

Research article

Complexes between the LKB1 tumor suppressor, STRAD α/β and MO25 α/β are upstream kinases in the AMP-activated protein kinase cascade

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Abstract

Background: The AMP-activated protein kinase (AMPK) cascade is a sensor of cellular energy charge that acts as a 'metabolic master switch' and inhibits cell proliferation. Activation requires phosphorylation of Thr172 of AMPK within the activation loop by upstream kinases (AMPKKs) that have not been identified. Recently, we identified three related protein kinases acting upstream of the yeast homolog of AMPK. Although they do not have obvious mammalian homologs, they are related to LKB1, a tumor suppressor that is mutated in the human Peutz-Jeghers cancer syndrome. We recently showed that LKB1 exists as a complex with two accessory subunits, STRAD α/β and MO25 α/β .

Results: We report the following observations. First, two AMPKK activities purified from rat liver contain LKB1, STRAD α and MO25 α , and can be immunoprecipitated using anti-LKB1 antibodies. Second, both endogenous and recombinant complexes of LKB1, STRAD α/β and MO25 α/β activate AMPK via phosphorylation of Thr172. Third, catalytically active LKB1, STRAD α or STRAD β and MO25 α or MO25 β are required for full activity. Fourth, the AMPK-activating drugs AICA riboside and phenformin do not activate AMPK in HeLa cells (which lack LKB1), but activation can be restored by stably expressing wild-type, but not catalytically inactive, LKB1. Fifth, AICA riboside and phenformin fail to activate AMPK in immortalized fibroblasts from LKB1-knockout mouse embryos.

Conclusions: These results provide the first description of a physiological substrate for the LKB1 tumor suppressor and suggest that it functions as an upstream regulator of AMPK. Our findings indicate that the tumors in Peutz-Jeghers syndrome could result from deficient activation of AMPK as a consequence of LKB1 inactivation.

Introduction

AMP-activated protein kinase kinase (AMPKK) and AMP-activated protein kinase (AMPK) are the upstream and downstream components, respectively, of a protein kinase cascade that acts as a sensor of cellular energy charge [1,2]. AMPK is activated by the elevation in cellular 5'-AMP that accompanies a fall in the ATP:ADP ratio due to the reaction catalyzed by adenylate kinase ($2\text{ADP} \leftrightarrow \text{ATP} + \text{AMP}$). This occurs during metabolic stresses such as hypoxia, ischaemia, glucose deprivation and, in skeletal and cardiac muscle, during contraction or exercise [1-3]. Once activated by stress, AMPK switches on the uptake of glucose and fatty acids and the oxidative metabolism of these fuels to generate ATP, while switching off biosynthetic pathways that consume ATP. It achieves this metabolic switching both by direct phosphorylation of metabolic enzymes and by longer-term effects on gene expression [1,2].

We have previously partially purified from rat liver an upstream kinase (AMPKK) that activates AMPK by phosphorylation of AMPK residue Thr172 within the activation loop of the kinase domain [4], but we have been unable to identify the activity as a defined gene product. As an alternative approach, we searched for kinases upstream of the *Saccharomyces cerevisiae* homolog of AMPK (the SNF1 complex), taking advantage of genome-wide approaches available in that organism. This identified Elm1, Pak1 and Tos3 as alternative upstream kinases in yeast that can activate the SNF1 complex *in vivo* in a partially redundant manner [5]. The nearest relatives encoded by the human genome are calmodulin-dependent protein kinase kinase (CaMKK) and LKB1 (see Additional data file 1 with the online version of this article). We have previously shown that CaMKK purified from pig brain could activate AMPK in cell-free assays (albeit poorly in comparison to the extent to which it activates its known substrate, calmodulin-dependent protein kinase I); but the AMPKK previously purified from rat liver was not calmodulin-dependent [6]. LKB1 is a 50 kDa serine/threonine kinase that was originally discovered as the product of the gene mutated in the autosomal dominant human disorder, Peutz-Jeghers syndrome (PJS) [7,8]. People with PJS develop benign polyps in the gastrointestinal tract but also have a 15-fold increased risk of developing malignant tumors in other tissues [9,10]. Nearly 100 different PJS mutations have been reported, and most are expected to impair the kinase activity of LKB1 [11]. Several human tumor cell lines, including HeLa and G361 cells, lack expression of LKB1. Expression of wild-type LKB1, but not catalytically inactive LKB1 or PJS mutants, in G361 cells caused a G1-phase cell-cycle arrest [12] that was associated with the induction of the cyclin-dependent kinase inhibitor, p21, and was dependent on p53 [13]. Homozygous *LKB1* knockout mice die of multiple defects at mid-gestation [14].

Heterozygotes are viable, but most develop polyps similar to those found in people with PJS by 45 weeks of age [15-18], although it is controversial as to whether these are caused by haploinsufficiency or loss of heterozygosity (reviewed in [11]). It has also been reported that a significant number of *LKB1*^{+/-} mice over 50 weeks of age develop hepatocellular carcinomas that are associated with loss of *LKB1* expression [19]. These results show that LKB1 acts as a tumor suppressor and that the catalytic activity of LKB1 is essential for this function, but the downstream substrate(s) that LKB1 phosphorylates to mediate the suppression of cell proliferation remained unknown.

Recently, we reported that LKB1 is associated with two accessory proteins called Ste20-related adaptor protein- α (STRAD α) [20] and mouse protein 25- α (MO25 α) [21], for each of which there is also a closely related isoform (STRAD β and MO25 β) encoded in the human genome. Although STRAD α and β are related to the Ste20 protein kinases, several of the residues expected in active protein kinases are not conserved, and they appear to be inactive 'pseudokinases' [20]. MO25 α binds to the carboxyl-terminus of STRAD α and stabilizes the association between STRAD α and LKB1 [21]. The association of LKB1 with STRAD α and MO25 α increased the kinase activity of LKB1 against an artificial substrate (myelin basic protein) and also enhanced its cytoplasmic localization [20,21], which was previously implicated in the tumor suppressor function of LKB1 [13]. Here, on the basis of the sequence similarity between LKB1 and the upstream kinases identified for the yeast homolog of AMPK [5], we investigate whether LKB1:STRAD:MO25 complexes could play a role in activating AMPK in mammalian cells.

Results

Resolution of two AMPKKs from rat liver that both contain LKB1, STRAD α and MO25 α

While experimenting with different conditions to optimize recovery at the Q-Sepharose step of our previous purification protocol for AMPKK [4], we found that we were able to resolve two peaks of activity (Figure 1a). Because the second peak corresponds to the AMPKK originally purified [4], we refer to it as AMPKK1, with the first peak being termed AMPKK2. On size-exclusion chromatography on Sephacryl S-200, AMPKK1 and AMPKK2 eluted as proteins of large but distinct size, with estimated Stokes radii of 5.7 and 5.2 nm respectively. We probed blots of fractions across the Q-Sepharose column using antibodies against LKB1, STRAD α and MO25 α (Figure 1b). This revealed that the activity of AMPKK2 correlated with the presence of the LKB1 polypeptide (around 50 kDa), as well as those of STRAD α (around 45/48 kDa) and MO25 α (around 40 kDa). The monoclonal

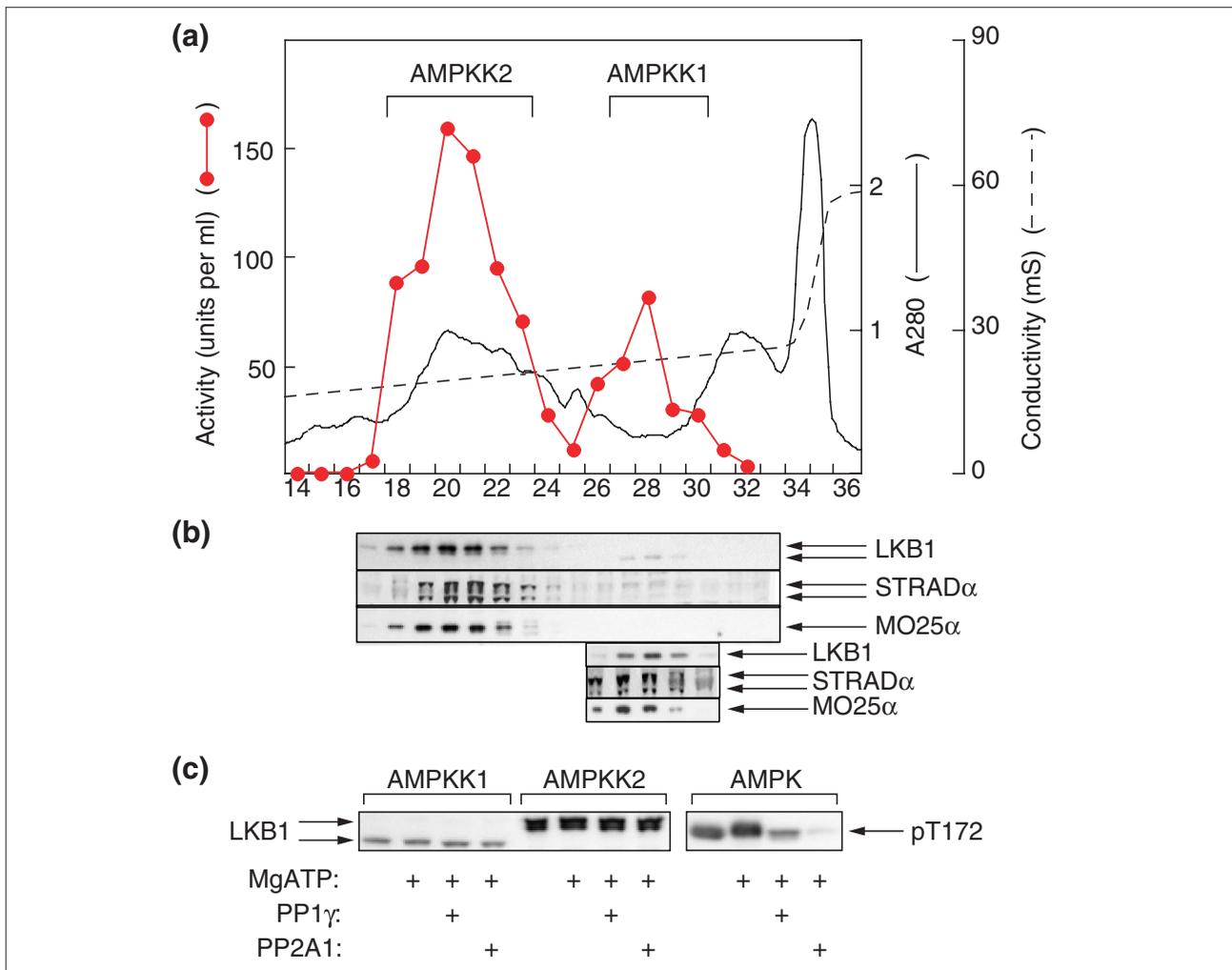
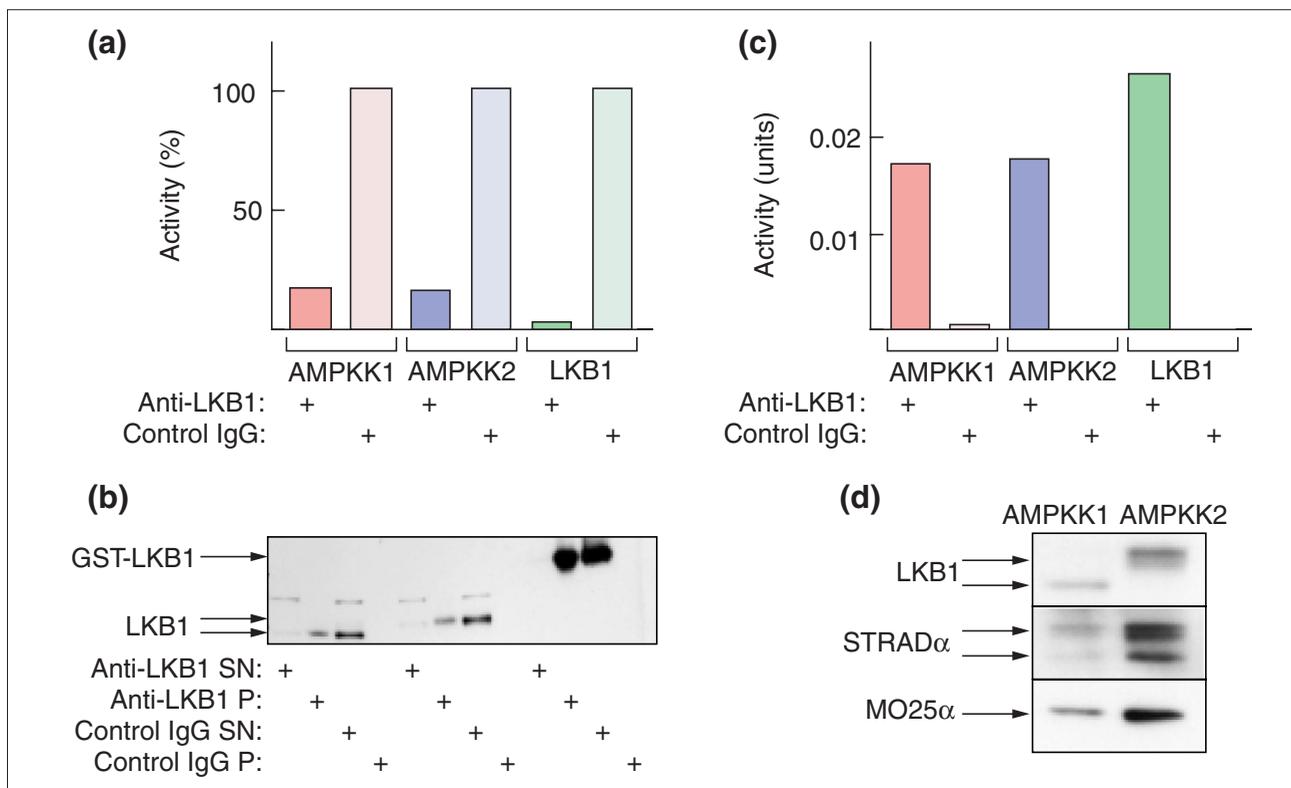


Figure 1

Two AMPKs can be resolved from rat liver extracts and both contain LKB1, STRAD α and MO25 α . **(a)** Separation of two activities that activate the GST-AMPK α 1 catalytic domain by Q-Sepharose chromatography. The graph shows AMPK activity in 4.5 ml fractions (red circles and red line), absorbance at 280 nm (continuous black line) and conductivity in the eluate (dashed black line) plotted against fraction number. **(b)** Probing of blots of column fractions after SDS gel electrophoresis (1 μ l per lane) using anti-LKB1, anti-STRAD α or anti-MO25 α antibodies. In the three bottom panels, fractions 26-30 were concentrated from 4.5 ml to 250 μ l using Amicon Ultra-4 30,000 MWCO centrifugal concentrators, and reanalyzed by western blotting using 2 μ l per lane. **(c)** The effect of protein phosphatase treatment on the mobility of LKB1. The peak fractions of AMPK1 (0.2 units) or AMPK2 (0.8 units) were incubated in a final volume of 20 μ l with or without 5 mM MgCl₂ and 200 μ M ATP for 15 min at 30°C. Protein phosphatases (PP1 γ , 8 mU; or PP2A₁, 1 mU) or buffer were added and incubation continued for a further 15 min before stopping the reactions in SDS sample buffer and analyzing by SDS gel electrophoresis and western blotting using anti-LKB1 antibody.

antibody against STRAD α , which is specific for the α isoform, detected a doublet, as reported previously [20]; the explanation for this is not known. We did not obtain any signal of the correct molecular mass in these fractions using anti-MO25 β antibody (not shown), consistent with previous observations that MO25 β is not expressed in mouse liver [21]. We also obtained a faint signal for LKB1 and STRAD α in fractions containing AMPK1, but at this loading MO25 α was below the limit of detection. However,

the presence of LKB1, STRAD α and MO25 α in these fractions was confirmed by analyzing a higher loading (Figure 1b, bottom three panels). An interesting finding was that the LKB1 polypeptide migrated with a significantly faster mobility in AMPK2, while LKB1 in AMPK1 appeared to run as a doublet (Figure 1b; see also Figures 1c, 2b and 2d). The results in Figure 1c suggest that this difference in mobility was not due to a difference in phosphorylation state of the LKB1 polypeptide. Incubation

**Figure 2**

AMPKK activity (that is, the ability to activate AMPK α catalytic domain), and LKB1, STRAD α and MO25 α polypeptides, can be immunoprecipitated from rat liver AMPKK1 and AMPKK2 using anti-LKB1 antibody. **(a)** Depletion of AMPKK activity from supernatant. Sheep anti-human LKB1 or pre-immune control immunoglobulin (IgG) was prebound to Protein G-Sepharose beads and cross-linked with dimethylpimelimidate as described [47], except that a final wash of the beads with 100 mM glycine, pH 2.5, was performed. Bead-bound antibodies (40 μ l) were incubated with the peak fraction of AMPKK1 (0.04 units), AMPKK2 (0.03 units) or recombinant GST-LKB1:STRAD α :MO25 α complex (0.06 units) for 120 minutes and the beads removed in a microcentrifuge (14,000 \times g for 2 min). AMPKK activity was determined in the supernatants and is expressed as a percentage of the value obtained using the control IgG. **(b)** The pellets from the experiment in (a) were resuspended in the original volume and samples of the supernatants and pellets analysed by western blotting with anti-LKB1 antibody. The recombinant LKB1 migrates at a higher molecular mass because of the GST tag. **(c)** As in (a), except that the amounts of AMPKK1, AMPKK2 and recombinant GST-LKB1:STRAD α :MO25 α complex were increased to 0.44, 0.70 and 1.4 units, respectively, and the activities were determined in the resuspended pellets. In this experiment the amount of antibody was limiting, so only a fraction of the activity was precipitated. **(d)** The pellets from the experiment in (c) were resuspended and samples analyzed by western blotting with anti-LKB1, anti-STRAD α and anti-MO25 α antibodies.

of the AMPKK1 and AMPKK2 fractions with MgATP, followed by treatment with or without the catalytic subunit of protein phosphatase 1 γ (PP1 γ) or the protein phosphatase 2A $_1$ (PP2A $_1$) holoenzyme, did not alter the mobility of any of the LKB1 polypeptides. The right-hand panel in Figure 1c shows that these protein phosphatases did dephosphorylate Thr172 on the α subunit of AMPK when incubated under identical conditions.

AMPKK activity can be immunoprecipitated from AMPKK1 and AMPKK2

Using anti-LKB1 antibody but not a pre-immune control immunoglobulin, we were able to immunoprecipitate AMPKK activity from fractions containing both AMPKK1

and AMPKK2. Figure 2a shows results of an experiment where the amount of AMPKK1 or AMPKK2 was limiting and the antibody was in excess, and shows that we were able to remove more than 80% of the activity from the peak fractions containing AMPKK1 and AMPKK2 by immunoprecipitating with anti-LKB1 antibody, while no activity was removed using a pre-immune control immunoglobulin. We could remove more than 95% of the AMPKK activity of a recombinant tagged LKB1:STRAD α :MO25 α complex (see below) under the same conditions (Figure 2a). The small amount of activity remaining in the supernatants of the AMPKK1 and AMPKK2 immunoprecipitates could be accounted for by the fact that the immunoprecipitation was not quantitative, with a small amount of the LKB1

polypeptide remaining in the supernatant. No LKB1 polypeptide was precipitated using the pre-immune control immunoglobulin (Figure 2b).

Because of the small amount of AMPKK1 and AMPKK2 used in this experiment, it proved difficult to analyze the pellets for AMPKK activity and the presence of the other polypeptides. We therefore repeated the experiment with more AMPKK (the amount of antibody was now limiting) and analyzed the pellets only. This showed that we could recover a similar amount of AMPKK activity in the pellet from the peak fractions containing AMPKK1 and AMPKK2 as we could from the recombinant LKB1:STRAD α :MO25 α complex, with no activity being recovered in the pellet using the pre-immune control immunoglobulin (Figure 2c). Western blotting of the AMPKK1 and AMPKK2 pellets showed that they contained LKB1, STRAD α and MO25 α (Figure 2d).

Recombinant LKB1:STRAD α :MO25 α complexes activate AMPK α 1 catalytic domain in cell-free assays

To examine whether LKB1 activated AMPK on its own or whether the accessory subunits STRAD α/β and MO25 α/β were required, we expressed LKB1 tagged with glutathione-S-transferase (GST), FLAG-tagged STRAD α/β and Myc-tagged MO25 α/β in various combinations in HEK-293T cells, and purified the complexes on glutathione-Sepharose. We also used a GST-tagged kinase-inactive mutant of LKB1 (D194A), and a plasmid expressing GST alone, as controls. The complexes were purified on glutathione-Sepharose and incubated with the AMPK α 1 catalytic domain in the presence of MgATP, and activation of the catalytic domain as well as phosphorylation of Thr172 (using a phosphospecific anti-pT172 antibody) was measured. Figure 3a shows that LKB1 alone did not significantly increase the activity, or phosphorylation of Thr172, of the AMPK α 1 catalytic domain above the basal activity observed in the presence of GST alone (compare lanes 1 and 14). The same result was obtained with LKB1 that had been co-expressed with MO25 α or MO25 β (lanes 4 and 5), which was expected as these proteins do not interact with LKB1 in the absence of STRAD α/β [21]. An LKB1:STRAD α complex did give a small but significant activation, and Thr172 phosphorylation, of the AMPK α 1 catalytic domain above the basal value (compare lanes 1 and 2). To produce, however, a large activation and phosphorylation of the AMPK α 1 catalytic domain, a heterotrimeric complex containing LKB1, STRAD α or STRAD β , and MO25 α or MO25 β was required (lanes 6 to 9). With the heterotrimeric complexes the degree of activation was in the order LKB1:STRAD α :MO25 α > LKB1:STRAD α :MO25 β \approx LKB1:STRAD β :MO25 α > LKB1:STRAD β :MO25 β . The ability of LKB1:STRAD:MO25 complexes to activate AMPK α 1 was dependent on LKB1 catalytic activity, because complexes of a catalytically inactive

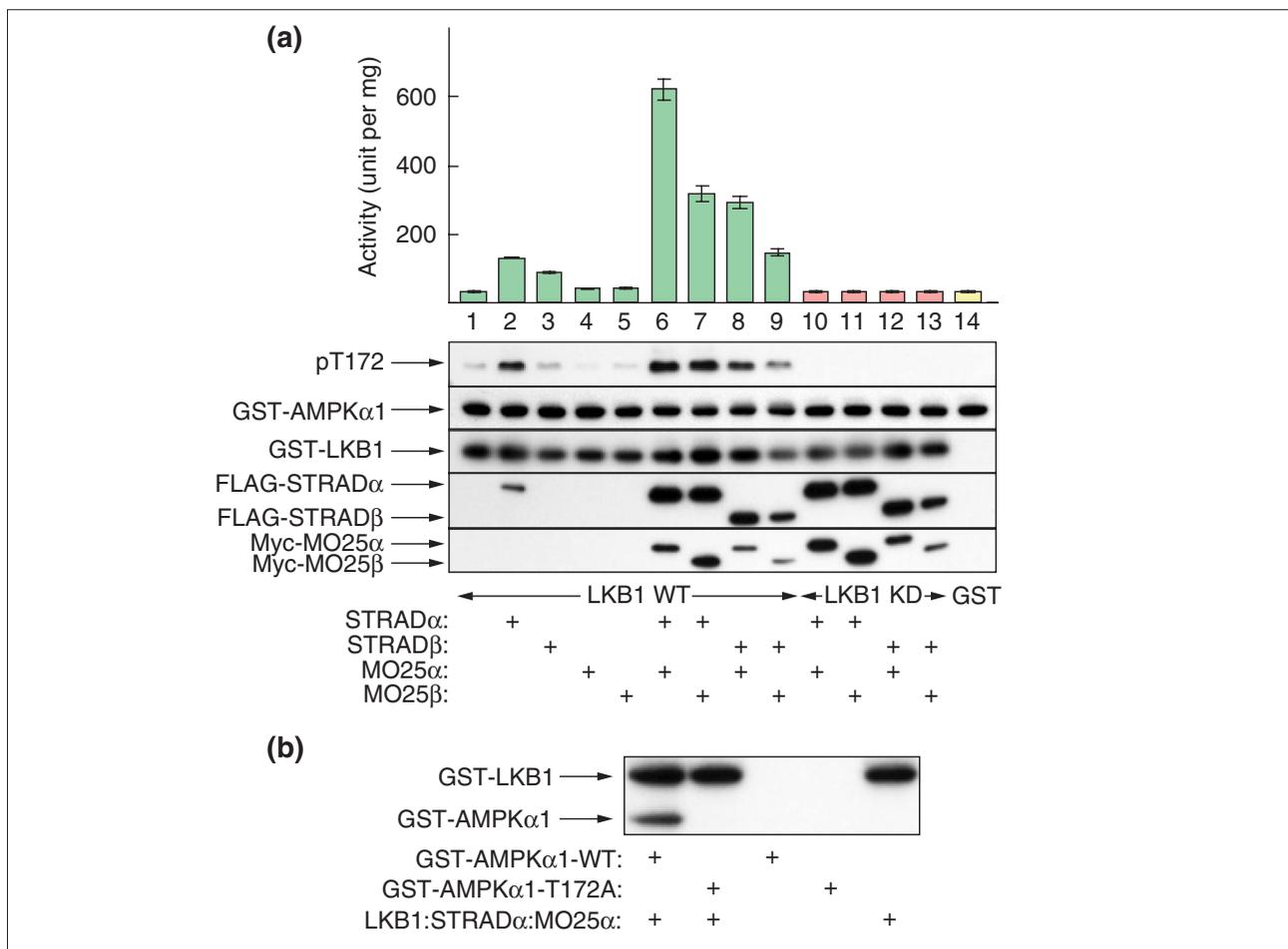
mutant of LKB1 (D194A) with the various combinations of STRAD α/β and MO25 α/β (lanes 10-13) were unable to activate or phosphorylate AMPK α 1. The degree of activation obtained with the various complexes of wild-type LKB1 correlated well with the phosphorylation of Thr172, as assessed by probing blots with a phosphospecific antibody (pT172). The bottom three panels in Figure 3a, probed with anti-GST, anti-FLAG or anti-Myc antibodies, confirm that the relevant STRAD and MO25 subunit co-precipitated with LKB1 when DNAs encoding these subunits had been co-transfected. When STRAD α was co-expressed with LKB1 in the absence of a MO25 subunit, the amount of STRAD α subunit co-precipitated with LKB1 was reduced (compare lanes 2 and 3 with lanes 6 and 7).

Figure 3b provides evidence that Thr172 was the only site on the AMPK α 1 catalytic domain phosphorylated by the LKB1:STRAD α :MO25 α complex. When the two proteins were incubated together in the presence of [γ - 32 P]ATP, the wild-type AMPK α 1 catalytic domain became 32 P-labeled, but a T172A mutant of the AMPK α 1 catalytic domain did not.

AMPKK1, AMPKK2 and recombinant LKB1:STRAD:MO25 complexes also activate heterotrimeric AMPK complexes

Although most of the AMPKK assays in this study were conducted using the AMPK α 1 catalytic domain as substrate, AMPKK1, AMPKK2 and the recombinant GST-LKB1:STRAD α :MO25 α complex also activated heterotrimeric AMPK complexes. We incubated rat liver AMPK (a mixture of α 1 and α 2 in complexes with β 1 and γ 1) with MgATP with or without each of the three AMPKK preparations. We then immunoprecipitated with anti-AMPK α 1 or anti-AMPK α 2 antibodies, and measured the activation of each isoform in the precipitate. The results (Figure 4a) show that the AMPK α 1 and AMPK α 2 complexes were activated by all three AMPKK preparations. Blotting of the three AMPKK preparations using anti-LKB1, anti-STRAD α and anti-MO25 α antibodies (Figure 4b) showed that activation of the heterotrimers was not simply proportional to the amount of these polypeptides in the preparation. Although the amounts of each AMPKK preparation used for Figure 4a had been chosen to yield a comparable degree of AMPK activation, there was much more LKB1, STRAD α and MO25 α in the recombinant LKB1:STRAD α :MO25 α complex than in either of the native complexes, and more of all three subunits in AMPKK2 than in AMPKK1. All three AMPKK preparations also activated recombinant α 1 β 1 γ 1 and α 2 β 1 γ 1 complexes prepared [22] by co-expression of recombinant DNA in CCL13 cells (not shown).

The assays in Figure 4a were conducted in the presence of 200 μ M AMP. Figure 4c shows that when the AMPK α 1 β 1 γ 1

**Figure 3**

Recombinant LKB1:STRAD:MO25 complexes can efficiently activate the AMPK α 1 catalytic domain via phosphorylation at Thr172. **(a)** The indicated combinations of GST-tagged wild-type LKB1 (WT, lanes 1-9), or kinase-dead (D194A; KD, lanes 10-13) LKB1 mutant, or GST-alone (lane 14), FLAG-tagged STRAD α or STRAD β , and Myc-tagged MO25 α or MO25 β were coexpressed in HEK-293T cells, purified on glutathione-Sepharose and tested for their ability to activate GST-AMPK α 1 catalytic domain (top panel). The results are expressed as the increase in the units of AMPK activity generated per mg full-length GST-AMPK α 1 catalytic domain. Samples from each incubation were also analyzed by western blotting and probed using the indicated antibodies (from top to bottom): anti-pT172; anti-AMPK α 1 catalytic domain (GST-AMPK α 1); anti-GST to detect GST-LKB1; anti-FLAG to detect STRAD α and STRAD β , and anti-Myc to detect MO25 α and MO25 β . All proteins migrated with the expected mobility, taking into account the epitope tags. The bottom three blots were conducted on blank reactions lacking GST-AMPK α 1 catalytic domain, as the latter appeared to cause some interference with detection. **(b)** Recombinant GST-LKB1:STRAD α :MO25 α complex was used to phosphorylate wild-type GST-AMPK α 1 catalytic domain (GST- α 1-WT) or a T172A mutant (GST- α 1-T172A) using [γ - 32 P]ATP as described in Materials and methods. The reaction was analyzed by SDS gel electrophoresis and autoradiography. Arrows show the migration of GST-LKB1 (which autophosphorylates) and GST-AMPK α 1 catalytic domain.

or AMPK α 1 β 1 γ 1 heterotrimer were used as substrate, the activation of all three AMPKK preparations was stimulated from 2- to 3.5-fold by AMP. When the AMPK α 1 catalytic domain was used as substrate, however, the activation was not affected, or was even slightly inhibited, by AMP. The activity of the three AMPKK preparations was not significantly affected by the direct addition of phenformin to the assays up to 1 mM concentration, although concentrations above that started to inhibit AMPKK activity (not shown).

These results indicate that neither AMP nor phenformin directly stimulates the LKB1:STRAD α :MO25 α complex.

Endogenous LKB1 that activates AMPK can be immunoprecipitated from 293 cells but not from HeLa cells

Figure 5a shows that AMPKK activity that activated the AMPK α 1 catalytic domain above the basal activity, and phosphorylated Thr172, could be immunoprecipitated

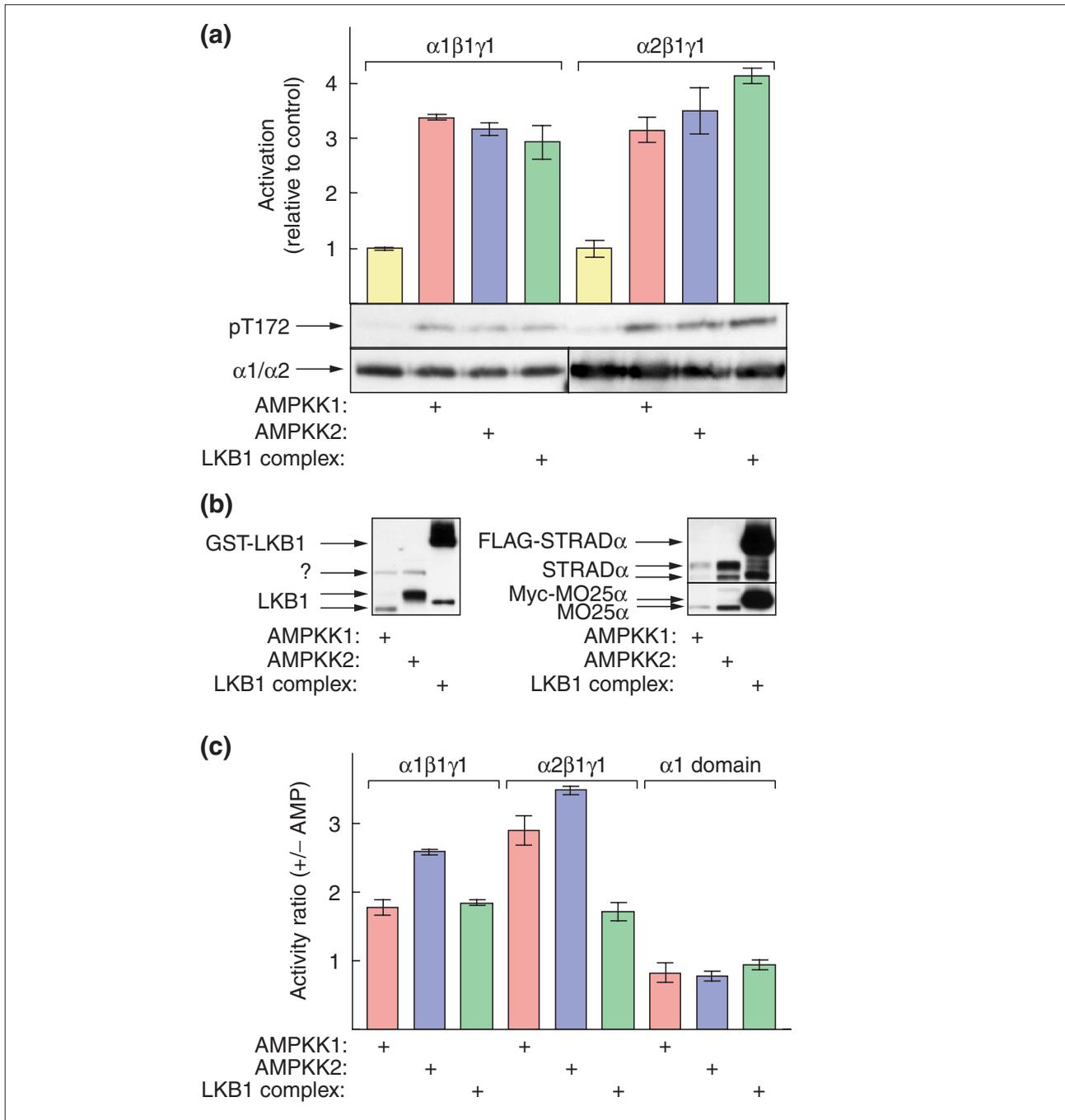


Figure 4

Activation and phosphorylation of heterotrimeric AMPK complexes by AMPKK1, AMPKK2 and recombinant GST-LKB1:STRAD α :MO25 α complexes, and the effect of AMP. **(a)** Activation of $\alpha 1\beta 1\gamma 1$ and $\alpha 2\beta 1\gamma 1$ complexes separated from purified rat liver AMPK. The AMPK $\alpha 1$ - or AMPK $\alpha 2$ -containing complexes were purified by immunoprecipitation and activation of the resuspended immunoprecipitates by the three AMPKK preparations examined. The results are expressed as activation relative to the control without added AMPKK. **(b)** Quantification by western blotting of the relative amounts of LKB1, STRAD α and MO25 α polypeptides in the three AMPKK preparations used in (a). A small amount of degradation is detectable due in part to the heavy loadings of the GST-LKB1 and FLAG-STRAD α . The identity of the polypeptide labeled '?' in the anti-LKB1 blot is not known. **(c)** Effect of AMP on the activation of $\alpha 1\beta 1\gamma 1$ and $\alpha 2\beta 1\gamma 1$ heterotrimers of AMPK, and of GST-AMPK $\alpha 1$ catalytic domain, by AMPKK1, AMPKK2 and the recombinant GST-LKB1:STRAD α :MO25 α complex. AMPKK activity was measured as in Figure 3 with or without 200 μ M AMP. The results are expressed as ratios of the activities obtained with and without AMP.

from untransfected HEK-293T cell extract using anti-LKB1 antibody (lane 1), but not pre-immune control immunoglobulin (lane 2). As reported previously [20,21], immunoprecipitation of endogenous LKB1 resulted in the co-precipitation of STRAD α and MO25 α (lane 1). As a further control, we employed normal HeLa cells as an LKB1-null cell line, as it is known that LKB1 is not expressed in these cells [12]. Consistent with this, no LKB1, STRAD α and MO25 α subunits or AMPKK activity were immunoprecipitated from the same amount of HeLa cell-extract protein using anti-LKB1 antibody (lane 3). AMPKK activity and Thr172 phosphorylation, as well as detectable STRAD α and MO25 α subunits, were recovered following immunoprecipitation of LKB1 from a line of HeLa cells that stably express wild-type LKB1 [23] (lane 5). The LKB1, STRAD α and MO25 α polypeptides were still recovered in cells expressing a catalytically inactive mutant of LKB1, but AMPKK activity was not (lane 7). Although the LKB1 polypeptide was overexpressed to a large extent in the HeLa cells compared to the endogenous levels observed in 293 cells (compare lane 1 with lane 5 or 7), it is clear that the availability of STRAD α and/or MO25 α limits the activity in these cells. There was less AMPKK activity and Thr172 phosphorylation, as well as less co-precipitated STRAD α and MO25 α , in HeLa cells expressing LKB1 than in 293 cells, even though the LKB1 polypeptide was overexpressed. The AMPKK activity in the immunoprecipitates from 293 cells and HeLa cells expressing wild-type LKB1 correlated with the levels of STRAD α and MO25 α in the complex, rather than with the levels of LKB1.

Figure 5b shows western blots of total lysates of the same cells. Although the expression of MO25 α in HeLa cells was lower than in 293 cells, it was unaffected by overexpression of either wild-type or kinase-dead LKB1, as was expression of the protein kinases ERK1 and ERK2, used as loading controls. Interestingly, however, expression of the STRAD α doublet was almost undetectable in the control HeLa cells but was readily detectable in cells stably expressing wild-type or kinase-dead LKB1.

Expression of LKB1 restores activation of AMPK in HeLa cells

The drug 5-aminoimidazole-4-carboxamide (AICA) riboside activates AMPK in intact cells by being taken up and immediately converted by adenosine kinase to AICA riboside monophosphate (ZMP), which mimics the effect of AMP on the AMPK system [24]. The anti-diabetic drug metformin activates AMPK in intact cells by a mechanism that is not known, although it does not involve changes in cellular adenine nucleotide content [25-27]. We have previously found (unpublished observations) that, although AMPK is expressed in HeLa cells, it is not activated either by AICA riboside or by metformin. A potential explanation for this is

that HeLa cells do not express LKB1 ([12]; see also above). To examine whether expression of recombinant LKB1 might restore the ability of HeLa cells to respond to these drugs, we used the HeLa cell line that stably expresses wild-type LKB1 [23]. In these experiments we used phenformin, a close relative of metformin that we have found to activate AMPK more rapidly than metformin in other cell types. Figure 6a shows that neither AICA riboside nor phenformin activated AMPK above the basal level in control HeLa cells. In cells expressing wild-type LKB1 but not the kinase-inactive mutant, however, both AICA riboside and phenformin caused a robust activation, as well as a small increase in basal activity. The AMPK activity also correlated with the phosphorylation of Thr172 on AMPK α (shown by probing with the anti-pT172 antibody, Figure 6b) and with the phosphorylation of a downstream target of AMPK, acetyl-CoA carboxylase (ACC; shown by probing with a phosphospecific antibody against Ser-79, the primary AMPK site on that protein; Figure 6c). Interestingly, stable expression of wild-type LKB1 in the HeLa cells caused a small but reproducible degree of upregulation of expression of AMPK α 1 and a marked down-regulation of expression of ACC (data not shown). These effects may be a consequence of the increase in basal AMPK activity shown in Figure 6a. Because the expression of these proteins was not uniform in these cells, in order to accurately quantify their phosphorylation status we simultaneously probed single blots of lysates using either anti-pT172 and anti- α 1/ α 2 antibodies (to detect Thr172 phosphorylation and total AMPK α), or with anti-pACC and streptavidin (to detect Ser79 phosphorylation and total ACC). The two probing reagents used in each of these dual-labeling protocols were labeled with fluorescent dyes emitting in different regions of the infra-red spectrum, and the results were quantified in two separate channels using an infra-red laser scanner. In Figure 6b, these results are expressed as ratios of the signal obtained using the phosphospecific antibody to the signal obtained for the total protein, which corrects for different levels of expression of the proteins. This revealed that there was a good correlation between activation of AMPK and phosphorylation of Thr172. There was also a correlation with phosphorylation of ACC, although in this case AICA riboside appeared to have a larger effect than phenformin.

AMPK activation is defective in immortalized fibroblasts from LKB1^{-/-} mouse embryos

We performed further experiments with immortalized mouse embryo fibroblasts (MEF cells) from embryonic-day (E) 9.5 embryos of LKB1^{-/-} knockout mice. In cells from control LKB1^{+/+} embryos, AICA riboside and phenformin caused two-fold and three-fold activation of endogenous AMPK, but this was completely absent from the LKB1^{-/-} cells (Figure 7). The basal activity of AMPK was also about 60% lower in the

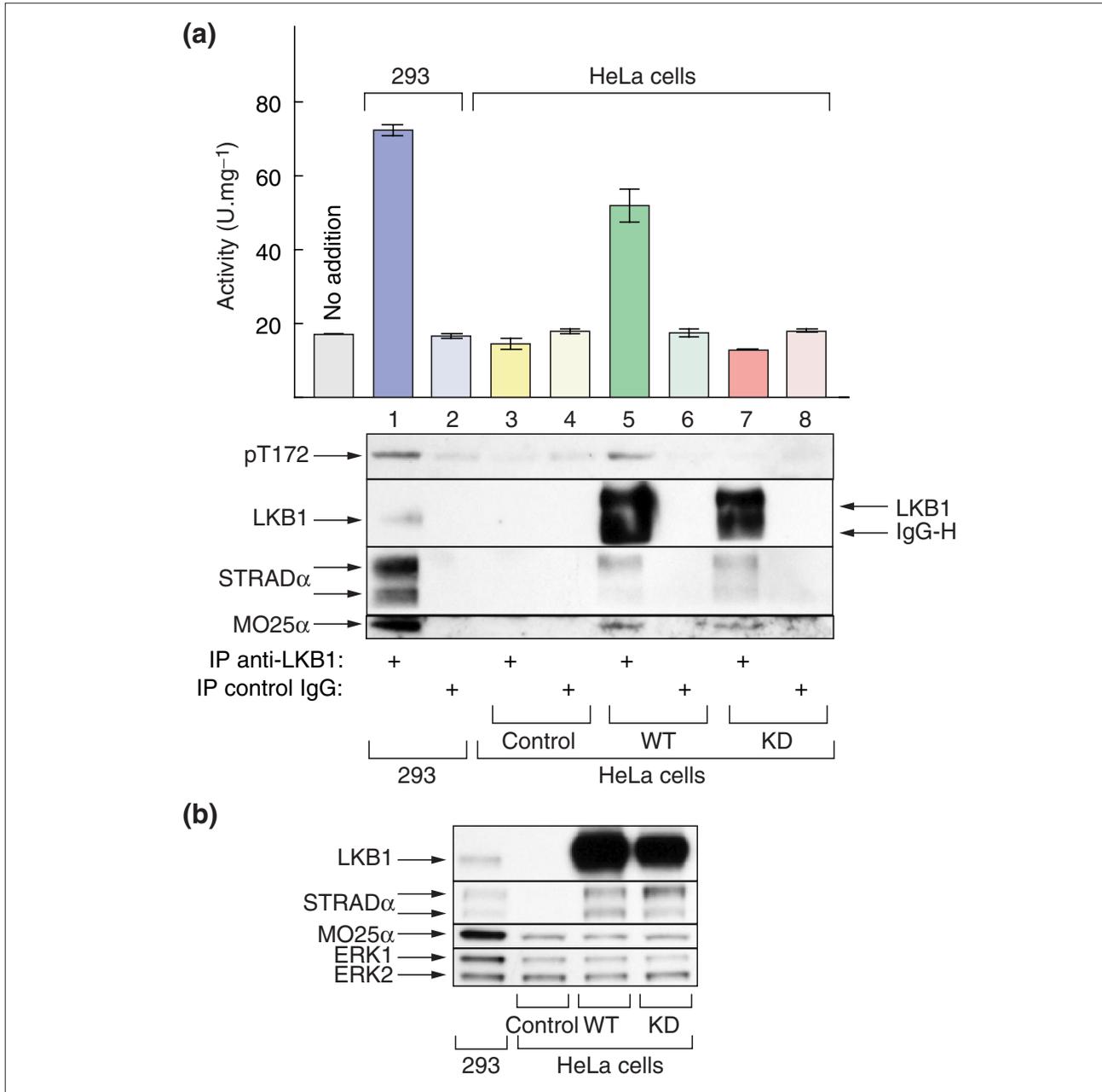
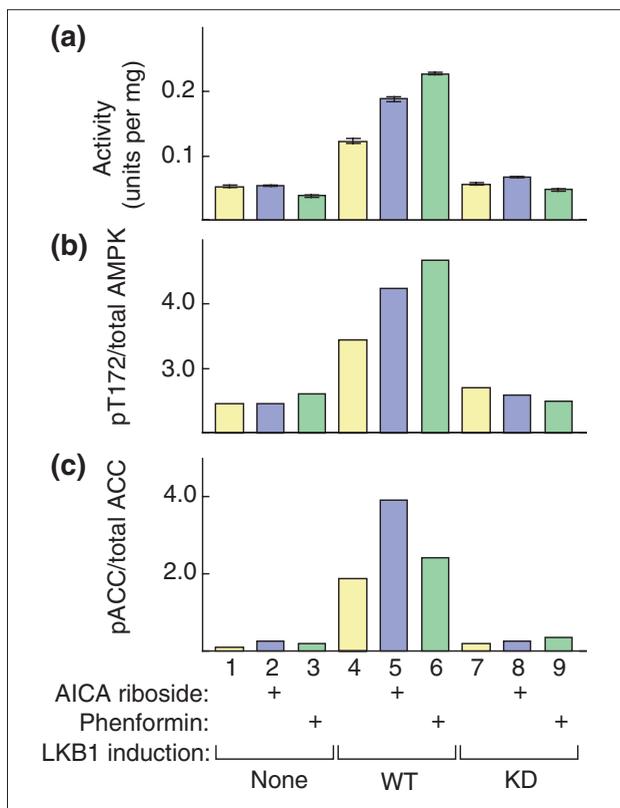


Figure 5

Endogenous AMPKK activity (that is, ability to activate AMPK α I catalytic domain) can be immunoprecipitated from 293 cells using anti-LKB1 antibody, but activity can only be immunoprecipitated from HeLa cells if they stably express wild-type LKB1, but not a catalytically-inactive mutant. **(a)** LKB1 was immunoprecipitated from 0.5 mg cell extract derived from untransfected HEK-293T cells (lanes 1,2), untransfected HeLa cells (control; lanes 3,4), or HeLa cells stably expressing wild-type LKB1 (WT; lanes 5,6) or a kinase-dead LKB1 mutant (D194A; KD, lanes 7,8). Immunoprecipitation used anti-LKB1 (lanes 1, 3, 5, 7) or a pre-immune control immunoglobulin (IgG; lanes 2, 4, 6, 8). Samples of each immunoprecipitate were used to assay activation of GST-AMPK α I catalytic domain, to analyze phosphorylation of GST-AMPK α I catalytic domain on Thr172 (middle panel), and to determine by western blotting the recovery of LKB1 and its accessory subunits (bottom panels). In lanes 5 and 7 some immunoglobulin heavy chain (IgG-H) had eluted from the protein G-Sepharose despite the fact that it had been cross-linked: this explains why LKB1 may not appear to comigrate in lanes 1, 5 and 7. Also shown at left in the top panel is the basal activity obtained when the GST-AMPK α I-catalytic domain was incubated with MgATP on its own (no addition). **(b)** Whole cell lysates from the same cells were analyzed by SDS gel electrophoresis and blots probed using anti-LKB1, anti-STRAD α , and anti-MO25 α antibodies. They were also probed with anti-ERK1/2 antibodies as loading controls.

**Figure 6**

Restoration of the ability of AMPK to be activated, and AMPK and acetyl-CoA carboxylase to be phosphorylated, by AICA riboside and phenformin in HeLa cells following expression of LKB1. Control HeLa cells (lanes 1,2,3), HeLa cells expressing wild-type LKB1 (WT; lanes 4,5,6) or kinase-inactive mutant LKB1 (D194A; KD, lanes 7,8,9) were incubated for 60 min with no further addition, with 2 mM AICA riboside or 10 mM phenformin, and lysed. **(a)** Endogenous AMPK was immunoprecipitated from the cell extracts and assayed. **(b)** The cell lysates were immunoblotted with antibodies recognizing AMPK α 1 phosphorylated at Thr172 or total AMPK α 1; the results were analyzed using the LI-COR Odyssey™ IR imager as described in the Materials and methods section, and are expressed as a ratio of the two signals. **(c)** The cell lysates were analyzed by western blotting and the membranes probed with antibodies recognizing ACC phosphorylated at Ser79, or streptavidin to determine total AMPK α 1. The results were analyzed using the LI-COR imager as for (b).

LKB1^{-/-} cells. Figure 7 also confirms, by western blotting of cell lysates, that the expression of LKB1 was absent from *LKB1*^{-/-} cells, that the expression of the AMPK α subunits was normal, and that the phosphorylation of Thr172 on the AMPK α subunits correlated with AMPK activity.

Discussion

Our results provide strong evidence that LKB1:STRAD:MO25 complexes represent the major upstream kinases acting on

AMPK, although they do not rule out the possibility that the complex might contain additional components. The key evidence may be summarized as follows. First, during previous extensive efforts to purify from rat liver extracts activities that activate dephosphorylated AMPK, ([4] and subsequent unpublished work), we have not detected any activities other than AMPKK1 and AMPKK2, at least under the assay conditions used. Second, both AMPKK1 and AMPKK2 purified from rat liver contained LKB1, STRAD α and MO25 α that were detectable by western blotting and whose presence correlated with AMPKK activity across the column fractions (Figure 1). Third, the ability of the AMPKK1 and AMPKK2 fractions to activate AMPK was almost completely eliminated by immunoprecipitation with anti-LKB1 antibody, but not a control immunoglobulin. Activity was also detected, along with the LKB1, STRAD α and MO25 α polypeptides, in the anti-LKB1 immunoprecipitates but not in the control immunoprecipitates (Figure 2). Fourth, the AMPKK activity in AMPKK1 and AMPKK2 was not a contaminant that co-precipitated with anti-LKB1 antibody, because recombinant complexes of GST-LKB1, STRAD and MO25 expressed in 293 cells and purified on glutathione-Sepharose also activated the AMPK α 1 catalytic domain efficiently, and phosphorylated Thr172 (Figure 3). Complexes formed from a catalytically inactive mutant LKB1 failed to activate or phosphorylate AMPK. Phosphorylation of the AMPK α 1 catalytic domain by this recombinant complex occurred exclusively at Thr172, because the wild-type AMPK α 1 catalytic domain, but not a T172A mutant, could be phosphorylated using [γ -³²P]ATP and the GST-LKB1:STRAD α :MO25 α complex. Fifth, although most of the experiments in this study were conducted using the bacterially expressed AMPK α 1 catalytic domain as substrate, AMPKK1, AMPKK2 and recombinant LKB1-STRAD α -MO25 α complexes also efficiently activated heterotrimeric AMPK complexes, both the α 1 β 1 γ 1 and α 2 β 1 γ 1 isoforms (Figure 4). Sixth, HeLa cells, unlike HEK 293T cells, do not express LKB1 (Figure 5) and therefore represent a natural 'knockout' cell line. The drugs AICA riboside and phenformin, which activate AMPK in other cell types via distinct mechanisms [24,27], did not activate AMPK in HeLa cells. In cells stably transfected with DNA that expressed wild-type LKB1 (but not a catalytically inactive mutant), however, the ability of AICA riboside and phenformin to activate AMPK, to phosphorylate Thr172 on the AMPK α subunit, and to cause phosphorylation of a downstream target (ACC) was restored (Figure 6). This experiment proves that (in the presence of STRAD α and MO25 α) LKB1 is sufficient for AMPK activation, but does not prove that it is necessary, because expression of upstream kinases other than LKB1 might also be defective in HeLa cells. Figure 5 also confirms that STRAD α and MO25 α are necessary to generate an active complex because, although the LKB1

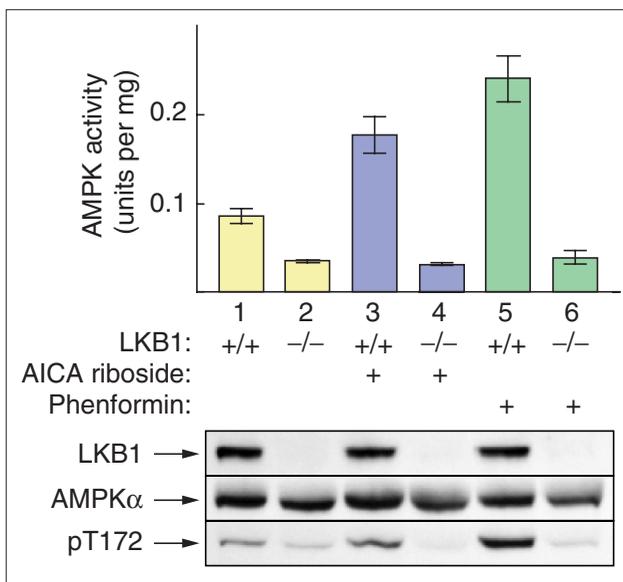


Figure 7

AMPK is activated and phosphorylated in response to AICA riboside and phenformin in *LKB1*^{+/+} but not in *LKB1*^{-/-} MEF cells. Cells immortalized from control embryos *LKB1*^{+/+} and *LKB1*^{-/-} knockout embryos [14], were incubated with AICA riboside (2 mM) or phenformin (10 mM) for 1 hour. Lysates were prepared and AMPK activity (expressed as units per mg total lysate protein) determined in immunoprecipitates made using a mixture of anti-AMPK α 1 and anti-AMPK α 2 antibodies. Lysates were also analyzed by SDS gel electrophoresis and blots probed using anti-LKB1, anti-AMPK- α 1/ β 2, and anti-pT172 antibodies.

polypeptide was greatly overexpressed in the stably transfected HeLa cells compared to the endogenous level in 293 cells, the AMPKK activity, and the amounts of STRAD α and MO25 α , in the anti-LKB1 immunoprecipitate, were actually less. This suggests that the amount of active LKB1 was limited by the availability of STRAD α and MO25 α . Seventh, in *LKB1*^{+/+} MEF cells, AMPK became activated in response to both AICA riboside and phenformin. In *LKB1*^{-/-} MEF cells, however, the basal activity of AMPK was lower and AICA riboside and phenformin failed to activate AMPK. These results show that LKB1 is both necessary and sufficient for AMPK activation, at least in MEF cells.

All of the assays of the activity of LKB1 and its complexes described in this article, whether using the AMPK α 1 catalytic domain or AMPK heterotrimers as substrate, utilized MgATP as the co-substrate. Previous studies of the kinase activity of LKB1, whether utilizing autophosphorylation [12], or p53 [28] or myelin basic protein [20] as substrates, had used MnATP as co-substrate and had reported that there was no activity with the more physiological MgATP complex. Thus, unlike previously used substrates, AMPK is a

good substrate for LKB1 complexes even using the physiologically relevant divalent metal ion.

We have previously reported that the activation of AMPK by AMPKK1 (called at that time AMPKK) was stimulated by AMP, and presented evidence favoring the hypothesis that AMP acted not only by binding to the downstream kinase and making it a better substrate, but also by activating the upstream kinase [6]. The results in Figure 4c support the first hypothesis but do not support the second. Using α 1 β 1 γ 1 or α 2 β 1 γ 1 AMPK complexes as substrate, activation by AMPKK1, AMPKK2 or LKB1 was stimulated from 2- to 3.5-fold by AMP. When using the AMPK α 1 catalytic domain as substrate, however, AMP had no effect, or even slightly inhibited activation. The AMPK α 1 catalytic domain is not allosterically activated by AMP [29], and AMP binding appears to be a function of the γ subunit ([30], and unpublished observations). Taken together with previous results [6,24,31], these data support the idea that the effects of AMP on the kinase cascade are all mediated through binding to the downstream kinase, AMPK. The previous report that AMP stimulated the upstream kinase was obtained using a less pure AMPKK preparation [6], and we have been unable to reproduce this with the more purified preparations utilized here.

Both AMPKK1 and AMPKK2 appear to contain LKB1, STRAD α and MO25 α , and thus it is not clear at present why they resolve on Q-Sepharose chromatography. One interesting difference is that the LKB1 polypeptide in AMPKK1 migrated significantly faster on SDS gels than that in AMPKK2 (Figures 1 and 2). LKB1 is known to be phosphorylated at up to eight sites, and is also farnesylated at Cys433, near the carboxyl-terminus [23,28,32,33], suggesting that the difference in mobility might be due to a difference in covalent modification. It did not appear to be due to differential phosphorylation, however, because neither incubation with MgATP, nor protein phosphatase treatment, produced a shift in mobility of the LKB1 polypeptides in either AMPKK1 or AMPKK2 (Figure 1c). Another difference between AMPKK1 and AMPKK2 was their Stokes radii estimated by size exclusion chromatography (5.7 versus 5.2 nm respectively). By combining estimates of Stokes radius and sedimentation coefficient, we previously estimated the molecular mass of AMPKK1 to be 195 kDa [4], and assuming a similar shape our estimate of the Stokes radius of AMPKK2 would suggest a mass of about 175 kDa. These values are close to, although slightly larger than, the calculated mass of 140 kDa for a 1:1:1 LKB1:STRAD α :MO25 α complex. Although we cannot rule out the possibility that AMPKK1 and/or AMPKK2 contain additional associated protein(s) other than LKB1, STRAD α / β and MO25 α / β , it is also possible that differences in covalent modification

might affect the shape of the complex and hence the Stokes radius. Whatever the reason for the difference in electrophoretic and chromatographic behavior of AMPKK1 and AMPKK2, a clear conclusion from Figure 4 is that, for the same amount of LKB1, STRAD α and MO25 α polypeptides, the former was more active than the latter. Although further work is required to explain these differences, they might be caused by the same covalent modifications that alter the mobility on SDS gels. Figure 4 also shows that, for the same amount of LKB1, STRAD α and MO25 α polypeptides, both AMPKK1 and AMPKK2 were much more active than the recombinant complex. The low activity of the latter might be explained by the presence of the purification tag on each subunit, by imperfect folding or assembly, or by an altered level of covalent modification, when the complex is overexpressed. As mentioned above, our data do not rule out the possibility that the recombinant LKB1 complex may be lacking additional subunit(s) present in the endogenous AMPKK1 and AMPKK2 complexes.

Our present results confirm, using a probable physiological substrate, previous findings using an artificial substrate (myelin basic protein) that a STRAD subunit stimulates the kinase activity of LKB1 [20], and that the MO25 subunit stimulates the activity further, probably by stabilizing the LKB1:STRAD complex [21]. No AMPKK activity was obtained with recombinant LKB1 unless a STRAD subunit was also expressed, and the activity was increased substantially by the additional presence of a MO25 subunit (Figure 3). It was also noticeable that the amount of STRAD α and STRAD β that co-precipitated with LKB1 was greatly enhanced by the co-expression of MO25 α or MO25 β (Figure 3), consistent with previous findings [21]. Another new result in this article is that STRAD α protein (unlike MO25 α) was not detectable in HeLa cells unless either wild-type or kinase-dead LKB1 was stably expressed (Figure 6b). These results suggest that STRAD α is normally complexed with LKB1 in the cell, and that STRAD is unstable in the absence of LKB1. The exact mechanism by which the STRAD and MO25 subunits activate LKB1 remains unclear, but these accessory subunits introduce scope for additional regulation of the kinase. It is already known that LKB1 phosphorylates STRAD α at two distinct sites [20], and that STRAD α and MO25 α form a complex that retains LKB1 in the cytoplasm [21].

People with PJS are heterozygous for mutations in LKB1, and further work is required to establish whether loss of one allele of *LKB1* could affect AMPK activation in these patients. An interesting unanswered question is whether activation of AMPK can explain the ability of LKB1 to act as a tumor suppressor and to arrest cell growth and proliferation. This certainly seems plausible, because apart from the

fact that AMPK is a general inhibitor of biosynthesis [1,2], there is accumulating evidence that it can regulate cell proliferation and apoptosis. For example, activation of AMPK inhibits proliferation of HepG2 cells by stabilizing p53 [34]. Interestingly, expression of LKB1 in G361 cells that normally lack expression of the kinase causes an arrest in G1 phase of the cell cycle that is associated with an induction of p21 and is dependent on p53 [12,13].

Another exciting possibility is that LKB1:STRAD:MO25 complexes might also act as upstream kinases for other protein kinases, in the same manner that PDK1 phosphorylates threonine residues in the activation loop of a number of kinases of the 'AGC' subfamily [35]. A dendrogram showing the relationships between catalytic domain sequences of 518 human protein kinases encoded in the human genome [36] shows that the AMPK α 1 and AMPK α 2 subunits lie on a small sub-branch also containing eight other protein kinases (NuaK1, NuaK2, BrsK1, BrsK2, SIK, QIK, QSK and MELK), most of which either have not been studied previously or have very little known about them. An alignment of the activation loop sequences of these kinases is shown in Additional data file 2 with the online version of this article and show that, as well as conservation of the threonine residue phosphorylated by LKB1 in AMPK, they have other conserved motifs that are not present in other protein kinases known to be activated by other upstream kinases. It remains to be determined whether the other kinases in the AMPK subfamily are activated by phosphorylation of the conserved threonine residue by LKB1:STRAD:MO25 complexes, but if this is the case these other kinases might mediate some of the tumor suppressor functions of LKB1.

A significant number of inherited forms of PJS found in certain families do not exhibit mutations in the LKB1 gene [37,38], indicating that there could be other causative loci for PJS. On the basis of the results presented here it would be very interesting to examine whether mutations in the genes encoding STRAD α or β , MO25 α or β , or any of the subunits of AMPK or of the AMPK-like subfamily of kinases, are found in PJS patients who do not have mutations in the LKB1 gene.

While this article was under review, two papers were published that are relevant to our results. Hong *et al.* [39] reported that FLAG-tagged LKB1 expressed in, and purified from, COS7 cells would activate a recombinant AMPK heterotrimer, and phosphorylate the α subunit at Thr172, in cell-free assays. This is consistent with our results, although these authors provided no evidence that LKB1 acts on AMPK *in vivo*, or that LKB1 required the presence of the STRAD and MO25 subunits to phosphorylate AMPK. Spicer

et al. [40] reported evidence, based on expression of recombinant LKB1 in cultured cells, suggesting that it might act upstream of the PAR1A protein kinase. PAR1A (also known as MARK-3 [41]) lies with three closely related protein kinases (MARK-1, MARK-2, MARK-4) on a branch of the human kinase tree [36] immediately adjacent to AMPK- α 1 and - α 2 and the eight AMPK-like kinases discussed above. Although Spicer *et al.* [40] did not provide evidence that LKB1 directly phosphorylated PAR1A, the results of our study suggest that this might be the case. The sequence of the activation segment of PAR1A is given in Additional data file 2 (available with the online version of this article).

Conclusions

Our results provide strong evidence, both in cell-free assays and in intact cells, that complexes between LKB1, STRAD α / β and MO25 α / β constitute the long sought-after upstream kinases that activate AMPK via phosphorylation at Thr172 in the activation loop. Because it is already known that pharmacological activation of AMPK causes a general inhibition of biosynthesis, as well as a p53-dependent arrest in G1 phase of the cell cycle, activation of AMPK by LKB1 might explain, at least in part, the ability of LKB1 to act as a tumor suppressor. LKB1 may also act as an upstream kinase for other members of the AMPK-like subfamily of protein kinases.

Materials and methods

Materials, proteins and antibodies

Protein G-Sepharose, glutathione-Sepharose and prepacked Q-Sepharose columns were from Amersham Pharmacia Biotech, Little Chalfont, UK. The GST-AMPK α 1 catalytic domain, and a T172A mutant, were expressed in *Escherichia coli* and purified as described previously [29]. Sheep antibodies against the α 1 and α 2 subunits of AMPK [22], human LKB1, MO25 α and MO25 β [21], and phosphospecific antibody against the Thr172 site on the AMPK α subunit (anti-pT172) [42] were described previously. Sheep antibody against AMPK α 1 catalytic domain was raised against the peptide CDPMKRATpIKDIRE (cysteine + residues 252-264 of rat AMPK α 1 given in the single-letter code for amino acids; Tp, phosphothreonine) using methods described for anti-pT172 [42]. Although designed as a phosphospecific antibody, it recognizes the GST-AMPK α 1 catalytic domain expressed in bacteria and recognition is not affected by protein phosphatase treatment. The monoclonal antibody against STRAD α was described previously [20]. Monoclonal anti-GST and anti-FLAG epitope antibodies were from Sigma (Poole, UK). Anti-Myc antibodies were prepared by ammonium sulfate precipitation of medium from Myc1-9E10 hybridoma cells grown in RPMI 1640 medium supplemented with 2 mM glutamine and

15% (v/v) fetal bovine serum. Anti-Erk1/2 antibodies were from Cell Signaling Technology (New England Biolabs, Hitchin, UK). The DNA constructs encoding GST-LKB1 (wild-type and kinase-dead) in the pEBG-2T vector [28], and FLAG-STRAD α , FLAG-STRAD β , Myc-MO25 α and Myc-MO25 β in the pCMV5 vector [21] have been described previously. PP1 γ was expressed in *E. coli* [43], and PP2A $_1$ was purified from rabbit skeletal muscle [43]. Sources of other materials and proteins were as described previously [4].

Enzyme assays

AMPK [4], PP1 γ and PP2A $_1$ [43] were assayed, and units defined, as described previously. AMPKK was assayed as follows (based on [27]). A fusion protein between the kinase domain of the α 1 subunit of AMPK and glutathione-S-transferase (GST-AMPK α 1) was expressed in *E. coli* [29]. Although some preparations of GST-AMPK α 1 show evidence of proteolytic degradation, only the full length GST-AMPK α 1 is phosphorylated (J.L.R., unpublished observations). The amount of full-length GST-AMPK α 1 was quantified by densitometry of Coomassie-Blue-stained gels, using bovine serum albumin as standard. The *E. coli* lysate expressing GST-AMPK α 1 was adsorbed onto glutathione-Sepharose beads (Amersham-Pharmacia) such that the final concentration of kinase after maximal activation using MgATP and AMPKK in the assay below was 1 unit in the standard kinase assay per 5 μ l of beads. The slurry was washed with 4 \times 1 ml of IP buffer (50 mM Tris-HCl, pH 7.4 at 4°C, 50 mM NaF, 5 mM Na pyrophosphate, 1 mM EDTA, 1 mM EGTA, 1% Triton X-100, 1 mM dithiothreitol (DTT), 1 mM benzamidine, 0.1 mM phenylmethane sulfonyl fluoride, 1 M NaCl) to remove unbound proteins. It was then washed in 3 \times 1 ml of assay buffer (50 mM Na HEPES, pH 7.4, 1 mM DTT, 0.02% Brij-35).

For the kinase assay, the AMPKK preparation was incubated with 10 μ l of a 50% slurry of the glutathione-Sepharose beads with bound GST-AMPK α 1, plus 200 μ M AMP, 200 μ M ATP, 5 mM MgCl $_2$ in assay buffer in a final volume of 25 μ l. After incubation for 20 min at 30°C on a rotary shaker, the beads were washed with 4 \times 1 ml of IP buffer and 3 \times 1 ml of assay buffer prior to a standard AMPK assay. The units of AMPKK are the units of AMPK generated in the assay, expressed per mg of full length GST-AMPK α 1 protein used. Rapid lysis of cells for AMPK assays was as described previously [44]. AMPK and AMPKK assays were carried out in triplicate and results are expressed as mean \pm standard deviation.

Purification of AMPKK1 and AMPKK2

AMPKK was purified to the Blue-Sepharose stage as described previously [4]. The flow-through from this column was adjusted to 160 mM NaCl by dilution in buffer

A (50 mM Hepes, 10% (w/v) glycerol, 0.02% (w/v) Brij-35, 1 mM EDTA, 1 mM EGTA, 1 mM DTT, 1 mM benzamidine, 0.1 mM PMSF, 1 µg/ml soybean trypsin inhibitor), and applied to a high performance Q-Sepharose HiLoad 16/10 column in buffer A plus 160 mM NaCl at 3 ml/min. The column was washed in buffer A plus 160 mM NaCl until the A_{280} was < 0.05, and AMPKK activity was then eluted with a linear gradient (120 ml) from 160-400 mM NaCl in buffer A.

Expression of recombinant LKB1 complexes in HEK-293T cells

Various combinations of GST-tagged LKB1, FLAG-tagged STRAD α or STRAD β , and Myc-tagged MO25 α or MO25 β were expressed in HEK293 cells and the complexes purified on glutathione-Sepharose as described previously [21].

Phosphorylation of GST- α 1 catalytic domain using [γ - 32 P]ATP

GST-AMPK α 1 catalytic domain (50 µg/ml), either wild-type or a T172A mutant [29] was incubated for 30 min at 30°C with 5 mM MgCl₂ and [γ - 32 P]ATP (200 µM; approximately 750 cpm/pmole) in the presence or absence of the GST-LKB1:STRAD α :MO25 α complex (20 units/ml). The reaction was terminated by the addition of SDS sample buffer (Invitrogen, Paisley, UK), the polypeptides resolved by SDS gel electrophoresis and the dried gel subjected to autoradiography.

Preparation of and activation of AMPK heterotrimer

AMPK was purified from rat liver as described previously [4]. Dephosphorylation, with PP2A, addition of okadaic acid to inhibit the phosphatase, and incubation with AMPKK was as described previously [4]. The reaction was stopped by adding 5 µl of 0.5 M EDTA to 20 µl of the dephosphorylated AMPK, and 20 µl of the mixture was then incubated for 2 h at 4°C with 75 µl of a 15% suspension of anti-AMPK α 1 or anti-AMPK α 2 antibodies bound to protein G-Sepharose [44] plus 200 µl of IP buffer. The beads were recovered by centrifugation (14,000 × g for 2 min) and washed twice with IP buffer and twice with 50 mM Na Hepes buffer, pH 7.4. AMPK assays were then carried out on the resuspended immunoprecipitates [44]. To obtain recombinant AMPK, plasmids encoding Myc-AMPK α 1 or Myc-AMPK α 2, AMPK β 1 and AMPK γ 1 were co-expressed in CCL13 cells [22], and cells harvested by the rapid lysis method [44]. Lysates were immunoprecipitated with anti-Myc antibody and resuspended in 50 mM Na HEPES, 1 mM dithiothreitol, 0.02% (w/v) Brij-35, pH 7.5, and assayed as above.

Immunoprecipitation of endogenous LKB1

Immunoprecipitation of endogenous LKB1 using anti-human antibody and protein G-Sepharose has been

described previously [21]. The kinase assays were conducted using GST-AMPK α 1 catalytic domain as substrate in shaking incubators as described previously for immunoprecipitate assays of AMPK [44].

HeLa cells expressing LKB1

The generation and culture conditions of HeLa cells stably expressing inducible (Tet-ON) wild-type or kinase-inactive mutant LKB1, and conditions for their culture, has been described previously [23].

Production of immortalized mouse embryo fibroblasts

Wild-type and *LKB1*^{-/-} E9.5 embryos [14] were minced into small fragments and placed in culture in Dulbecco's modified Eagle's Medium supplemented with penicillin, streptomycin, glutamine, 10% fetal bovine serum (AutogenBioclear, Santa Cruz, USA), and 10% conditioned medium collected from day-3 cultures of wild-type fibroblasts. The cultures were subsequently allowed to expand for 5 days, after which they were passaged according to a modified 3T3 protocol [45]. High-passage cultures that expanded were considered immortalized.

Protein analysis and electrophoresis

Protein concentration was determined using the dye-binding method of Bradford [46]. SDS gel electrophoresis used precast Bis-Tris 4-12% gradient polyacrylamide gels, in the MOPS buffer system (Invitrogen), except for analysis of acetyl-CoA carboxylase, where pre-cast 3-8% Tris-acetate gels (Invitrogen) were used. Proteins were transferred to nitrocellulose membranes (BioRad, Hemel Hempstead, UK) using the Xcell II Blot Module (Invitrogen).

Detection of western blots by infra-red imaging

To analyze phosphorylation of ACC, membranes were incubated in LI-COR Odyssey™ Blocking buffer for 1 h. Anti-pACC antibody (1.46 µg/ml in blocking buffer containing Tween-20 0.2% v/v) was then added and left shaking for 1 h. The membranes were washed 6 × 5 min with TBS (10 mM Tris-HCl, pH 7.4, 0.5 M NaCl) plus Tween-20 (0.2% v/v). The membranes were immersed in blocking buffer containing Tween-20 (0.2% v/v) and 1 µg/ml anti-sheep IgG conjugated to IR dye 680 (Molecular Probes, Leiden, The Netherlands) and 1 µg/ml streptavidin conjugated to IR Dye 800 (Rockland Inc., from Lorne Laboratories, Reading, UK) and left shaking for 1 h, protected from light. The membranes were then washed 6 × 5 min using TBS-Tween (0.2%) and 1 × 5 min in PBS. The membranes were scanned in two different channels using the Odyssey IR imager, the results quantified using Odyssey software and expressed as a ratio of the signal obtained with the pACC antibody to that obtained with streptavidin. Analysis of

phosphorylation of GST- α 1 catalytic domain was similar except that the 4-12% Bis-Tris gels were used, and the membranes were simultaneously probed for 1 h with the sheep anti-pT172 and anti-AMPK α 1 catalytic domain antibodies, directly labeled with the IR dye 680 and IR dye 800 respectively, according to manufacturers' instructions.

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Additional data files

The following additional materials are available with the online version of this article: Additional data file 1, showing an alignment of the kinase domains of Tos3, Pak1, CaMKK β , LKB1 and Elm1, and Additional data file 2, showing an alignment of the activation loop of the kinase subgroup phylogenetically close to LKB1.

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