Fig. 1. Selective binding of JIP-1 to the MAP kinase INK and the MAP kinase kinase MKK7. (A) Epitope-tagged JIP-1 (T7-Tag) was expressed in cells with the HA-tagged MAP kinases ERK2, p38α, JNK1, and JNK2 (15, 16). The MAP kinases were immunoprecipitated with an antibody to HA. The presence of JIP-1 in the immunoprecipitates (IP) was detected on immunoblots probed with an antibody to T7-Tag. The amount of JIP-1 and MAP kinases in the cell lysates was examined by protein immunoblot analysis. (B) JIP-1 was expressed in cells as a GST fusion protein together with epitopetagged MEK1, MKK3, MKK4, MKK6, or MKK7 (15, 16). JIP-1 was precipitated from cell lysates with glutathione-agarose, and the MAPKKs present in the pellet were detected by protein immunoblot analysis. The amount of the MAPKKs in the cell lysates was examined by protein immunoblot analysis. (C) Epitope-tagged JIP-1 (T7-Tag) was expressed in cells with Flagtagged MKK4 or MKK7 (15, 16). The presence of JIP-1 in Flag IP was detected by protein immunoblot analysis with an antibody to T7-Tag. The amount of the MAPKKs in the cell

🗲 JIP-1 JIP-1 Lysate MAP Lysate Kinase JNK2 Control JNK1 ERK2 p380 в JIP-1 Pellet Lysate MEK1 MKK3 MKK6 MKK7 MKK4 MKK7 MKK4 JIP-1 ◄ JIP-1 IP JIP-1 ► JIP-1 Lysate MKK7 🕨 Lysate — MKK4

Experimental approach to protein-protein interaction



of tagged proteins



Differenza? BCMA - 2011 - 04 Fig. 1. Selective binding of JIP-1 to the MAP kinase JNK and the MAP kinase kinase MKK7. (A) Epitope-tagged JIP-1 (T7-Tag) was expressed in cells with the HA-tagged MAP kinases ERK2, p38 α , JNK1, and JNK2 (15, 16). The MAP kinases were immunoprecipitated with an antibody to HA. The presence of JIP-1 in the immunoprecipitates (IP) was detected on immunoblots probed with an antibody to T7-Tag.

JIP-1 (endogena)



Experimental approach to protein-protein interaction



PULL-DOWN



• metto in agitazione (rotazione) a 4°C 2h o O/N affinché la proteina "esca", (fusa con la glutatione transferasi) vada in contatto con tutte le proteine presenti nell'estratto



• centrifugo a bassa velocità (3000 rpm, 1 min, 4°C). Sul fondo della provetta si depositano:sferette di sepharoseglutatione--glutationetransferasi-proteina esca; in soluzione restano:proteine non legate alla proteina "esca"

•procedo come per l'immunoprecipitazione



Fig. 1. Selective binding of JIP-1 to the MAP kinase INK and the MAP kinase kinase MKK7. (A) Epitope-tagged JIP-1 (T7-Tag) was expressed in cells with the HA-tagged MAP kinases ERK2, p38α, JNK1, and JNK2 (15, 16). The MAP kinases were immunoprecipitated with an antibody to HA. The presence of JIP-1 in the immunoprecipitates (IP) was detected on immunoblots probed with an antibody to T7-Tag. The amount of JIP-1 and MAP kinases in the cell lysates was examined by protein immunoblot analysis. (B) JIP-1 was expressed in cells as a GST fusion protein together with epitopetagged MEK1, MKK3, MKK4, MKK6, or MKK7 (15, 16). JIP-1 was precipitated from cell lysates with glutathione-agarose, and the MAPKKs present in the pellet were detected by protein immunoblot analysis. The amount of the MAPKKs in the cell lysates was examined by protein immunoblot analysis. (C) Epitope-tagged JIP-1 (T7-Tag) was expressed in cells with Flagtagged MKK4 or MKK7 (15, 16). The presence of JIP-1 in Flag IP was detected by protein immunoblot analysis with an antibody to T7-Tag. The amount of the MAPKKs in the cell

🗲 JIP-1 JIP-1 Lysate MAP Lysate Kinase JNK2 Control JNK1 ERK2 p380 в JIP-1 Pellet Lysate MEK1 MKK3 MKK6 MKK7 MKK4 MKK7 MKK4 JIP-1 ◄ JIP-1 IP JIP-1 ► JIP-1 Lysate MKK7 🕨 Lysate — MKK4







IP

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(B) JIP-1 was expressed in cells as a <u>GST fusion protein</u> together with epitopetagged MEK1, MKK3, MKK4, MKK6, or MKK7 (15, 16). JIP-1 was precipitated from cell lysates with <u>glutathione-agarose</u>, and the MAPKKs present in the pellet were detected by protein immunoblot analysis. The amount of the MAPKKs in the cell lysates was examined by protein immunoblot analysis. (C) Epitope-tagged JIP-1 (T7-Tag) was expressed in cells with Flagtagged MKK4 or MKK7 (15, 16). The presence of JIP-1 in Flag IP was detected by protein immunoblot analysis with an antibody to T7-Tag. The amount of the MAPKKs in the cell hysates was examined by protein immunoblot







MAPK



MAP3K





Fig. 2. Selective binding of JIP-1 to the mixedlineage group of MAPKKKs. (A) JIP-1 was expressed in cells as a GST fusion protein together with the epitope-tagged MAPKKKs (15, 16). The presence of MAPKKKs in glutathione-agarose precipitates (pellet) was assayed by protein immunoblot analysis. The amount of the MAPKKKs in the cell lysates was examined by protein immunoblot analysis. (B) Epitopetagged JIP-1 was coexpressed in cells with epitope-tagged MLK3 or DLK (15, 16). The presence of JIP-1 in the MLK3 and DLK immunoprecipitates (IP) was examined by protein immunoblot analysis. The amount of the MAPKKKs in the cell lysates was examined by protein immunoblot analysis.

B: immunoprecipitation

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MAP3K



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Mitogen-activated protein kinase modules. The MAPK module consists of an MKKK, an MKK, and a MAPK. MKKKs respond to a variety of extracellular signals, including growth factors differentiation factors and stress. The activated MKKKs can then activate one or several MKKs. In contrast, the MKKs are relatively specific for their target MAPKs. Once activated, MAPKs can then phosphorylate transcription factors (for example ATF-2, Chop, c-Jun, c-Myc, DPC4, Elk-1, Ets1, Max, MEF2C, NFAT4, Sap1a, STATs, Tal, p53), other kinases (MAPKAP kinase, p90^{rsk} S6 kinase), upstream regulators (EGF receptor, son of sevenless [Sos] Ras exchange factor), and other regulatory enzymes such as phospholipase A2. These downstream targets then control cellular responses including growth, differentiation, and apoptosis [1**,2,3].

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Each of these MAPK cascade member interacts with JIP-1but is it a competitive or a cooperative interaction?



Binding of JIP-1 to MKK7, MLK and HPK1 independently of JNK

Fig. 3. Binding of JIP-1 to MKK7, MLK, and HPK1 independently of JNK. (**A**) The binding of JIP-1 to HPK1, MLK3, DLK, and MKK7 is independent of JNK. GST (Control), GST-tagged JIP-1, and a GST-tagged JIP-1 mutant with an inframe deletion of the



JNK binding domain (JIP-1 Δ JBD) were coexpressed in cells together with HPK1 and epitope-tagged JNK1, MKK7, MLK3, and DLK (15, 16). The presence of kinases in the reduced glutathione-agarose precipitates (pellets) and cell lysates was examined by protein immunoblot analysis.



(B) Deletion analysis of the binding of JIP-1 to JNK1, MKK7, MLK3, and DLK. JIP-1 was expressed in cells as a GST fusion protein together with HPK1 or epitope-tagged JNK1, MKK7, MLK3, and DLK (15, 16). The presence of these kinases in glutathione-agarose precipitates was examined by protein immunoblot analysis. (C) Kinase assay: JIP1 enhances the activation of JNK by MKK7 and MLK3



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A Cytoplasmic Inhibitor of the JNK Signal Transduction Pathway

Martin Dickens, Jeffrey S. Rogers, Julie Cavanagh, Art Raitano, Zhengui Xia, Jocelyn R. Halpern, Michael E. Greenberg, Charles L. Sawyers, Roger J. Davis*

The c-Jun amino-terminal kinase (JNK) is a member of the stress-activated group of mitogen-activated protein (MAP) kinases that are implicated in the control of cell growth. A murine cytoplasmic protein that binds specifically to JNK [the JNK interacting protein-1 (JIP-1)] was characterized and cloned. JIP-1 caused cytoplasmic retention of JNK and inhibition of JNK-regulated gene expression. In addition, JIP-1 suppressed the effects of the JNK signaling pathway on cellular proliferation, including transformation by the *Bcr-Abl* oncogene. This analysis identifies JIP-1 as a specific inhibitor of the JNK signal transduction pathway and establishes protein targeting as a mechanism that regulates signaling by stress-activated MAP kinases.

Overexpression of JIP1 inhibits JNK traslocation to the nucleus and in vivo activity



Experimental approach to protein-protein interaction

Two-hybrid system



Y2H systems exploit the modular nature of eukaryotic transcription factors, which consist of a sequence-specific DNA-binding domain (DBD) and an RNA Pol II-recruiting, transcription activation domain (AD).





Two-hybrid system: two types of hybrids



Two-hybrid system: two types of hybrids



Pairs of bait and prey fusion proteins are coexpressed in yeast cells.



Pairs of bait and prey fusion proteins are coexpressed in yeast cells.



When pairs of interacting bait and prey fusion proteins are coexpressed in a yeast cell, the interacting fusion proteins are able to activate transcription of the reporter genes.



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Yeast Two-Hybrid System

Yeast two-hybrid system design. Library-derived, transcription-activating prey fusion proteins that interact with the DNA-binding bait fusion protein activate the expression of reporter genes.



a known protein of interest is fused to the DNA-BD of the yeast GAL4 transcription factor to create a "bait" protein. Interacting partner proteins, often derived from a library, are expressed as fusions to the AD of yeast GAL4, to create "prey" proteins

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Four reporters give high stringency. Interacting bait and prey fusion proteins drive the expression of four different reporters from three different GAL4-responsive promoters (M1, G1, and G2), which are stably integrated in the genome of the reporter strain, Y2HGold. Aureobasidin A (AbA) resistance and the two auxotrophic reporters for histidine and adenine biosynthesis confer growth selection in the presence of AbA and on histidine- and adenine-deficient media, while the α -galactosidase reporter produces blue colonies in the presence of X-alpha-Gal.



Figure 3. The Mate & Plate Protocol. To screen a Matchmaker Mate & Plate Library, an aliquot of the library in the Y187 strain (*MAT*α) is simply mixed with a bait-expressing culture of the Y2HGold strain (*MATa*). The mated strains are cultured overnight and plated on selective agar medium containing AbA.

X- α -Gal detects secreted α -galactosidase activity following a GAL4-based two-hybrid interactions in Y2HGold yeast patches and colonies.

Rescuing plasmid DNA from yeast (Saccharomyces cerevisiae).positive clones



The protocol uses Zymolyase to efficiently digest the cell walls of the yeast and generate spheroplasts, which are then subjected to SDS/alkaline lysis. A spin column purifies the plasmid DNA, which can then be analysed directly or used to transform E. coli for propagation and scaled-up plasmid preparations, or used as a template for PCR.

Analysis of positive candidate clones.



Lane 2: No template control. Lanes 3-17: randomly selected colonies containing candidate clones Lanes M1: 1 kb ladder. Lane M2: 100 bp ladder.

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Performing two-hybrid screens in yeast is a powerful method of identifying novel protein binding relationships that involve a particular protein of interest. However, the conformation of a mammalian protein expressed in yeast may be quite different from its normal conformation in a mammalian cells. Thus, it is important to perform a two-hybrid assay in mammalian cells to confirm that the suspected interactions also take place when the proteins are folded and modified as they would be in their native environment. The mammalian assay often reflects interactions between mammalian proteins with greater authenticity than can be achieved in yeast.



The mammalian two-hybrid principle. The bait protein is fused to the DNA binding domain of yeast GAL4 and the prey protein is fused to the transcriptional activation domain of HSV VP16. If the two proteins interact at the PGAL4-E1b promoter (GAL promoter), SEAP is secreted into the growth medium.



secreted alkaline phosphatase (SEAP), which is readily detected in the culture medium (chemiluminescence).