

Physiological regulation by protein dephosphorylation

Phosphorylation of tyrosine residues in proteins is a major mechanism for regulation of protein structure and function, and directly affects cellular function. Tyrosine phosphorylation is a reversible process, and is controlled by the opposing activities of two major and entirely distinct families of enzymes - protein tyrosine kinases and protein tyrosine phosphatases (PTPs).

Our long-term goal is to clarify the roles of PTPs in regulating specific physiological processes at the levels of individual molecules, cells, and whole animals.

Our group studies two related PTPs - PTP Epsilon (PTP ϵ) and PTP Alpha (PTP α). The four protein forms of PTP ϵ are all produced from the single PTP ϵ gene through steps regulated at the levels of transcription, translation, and post-translational proteolytic processing. All forms of PTP ϵ share the same catalytic domains, but have unique amino termini that determine their individual subcellular locations and physiological roles.

We have shown that the receptor-type form of PTP ϵ (RPTP ϵ) is an assists Neu-mediated **mammary tumorigenesis**

in mice. RPTP ϵ is specifically expressed in this type of mammary tumors, and expression of RPTP ϵ in transgenic mice causes massive mammary hyperplasia and associated tumorigenesis. In agreement, mammary tumors induced by Neu in mice genetically lacking PTP ϵ grow slower in culture and produce smaller tumors when implanted in nude mice than do PTP ϵ -expressing tumors. At the molecular level, the Neu kinase phosphorylates RPTP ϵ , which then specifically dephosphorylates Src and activates it. Src is a well-known collaborator of Neu in mammary cell transformation. In the absence of RPTP ϵ this process is less efficient, Src is less activated, and the resulting tumor cells appear less transformed.

PTP ϵ also dephosphorylates the adaptor protein Shc, thereby sending an anti-mitogenic signal and illustrating that PTP ϵ plays roles that are context-specific (as do many other phosphatases and kinases). In Neu-transformed mammary tumor cells, this signal would counter the pro-mitogenic effect of PTP ϵ via activation of Src, and would create a signaling "traffic jam". We have shown that in this particular case, the dominant kinase Neu physically binds Shc and phosphorylates it,

thereby preventing PTP ϵ from gaining access to Shc. Neu therefore introduces order into its downstream signaling events and ensures that PTP ϵ plays a coherent role that is free from internal contradiction.

A second, distinct isoform of PTP ϵ , cyt-PTP ϵ , is predominantly cytosolic. We have shown that cyt-PTP ϵ is critical for **maintaining proper bone mass** by regulating the adhesion and activity of osteoclasts, the specialized cells that degrade bone *in vivo*. Cyt-PTP ϵ is required for proper organization and function of podosomes, the adhesion structures of osteoclasts. At the molecular level cyt-PTP ϵ participates in activating the Src kinase downstream of integrin receptor molecules. Accordingly, female mice lacking PTP ϵ exhibit increased bone mass.

Previous studies in our lab showed that cyt-PTP ϵ also affects **Schwann cells, which myelinate axons in the peripheral nervous system**. Using substrate-trapping technology we established that the voltage gated potassium channels Kv1.5 and Kv2.1 are substrates of PTP ϵ , and that dephosphorylation of Kv2.1 predominantly at its Y124 by PTP ϵ counters phosphorylation and upregulation of Kv2.1 by the Src and Fyn tyrosine kinases. These findings correlate with severe transient hypomyelination observed in sciatic nerves of newborn mice lacking PTP ϵ .

Interestingly, the closely-related PTP α performs similar roles in Schwann cells vis-à-vis Kv channels, and affects myelination in the peripheral nervous system even more than cyt-PTP ϵ . The molecular details of this activity, however, differ somewhat from those

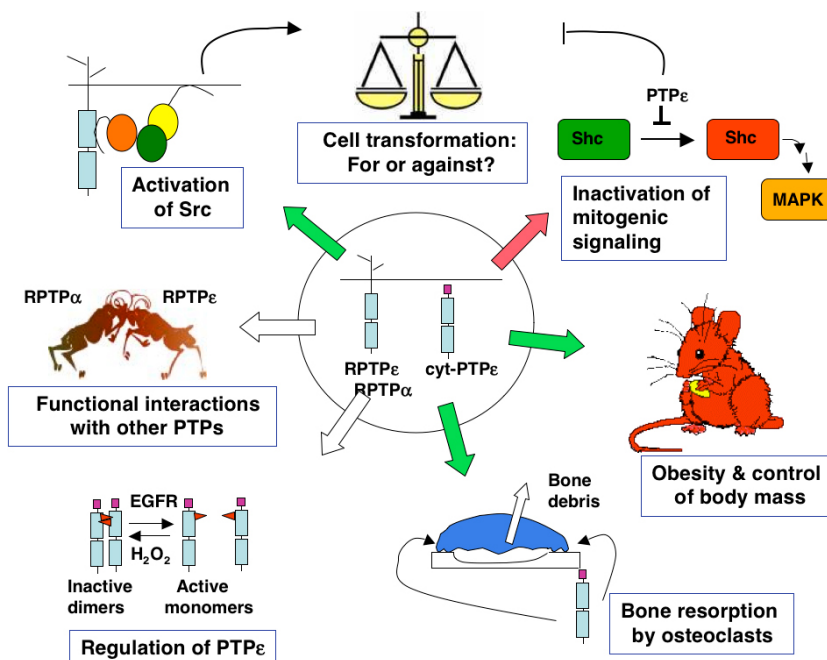
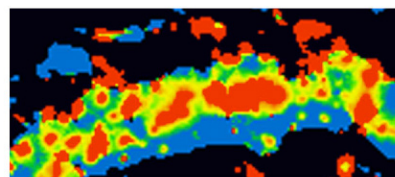
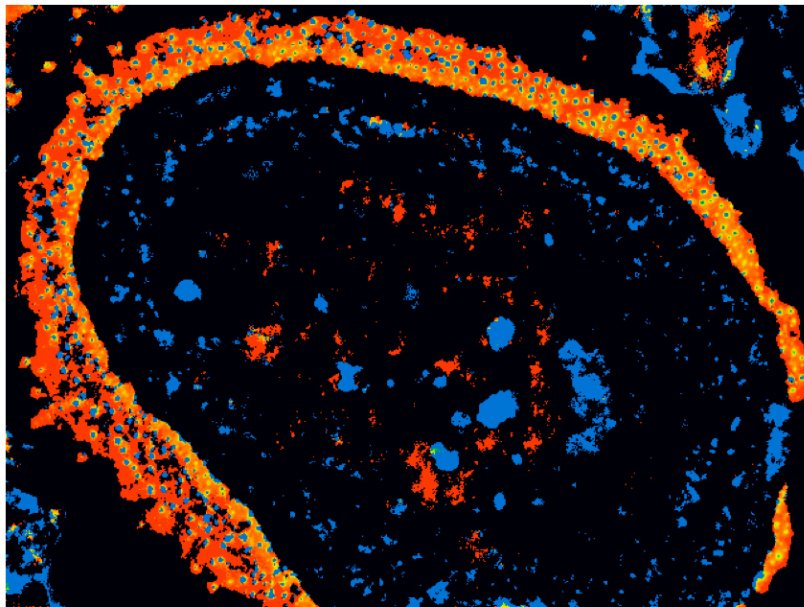


Fig. 1 Overview of physiological systems and topics studied in our laboratory. Colored arrows indicate processes that PTP epsilon activates (green) or inhibits (red).



Podosomes from wild-type osteoclasts Podosomes from PTP ϵ -deficient osteoclasts

Fig. 2 Podosomes – adhesion structures of bone-resorbing osteoclasts – are disrupted in cells from mice lacking PTP epsilon. Top: mature, bone resorbing osteoclast, in which podosomes are arranged as an array at the cell periphery. Podosomes contain an actin core (Blue) surrounded by proteins such as vinculin (Red). Bottom: magnified image of podosomes from osteoclasts of wild-type (left) and PTP epsilon-deficient (right) mice. Note evenly sized- and spaced podosomes in WT sample vs. total disarray in PTP ϵ -deficient sample. Red-actin, blue-vinculin. (in collaboration with Chen Luxenburg/Benny Geiger).

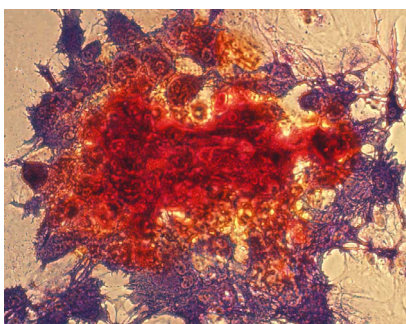


Fig. 3 Osteoblasts – the cells that produce bone matrix – as viewed in culture. Along with osteoclasts, osteoblasts determine overall bone mass and turnover. Bone marrow cells were grown for three weeks in the presence of dexamethasone and ascorbic acid. Cells were stained for alkaline phosphatase (purple, a marker of osteoblasts in this system) and Alizarin Red (red, bone matrix secreted by osteoblasts).

of cytosolic cyt-PTP ϵ and are caused by PTP α being an integral receptor-type molecule. This study illustrates that the physiological roles of these closely-related PTPs *in vivo* overlap in some aspects, but are distinct in others.

Regulation of PTP activity is not properly understood at present. We have characterized novel mechanisms for regulation of this PTP – **inhibitory dimerization** and **inhibitory interactions with microtubules** *in vivo*. Dimerization and interaction with tubulin are regulated by physiological processes in cells, such as increased oxidative stress or activation of the epidermal growth factor (EGF). PTP ϵ is also regulated by tyrosine phosphorylation at its C-terminal – phosphorylation drives PTP ϵ to

activate Src and related kinases, thereby providing PTP ϵ with the ability to influence indirectly multiple cellular processes via Src. PTP ϵ is phosphorylated by integrins, as well as by Neu and the related EGF receptor.

In all, these and other studies indicate that PTP ϵ and PTP α participate in diverse physiological processes. Our future studies are aimed at understanding at the molecular level how PTPs regulate processes such as bone homeostasis, obesity, and malignant transformation, while addressing broader issues of regulation of PTP activity and uniqueness vs redundancy between related PTPs.

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Acknowledgements

Studies in our group are supported by the Israel Science Foundation, the European Union, The Minerva Foundation (Germany), The Israel Cancer Research Foundation, the Osteogenesis Imperfecta Foundation (USA), and by the Fritz Thyssen Stiftung (Germany).

INTERNAL support

We are also supported by the David and Fela Shapell Family Center for Genetic Disorders Research, the Kekst Family Center for Medical Genetics, the Women's Health Research Center, and by the Leo and Julia Forchheimer Center for Molecular Genetics.