A two-dimensional screen for AMPK substrates identifies tumor suppressor fumarate hydratase as a preferential AMPKa2 substrate

Anna Klausa, b, 1, Cécile Polgea, b, 1, 2, Sarah Zorman a, b, Yolanda Auchlic, René Brunisholzc, Uwe Schlattnera, b,⁎

a University Joseph Fourier, Laboratory of Fundamental and Applied Bioenergetics, Grenoble, France
b Inserm, U1055, Grenoble, France
c Functional Genomics Center Zurich, ETH Zurich/University of Zurich, Switzerland

ARTICLE INFO

Article history:
Received 12 December 2011
Accepted 25 March 2012
Available online 3 April 2012

Keywords:
AMP-activated protein kinase
cell signaling
fumarate hydratase
protein kinase substrates
protein phosphorylation
surface plasmon resonance

ABSTRACT

AMP-activated protein kinase (AMPK) is emerging as a central cellular signaling hub involved in energy homeostasis and proliferation. The kinase is considered as a suitable target for pharmacological intervention in several energy-related pathologies like diabetes type II and cancer, although its signaling network is still incompletely understood. Here we apply an original two-dimensional in vitro screening approach for AMPK substrates that combines biophysical interaction based on surface plasmon resonance with in vitro phosphorylation. By enriching for proteins that interact with a specific AMPK isoform, we aimed to identify substrates that are also preferentially phosphorylated by this specific AMPK isoform. Application of this screen to full-length AMPKα2β2γ1 and soluble rat liver proteins identified the tumor suppressor fumarate hydratase (FH). FH was confirmed to interact with and to be preferentially phosphorylated by the AMPKα2 isoform by using yeast-two-hybrid and in vitro phosphorylation assays. AMPK-mediated phosphorylation of FH significantly increased enzyme activity in vitro and in vivo, suggesting that it is a bona fide AMPK substrate. In vivo, AMPKα2 is supposed to target the cytosolic/nuclear pools of FH, whose tumor suppressor function relies on DNA damage repair and inhibition of HIF-1α-signaling.

© 2012 Elsevier B.V. All rights reserved.

1. Introduction

AMP-activated protein kinase (AMPK) is member of a Ser/Thr kinase family conserved across the eukaryotic kingdom, including SNF1 complex in yeast and SnRK1 in plants. These kinases function as heterotrimeric complexes composed of one catalytic α-type subunit and two regulatory β- and γ-type subunits [1-4]. Subunits of mammalian AMPK occur as different isoforms (α1, α2, β1, β2, γ1-3) and splice variants (of γ2 and 3), potentially generating multiple different heterotrimeric complexes.

In mammals, AMPK functions mainly as an energy sensor, integrating signals from inside the cell, the cellular
environment, and the whole organism (for reviews see [5–8]). The activation mechanism involves AMP-induced conformational changes, covalent activation by the upstream kinases LKB1 or CamKKβ [9,10], and AMP- and ADP-dependent inhibition of AMPK dephosphorylation. Altered AMPK signaling has been associated with different human pathologies like diabetes and cancer, and the kinase is a promising drug target for these pathologies [11,12]. Two of the major drugs used for treating diabetes type II, metformin and thiazolidinediones, activate AMPK [13,14] and many of their therapeutic effects are mediated by AMPK signaling [15]. The identification of LKB1, a known tumor suppressor, as an upstream kinase of AMPK [10] and the effect of metformin reducing cancer incidence [16] have generated substantial interest for the role of AMPK in cancer development. Activated AMPK negatively regulates cell proliferation and the cell cycle, mostly mediated by mTOR and p53, respectively [17–19]. However, treatments based on a systemic activation of AMPK may not only be beneficial, given the largely pleiotropic effects to be expected from a growing number of AMPK substrates.

Systemic activation may be avoided to some degree by targeting specific AMPK isoform combinations, since they show a partial tissue-specificity [20] or may recognize specific substrates. However, information on putative determinants of kinase-substrate interaction is scarce. Few AMPK interactors have been independently verified by more than one method [21–23], and most interaction data come from large-scale screening like immunoprecipitation-MS analysis with tagged AMPK [24], which do even not proof direct interactions. The variable N-terminal region of the β-subunits has been proposed to mediate interaction of the kinase with its substrates in yeast [25] and plants [26]. In mammals, the α1 and α2 subunits were shown to exhibit subtle different substrate preferences when using variants of the SAMS peptide, suggesting that the two α isoforms could phosphorylate different substrates within the cell [27], but this could not be confirmed so far for known AMPK substrates.

To identify substrates that interact with a specific AMPK isoform combination and thus potentially represent preferential substrates of this AMPK species, we have set up a protocol involving prefractionation and a two-dimensional in vitro screening. This combines biophysical interaction assays using surface plasmon resonance (SPR) with in vitro phosphorylation assays and protein identification by mass spectrometry (MS) as successfully applied already in an earlier study [28]. This approach identified the tumor suppressor fumarate hydratase (FH) as an interactor and preferential substrate of α2-containing AMPK complexes, with phosphorylation leading to enzymatic activation.

2. Material and methods

2.1. Material

AICA-Riboside (AICAR) was from Biotrend Chemicals (Zurich, Switzerland), rabbit polyclonal anti-P-Thr172 AMPKα and anti-His-tag antibodies from Cell Signaling Technology (Danvers, MA, USA), goat polyclonal anti-GSTipi and rabbit polyclonal anti-FH antibody from Abcam (Cambridge, UK), secondary antibodies coupled to horseradish peroxidase were from GE Healthcare Life Science (Buckinghamshire, UK) for rabbit IgG and Thermo Scientific (Rockford, USA) for goat IgG.

2.2. Cloning and purification of proteins

Plasmids pγ1/γ1His-a1, pγ1/γ1His-a1T172D, pγ1/γ1His-a2 and pγ1/γ1His-a2T172D [29] were used for bacterial expression and purification as published previously [29,30]. For Y2H experiments, PCR-amplified inserts were introduced into Y2H vectors pCab and pDSL (Dualsystems Biotech AG, Schlieren, Switzerland). FH (mature form lacking signal peptide, GenelD: 24358) and fatty acid binding protein 1 (FABP1, GenelD: 24360) were amplified from rat liver cDNA and introduced into yeast two-hybrid vectors or bacterial expression vectors pET-52b (+) (Merck KgaA, Darmstadt, Germany) and pGEF 4 T-1 (GE Healthcare). The fusion constructs Strep-FH, Strep-FABP1, GST-FH, GST-FABP1, GST-ACC (plasmid kindly provided by G. Hardie, Univ. of Dundee, UK) [31] and GST-CamKKβ (plasmid kindly provided by H. Tokumitsu, Kagawa Medical University, Japan) were bacterially expressed and purified according to standard procedures and the tag proteolytically removed where necessary. For further details see the online Supplementary Material 1.

2.3. Preparation and prefractionation of liver extract

Total liver from one rat was snap-frozen in liquid nitrogen and homogenized in 15 ml ice-cold extraction buffer A (20 mM HEPES, pH 7.4, 100 mM NaC1, 50 μM EDTA, and anti-protease cocktail, 1 tablet per 50 ml solution, Roche Diagnostics, Basel, Switzerland) using a Polytron PT 3000 homogenizer at 24 000 rpm for 20 s. After centrifugation at 15000 g for 30 min at 4 °C, the supernatant was filtered (0.22 μm filter). Prefractionation was carried out on an Äkta Explorer 100 Air HPLC system (GE Healthcare). Three ml of liver extract were applied to a Ni-NTA column (2 ml bed volume; Qiagen) pre-equilibrated in buffer A. The column was then washed at a flow rate of 1 ml/min with 2 column volumes (CV) of buffer A. Proteins were eluted with imidazole buffer (20 mM HEPES, pH 7.4, 100 mM NaC1 and 250 mM imidazole) and the first 5 ml collected. This process was repeated 3 times. Between each load, the column was washed with 4 CV imidazole buffer, 1 CV water, 1 CV NaOH 0.5 M and 5 CV buffer A. To reduce the volume, collected proteins were precipitated with 80% (w/v) ammonium sulfate for 2 hours at 4 °C. The pellet was resuspended in 5 ml buffer A and further centrifuged at 15 000 g for 10 min at 4 °C. The supernatant was filtered (0.22 mm filter) and applied to a Superdex 200 size exclusion column (separation range Mr = 10 000–600 000; volume 120 ml; GE Healthcare) pre-equilibrated in buffer A. Proteins were then separated at a flow rate of 1 ml/min and collected in 12 fractions of 5 ml each (S1 to S12) supplemented with anti-protease cocktail (Roche, 1 tablet per 50 ml solution) was added.

2.4. Surface plasmon resonance interaction screening and yeast two-hybrid assays

The SPR screening was performed with a BIACore 2000 (GE Healthcare) using a NTA sensor chip (GE Healthcare) and as running buffer 10 mM HEPES pH 7.4, 100 mM NaCl, 50 μM
EDTA and 0.005% Surfactant P20. In each measurement cycle, the NTA surface was activated by a 1 min-pulse of 500 μM NiCl₂ and 50 nM His-tagged AMPK α2(γ2γ1) (AMPK221) was injected at 5 μl/min until reaching 400 response units (RU) of immobilization. An HPLC fraction was then injected onto the AMPK221 surface at 20 μl/min for 120 s. Interacting protein was quantified at a reporting point 80 s after dissociation start, since the association phase was biased by an SPR signal caused by the chromatography sample buffer. After 120 s of dissociation, a protein-free surface was regenerated by injection of 10 mM HEPES, pH 8.3, 150 mM NaCl, 350 mM EDTA and 0.005% Surfactant P20. Binary protein-protein interactions were analyzed in vivo using the Cyto-Y2H system (Dualsystems BioTech) [32] based on the split-ubiquitin system [33,34] (see online Supplementary Material 1).

2.5. Co-immunoprecipitation

Strep-tagged FH (1 μg) and His-tagged AMPK 221TD (1 μg) were co-immunoprecipitated with anti-His-tag antibody (1:200) and protein G Sepharose (10% w/v) in IP buffer (30 mM Hepes pH 7.3, 300 mM NaCl, 6 g/l BSA, 0.5% w/v dodecylmaltoside) overnight at 4 °C. Sepharose was washed twice (30 mM Hepes pH 7.3, 300 mM NaCl, 6 g/l BSA, 0.5% w/v dodecylmaltoside) and resuspended in SDS-PAGE sample buffer. Proteins separated by SDS-PAGE were probed for FH by immunoblotting.

2.6. AMPK substrate phosphorylation screening

AMPK phosphorylation assays were performed at 37 °C in a final volume of 25 μl containing 12.5 μl of chromatography fractions and kinase buffer (200 μM [γ-32P]ATP (400 mCi/mmol ATP), 50 μM AMP, 5 mM MgCl₂, 1 mM DTT and 10 mM HEPES pH 7.4), with or without recombinant constitutively active AMPK221 (50 pmol). The kinase reactions were stopped after 2 min by addition of 10 μl SDS sample buffer (105 mM Tris–HCl, pH 6.8, 4% (w/v) SDS, 15% (w/v) glycerol, 1.2 M β-mercaptoethanol, and 0.02% (w/v) bromophenol blue), heated to 95 °C for 5 min, and separated by SDS-PAGE. Following colloidal Coomassie staining, gels were air-dried and exposed to autoradiography films (GE Healthcare) for up to 2 weeks or to Typhoon imager (GE Healthcare).

2.7. Trypsin digestion and mass spectrometry

Radioactively labeled AMPK-specific bands were cut from the gels, in-gel trypsin-digested (Promega), and extracted peptides analyzed by MALDI MS and MALDI MS/MS using an Ultraflex TOF/TOF II (Bruker Daltonics, Bremen, Germany). Processed spectra were combined through BioTools software (Bruker Daltonics) to search the Uniref100 database (release 6.0), non-restricted to the taxonomy, using Mascot software v. 2.0 (Matrix Science, London, UK). Probability-based MOWSE scores greater than 50 were considered significant. For details see the online Supplementary Material 2.

2.8. In vitro analysis of AMPK substrate phosphorylation

To compare phosphorylation kinetics, purified FABP1, FH and ACC Strep- or GST-constructs (200 pmol) were incubated for 5, 10, 20, 30 and 60 min at 37 °C with 200 μM [γ-32P]ATP (specific activity 650 mCi/mmol ATP) and AMPK221 (4 pmol) previously activated by incubation with 1 pmol CamKKβ for 20 min at 30 °C in kinase buffer (200 μM ATP, 50 μM AMP, 5 mM MgCl₂, 1 mM DTT, 10 mM HEPES pH 7.4). To compare phosphorylation by different AMPK isoforms, purified Strep-FH and GST-ACC (200 pmol) were incubated for 8 min at 37 °C in the presence or absence of 3 pmol previously activated AMPK (AMPK221, -211 or -111) in kinase buffer containing 200 μM [γ-32P]ATP (specific activity 650 mCi/mmol ATP). For negative controls, AMPK substrates were incubated with 1 pmol CamKKβ alone without AMPK. Kinase reactions were stopped by addition of SDS-PAGE sample buffer and subjected to SDS-PAGE and Typhoon phosphoimager (GE Healthcare).

2.9. AMPK activation in cell culture

HeLa cells were cultured in DMEM/F12 high glucose medium supplemented with 10% inactivated fetal calf serum (FCS) and 1% glutamate/streptomycin/penicillin. Endogenous AMPK of HeLa cells was activated by treatment with 1 mM AICAR for 1 h at 37 °C. Cells were then trypsinated, collected by centrifugation (1200 g, 5 min), and resuspended in lysis buffer (50 mM Tris/HCl pH 7.5, 100 mM NaCl, 5 mM MgCl₂, 1% NP-40, 0.1% SDS) supplemented with protease (Roche) and phosphatase (Thermo Scientific) inhibitor cocktail. Cells were lysed by sonication and insoluble material was removed by centrifugation (10 min, 10 000 g, 4 °C). AMPK activation was verified by immunoblotting using anti P-Thr172 AMPK antibody. Immunoblot against GSTpi was used as a loading control.

2.10. Fumarate hydratase enzyme activity

AMPK221 was activated by CamKKβ and incubated with GST-FH in kinase buffer for 30 min at 37 °C prior to activity measurements. Enzyme activity of FH and phospho-FH was then determined at 25 °C by a spectrophotometric assay measuring fumarate formation (240 nm) in 0.1 M potassium phosphate buffer pH 7.6 using 0.5 to 8 mM malate. Data were analyzed by direct fitting to Michaelis-Menten kinetics and secondary plots using SigmaPlot 10 (Systat Software, USA). FH activity of HeLa extracts was measured under the same conditions using 2.5 mM malate.

3. Results

3.1. Setup of an in vitro AMPK substrate screen

With the rationale to use the affinity between the kinase and its substrates as an additional parameter in a two-dimensional screening matrix for new substrates, we set out the following strategy (Fig. 1): Starting with soluble proteins within a cell extract of rat liver, we (i) eliminated proteins that non-specifically interact with Ni-NTA matrix, (ii) reduced complexity via size exclusion chromatography, (iii) screened for fractions containing AMPK interactors by using Biacore SPR with His-tagged AMPK221 immobilized on an NTA sensor chip, and finally (iv) screened SPR-positive fractions with in vitro phosphorylation assays using constitutively active AMPK221.
Preliminary experiments had revealed a high degree of non-specific protein binding to the NTA surface during SPR (not shown), which could be eliminated by an initial Ni-NTA chromatography step. Prefractionation with size exclusion chromatography on a Superdex 200 column had the additional advantage that eluted fractions contained proteins of similar size. This is an important prerequisite for the subsequent SPR experiments, since the SPR signal directly correlates with the mass bound at the chip surface, and thus not only with the number but also with the size of the bound protein. The unprocessed protein chromatography fractions were individually analyzed by Biacore SPR on surfaces covered with AMPK221 or left blank (Fig. 2). Fractions were considered interaction-positive when 80 s after dissociation start the SPR response on the AMPK221 surface was still higher as compared to the blank surface (fractions S1, S2, S3, S4, S10, S11 and S12). Fraction S1 contained mainly aggregates and was discarded; all other positive fractions were subjected to phosphorylation assays with or without constitutively active AMPK221 and separated by SDS-PAGE (Fig. 3). Nine AMPK-specific bands could be identified in these interaction-positive fractions.

### 3.2. Identification of candidate substrates of AMPK

MALDI-MS/MS mass spectrometry of AMPK-specific phospho-bands identified several proteins with significant MASCOTT score (Table 1, online Supplementary Material 2). Three of them are at least partially localized in the cytosol and are thus the most likely candidate substrates of AMPK in vivo. The γ-actin was already identified as a putative AMPK substrate in our earlier in vitro AMPK substrate screen [28]. Fumarate hydratase (FH) and fatty-acid binding protein 1 (FABP1 or FABPL) are newly identified AMPK candidate substrates. FH occurs in identical form in mitochondria and cytosol, but has different functions in the two compartments [35]. FABP1, as a mal protein of 14.6 kDa, is the liver isoform of a family of nine different FABPs in mammals [36]. These proteins were analyzed for putative AMPK phosphorylation sites, either corresponding to the stringent consensus motif [31,37] or to recognition sequences identified by peptide library profiling [38]. While γ-actin did not contain a stringent AMPK site and was not further analyzed, FH preprotein and mature protein, as well as FABP1, contained at least one stringent AMPK site and additional less stringent sites.

Fig. 1 – Flow chart of the in vitro screening procedure. A tissue-derived extract containing soluble proteins is pre-fractionated by two step column chromatography with different sorbent chemistries. Each fraction is then analyzed by SPR for the presence of AMPK221 interacting proteins. Positive fractions are subjected to in vitro phosphorylation assays for detection of potential downstream substrates. After SDS-PAGE separation and autoradiography, positive lanes are excised and proteins identified by mass spectrometry.

### 3.3. FH and FABP1 preferentially interact with AMPKα2

We next wanted to confirm whether FH and FABP1 are indeed those proteins that were directly interacting with AMPK221 in the first dimension and phosphorylated by AMPK221 in the second dimension of our screen. A cytosolic yeast two-hybrid (Y2H) assay, the Cyto-Y2H [32,39], confirmed a direct protein-protein interaction in vivo between FH and the α2 and β2 AMPK subunits, but not the α1 and β1 subunits (Fig. 4). Direct interaction of AMPK221 with FH could be confirmed by co-immunoprecipitation (Fig. 5). FABP1 showed the same specificity for α2, while it interacted only very weakly with both β1 and β2 (Fig. 4). These results confirm that FH and FABP1 are true interactors of AMPK. Importantly, they show specific interactions with the AMPK subunits used in the initial SPR screen: the AMPKα2 catalytic subunit (in case of FH and FABP) and the AMPKβ2 regulatory subunit (in case of FH).
3.4. FH is directly phosphorylated by AMPK221

Direct phosphorylation of FH and FABP1 by AMPK was verified by in vitro phosphorylation assays with purified recombinant proteins. In principle, phosphorylation in complex mixtures could also occur by another protein kinase which is itself activated by AMPK. FH and FABP1 were therefore expressed in *E. coli* as GST- and Strep-tagged proteins. GST-FH incorporated γ-32P ATP presence of CamKKβ-activated AMPK in a time-dependent manner (Fig. 6). Kinetics and extent of 32P incorporation were comparable to the reference AMPK substrate acetyl-CoA carboxylase (ACC). Similar results were obtained with Strep-tagged FH (Suppl. Fig. 1), showing that FH phosphorylation was not due to an interaction of AMPK with the GST-tag (Klaus & Schlattner, unpublished data). By contrast, FABP1 constructs were not phosphorylated under these conditions (not shown). Thus, the screen correctly identified FH as a true and direct substrate of AMPK in vitro.

Fig. 2 – SPR interaction screening. Representative association/dissociation kinetics of different fractions from size exclusion chromatography injected onto immobilized AMPK221 (full lines) or empty surface (control, dotted lines).

Fig. 3 – Phosphorylation assay screening. SPR positive fractions were subjected to in vitro phosphorylation assays with or without constitutively active αT172D AMPK221 using incubation with [γ-32P]ATP for 2 min at 37 °C. Assay mixtures analyzed by SDS-PAGE and Typhoon phospho-imager revealed AMPK auto-phosphorylation of α and β subunits and phosphorylation of putative AMPK substrates (bands indicated by small letters). Phosphorylation patterns of fractions S10 and S11 were similar to S12 and are not shown.
3.5. FH is preferentially phosphorylated by α2-containing AMPK complexes

We then wanted to know whether FH not only interacts specifically with AMPK221, but is also specifically phosphorylated by this AMPK isoform combination. Like above, in vitro phosphorylation assays were conducted with FH and ACC, using three different AMPK complexes: AMPK221, AMPK211, and AMPK111, all previously activated by CamKKβ. ACC phosphorylation served to account for different specific activities of the AMPK complexes, since the ACC-derived SAMS peptide is an equally good substrate for α1- and α2-containing AMPK complexes [27]. We first investigated the effect of different α-subunits on FH phosphorylation (Fig. 7A). The ratio P-ACC(221)/P-ACC(111) was 1.5, while the ratio P-FH(221)/P-FH(111) was 5.0. If normalized to ACC, FH is still 3.3 times more phosphorylated by AMPKα2 as compared to AMPKα1. Complexes containing different β-subunits (AMPK221 and AMPK211) phosphorylated both ACC and FH with similar efficiency (ratios of 1.1 for P-ACC(221)/P-ACC(211) and 0.9 for P-FH(221)/P-FH(211); Fig. 7B). Thus, at least in vitro, AMPK β-subunits have no effect on FH phosphorylation. These results strongly suggest that AMPK isoform composition can determine preference for specific substrates. FH interacts with AMPKα2 and is preferentially phosphorylated by α2-containing complexes. Although FH also interacts with the β2-subunit, this does not affect phosphorylation efficiency.

3.6. FH phosphorylation by AMPK increases its enzyme activity in vitro and in vivo

We have finally addressed the effect of FH phosphorylation on its enzymatic function, which catalyzes the reversible hydration/dehydration of fumarate to malate. Enzyme kinetics of FH were determined before and after in vitro phosphorylation by CamKKβ-activated AMPK221, using malate as substrate and measuring fumarate formation by spectrophotometry. FH phosphorylation led to a 37% increase in $k_{cat}$ whereas the apparent $K_m$ remained almost unaffected (Fig. 8; Table 2). To investigate whether AMPK could also affect FH activity in vivo, we examined the effect of AMPK activation by its pharmacological agonist AICAR on FH activity in HeLa cells. Treatment of HeLa cells with 1 mM AICAR for 1 h led to a strong increase in AMPKα1 Thr172 phosphorylation (Fig. 9A). This AMPK activation led to an average increase in FH activity by 31.3±6.4% (Fig. 9B). Similar results were obtained by activating AMPK with the Abbott compound A-769662 (not shown).

4. Discussion

The original two-dimensional in vitro screen for protein kinase substrates presented here combines biophysical interaction based on SPR with phosphorylation assays. Our data provide proof of principle that such a screening protocol can reveal...
AMPK substrates that are phosphorylated in an AMPK isoform-specific manner. We identified FH (or fumarase) as a novel AMPK substrate, and show that mainly the α2-subunit of AMPK is involved in FH interaction and recognition, as well as in FH phosphorylation. This phosphorylation increases FH enzymatic turnover in vitro and in vivo.

SPR technology has so far not been used to explore kinase/substrate interaction for screening of novel kinase substrates. It has only been applied as high-throughput readout device to measure interactions between phosphorylated kinase substrates and anti-phospho antibodies [40]. High-throughput procedures have also been developed to screen for AMPK activators or inhibitors (e.g. [41]). We show here that SPR can detect AMPK interactors in complex protein mixtures when different conditions are satisfied: (i) availability of highly pure, active kinase, as we have established by polycistronic bacterial expression of full-length AMPK complex [29]; (ii) reversible, high density immobilization of the kinase on the chip surface for repeated use with fresh protein (e.g. by using Ni-NTA); (iii) the use of prefractionated extracts as source of soluble protein to reduce
complexity; and in particular (iv) prior removal of proteins with non-specific affinity to the chip surface (especially relevant for Ni-NTA). We have assembled these conditions in a protocol (Fig. 1) that provides useful data for AMPK and soluble liver proteins. The resolving power of the screen could be further improved by using multidimensional prefractionation (e.g. by additional ion exchange chromatography) or detection approaches (e.g. 2D-PAGE of interaction-positive fractions).

From SPR-positive fractions, FH and FABP1 were identified as direct AMPK221-interacting proteins. Another FABP family member, the epidermal FABPS, and FH were also part of AMPK-containing complexes in an earlier large-scale anti-bait co-immunoprecipitation study using AMPK-α1 [24]. However, here we show that both proteins exclusively interact with subunits used in our SPR screen: the α2- and (in case of FH) the β2-subunits. In addition, recombinant FH, but not FABP1, was also phosphorylated by AMPK in vitro. Possibly, FABP1 phosphorylation by AMPK requires additional factors (i.e. fatty acids) or secondary modifications missing in the bacterially expressed FABP1 but present in endogenous liver protein. Phosphorylation of FH constructs by AMPK221 occurred with kinetics and a degree of 32P-incorporation per mol of protein that were similar to the classical α1-complexes. This is one of the first reports showing a clear preference of mammalian AMPK complexes for one of its substrates [27]. Such substrate specificity may contribute to tissue- and compartment-specific AMPK signaling whose mechanisms are so far largely unsolved.

FH or fumarase is encoded by a single gene, but dual isoforms of FH exist in mammalian systems [43]. While mitochondrial FH is well known for its participation in the tricarboxylic acid cycle (TCC), converting fumarate into malate, the role of cFH is emerging only more recently. Recent research is driven by the tumor suppressor function of FH which suggests that metabolic signals can regulate carcinogenesis (reviewed in [42]). Cancer incidence is linked to cFH inhibition and/or the resulting pseudohypoxic fumarase accumulation, which may act via different mechanisms. These include induction of pseudohypoxia via stabilization of HIF-1α [43], signaling via serum responsive factor [44], up-regulation of antioxidant-response element-controlled genes [45,46], or inhibition of DNA damage response [47]. In the latter mechanism, cellular stressors leading to DNA damage, induce cFH translocation to the nucleus, where its enzymatic activity is required to activate the DNA repair machinery, thus avoiding genomic instability. Our study together with literature data suggest that phosphorylation and activation of cFH by AMPK could play an important role in this sequence of events. AMPK signaling is known to respond to DNA damage and genotoxic stress transmitted via p53 and the nuclear sensor ataxia-telangiectasia mutated protein (ATM) [49]. Furthermore, the nuclear functions of AMPK are mediated by p53 targets Sestrin1 and Sestrin2 [48] or the cellular damage sensor ataxia-telangiectasia mutated protein (ATM) [49]. cFH is also a substrate of AMPK, and the α2-isozyme is preferentially phosphorylated by AMPK [27]. Hence, the nuclear functions of AMPK are dependent on the preferential phosphorylation of cFH isoforms [27].

In summary, we provide proof of concept that combining classical in vitro AMPK phosphorylation assays with SPR-based AMPK-protein interaction screening can not only identify novel AMPK substrates but also enrich for AMPK isoform-specific substrates. The newly identified AMPK substrate FH is exclusively interacting with and preferentially phosphorylated by α2-containing AMPK complexes. Both phosphorylation and activation of FH could contribute to the tumor suppressor function of FH.

Supplementary data to this article can be found online at doi:10.1016/j.jprot.2012.03.040.

Acknowledgements

This work was supported by EU FP6 contract LSHM-CT-2004-005272 (EXGENESIS), the French Fondation pour la Recherche Médicale (to A. Klaus, nee Brückner) and the French Agence Nationale de Recherche (“chair d’excellence” to U.S.). We thank Daniel Auerbach (Dualsystems Schlieren, Switzerland) for providing an unpublished version of the Cyto-Y2H system, and Grahame Hardie (University of Dundee) and H. Tokumitsu (Kagawa Medical University) for providing GST-ACC and CamKKβ expression vectors. The abbreviations used are: ACC, acetyl-CoA carboxylase; AICAR, aminoimidazole carboxamide ribonucleotide; AMPK, AMP-activated protein kinase; CaMKKβ, CaMKKβ,
Ca^{2+}/calmodulin-dependent protein kinase kinase; FABP, fatty acid binding protein; FH, fumarate hydratase; cFH, cytosolic FH; MS, mass spectrometry; Ni-NTA, nickel-nitrilotriacetic acid; SPR, surface plasmon resonance; TCC, tricarboxylic acid cycle; Y2H, yeast two-hybrid.

REFERENCES


