

# Ezrin silencing remodulates the expression of Phosphoinositide-specific Phospholipase C enzymes in human osteosarcoma cell lines

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**Abstract** Ezrin, a protein belonging to the Ezrin, radixin and moesin (ERM) family, was engaged in the metastatic spread of osteosarcoma. The Protein 4.1, Ezrin, radixin, moesin (FERM) domain of Ezrin binds the membrane Phosphatidylinositol (4,5) biphosphate (PIP<sub>2</sub>), a crucial molecule belonging to the Phosphoinositide (PI) signal transduction pathway. The cytoskeleton cross-linker function of Ezrin largely depends on membrane PIP<sub>2</sub> levels, and thus upon the activity of related enzymes belonging to the PI-specific phospholipase C (PI-PLC) family. Based on the role of Ezrin in tumour progression and metastasis, we silenced the expression of *Vil2* (OMIM \*123900), the gene which codifies for Ezrin, in cultured human osteosarcoma 143B and Hs888 cell lines. After Ezrin silencing, the growth rate of both cell lines was significantly reduced and morphological changes were observed. We also observed moderate variations both of selected PI-PLC enzymes within the cell and of expression of the corresponding *PLC* genes. In 143B cell line the transcription of *PLCB1* decreased, of *PLCG2* increased and of *PLCE* differed in a time-dependent manner. In Hs888, the expression of *PLCB1* and of *PLCD4* significantly increased, of *PLCE* moderately increased in a time dependent manner; the expression of *PLCG2* was up-regulated. These observations indicate that Ezrin silencing affects the transcription of selected *PLC* genes, suggesting that Ezrin might influence the expression regulation of PI-PLC enzymes.

**Keywords** Signal transduction · PLC · Ezrin · Cytoskeleton · Osteosarcoma · Metastasis

## Introduction

Osteosarcoma, the most common primary bone tumour in childhood and adolescence, includes several pathological entities, differing in clinical, radiological, and histological features (Mirabello et al. 2009a, b; Gatta et al. 2005). The presence of metastasis confers worse prognosis to the clinical outcome of osteosarcoma affected patients (Meyers et al. 2005). The identification of molecules involved in the metastasizing process is crucial in order to understand the mechanisms of tumour dissemination, possibly opening the way to novel therapeutic strategies.

Ezrin, a protein involved in the metastatic spread of osteosarcoma (Khanna et al. 2004), belongs to the Ezrin-radixin-moesin (ERM) family proteins, which play structural and regulatory roles (Khanna et al. 2004; Ferrari et al. 2008; Hunter 2004). The reduction of Ezrin significantly reduced the metastatic dissemination in osteosarcoma animal models (Khanna et al. 2004). Despite a number of observations following great research efforts, the mechanisms by which Ezrin mediates the metastatic process remain to be fully delineated.

The Protein 4.1, Ezrin, radixin, moesin (FERM) domain (Chishti et al. 1998) present in Ezrin is involved in the recognition of Phosphatidylinositol (4,5) biphosphate (PIP<sub>2</sub>), a crucial molecule belonging to the Phosphoinositide (PI) signal transduction pathway (Gautreau et al. 1999; Martin 2003; Pujuguet et al. 2003; Zhao et al. 2004; Tsukita and Yonemura 1997; Fievet et al. 2007). The role of Ezrin in actin assembly (Defacque et al. 2000, Defacque et al. 2002) largely depends on the membrane PIP<sub>2</sub> levels (Hao et al. 2009). ERM proteins bind actin and, by means of their N-terminal domains, simultaneously the PIP<sub>2</sub> located at the plasma membrane

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(Niggli, V et al. 2008, Gilmore and Burridge 1996 Isenberg and Niggli 1998, Nakamura et al. 1999, Eberle et al. 1990, Dobos et al. 1992, Apgar 1995, Gachet et al. 1997, Gratacap et al. 1998). Once activated, Ezrin, commonly localized in the cytoplasm in its inactive form, moves and tethers actin to the cortical membrane, thus promoting cytoskeleton reorganization and subsequent cell morphology alterations (Dard et al. 2004; Zhu et al. 2007; Di Cristofano et al. 2010; Yang et al. 2012; Zhao et al. 2011; Tan and Yang 2010). Beside phosphorylation, activation of ERM proteins also occurs after interaction with PIP2 (Gilmore and Burridge 1996, Hirao et al. 1996, Legg and Isacke 1998, Nakamura et al. 1999). The levels of PIP2 are regulated by means of the PI-specific Phospholipase C family of enzymes Berridge and Dupont (1994); Divecha and Irvine 1995; Hisatsune et al. 2005; Rhee 2001 Bunney and Katan 2011). The reduction of PIP2 levels induces ERM protein dissociation from the membrane, and PI-PLC activity is required for this chemokine-mediated event (Brown et al. 2011).

In mammals, thirteen PI-PLC enzymes were divided into six sub-families on the basis of amino acid sequence, domain structure and mechanism of recruitment (Suh et al. 2008). Regulatory domains specific to each subfamily determine the susceptibility to different mechanisms of activation (Suh et al. 2008). The distribution of PI-PLC enzymes seems strictly tissue specific (Suh et al. 2008; Lo Vasco 2010; Lo Vasco 2012), and probably each cell type owns a specific panel of expression, which differs under different stimulation conditions (Suh et al. 2008, Lo Vasco et al. 2012, Lo Vasco et al. 2007a, Lo Vasco et al. 2010b; Lo Vasco et al. 2010c, Lo Vasco et al. 2007b).

In order to investigate the PI-PLC isoforms specifically involved in the PIP2-mediated regulation of Ezrin activity, we silenced the transcript of *Vil2*, the gene which codifies for Ezrin (OMIM \*123900) by transfecting cultured human osteosarcoma cell lines, 143B and Hs888, with specific antisense silencing RNA (siRNA). We analysed the effects of Ezrin silencing upon the survival and morphology of the cells, upon the expression of *PLC* genes, which codify for PI-PLC enzymes, and upon the localization PI-PLC enzymes both in transfected and in control cells.

## Materials and methods

### Cell cultures

Two human osteosarcoma cell lines were analysed, 143B and Hs888, obtained from the American Type Culture Collection (ATCC, Rockville, MD, USA). Cells were cultured in Dulbecco's modified Eagle's medium (DMEM)

supplemented with 10–15 % foetal bovine serum (FBS), 1 mM sodium pyruvate, 100 U/mL of penicillin, and 100 mg/mL of streptomycin, at 37 °C and 5 % CO<sub>2</sub> according to ATCC recommendations.

Cells were grown at 37°C in a humidified 5 % CO<sub>2</sub> atmosphere in an incubator (Forma Scientific, USA). Confluent monolayer of cells was rinsed with phosphate-buffered saline (PBS) and 0.25 % Trypsin/EDTA (disodium ethylene diaminetetraacetate) was added for 3–5 min at 37°C, gently shaking the flask, then neutralised using growth medium. Cells were counted using a Neubauer haemocytometer (Weber Scientific International Ltd., Middlesex, UK). Cells were stored at –20 °C until use.

### Cell survival Trypan Blue test

Cells were diluted 1:1 in trypan blue (Sigma Aldrich, Dorset, UK) for survival quantification. A growth curve was designed counting the quantity of cells by cm<sup>2</sup> at different times. The number of viable cells was determined by adding 0.4 % Trypan blue staining to an equal volume of cell suspension. Viable cells were counted using a Neubauer haemocytometer and a phase contrast microscope. The following equation was used to calculate the total number of viable cells in 1 ml suspension: number of total viable cells in 1 ml (TC) =  $2 \times 10^4$  (=average of the cell counts from the squares of the haemocytometer grid, 2=dilution factor 1:1). The number of live cells was used to determine the growth rate and experiments were repeated three times.

### Cells transfection for Ezrin silencing

143B and Hs888 cells were transiently transfected with Ezrin silencing RNA using METAFECTENE SI+ (Biontech Laboratories GmbH, Munich, Germany). siRNA sequences targeting Ezrin and negative control siRNA, were designed and synthesized by Invitrogen (Life Technologies, Foster City, CA, USA). The siRNA was designed according to Ezrin complementary DNA (cDNA) sequence (EZR Gene ID: 7430). Briefly, 2.2 ml cell suspension were prepared in complete cell culture medium with a concentration of  $1.5 \cdot 10^5$  cells/ml of 143B cells and  $3 \cdot 10^5$  cells/ml of Hs888. Cells were seeded, in 6-well plates, shortly before the addition of the lipoplex, according to the manufacturer's instructions. Then cells were incubated under normal culture conditions (37 °C in CO<sub>2</sub>-containing atmosphere) until the lipoplex addition. Before transfection, 150 µl of 1× SI+buffer were mixed with 72 µl of METAFECTENE® SI+ and 540 pMol of RNA stock solution. The mixture was incubated for 15 min at room temperature and then added to the cells within one hour from seeding. Cells were incubated 72 h. Functional siRNA was measured by reverse transcription–polymerase chain reaction (RT-PCR) and western blot analysis 24, 48 and 72 h after

transfection. Contemporarily, a growth curve was designed counting cells using a Neubauer haemocytometer.

#### RNA extraction

Total RNA was extracted with a SV Total RNA Isolation System (Promega, Madison, WI, USA) according to the manufacturer's instructions. The cells were transferred to a microcentrifuge tube containing 175  $\mu\text{L}$  of SV RNA Lysis Buffer and were passed through a 20-gauge needle to shear the genomic DNA for 4 to 5 times. 350  $\mu\text{L}$  of SV Dilution Buffer was then added, mixed by inverting 4 times, and placed in a heating block at 70  $^{\circ}\text{C}$  for 3 min. The sample was centrifuged for 10 min at  $14,000 \times g$ . The lysate solution was transferred to a new microcentrifuge tube, 200  $\mu\text{L}$  of 95 % ethanol were added, and the mixture was transferred to a spin column assembly, and centrifuged at  $14,000 \times g$  for one minute. The liquid was discarded from the collection tube, 600  $\mu\text{L}$  of SV RNA Wash Solution was added to the column, centrifuged at  $14,000 \times g$  for one minute, and the collection tube was emptied. A DNase incubation mixture was prepared per sample by combining 40  $\mu\text{L}$  Yellow Core Buffer (Promega), 5  $\mu\text{L}$  0.09 M  $\text{MnCl}_2$  and 5  $\mu\text{L}$  of DNase I enzyme. The DNase incubation mixture was added directly to the membrane of the spin basket. The mixture was incubated for 15 min at room temperature, 200  $\mu\text{L}$  of SV DNase Stop Solution was added to the spin basket, and centrifuged at  $14,000 \times g$  for one minute. Next, 600  $\mu\text{L}$  of SV RNA Wash Solution was added and centrifuged at  $14,000 \times g$  for one minute. The collection tube was emptied, 250  $\mu\text{L}$  of SV RNA Wash Solution was added, and centrifuged at  $14,000 \times g$  for two minutes. The spin basket was transferred from the collection tube to an elution tube, 100  $\mu\text{L}$  of Nuclease-Free Water was added to the membrane and centrifuged at  $14,000 \times g$  for one minute. Finally, RNA was eluted into a sterile collection tube with RNase-free water. The procedure was carried out for each sample. The concentration and quality of the RNA obtained was monitored using a NanoDrop ND-1000 Spectrophotometer (Thermo Fisher Scientific, Inc. USA).

#### Reverse Transcriptase (RT)-Polymerase Chain Reaction (PCR)

RNA was reverse-transcribed into cDNA using High-Capacity cDNA Reverse Transcription Kit (Life Technologies, Foster City, CA, USA). Briefly, 2  $\mu\text{g}$  RNA were incubated with the master mix (2  $\mu\text{L}$  of  $10 \times$  Reverse Transcription Buffer, 0.8  $\mu\text{L}$  of  $25 \times$  dNTPs (100 mM), 2  $\mu\text{L}$  of  $10 \times$  random primers, 1  $\mu\text{L}$  of MultiScribe<sup>TM</sup> Reverse Transcriptase (50 U/ $\mu\text{L}$ ) and 3.2  $\mu\text{L}$  of DNase-free water). 10  $\mu\text{L}$  of diluted RNA was then added to make a final volume of 20  $\mu\text{L}$ . The RNA mix was then amplified for 10 min at 25  $^{\circ}\text{C}$ , 120 min at 37  $^{\circ}\text{C}$  and 5 min

at 85  $^{\circ}\text{C}$  in a Gene Amp<sup>®</sup> PCR System 9700 (Applied Biosystems) thermocycler.

The primer pairs (Bio Basic Inc, Amherst, New York, USA) are listed in Table 1. To amplify glyceraldehyde 3 phosphate dehydrogenase (GAPDH) (Bio Basic Inc, Amherst, New York, USA) the following primer pair was used: forward 5' -CGAGATCCCTCCAAAATCAA-3' reverse 5'-GTCTTCTGGGTGGCAGTGAT-3'. The specificity of the primers was verified by searching in the NCBI database for possible homology to cDNAs of unrelated proteins. RNA samples were also amplified by PCR without RT to exclude possible contamination.

Standard analytical PCR reaction was performed with GoTaq Master Mix (Promega). Each PCR tube contained the following reagents: 5X GoTaq buffer, 0.2  $\mu\text{M}$  forward primer, 0.2  $\mu\text{M}$  reverse primer, 0.2 mM dNTPs, 0.5 mM  $\text{MgCl}_2$ , 1.25 U GoTaq and 3.5  $\mu\text{L}$  of (about 35  $\mu\text{g}$ ) template cDNA at a 50  $\mu\text{L}$  final volume. Cycling conditions were performed with 95  $^{\circ}\text{C}$  initial denaturation step for 1 min was followed by 40 cycles consisting of 95  $^{\circ}\text{C}$  denaturation (30s), annealing (30 s) at the appropriate temperature for each primer pair and 72  $^{\circ}\text{C}$  extension (1 min) in Gene Amp<sup>®</sup> PCR System 9700 (Applied Biosystems) thermocycler. Amplified PCR products were visualized by 1.5 % TAE ethidium bromide-stained agarose gel electrophoresis for 1 h at 100 V using UV light transilluminator PC-assisted CCD camera UVB lamp (Vilber Lourmaret, France) was used for gel documentation. Gel electrophoresis of the amplification products revealed single DNA bands with nucleotide lengths as expected for all primer pairs.

#### Real-time PCR

The messenger RNA (mRNA) transcription of transfected 143B and Hs888 cells and normal controls was measured. Gene expression was analysed by real-time PCR using the 7500 Real-Time PCR instrument from Applied Biosystems<sup>TM</sup>. TaqMan<sup>®</sup> primers and probes for each gene, as well as the GAPDH reference gene, were obtained from Applied Biosystems<sup>TM</sup>. Briefly, total RNA was extracted with a SV Total RNA Isolation System (Promega, Madison, WI, USA) according to the manufacturer's instructions. The purity and quantity of RNA was assessed by NanoDrop ND-1,000 Spectrophotometer (Thermo Fisher Scientific, Inc. USA). The RNA was reverse transcribed into cDNA with High Capacity cDNA Reverse Transcription Kit (Life Technologies, Foster City, CA, USA).

Amplification products were detected using gene-specific primers and probes labelled with reporter dye FAM which yielded a predicted amplicons of 82, 84, 61, 78, 64, 93 and 62 base pairs respectively; glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was used as an internal standard, which yielded a predicted amplicon of 58 base pairs. Reaction

**Table 1** Primers' pairs for Polymerase Chain Reaction

PI-PLC $\beta$ 1 (PLCB1; OMIM *607120)	forward 5'-AGCTCTCAGAACAAGCCTCCAACA-3' reverse 5'-ATCATCGTCGTCGTCACACTTCCGT-3'
PI-PLC $\beta$ 2 (PLCB2; OMIM *604114)	forward 5'-AAGGTGAAGGCCTATCTGAGCCAA-3' reverse 5'-TTGGCAAACCTCCCAAAGCGAGT-3'
PI-PLC $\beta$ 3 (PLCB3; OMIM *600230)	forward 5'-TATCTTCTTGGACCTGCTGACCGT-3' reverse 5'-TGTGCCCTCATCTGTAGTTGGCTT-3'
PI-PLC $\beta$ 4 (PLCB4; OMIM *600810)	forward 5'-GCACAGCACACAAAGGAATGGTCA-3' reverse 5'-CGCATTTCCTTGCTTCCCTGTCA-3'
PI-PLC $\gamma$ 1 (PLCG1; OMIM *172420)	forward 5'-TCTACCTGGAGGACCCTGTGAA-3' reverse 5'-CCAGAAAGAGAGCGTAGTTCG-3'
PI-PLC $\gamma$ 2 (PLCG2; OMIM *600220)	forward 5'-AGTACATGCAGATGAATCACGC-3' reverse 5'-ACCTGAATCCTGATTTGACTGC-3'
PI-PLC $\delta$ 1 (PLCD1; OMIM *602142)	forward 5'-CTGAGCGTGTGGTTCCAGC-3' reverse 5'-CAGGCCCTCGGACTGGT-3'
PI-PLC $\delta$ 3 (PLCD3; OMIM *608795)	forward 5'-CCAGAACCCTCTCAGCATCCA-3' reverse 5'-GCCA TTGTTGAGCACGTAGTCAG-3'
PI-PLC $\delta$ 4 (PLCD4; OMIM *605939)	forward 5'-AGACACGTCCCAGTCTGGAACC-3' reverse 5'-CTGCTTCTCTTCTCCTCATATTC-3'
PI-PLC $\epsilon$ (PLCE; OMIM *608414)	forward 5'-GGGGCCACGGTCATCCAC-3' reverse 5'-GGGCCTTCATACCGTCATCCTC-3'
PI-PLC $\eta$ 1 (PLCH1; OMIM *612835)	forward 5'-CTTTGGTTTCGGTTCCTTGTGTGG-3' reverse 5'-GGATGCTTCTGT CAGTCCTCC-3'
PIPLC $\eta$ 2 (PLCH2; OMIM *612836)	forward 5'-GAAACTGGCCTCCAAACACTGCCCGCCG-3' reverse 5'-GTCTTGTGGAGATGCACGTGCCCTTGC-3'

mixtures for all gene expression assays contained: 5  $\mu$ l TaqMan<sup>®</sup> mastermix (2X; Applied Biosystems<sup>™</sup>), 0,5  $\mu$ l primer/probe mix specific for each analysed gene and 1  $\mu$ l PCR grade water. 3,5  $\mu$ l of cDNA (35 ng) were added. PCR reaction was carried out in triplicate on 96-well plate with 10  $\mu$ l per well using 1X TaqMan Master Mix. After 2 min incubation at 50 °C and 10 min at 95 °C, the reaction was carried out for 40 cycles at 95 °C for 15 s and 60 °C for 1 min. At the end of the reaction, the results were evaluated using the ABI PRISM 7500 software. The Ct (Cycle threshold) values for each set of three reactions were averaged for calculations. The  $2^{-\Delta\Delta C_t}$  method was used to calculate relative changes in gene expression.

#### Western blot

Western blot analyses were conducted 24 and 48 h from transfection and in normal controls. Cells were washed with cold PBS, then were processed in cell lysis buffer (50 mM Tris-HCl, 150 mM NaCl, 2 mM EDTA, 1 % NP-40, 2 mM sodium fluoride, 0.5 % sodium deoxycholate, and 0.1 % SDS) containing protease inhibitors. 50  $\mu$ g of protein was separated by 10 % sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred onto nitrocellulose membranes (Invitrogen, Life Technologies, CA, USA). The membranes were blocked in PBS with 5 % skim milk for 1 h

and incubated overnight with the primary antibodies. Finally, membranes were visualized by the addition of anti-mouse immunoglobulin G (Jackson ImmunoResearch, UK) and anti-rabbit immunoglobulin G (Jackson ImmunoResearch, UK) enhanced chemiluminescence. Expression of  $\beta$ -actin was used as an internal control to normalize results. The densities of the bands on the membrane were scanned and analysed with ImageJ software.

#### Immunofluorescence analysis of subcellular distribution of target molecules

Immunofluorescence detection of Ezrin, PI-PLC  $\epsilon$ , PI-PLC  $\beta$ 1, PI-PLC  $\gamma$ 2, PI-PLC  $\delta$ 4 expression was performed on coverslips cultured transfected and non-transfected cells. Cells were washed three times with PBS and fixed with 4 % paraformaldehyde (PFA) in phosphate buffer saline (PBS) for 10 min at 4 °C, followed by three washes with PBS. Cells were incubated with primary antibodies diluted in PBS for 1 h at room temperature. Cover-slips were then incubated with the specific secondary antibody Texas Red or fluorescein-conjugated for 1 h at room temperature. Cells were washed twice with 1X PBS 5 min, then counterstained with 4',6-diamidino-2-phenylindole (DAPI) fluorescent staining. The slides were visualized using an inverted microscope.

## Statistical analysis

For in vitro studies, differences were determined either with two-way repeated measures analysis of variance (ANOVA) with Bonferroni's multiple comparison test, and by student's one tailed *t*-test, using Prism 5.0a software (GraphPad Software, San Diego, CA, USA). A *p* value <0.05 was considered significant.

## Results

Silencing of Ezrin was validated by western blot, RT-PCR and gel electrophoresis, and real-time PCR of mRNA extracts and compared to non-targeting control siRNA (Fig. 1, I. Western blot assay showed no change in the expression of  $\beta$ -actin as internal control; the expression of Ezrin protein was significantly decreased in Ezrin siRNA transfected 143B cells compared to the transfected cells (Fig. 1, I b). Ezrin transcription was compared in cells transfected with Ezrin-silencing specific siRNA to control group, comprising untransfected cells and cells transfected with the carrier metefectamine. The transcription of Ezrin was suppressed in transfected 143B compared to the control group (not transfected and siRNA transfected), which correctly expressed Ezrin mRNA. The mRNA expression level of Ezrin in transfected cells was significantly reduced with respect to untreated cells ( $p < 0.001$ ) (Fig. 1, a).

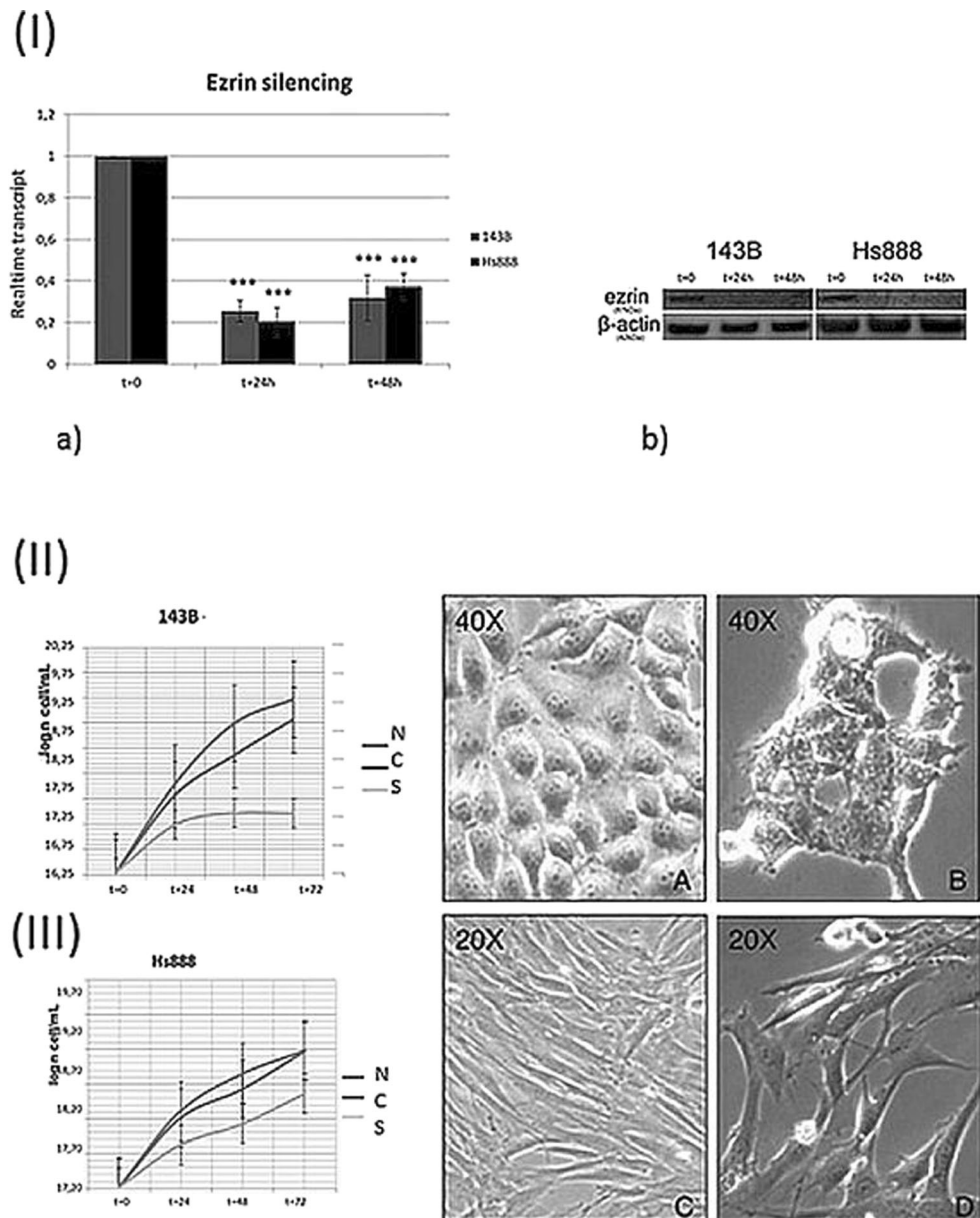
In 143B Cells, survival Trypan Blue test indicated decrease of the growth rate of Ezrin siRNA-transfected cells (Fig. 1, II) with respect to control cells ( $p < 0.5$ ). The growth rate was reduced in Ezrin siRNA transfected cells (S) in the 0–72 h interval with respect to untransfected control cells (N) and in metefectamine transfected control cells (C). The cell growth was reduced in 143B cells in which Ezrin was silenced with respect to controls since 3–6 h from silencing. The growth rate of S cells was reduced after 24 h from Ezrin silencing (Fig. 1, II), and remained constant during the remaining 24–72 h interval. The growth rate of N and C cells had a significant exponential progression after 24 h. In 143B transfected cells the expression of *PLCG2* gene increased about 40 % after 24 h from the transfection and about 25 % after 48 h; the expression of *PLCB1* decreased about 55 % (Fig. 2). The expression of *PLCE* was moderately (about 15 %) reduced after 24 h from the silencing and moderately increased after 48 h (Fig. 2). *PLCB1* was expressed in control cells in low concentration. *PLCD4*, undetected in 143B, increased about two folds after 24 h from Ezrin silencing (Fig. 2). There was a statistically significant difference in the mRNA expression levels of *PLCB1*, which was decreased both after 24 ( $p < 0.0005$ ) and 48 ( $p < 0.0125$ ) hours from Ezrin silencing. The expression of GAPDH mRNA in the considered interval did not differ in a statistically significant manner, as expected.

Immunofluorescence microscopy showed moderate signal intensity of Ezrin localized in the cytoplasm, with membrane signal enhancement in 143B cell controls. PI-PLC  $\epsilon$  was also localized in the cytoplasm, with weak signal intensity. A focal cytoplasmic co-localization of Ezrin and PI-PLC  $\epsilon$  was observed (Fig. 3). In the cytoplasm, PI-PLC  $\beta 1$  and PI-PLC  $\gamma 2$  were respectively strongly and weakly detected (Fig. 4). In 143B cells transfected with Ezrin siRNA, irregular outline of the plasma membrane was associated with reduced intercellular adhesion and micro-vacuolization of the cytoplasm was also observed at optic microscope (Fig. 1, II A and B). Significant reduction of the signal intensity of PI-PLC  $\beta 1$  in the cytoplasm was also detected (Fig. 4). For PI-PLC  $\gamma 2$  stronger cytoplasmic signal with membrane staining reinforcement were observed (Fig. 4). Moderate increase and of PI-PLC  $\epsilon$  signal intensity, localized in cytoplasm was observed (Fig. 3).

In Hs888 Cells, survival Trypan Blue test indicated that the growth rate of the Ezrin siRNA-treated cells decreased in a time-dependent manner (Fig. 1) with respect to control cells ( $p < 0.5$ ). The growth rate was reduced in Ezrin siRNA transfected cells (S) in the 0–24 h interval with respect to untransfected control cells (N) and in metefectamine transfected control cells (C) (Fig. 1, III).

The expression of *PLCE* was comparable to the untreated cells after 24 h, and increased about 80 % after 48 h (Fig. 2); *PLCG2* was moderately increased; *PLCB1*, weakly expressed in untreated controls, significantly increased (from 12 to 16 folds) in the 24–48 h interval (Fig. 2); *PLCD4* increased after 24 h from silencing (Fig. 2). A statistically significant difference in the mRNA expression levels of *PLCE* ( $p < 0.005$ ) was calculated comparing Ezrin siRNA transfected Hs888 and control cells (both untransfected and metefectamine transfected cells). After 48 h from Ezrin silencing a statistically significant difference of mRNA expression levels of *PLCB1* both after 24 ( $p < 0.0005$ ) and 48 ( $p < 0.0125$ ) hours from transfection was also calculated. The expression of GAPDH mRNA in the considered interval did not differ in a statistically significant manner, as expected. Immunofluorescence microscopy showed focal cytoplasmic co-localization of Ezrin and PI-PLC  $\epsilon$  in Hs888 control cells (Fig. 3). After Ezrin silencing, the quantitative reduction of cellular elements was accompanied by substantially well-preserved structure (Fig. 1, c and d). Ezrin was mildly localized in the cytoplasm. PI-PLC  $\epsilon$  was weakly localized in the cytoplasm (Fig. 3). PI-PLC  $\beta 1$  was localized in the cytoplasm in control cells, and Ezrin silencing induced a significant increase of the signal intensity (Fig. 4). Moderate signal intensity for PI-PLC  $\gamma 2$  was detected in the cytoplasm, with strong perinuclear enhancement (Fig. 4). After Ezrin silencing, a slight increase of PI-PLC  $\epsilon$  signal intensity was observed, mainly localized in the cytoplasm (Fig. 3).

**Fig. 1** Effectiveness of Ezrin silencing. **a** Histogram of mRNA transcript concentrations after 0, 24 and 48 h from Ezrin silencing in 143B (gray) and Hs888 (black) cell lines. **b** Gel electrophoresis from Western blot of Ezrin protein in 143B and Hs888 cell lines compared to actin protein loading control. Growth curve after Ezrin silencing (left) effect of Ezrin siRNA on cell morphology (right) in 143B cells: the growth of silenced cells is significantly slowed with respect to untreated cells ( $p < 0,5$ ). Bar errors are indicated. N= untransfected control 143B cells; C=metafektamine transfected control 143B cells; Ezrin siRNA transfected 143B cells. **II a** and **b** - morphological changes in 143B cells (40X, contrast-phase microscopy). Irregular outline of the plasma membrane, reduced intercellular adhesion and cytoplasm micro-vacuolization. Growth curve after Ezrin silencing (left) effect of Ezrin siRNA on cell morphology (right) in Hs888 cells: the growth of silenced cells is slowed with respect to untreated cells. Bar errors are indicated. N= untransfected control Hs888 cells; C=metafektamine transfected control Hs888 cells; Ezrin siRNA transfected Hs888 cells. **III c** and **d** - morphological changes in Hs888 cells (20, contrast-phase microscopy). Quantitative reduction of cells displaying substantially well-preserved structure



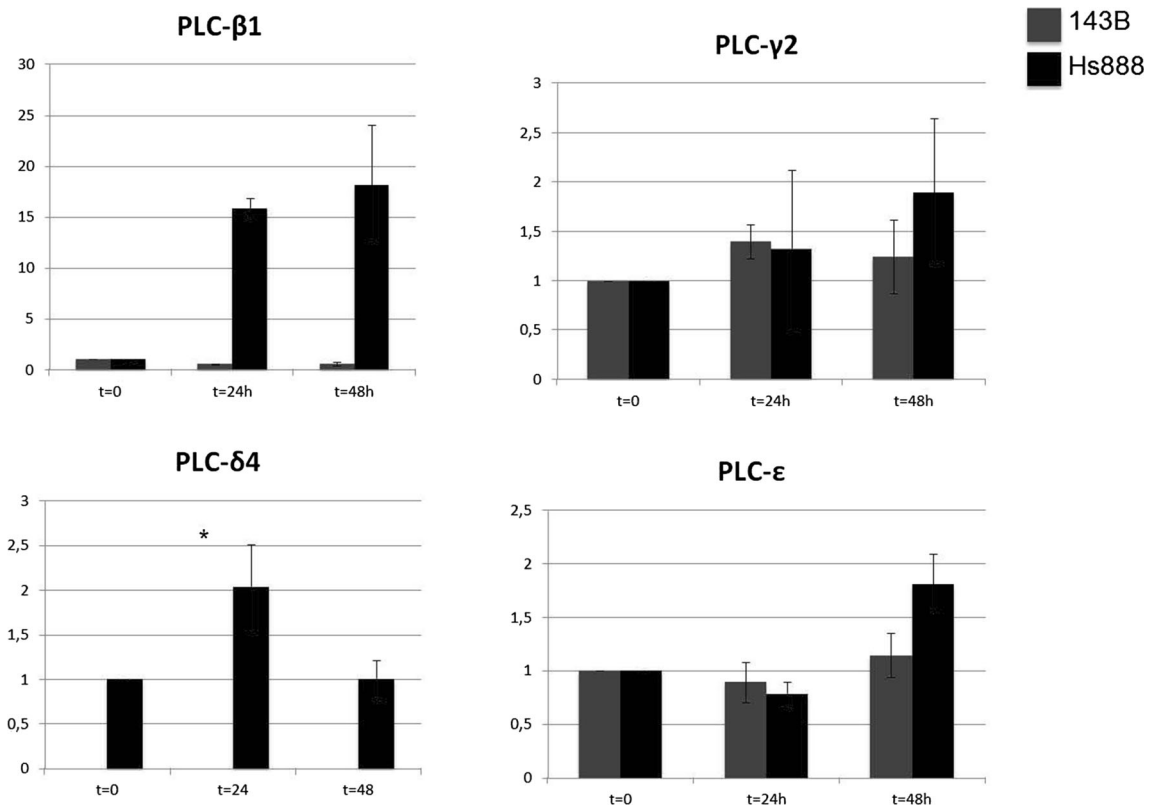
## Discussion

The present results in 143B cells and Hs888 are not comparable, probably due to the different origins of the cells. 143B thymidine kinase negative human osteosarcoma cells, originating from highly aggressive primary tumour, develop osteolytic tumours (Kaminski et al. 2003). Hs888 cells derived from lung metastasis of osteosarcoma. Ezrin silencing induced cell growth rate reduction more marked in 143B than in Hs888 cells.

Ezrin silencing reduced the growth rate of cells. That was more marked in 143B line, as well as morphological changes, probably related to the cytoskeleton-linker activity of Ezrin, and microvacuolization of the cytoplasm. The quantitative

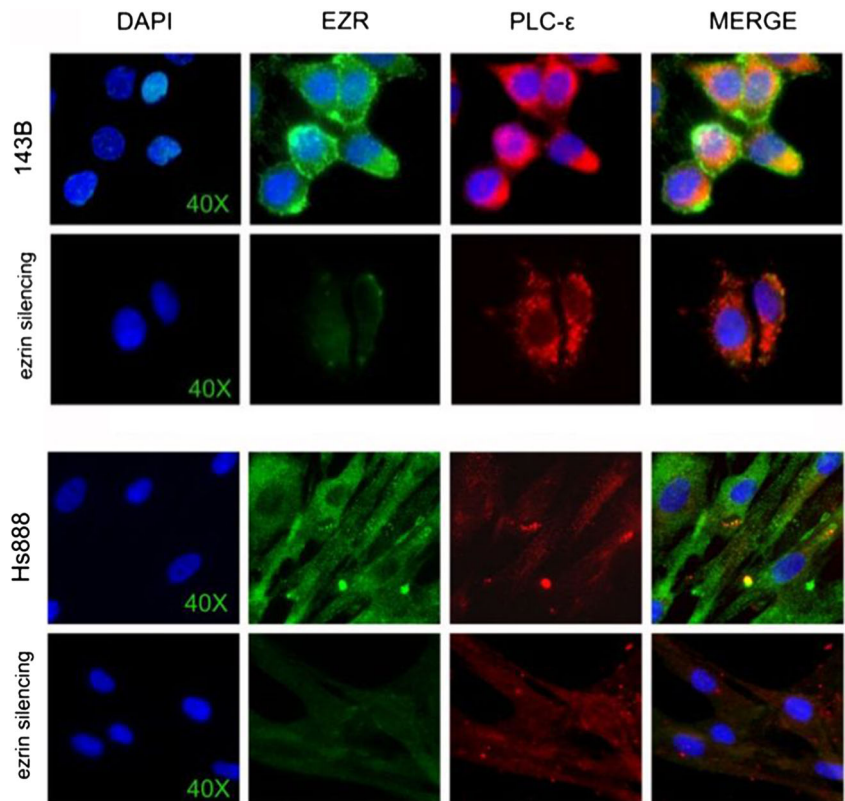
changes of PI-PLC enzymes occurring after 24 h from Ezrin silencing might indicate that lack of Ezrin affects the regulation of the PI signal transduction pathway. The changes of the quantity and localization of PI-PLC  $\gamma 2$  corroborate our previous hypothesis that this isoform might play an important role in osteosarcoma.

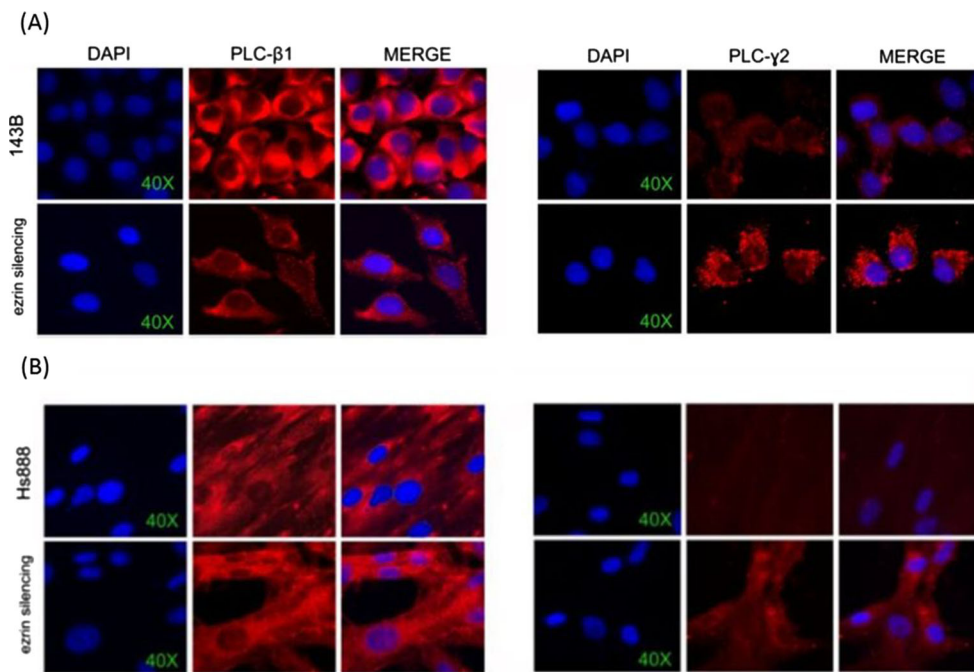
The differences of intracellular PI-PLC enzymes accorded to the expression of the corresponding *PLC* genes (Fig. 2). In both cell lines, basal PI-PLC  $\beta 1$  is mildly expressed (2–4.5 ng/ml), according to previous observations (Lo Vasco et al. 2014). PI-PLC  $\beta 1$  is selectively increased during myoblast and adipocyte differentiation (Faenza et al. 2004, O'Carroll et al. 2009), and might be altered in breast cancer (Molinari et al. 2012, Abalsamo et al. 2012). Evidences



**Fig. 2** Real-time results after Ezrin silencing. Histograms of the transcript concentrations of PLC genes after 0, 24 and 48 h from Ezrin silencing in 143B (gray) and Hs888 (black) cell lines

**Fig. 3** Partial co-localization of Ezrin and PI-PLC ε Fluorescence immunocytochemistry of Ezrin (green) and PI-PLC ε (red) in 143B (upper) and Hs888 (lower) cell lines. Diaminophenyl indole (DAPI, blue) counterstain for nuclei (60X)





**Fig. 4** Immunofluorescence analyses. **a** Localization of PI-PLC  $\beta 1$  and PI-PLC  $\gamma 2$  in 143B cell line. **LEFT.** Fluorescence immunocytochemistry of PI-PLC  $\beta 1$  (red) in 143B (upper) and in 143B cells after Ezrin silencing (lower). Diaminophenyl indole (DAPI, blue) counterstain for nuclei (60X). **RIGHT.** Fluorescence immunocytochemistry of PI-PLC  $\gamma 2$  (red) in 143B (upper) and in 143B cells after Ezrin silencing (lower). Diaminophenyl indole (DAPI, blue) counterstain for nuclei (60X). **b**

Localization of PI-PLC  $\beta 1$  and PI-PLC  $\gamma 2$  in Hs888 cell line **LEFT.** Fluorescence immunocytochemistry of PI-PLC  $\beta 1$  (red) in Hs888 (upper) and in Hs888 cells after Ezrin silencing (lower). Diaminophenyl indole (DAPI, blue) counterstain for nuclei (60X). **RIGHT.** Fluorescence immunocytochemistry of PI-PLC  $\gamma 2$  (red) in Hs888 (upper) and in Hs888 cells after Ezrin silencing (lower). Diaminophenyl indole (DAPI, blue) counterstain for nuclei (60X)

suggested that deletion of *PLCB1* favours cancer progression in the myeloid lineage (Lo Vasco et al. 2004, Kaminskis et al. 2005) and is involved in differentiation. Therefore, this isoform might contrast cancer progression. In Hs888, Ezrin silencing induced a very significant increase of *PLCB1* transcription (Fig. 2) and of cytoplasmic PI-PLC  $\beta 1$  (Fig. 4). The hypothesis that, in the metastatic Hs888 cell line, the expression of PI-PLC  $\beta 1$  might be under the control of Ezrin will require studies in order to investigate whether this mechanism occurs directly or involves further signalling molecules.

Ezrin silencing induced *PLCG2* transcription and cytoplasmic PI-PLC  $\gamma 2$  increase. The PI-PLC  $\gamma$  enzymes, detected at higher level in tumour than in normal tissues (Arteaga et al. 1991, Noh et al. 1995), are characterized by a unique region comprising two tandem SH2 and one SH3 domains (Katan and Williams 1997, Bunney and Katan 2011). Ezrin can interact with the SH2 domain, and might act as negative regulator of PI-PLC  $\gamma 2$ . The up-regulation of PI-PLC  $\gamma 2$  following Ezrin silencing might accord to the osteolytic nature of 143B cells (Kaminski et al. 2003). In fact, PI-PLC  $\gamma 2$  is involved in actin cytoskeleton reorganization (Cremasco V. 2999), and, in osteoclasts, is required for early phase differentiation (Kertész et al. 2012), adhesion, migration, bone resorption (Epple et al. 2008), regulation of the Proto-oncogene Src activation and membrane localization Mao

et al. (2006) PI-PLC  $\gamma 2$  was also indicated as a critical regulator in bone and immune cells during autoimmune inflammation (Faccio and Cremasco 2010). On the other hand, PI-PLC  $\gamma 2$ , usually absent in Hs888 cells, was detected in low concentration after Ezrin silencing. That suggests that PI-PLC  $\gamma 2$  might crucially network Ezrin. That observation might deserve great attention, as increasing evidences suggest that PI-PLC  $\gamma$  isoforms play key roles in cell migration and invasion (Lattanzio et al. 2013), as well as in cell growth and survival Mirabello et al. (2009a).

PI-PLC  $\delta 4$ , exclusively expressed in Hs888 cell line, accordingly to previous findings (Lo Vasco et al. 2013a), was up-regulated after Ezrin silencing. PI-PLC  $\delta$  enzymes, the most primitive and evolutionary conserved, are very sensitive to calcium and might play a key role in cell proliferation (Suh et al. 2008; Liu et al. 1996; Fukami et al. 2000). In fact, PI-PLC  $\delta 4$  is expressed more abundantly in high-rate proliferating cells (Santi et al. 2003, Ochocka and Pawelczyk 2003) and was associated to astrocytoma (Lo Vasco et al. 2007a, 2010a), and breast cancer (Leung et al. 2004). In the present experiments, the increase of *PLCD4* transcription might be related to the induced reduction of Ezrin, although the mechanism and the contemporary up-regulation of *PLCB1* will require further studies.

In both cell lines, the transcription of *PLCE* was affected by Ezrin silencing in a time-related manner. 24 h after Ezrin



silencing *PLCE* transcription was reduced and after 48 h increased, more markedly in Hs888 than in 143B cells. PI-PLC  $\epsilon$  enzyme is thought to play an important role in carcinogenesis. However, the mechanism of action is not completely understood, and controversial data were reported. A number of evidences indicate that PI-PLC  $\epsilon$  might favour cancer initiation and/or progression, as in bladder (Cheng et al. 2011; Ou et al. 2010), murine skin (Bai et al. 2004, Oka 2010, Li et al. 2009), head and neck cancers (Bourguignon et al. 2006). The rs 2274223 polymorphism was significantly associated to increased risk of squamous cell carcinoma and gastric cancer (Hao 2013). By contrast, tumour suppressive role for PI-PLC  $\epsilon$  was recently suggested in Ras-triggered cancers (Martins et al. 2014). Our present results suggest the existence of a relationship between Ezrin and PI-PLC  $\epsilon$ , corroborated by microscopy observations detecting focal and partial cytoplasmic colocalization (Figure 3).

Resuming, in the analysed osteosarcoma cell lines, Ezrin silencing reduced the growth rate and induced morphology changes, corroborating the hypothesis that it is involved in cell growth/survival and in cytoskeleton organization. The tight regulation of membrane PIP<sub>2</sub> levels might represent a mechanism of control of Ezrin activity, directly under the control of the PI signal transduction system by means of activated PI-PLC enzymes. Both Ezrin and PI-PLC enzymes bind PIP<sub>2</sub> in a competitive manner or, probably, in a more complex mechanism. Ezrin reduction or absence, induced by silencing the transcript of *Vil2*, increased the available PIP<sub>2</sub> that might explain the observed re-modulation of the PI-PLC enzymes panel. That suggests a possible connection in terms of reciprocal regulation that will require further studies. The present data might also partially contribute to explain the role of the PI-PLC family in the cytoskeleton organization, which might be related to the actin cross-linker role of Ezrin. Further studies, addressed to elucidate the relationship between Ezrin and cell line-specific PI-PLC enzymes, might help to identify the crosstalk among the molecules, opening the way to novel insights in the progression of the disease, with special regard to metastatic spread inputs, and, as far as one can see, to novel therapeutic strategies.

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