mob1aΔ/Δ1b/Δ2 or Mob1aαβ/Δ1bΔ2 mice results in tumor development. Because most of these cancers resembled trichilemmal carcinomas, we generated double-mutant mice bearing tamoxifen-inducible, keratinocyte-specific homozygous-null mutations of Mob1a and Mob1b (kDKO mice). kDKO mice showed hyperplastic keratinocyte progenitors and defective keratinocyte terminal differentiation and soon died of malnutrition. kDKO keratinocytes exhibited hyperproliferation, apoptotic resistance, impaired contact inhibition, enhanced progenitor self renewal, and increased centrosomes. Examination of Hippo pathway signaling in kDKO keratinocytes revealed that loss of Mob1a/b altered the activities of the downstream Hippo mediators LATS and YAP1. Similarly, YAP1 was activated in some human trichilemmal carcinomas, and some of these also exhibited MOB1A/1B inactivation. Our results clearly demonstrate that MOB1A and MOB1B have overlapping functions in skin homeostasis, and exert their roles as tumor suppressors by regulating downstream elements of the Hippo pathway.

Authorship note: Koichi Hamada and Kohichi Kawahara contributed equally to this work. Satoshi Itami and Akira Suzuki contributed equally as co-senior authors.

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MOB1 was originally shown in yeast to regulate mitotic exit and modulate cytokinesis (24–29). In Drosophila, dMOB1 (MATS) overexpression is tumor suppressive, while loss of dMOB1 triggers tumor development (17). In humans, 7 MOB homologs (hMOB1-A, 2A-C, 3, 4, where MOB indicates Mps one binder) have been identified (30), and hMOB1A (hMATS1, MOBKL1B) and hMOB1B (hMATS2, MOBKL1A) share 95% amino acid identity. Although no apparent functional domain has been found in hMOB1A/B, only these 2 MOB proteins can bind to and activate LATS1/2 (31). In vitro, hMOB1A overexpression inhibits cell proliferation, while suppression of hMOB1B or hMOB1A mediated by shRNA or siRNA increases proliferation (30) or impairs mitotic exit (32), respectively. In vivo, the hMOB1A gene is mutated in melanoma and breast cancer cell lines, and its expression is downregulated in human colon and non–small-cell lung cancers (17, 33, 34). However, the normal function of hMOB1 proteins in vivo is unknown. To assess whether MOB1 is an important functional component of mammalian Hippo signaling and to determine whether MOB1 is truly a tumor suppressor in vivo, we generated and characterized double-mutant mice lacking Mob1a and Mob1b.

Results

Embryonic lethality of Mob1a/1b-null mutant mice. We first generated single-mutant mice bearing a null mutation of Mob1a (Mob1aΔ/Δ) or a trapped mutation of Mob1b (Mob1bΔ/Δ) (Supplemental Figure 1, A–D; supplemental material available online with this article; doi:10.1172/JCI63735DS1) but no abnormalities were observed in morphology, body weight, histology, or life span (Supplemental Figure 1E and data not shown). We then attempted to generate double-homozygous–null mutant (Mob1aΔ/ΔMob1bΔ/Δ) mice, but no viable pups were obtained (Supplemental Table 1), indicating that complete loss of Mob1 is embryonic lethal. We next analyzed embryos from Mob1aΔ/ΔMob1bΔ/Δ intercrosses at various time points during gestation. By E6.5, although decidua were formed, 28% of embryos were absorbed too severely to genotype (Figure 1A and Table 1). Thus, MOB1A and MOB1B have overlapping functions, and MOB1 is essential for postimplantation embryogenesis.

To pinpoint the embryonic defect, we obtained individual blastocysts (E3.5) from Mob1aΔ/ΔMob1bΔ/Δ intercrosses and cultured them for 8 days. Mob1aΔ/ΔMob1bΔ/Δ blastocysts appeared normal at E3.5, but showed growth failure of the inner cell mass (ICM) by day 8 (Figure 1B). In contrast, the trophectoderm (TE) of Mob1aΔ/ΔMob1bΔ/Δ blastocysts developed normally.

To create conditional tamoxifen-inducible Mob1 mutants, we generated ERCreMob1aΔ/ΔMob1bΔ/Δ ES cells and established embryoid bodies (EBs) using the hanging drop method. Control and mutant EBs were cultured for 2 days with (or without) tamoxifen to delete Mob1 and then grown without leukemia inhibitory factor (LIF) for 3–4 days. Quantitative RT-PCR examination showed that Gata4 and Pdgfra mRNAs (essential for primitive endoderm formation) were markedly suppressed in Mob1aΔ/ΔMob1bΔ/Δ EBs, whereas Cdx2 and Eomesoderm mRNAs (essential for TE) were only slightly inhibited (Figure 1C). Levels of Oct3/4 (Pou5f1) and Sall4 mRNAs (essential for ICM), as well as Nanog, Fgf5, Pax6, and Sox2 mRNAs (essential for primitive ectoderm), were normal in the double-mutant EBs. Immunostaining of double-mutant blastocysts with antibodies recognizing CDX2 or Troma-1 (TE markers), NanOG or SOX2 (primitive ectoderm markers), or Oct3/4 confirmed that the levels of these proteins were also normal in the absence of Mob1. However, levels of GATA4 and PdGFRα proteins (primitive endoderm markers) were greatly reduced in the mutants (Figure 1D). Moreover, YAP1, which is usually expressed only in the nuclei of TE cells, was abnormally activated and expressed in the nuclei of ICM cells (Figure 1D). Thus, Mob1aΔ/ΔMob1bΔ/Δ embryos have a defect in primitive endoderm formation.

Mob1aΔ/ΔMob1bΔ/Δ and Mob1aΔ/ΔMob1bΔ/Δ mice show increased susceptibility to tumorigenesis. Mob1aΔ/ΔMob1bΔ/Δ and Mob1aΔ/ΔMob1bΔ/Δ mice were born alive and were healthy and fertile, but 52% of them had dental malocclusion (Supplemental Figure 2A). In addition, 25% of these heterozygotes exhibited disorganization due to disorganized inner ear hair bundles in the cochlear organ of Corti (Supplemental Figure 2B and Supplemental Video 1), and 31% showed histological evidence of increased trabeculae in femurs (Supplemental Figure 2C).

Because mutation or reduced expression of MOB1A occurs in cancer patients (33), we monitored tumorigenesis in Mob1aΔ/ΔMob1bΔ/Δ, Mob1aΔ/ΔMob1bΔ/Δ, and Mob1aΔ/ΔMob1bΔ/Δ (control) mice over 70 weeks. Various tumor types arose spontaneously in 100% of Mob1aΔ/ΔMob1bΔ/Δ and Mob1aΔ/ΔMob1bΔ/Δ mice, but in only 4% of controls (Figure 2, A and B, and Table 2). Southern blotting confirmed the loss of the WT Mob1 allele in all tumors (Figure 2C). In most mutants, skin tumors in the form of facial swellings (Figure 2A) were observed. Benign exos-
Figure 2
Loss of Mob1a/1b promotes tumorigenesis. (A and B) Tumor types arising in Mob1a<sup>Δ−/−</sup>1b<sup>tr/+</sup> or Mob1a<sup>Δ−/+1btr/tr</sup> mice. (A) Macroscopic or microscopic photographs of the indicated gross or H&E-stained tumors in mutant mice. Yellow arrows, tumor masses. Scale bars: 100 μm. (B) Kaplan-Meier analysis of tumor onset and survival for the Mob1a<sup>Δ−/−</sup>1b<sup>tr/+</sup> (<i>n</i> = 31), Mob1a<sup>Δ−/+1btr/tr</sup> (<i>n</i> = 48), and control Mob1a<sup>Δ−/+1btr/+</sup> (<i>n</i> = 22) mice in A. (C) Southern blots of tumor DNA showing loss of the WT Mob1 allele. Top (hybridized to probe A of Supplemental Figure 1A): lanes 1–3, control thymic DNA from Mob1a<sup>++</sup>, Mob1a<sup>Δ−/+</sup>, and Mob1a<sup>Δ−/Δ</sup> mice, respectively; lanes 4–5, osteosarcomas; 6–7, fibrosarcomas; 8–9, skin cancers; 10–11, breast cancers; 12–13, salivary gland cancers of Mob1a<sup>Δ−/Δ1btr/+</sup> mice. Bottom (probe C): 1–3, control tail DNA of Mob1b<sup>++</sup>, Mob1b<sup>tr/+</sup>, and Mob1b<sup>tr/tr</sup> mice, respectively; 4–5, osteosarcomas; 6–7, fibromyosarcomas; 8–9, skin cancers; 10–11, liver cancers of Mob1b<sup>Δ−/Δ1btr/+</sup> mice. Results shown are representative of at least 3 independent trials and at least 3 mice/group. Data are presented as the mean ± SEM, and <i>P</i> values were determined using the 2-tailed Student’s t test.
restricted to the basal epidermal layer. As these cells exit the cell cycle, they differentiate to form the spinous and granular skin layers as well as the dead, enucleated stratum corneum layers. The anagen phase of hair development thickens the skin until day 17, when the first catagen phase is triggered and skin thickness regresses until day 19. Hair remodeling then begins its lifelong cycle of spontaneous regrowth and regression (36). We saw this pattern clearly in our biopsy series from control mice (Supplemental Figure 4). However, the IFE and HFs of kdko(P1) mice showed hyperplastic multilayered epithelium at day 16 (Figure 3B), and impaired epidermal regression during catagen (Supplemental Figure 4; day 19). In addition, parakeratosis (reduced enucleation) was evident in the stratum corneum layer of kdko(P1) mice (Figure 3C).

To investigate keratinocyte differentiation, we used immunostaining to detect keratin markers in the fat pad epidermis, which allows easy analysis of epidermal layers. Keratin-15+ (KRT15+) cells, the most primitive in IFE, normally form a single basal layer attached to the IFE basement membrane (BM). This configuration was clearly visible in our controls, whereas the KRT15+ cells of kdko(P1) mice, although nearly normal in number, were scattered inside the IFE without attachment to the BM (Figure 3D). In control mice, KRT14+ and KRT5+ cells were present in 1 or 2 IFE layers (as expected), but appeared in multiple layers in kdko(P1) mice (Figure 3D). Moreover, there were increased numbers of irregularly organized KRT10+ cells in the suprabasal layers of kdko(P1) epidermis (Figure 3D). Filaggrin+ cells, the most highly differentiated keratinocytes, were present in kdko(P1) epidermis but at a reduced percentage (Figure 3D). Similar IFE alterations were observed in the back skin of kdko(P1) mice (Figure 3E and Supplemental Figure 5). KRT17+ outer root sheath cells were significantly increased in back skin HFs of kdko(P1) mice, and Trichohyalin+ inner root sheath cells were elevated slightly (Figure 3E). Thus, the phenotype of kdko(P1) mice may be largely due to abnormal expansion of immature stem/progenitor skin cells.

To try to overcome the early lethality of kdko(P1) mice, we waited until kdko mice reached 28 days of age before treating them with tamoxifen for 7 days. However, like kdko(P1) mice, all of these kdko(P28) mice showed keratinocyte hyperplasia (Figure 3F) and died within 15–55 days after treatment (Supplemental Figure 6). Thus, MOB1 deficiency in epidermal cells severely disrupts normal IFE and HF development and homeostasis.

### Table 2

<table>
<thead>
<tr>
<th>Tumor Type</th>
<th>kdkoΔ/Δ</th>
<th>kdkoΔ/ΔΔ</th>
<th>Overall</th>
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<tr>
<td>Skin cancer</td>
<td>23 (100%)</td>
<td>14 (100%)</td>
<td>37 (100%)</td>
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<tr>
<td>Exostosis</td>
<td>20 (87%)</td>
<td>14 (100%)</td>
<td>34 (92%)</td>
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<tr>
<td>Osteosarcoma</td>
<td>7 (30%)</td>
<td>2 (14%)</td>
<td>9 (24%)</td>
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<td>Fibrosarcoma</td>
<td>6 (26%)</td>
<td>2 (14%)</td>
<td>8 (22%)</td>
</tr>
<tr>
<td>Liver cancer</td>
<td>0 (0%)</td>
<td>7 (50%)</td>
<td>7 (19%)</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>5 (22%)</td>
<td>1 (7%)</td>
<td>6 (16%)</td>
</tr>
<tr>
<td>Lung cancer</td>
<td>0 (0%)</td>
<td>2 (14%)</td>
<td>2 (5%)</td>
</tr>
<tr>
<td>Salivary gland cancer</td>
<td>1 (4%)</td>
<td>1 (7%)</td>
<td>2 (5%)</td>
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Tumorogenic anomalies in MoBa/A-b double-homozygous mutant keratinocytes. To determine whether loss of MOB1 conferred tumorigenic properties on keratinocytes, we first immunostained kdko(P1) skin with anti-Ki67 Ab and found increased numbers of Ki67+ proliferating epithelial cells (Figure 4A). In control mice at P13, a few Ki67+ cells were located among basal IFE cells and outer root sheath cells, with more scattered among HF matrix cells. However, the incidence of Ki67+ cells in kdko(P1) skin at P13 was 1.5 times higher than in controls, and Ki67+ cells were also found in the suprabasal layers normally quiescent in control epidermis. In addition, TUNEL-positive apoptotic cells were reduced in kdko(P1) epidermis (Figure 4B). Thus, increased proliferation and repressed apoptosis may contribute to kdko(P1) epidermal hyperplasia. Cell-plating studies revealed that the saturation density of kdko(P1) keratinocytes was also increased (Figure 4C). Because the cell size (forward scatter) of control and mutant keratinocytes showed no difference by FACS analysis (data not shown), the increased saturation density of the mutant suggests impaired contact inhibition. Histological analysis confirmed that the mutant basal epidermal layer showed significantly increased cell density...
Figure 3
Characterization of keratinocyte-specific Mob1a/tb double-homozygous mutant mice. (A–C) Features of 16-day-old Krt14CreERMob1a<sup>+/-</sup> mice that were originally left untreated (control) or treated with tamoxifen (KDKO) at P1. (A) KDKO(P1) mice have a wrinkled-bear facial appearance (top left), ruffled, shaggy body hair (bottom left), abnormally large front paws (top right), and decreased survival (bottom right). (B) H&E-stained longitudinal and transverse sections of the back skin of the mice in a KDKO(P1) mice show hyperplasia of IFE and HF. Scale bars: 50 μm. (C) KDKO(P1) mice show parakeratosis (reduced enucleation) in stratum corneum layers. Scale bar: 20 μm. (D) Immunohistochemical analyses of fat pad epidermis of the mice in A using Alexa Fluor 488–tagged Abs recognizing the indicated differentiation markers corresponding to a specific skin layer. DAPI, nuclei. Scale bar: 50 μm. (E) Immunohistochemical analyses of back skin of the mice in A using Abs recognizing the indicated skin layer markers. For top panels, cells were stained with Alexa Fluor 568–tagged anti–KRT14 Ab; DAPI, nuclei. Scale bars: 20 μm. For bottom panels, cells were stained with Alexa Fluor 488–tagged anti–Trichohyalin Ab and Fluor 568–tagged anti–KRT17 Ab. Scale bar: 50 μm. (F) H&E-stained longitudinal sections of skin from 42-day-old Krt14CreERMob1a<sup>+/-</sup> mice that were left untreated (control) or treated with tamoxifen (KDKO) at P28. The KDKO(P28) mutant shows hyperplasia of IFE and HFs. Scale bar: 200 μm. Results shown are representative of at least 3 independent trials and at least 3 mice/group. Data are presented as the mean ± SEM.

To determine which mitotic stage was altered in KDKO(P1) keratinocytes, we divided the mitotic process into 4 parts based on cell morphology: part I, cells progressing from the round morphology of a resting cell to chromosome alignment (corresponding to pro-metaphase); part II, from chromosome alignment to ingestion of the cleavage furrow (metaphase/late anaphase); part III, from ingestion to furrow completion (late anaphase/telophase); and part IV, from furrow completion to cell division (cytokinesis). We used time-lapse video microscopy to measure the duration of each of parts I–IV in control and KDKO(P1) keratinocytes. Part IV was significantly accelerated in MOB1-deficient cells compared with controls, while part I was slightly faster in the mutant (Supplemental Figure 8, A and B). No significant differences were detected for parts II and III. Thus, loss of MOB1 accelerates a cell’s exit from mitosis.

We noted that KDKO(P1) mice had an apparent increase in the number of skin progenitors in the IFE (Figure 3D). We therefore performed RT-PCR to evaluate stem/progenitor cells in the HFs.
Discussion

We have demonstrated that mice completely deficient for Mob1 have the most severe phenotype among strains lacking a Hippo signaling component. Mob1a/1b double homozygous–null mutant mice die at gastrulation, much earlier than mice lacking Mst1/2 (15), Lats2 (21), Lats1 (14), Sav1 (20), or Nf2 (19). Our data further indicate that Mob1 is essential for embryogenesis and that functions of Mob1A and Mob1B overlap. In addition, the tumor spectrum observed in heterozygous Mob1-deficient mice is the broadest among mutants lacking Hippo components. These findings suggest both that Mob1 is the key molecule in the Hippo signaling pathway and that Mob1 may have molecular target(s) other than the Hippo pathway. This notion is consistent with the reduced expression or mutation of Mob1 frequently observed in a variety of human cancers (17, 33, 34), and with Mob1’s reported binding to a range of molecules, including TSSC1, NUP98, HDAC3, and DIPA (CCDD85B) (41, 42). Our results also imply that Mob1A may be more important than Mob1B, at least for embryogenesis and liver homeostasis, because Mob1b heterozygotes lacking Mob1a show partial embryonic lethality (Supplemental Table 1) and develop liver cancers (Table 2), whereas Mob1a heterozygotes lacking Mob1b are all viable and free of liver tumors.

The lethality of Mob1-deficient mice may stem from their failure to form primitive endoderm. The endodermal markers Pdx1 and Gata4 were markedly reduced in Mob1-deficient cells, whereas the primitive ectoderm markers Nanog, Sox2, Fgf5, and Pax6 were normal. Our mutant showed abnormal Yap1 activation, and activated Yap1 normally activates the transcription factor TEAD2. TEAD2 regulates primitive endoderm-specific genes such that sustained inhibition of TEAD2 enhances primitive endoderm-specific gene expression (43). Yap1 and Teads reportedly increase the expression of pluripotency genes such as Oct3/4 and Sox2 (43, 44), as well as the trophoblast gene Cdx2 (45, 46). However, levels of Oct3/4, Sox2, and CDX2 proteins were normal in our Mob1-deficient embryos. Thus, although we found Yap1 to be activated in the
MOB1-mediated regulation of the LATS1/2-YAP1 pathway controls skin homeostasis. (A) Immunostaining of keratinocytes from control and kDKO(P1) mice at P19 to detect YAP1 in the IFE (top) and HF (bottom). Scale bar: 50 μm. (B) Immunoblot of total extracts of control and kDKO(P1) keratinocytes to detect the indicated proteins. α-Tubulin, loading control. (C) Immunoblot of cytoplasmic and nuclear fractions of control and kDKO(P1) keratinocytes to detect the indicated proteins. α-Tubulin and Lamin, cytoplasmic and nuclear loading controls, respectively. (D) Immunostaining to detect YAP1 in keratinocytes from control and kDKO(P1) mice plated at low or high cell density. YAP1 is localized in the nucleus in mutant keratinocytes even at high cell density. (E) Immunoblot to detect the indicated proteins in total extracts of control (Cont) and kDKO(P1) keratinocytes that were left untreated (OA−) or treated with OA (OA+). Left: unadjusted lysates. Right: levels of LATS1 and LATS2 proteins in each sample were adjusted to equality before electrophoresis. Results shown are representative of at least 3 independent trials and at least 3 mice/group.

Figure 5

MOB1-mediated regulation of the LATS1/2-YAP1 pathway controls skin homeostasis. (A) Immunostaining of keratinocytes from control and kDKO(P1) mice at P19 to detect YAP1 in the IFE (top) and HF (bottom). Scale bar: 50 μm. (B) Immunoblot of total extracts of control and kDKO(P1) keratinocytes to detect the indicated proteins. α-Tubulin, loading control. (C) Immunoblot of cytoplasmic and nuclear fractions of control and kDKO(P1) keratinocytes to detect the indicated proteins. α-Tubulin and Lamin, cytoplasmic and nuclear loading controls, respectively. (D) Immunostaining to detect YAP1 in keratinocytes from control and kDKO(P1) mice plated at low or high cell density. YAP1 is localized in the nucleus in mutant keratinocytes even at high cell density. (E) Immunoblot to detect the indicated proteins in total extracts of control (Cont) and kDKO(P1) keratinocytes that were left untreated (OA−) or treated with OA (OA+). Left: unadjusted lysates. Right: levels of LATS1 and LATS2 proteins in each sample were adjusted to equality before electrophoresis. Results shown are representative of at least 3 independent trials and at least 3 mice/group.

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Figure 6
Characterization of skin cancers of Mob1-deficient mice and human trichilemmal carcinomas. (A) H&E-stained sections of representative tumors from Mob1a\textsuperscript{ΔΔ}1b\textsuperscript{tr/} or Mob1a\textsuperscript{ΔΔ}/+1b\textsuperscript{tr/tr} mice showing: (top left) characteristic trichilemmal keratinization (yellow arrows; also in right); (bottom left) atypical and highly mitotic cells; and (right) continuity with the epidermis. Scale bars: 50 μm (left); 500 μm (right). (B) Immunostaining of tumors from Mob1a\textsuperscript{ΔΔ}1b\textsuperscript{tr/} or Mob1a\textsuperscript{ΔΔ}/+1b\textsuperscript{tr/tr} mice to detect the indicated skin markers. White arrows, cancerous lesions; yellow arrow, nontumorous HF. Scale bar: 200 μm. (C) Immunoblot of total extracts of control and kDKO(P1) keratinocytes to detect ERK and AKT activation as well as the HF morphogenesis proteins GLI2 (FL; full length), LEF1 and HES1. β-Actin, loading control. (D) Immunostaining to detect GLI2 in HF s from control or kDKO(P1) mice. Scale bar: 25 μm. (E) Immunoblot to detect GLI2 in total extracts of control keratinocytes transfected with scramble siRNA (Control siSc) or GLI2 siRNA (Control siGLI2), as well as in samples of 4 trichilemmal carcinomas (Tumor 1, 2, 3, 4) from kDKO(P1) mice. (F) H&E staining of a human trichilemmal carcinoma viewed at low (scale bar: 200 μm) or high magnification (scale bar: 50 μm). (G) Immunostaining to detect YAP1 and MOB1A/1B in human trichilemmal carcinomas and nearby nontumorous tissues. Top: Both noncancerous and trichilemmal carcinoma (T) tissues can be seen in low-magnification images. Bottom: High-magnification images of human trichilemmal carcinomas. Scale bars: 100 μm. Results shown are representative of at least 3 independent trials and at least 3 mice/group.
formation. This difference may account for the development of IFE-derived squamous cell carcinomas in Yap1 transgenic mice, but HF-derived trichilemmal carcinomas in Mob1-deficient mutants.

At the biochemical level, Mob1-deficient keratinocytes exhibited reductions in not only phospho-LATS1/2, but also total LATS1/2 proteins. Lats1/2 mRNAs were comparable in control and mutant keratinocytes (data not shown), indicating that this surprising decrease in LATS1/2 proteins occurs posttranscriptionally. Like Mob1, SAV1 is a scaffolding protein in the Hippo pathway, but unlike Mob1 deficiency, Savr deficiency decreases phospho-MST, but does not affect total MST or LATS1/2 proteins (20). Another interesting biochemical observation was the activation of ERK in our Mob1-deficient keratinocytes: no connection between MOB1 and ERK has been reported to date. With respect to Hippo signaling, ERK can be activated by Yap1 (49) or suppressed by NF2 (50) or MST2 (51). Since NF2 and phospho-MST1/2 were not decreased in our Mob1-deficient keratinocytes (data not shown), we speculate that the increased Yap1 in these cells may have triggered their abnormal ERK activation.

Because all of our Mob1a/1b-deficient mice spontaneously developed tumors (and especially trichilemmal carcinomas), we believe that the loss of MOB1A/1B helps to both initiate and promote carcinoma onset. With respect to tumor initiation, the observed increase in the number of centrosomes and/or micronuclei in our mutant cells may have introduced detrimental alterations into their DNA. With respect to cancer promotion, the enhanced proliferation, apoptotic resistance, impaired contact inhibition, and increased progenitor self renewal associated with loss of Mob1a/1b may support the growth and progression of cells that have undergone tumor initiation events.

The very rare occurrence of trichilemmal carcinomas in humans has slowed the identification of genes involved in their development. Expression levels of MOB1A, LATS1/2, and SAV1 are more frequently reduced in the advanced stages of colon (33), breast (52), and renal cancers (53) than in the early stages of these malignancies. In lung cancers, the reverse is true, since MOB1A levels are frequently lower in the early pT1 stage of non-small-cell lung cancer as compared with later stages (34). These observations suggest that the loss of Hippo signaling molecules can be an important driver of cancer progression in humans. Further study of alterations to gene or protein expression or functions of Hippo signaling components in a broad range of human malignancies may increase our understanding of their involvement in tumorigenesis.

In conclusion, our results demonstrate that (a) MOB1 is a broadly-acting tumor suppressor in mice and (b) Hippo signaling drives trichilemmal carcinoma onset in the skin. Therapeutic strategies to control Hippo signaling or MOB1 expression might therefore benefit many cancer patients, particularly those with HF-derived cancers.

Table 3

<table>
<thead>
<tr>
<th>Trichilemmal carcinoma</th>
<th>Increased YAP1</th>
<th>Nuclear accumulation of YAP1</th>
<th>Decreased MOB1A/1B</th>
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<tr>
<td></td>
<td>11/14 (79%)</td>
<td>10/14 (71%)</td>
<td>5/10 (50%)</td>
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Methods

Generation of Mob1aα/α and Mob1bβ/β mice. A conditional targeting vector based on the Cre-loxP system was constructed to delete a genomic fragment containing exon 2 of the murine Mob1a gene (Supplemental Figure 1). This deletion generates a frame shift and early stop codon in exon 3. We introduced 1 loxP site into Mob1a intron 1 and 2 loxP sites into intron 2 to flank Mob1a exon 2. The PGK-Hyg resistance cassette was inserted in antisense orientation between the 2 loxP sites in intron 2. The resulting targeting vector was electroporated into E14K ES cells, and homologous recombinants were confirmed by Southern blotting using 5’ flanking probe A and a Hyg-specific probe. Correctly targeted Mob1a mutant clones were transiently transfected with pMC1-Cre (54) to delete the loxP-flanked Hyg gene. Progeny clones sensitive to hygromycin were subjected to Southern blotting to identify those retaining exon 2 flanked by 2 loxP sites (the Mob1αα allele) and those lacking exon 2 (Mob1aββ allele; equivalent to a knockout mutation). For Mob1b-deficient mice, an ES cell line bearing a gene trap mutation of intron 2 of the Mob1b gene was obtained from the Sanger Institute (Hinxton, United Kingdom). The single integration of the trapped site was confirmed by PCR and genomic Southern blotting using 5’ flanking probe C and a neospecific probe. Mob1aα/α, Mob1aβ/β, and Mob1bβ/β mice were generated from ES cell clones using standard procedures and backcrossed to C57BL/6 mice 3 times before intercrossing to generate Mob1aα/α, Mob1aβ/β, and Mob1bβ/β progeny. Primers used for genotyping are listed in Supplemental Table 2.

In vitro culture of preimplantation embryos. E3.5 embryos derived from the intercrossing of Mob1aα/α, Mob1aβ/β males and females were analyzed as described (55). Briefly, blastocysts were individually cultured in 24-well plates in ES cell medium without LIF and photographed every 24 hours. On day 8, the morphology of each embryo was recorded and its genotype determined by PCR.

Embryo immunostaining. Immunofluorescent staining of embryos was performed as described (45). Briefly, embryos (E3.5) were cultured overnight prior to fixation in 4% paraformaldehyde. Fixed tissues were permeabilized with 0.2% Triton X-100, blocked with 2% goat serum, and incubated overnight at 4°C with Abs recognizing CDX2 (Biocare Medical), Oct3/4 (gift of H. Niwa, Riken), PDGFRβ (eBiosciences), GATA4/6 (Santa Cruz), and YAP1 (Sigma-Aldrich). Secondary Abs were Alexa Fluor 488 goat anti-rabbit or Alexa Fluor 568 goat anti-mouse (Molecular Probes). Nuclei were visualized using DAPI (Dojindo). Stained embryos were examined by confocal microscopy.

Generation and differentiation of Mob1a/1b double-mutant ES cells. ES cells established from embryos derived from Mob1aα/α, Mob1aβ/β intercrosses were transfected with linearized CMV-Mer-Cre-Mer plasmid DNA (56) plus pApuo2 (57). To generate ERCreMob1aα/α, Mob1aβ/β ES clones, ES cells were selected by culture for 12 days in complete ES cell medium containing 1 μg/ml puromycin (Invivogen) on an irradiation-inactivated Puro MEF feeder layer. Tamoxifen (3.3 μM; Toronto Research Chemicals) was added (or not) for 2 days to completely delete the Mob1a gene (data not shown). Control and mutant EBs were generated from hanging drops of approximately 1,000 ES cells/20 μl medium as described (58).

Generation of keratinocyte-specific Mob1a/Mob1b double-mutant mice. Mob1aα/α, Mob1bβ/β mice were mated to Krt14CreER transgenic mice (35) in which Cre can be activated by tamoxifen under the control of the Krt14 promoter. Offspring carrying Krt14CreER plus 2 copies of the floxed Mob1a allele (Mob1aα/α) and 2 copies of the trapped Mob1b allele (Mob1bβ/β) were administered tamoxifen and used in the analysis as homozygous double mutant (Krt14CreERMob1aα/α, Mob1bβ/β +tamoxifen; KDKO) mice.
Primary keratinocytes isolated from control and KdKO mice were cultured as described (59). For cell saturation density assays, keratinocytes at passage 2 were seeded in 7-cm culture plates (0.3 × 10^5/well) and cultured for up to 12 days before counting cell numbers. For colony-forming assays, keratinocytes at passage 1 were seeded in 6-well plates (0.4 × 10^5/well). After 2 weeks, half the wells were fixed and stained with Giemsa (Muto Pure Chemicals), and the number of primary colonies was counted. Keratinocytes of an unfixed well were then trypsinized and reseeded so that each well of a 6-well plate received cells from 1 primary colony. Reseeded cells were cultured for 2 weeks to generate secondary colonies.

Clinical samples. Surgically obtained trichilemmal carcinoma samples containing noncancerous tissues were acquired from the Department of Regenerative Dermatology (Kyushu University). Resected cancerous tissues were fixed in formalin and stained with anti-YAP1 Ab (Cell Signaling) and anti-MOB1A/1B Ab (AP7031b; Abgent) using a standard protocol.

Statistics. KaleidaGraph software was used for statistical analyses. Data are shown as the mean ± SEM, and P values were determined using the Student’s t test unless otherwise stated. < 0.05 was considered statistically significant.

Study approval. The clinical sample study design was approved by the Institutional Review Board of Osaka University, and written informed consent was obtained from all patients. All animal experiments were approved by the Animal Experiment Review Boards of Kyushu University and Akita University. See Supplemental Methods for additional details.

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