

Dr. Mildred Scheel Memorial Lecture

Hamburg, June 18, 1988

Munk, Klaus

In Memoriam Dr. Mildred Scheel

Anders, Fritz

A Biologist's View of Human Being

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Ullrich, Axel

Growth Factor Receptors:

Role in Normal Mitogenic Signalling and Oncogenesis

In Memoriam Dr. Mildred Scheel

Klaus Munk



The Wilsede Meeting is also supported by the Wilsede Fellowship Programme of the Dr. Mildred Scheel Stiftung, which is part of the Deutsche Krebshilfe. Since that Foundation was established by Dr. Mildred Scheel, it is appropriate that we should reflect and comment on the great contribution which she made to cancer prevention, treatment and research.

Who was Mildred Scheel? What were her ideas and what did she achieve with her Foundation?

Mildred Scheel was born in Cologne in 1932, daughter of a physician and radiologist. She studied medicine and specialized in radiology. Later, she married Mr. Walter Scheel before he was appointed Minister for Foreign Affairs. When Mr. Scheel subsequently became President of the Federal Republic of Germany, she became the "First Lady" of this country. No doubt this helped her to fulfil her noble ambition to contribute to the fight against cancer. As a consequence of this, she founded the Deutsche Krebshilfe in 1974. From that time on, all

her efforts were directed towards encouraging people to contribute money for this crucial purpose. She developed many significant ideas for organizing cancer prevention, early diagnosis and treatment that was applicable on a large scale. She initiated the establishment of the first five cancer centers in this country. Once they were functioning successfully, she was able to convince the Government to assume full responsibility for maintaining them. She then prepared to launch new undertakings. It became apparent to people that she had unique qualities that enabled her to initiate new ideas for fighting cancer, and this added significantly to her personal success. She also supported in particular the treatment of childhood cancer in many hospitals, and initiated the psychosocial after-care of patients and their families. In addition, she aided individuals who were economically affected by having cancer.

The Dr. Mildred Scheel Stiftung was established to promote and support cancer research. It supports a great number

of research projects in many institutes and provides a fellowship programme for scientists to work and study at institutions abroad. Included in that programme is the Wilsede Fellowship Programme. The Dr. Mildred Scheel Stiftung is now an important body in the Federal Republic of Germany for the granting of fellowships. Many of Mildred Scheel's initiatives were not broadly accepted at first, but through her continued energy they are now accepted as common practices in the oncological field in this country.

When she had a particular goal in sight, no obstacles could prevent her from reaching it. Yet, for all her tenacity, Mildred Scheel was a warm, loving and sensitive person who had special understanding for cancer patients, together with a human touch. She was always very hard-working and enthusiastic, and stimulating for all of us. None of those who, like myself, had worked with her in the Foundation for over 10 years can

remember her ever missing a meeting of the board or the scientific councils of the Deutsche Krebshilfe or the Dr. Mildred Scheel Stiftung, until the last few weeks of her life. During those meetings she listened carefully to the experts, although sometimes she came to her own conclusions when she was convinced that a particular step forward had to be made. She never lost her enthusiasm for helping others, even when she realized what would be the consequence of her own illness. She always seemed to be positive in her attitude and could always stimulate others with her spirit and her personality. She could have done so much more in the future and she is sadly missed by all of us. We all will always remember her with great devotion.

The Mildred Scheel Memorial Lectures are our tribute. The second lecture will be held by Axel Ullrich, a classic molecular biologist, who has made important contributions to the understanding of cancer in the field of molecular biology.

Growth Factor Receptors: Role in Normal Mitogenic Signalling and Oncogenesis

A. Ullrich¹ and J. Schlessinger²

Growth factors, differentiation factors, and polypeptide hormones are crucial components of the regulatory system that coordinates development of multicellular organisms. Many of these factors mediate their pleiotropic actions by binding to and activating cell surface receptors with an intrinsic protein tyrosine kinase (PTK) activity. Figure 1 presents a schematic representation of the known growth factor receptors that bear PTK activity. Growth factor receptors with PTK activity, or receptor tyrosine kinases (RTKs), have a similar molecular topology. All possess a large, glycosylated, extracellular, ligand-binding domain, a single hydrophobic transmembrane region, and a cytoplasmic domain which contains a PTK catalytic domain (Hanks et al., 1988; Yarden and Ullrich 1988, Schlessinger 1988; Williams 1989).

Primary sequence homology and distinct structural characteristics of different RTKs allow the classification of these receptors into subclasses (Fig. 1). The structural features characteristic of the four subclasses include two cysteine-rich repeat sequences in the extracellular domain of monomeric subclass I receptors, disulfide-linked heterotetrameric $\alpha_2\beta_2$ structures with similar cysteine-rich sequences in subclass II RTKs, and five or three immunoglobulin-like repeats in the extracellular domains of subclass III

and IV RTKs, respectively. The tyrosine kinase domain of the latter is interrupted by hydrophilic insertion sequences of varying length. The availability of RTK cDNA clones has made it possible to initiate detailed structure-function analyses of the mechanisms of action of RTK family members. Numerous mutants of insulin, epidermal growth factor (EGF), platelet-derived growth factor (PDGF), insulin-like growth factor 1 (IGF-1), colony-stimulating factor 1 (CSF-1), and other receptors have been characterized in regard to their biological and biochemical properties. This has led to the establishment of a receptor domain function map and model for RTK-mediated signal generation (Fig. 2).

Ligand binding to the extracellular domain of the receptor results in conformational change and subsequent oligomerization [Schlessinger 1988]. Receptor oligomerization is a universal phenomenon among growth factor receptors. It has been detected in living cells, in isolated membranes, and in preparations of solubilized and purified receptors [Schlessinger 1986; Yarden and Schlessinger 1985, 1987a, b; Cochet et al., 1988]. It may be induced by either monomeric ligands, such as EGF, which cause receptor oligomerization by inducing conformational changes [Greenfield et al. 1989] resulting in receptor-receptor interactions [Lax et al. 1990] or by bivalent ligands, such as PDGF and CSF-1, which mediate dimerization of neighboring receptors [Seifert et al. 1989; Heldin et al. 1989; Hammacher et al. 1989]. Oligomerized growth factor receptors possess elevated PTK activity [Yarden and

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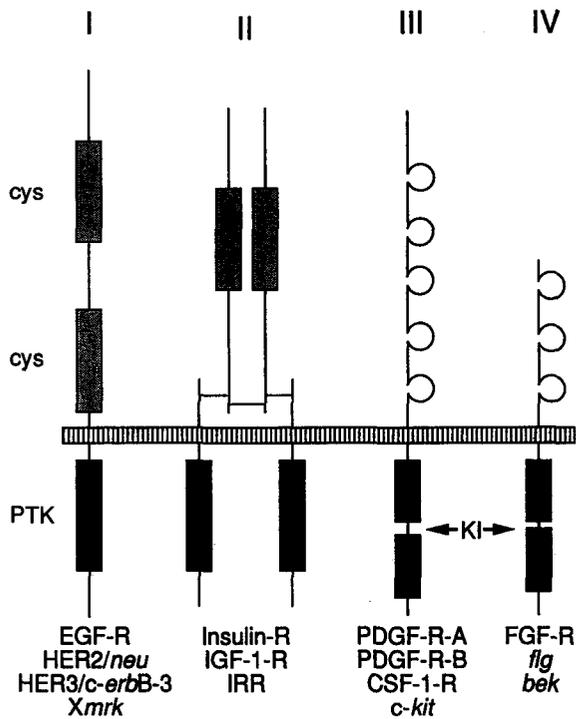


Fig. 1. Schematic representation of receptor tyrosine kinase subclasses. For details, see Ullrich and Schlessinger (1990)

Schlessinger 1987 a, b; Böni-Schnetzler and Pilch 1987], which leads to phosphorylation of tyrosine residues of the receptor polypeptide chain and of cellular substrates.

Receptor phosphorylation releases an internal constraint by stabilizing a conformation that is competent to interact with and phosphorylate cellular substrates [Honegger et al. 1988 a, b]. The recent observation that phosphorylation of EGF and insulin receptors can occur by intermolecular cross-phosphorylation both in vitro and in living cells [Honegger et al. 1989, 1990; Ballotti et al. 1989; Lammers et al. 1990] further supports the importance of receptor oligomerization in the process of receptor activation.

The chain of events that is initiated by tyrosine phosphorylation of cellular substrates is still poorly understood. Several RTK substates of potential biological importance have recently been identified (Figure 3). Both PDGF and EGF can induce tyrosine phosphorylation of phospholipase C γ (PLC- γ) in vitro and in living cells [Margolis et al. 1989; Meisenhelder et al. 1989; Wahl et al. 1989]. In addition, PLC- γ was observed to associate with the activated receptor kinases in a ligand- and kinase-dependent manner [Margolis et al. 1989, 1990 a; Kumjian et al. 1989]. However, growth factor-induced inositol triphosphate (IP₃) generation appears not to be the

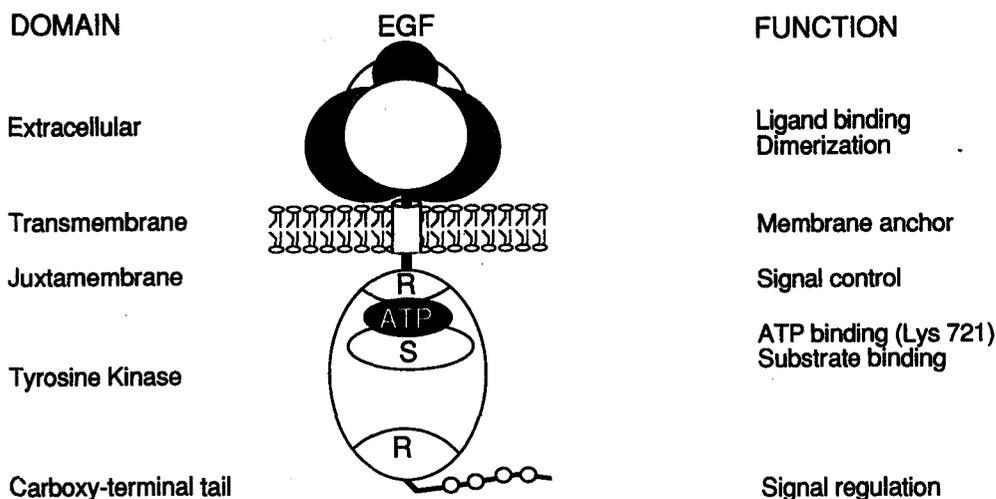


Fig. 2. Proposed structure-function topology of the EGF receptor. Subdomains II and IV (stippled) represent the cysteine-rich regions of the extracellular domain. Most of the structural determinants that define EGF binding affinity are proposed to be located in the cleft

formed by subdomains I and III. The symbols S and R within the PTK domain represent proposed interaction sites for substrates and regulatory factors [Ullrich and Schlessinger, 1990]

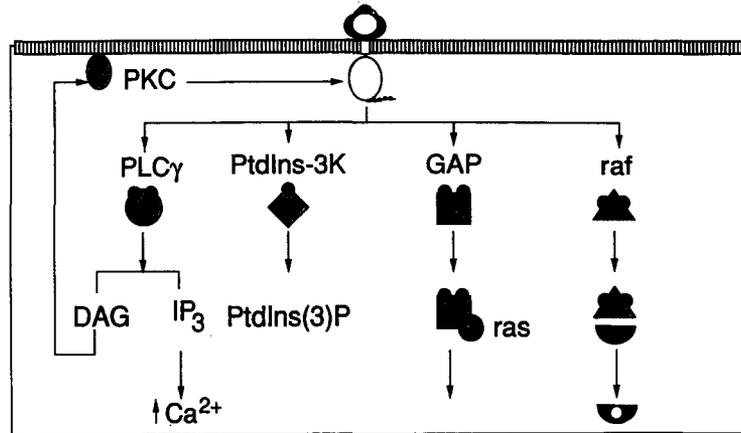


Fig. 3. Receptor-mediated multiple signalling pathways. Direct phosphorylation (*black dots* on symbols) of substrates, PLC- γ , PtdIns-3K, GAP, and *raf* leads to secondary events, including enzymatic activation and metabolite formation (DAG, IP₃, PtdIns(3)P), activation

of enzymatic functions by association, and Thr/Ser phosphorylation (*white dot* on symbol) of substrates [Ullrich and Schlessinger, 1990] PtdIns-3K: phosphatidylinositol 3-kinase; GAP: GTPase-activating protein; PtdIns(3)P: phosphatidylinositol 3-phosphate

sole mechanism leading to the initiation of DNA synthesis [Downing et al. 1989], which is compatible with the notion that the phosphatidylinositol (PI) signalling pathway does not play an essential role in the mitogenic response [Lopez-Rivas et al. 1987; L'Allemain et al. 1989; Margolis et al. 1990 b].

Other RTK substrates that have recently been identified include PI kinase and the *ras* binding protein GAP [Kaplan et al. 1987; Varticovski et al. 1989; Molloy et al. 1989] (Fig. 3). Similarly, it has been suggested that the *c-raf* protooncogene product becomes phosphorylated in response to PDGF receptor activation [Morrison et al. 1989]. Intriguingly, all proteins identified thus far as RTK targets are either components of second messenger pathways, protooncogene products, or factors that regulate the activity of protooncogene products.

The importance of allosteric regulation of receptor activation and signal transduction is further emphasized by the fact that a large variety of structural alterations found in RTK-derived oncogene products lead to constitutive kinase activation and, consequently, subversion of molecular control mechanisms and alteration of receptor signals. Thus, transforming RTK derivatives serve as valu-

able model systems not only for studying the mechanisms of oncogenesis but also for the analysis of normal structure-function relationships for these signal-transmitter molecules. Constitutive activation of RTK signalling functions can be achieved in a number of ways. For example, in the cases of *v-erb-B* and *v-kit*, deletion of the extracellular binding domain eliminates the negative control that this structure normally exerts on the cytoplasmic domain. Even point mutations within the extracellular domain can lead to intracellular activation, as in

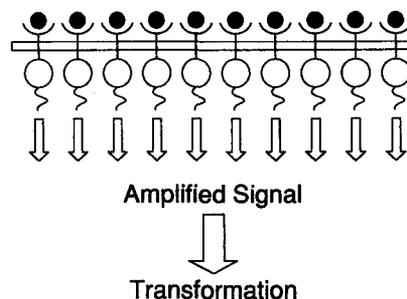


Fig. 4. Transformation by receptor amplification. Schematic representation of proposed transformation model by autocrine stimulation of overexpressed receptor tyrosine kinases. Ligand (*black dots*) is activating receptors in the plasma membrane of a tumor cell, resulting in an amplified transforming signal

the case of *v-fms* mutations at residues 301 and 374 [Woolford et al. 1988; Rousel et al. 1988] (Fig. 4). These mutations appear to induce and stabilize a conformational change equivalent to that triggered by ligand binding and possibly dimerization. Another dramatic effect of a single point mutation is exemplified by the Val/Glu conversion in the *neu* transmembrane domain [Bargmann et al. 1986], which suggests that this part of the putative receptor is involved in an overall conformational alteration that occurs upon interaction with the yet unidentified ligand. In this case, the transmembrane mutation results in constitutive receptor oligomerization [Weiner et al. 1989]. Another type of structural alteration has been identified in the EGF receptor/*erb-B* system and involves mutations in the PTK core region [Massoglia et al. 1990].

Despite the presence of an intact extracellular domain, these mutations render the EGF receptor competent for mitogenic and transforming signalling without autophosphorylation. RTK-derived oncogenes possess other structural lesions such as cytoplasmic point mutations, deletions, and C-terminal truncations which appear to enhance and modulate the transforming signal [Khaizaie et al. 1988; Woolford et al. 1988].

For human cancer, activating RTK mutations appear to be of minor importance. The most common cellular lesion found in human cancers involves autocrine activation in conjunction with receptor overexpression (Fig. 4). Many tumors and tumor cell lines have been found to coexpress growth factors and their receptors, including TGF- α , PDGF-A, PDGF-B, acidic fibroblast growth

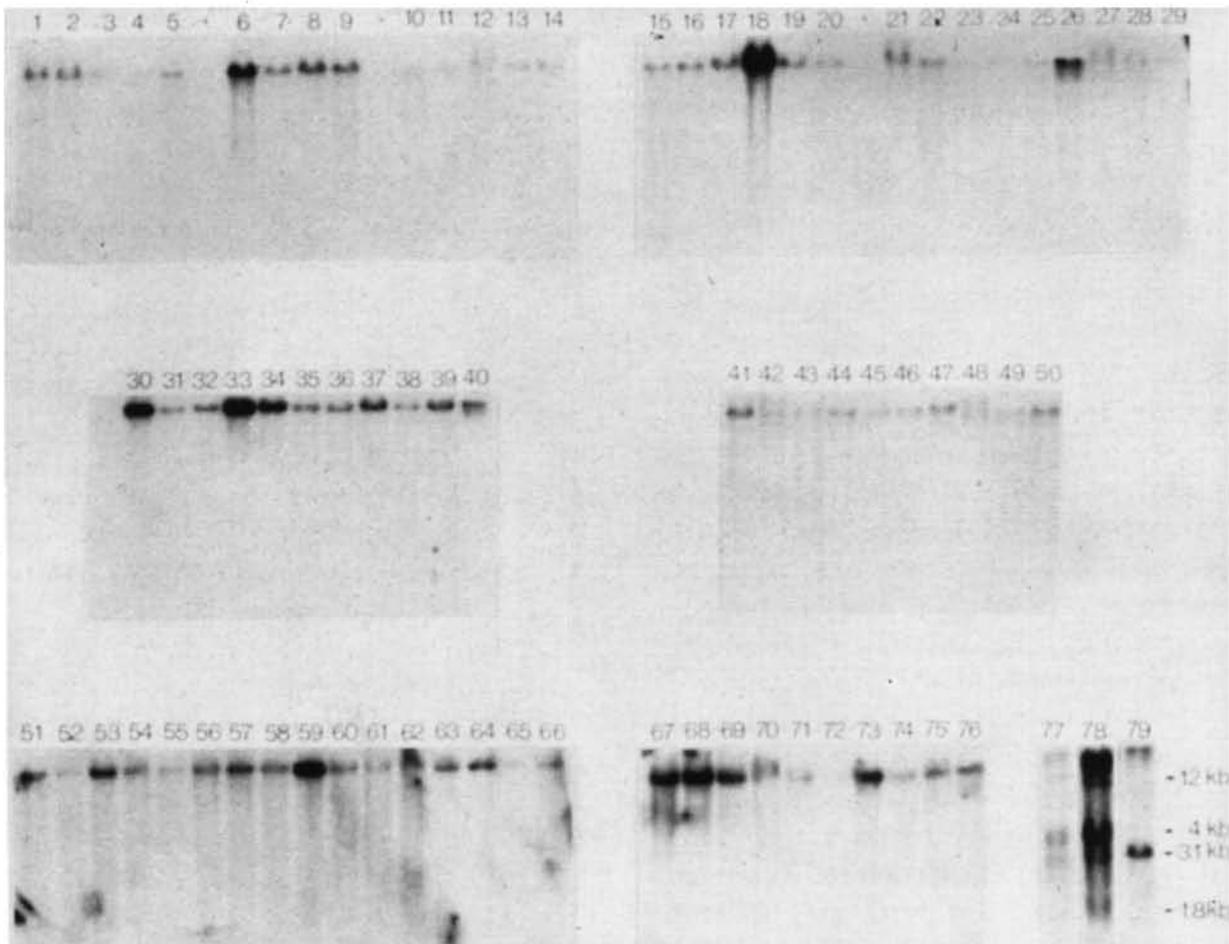


Fig. 5. HER2/*neu* gene amplification in mammary carcinoma. Southern blot hybridization analysis of chromosomal DNA from primary

mammary carcinoma tumors [Slamon et al. 1987]

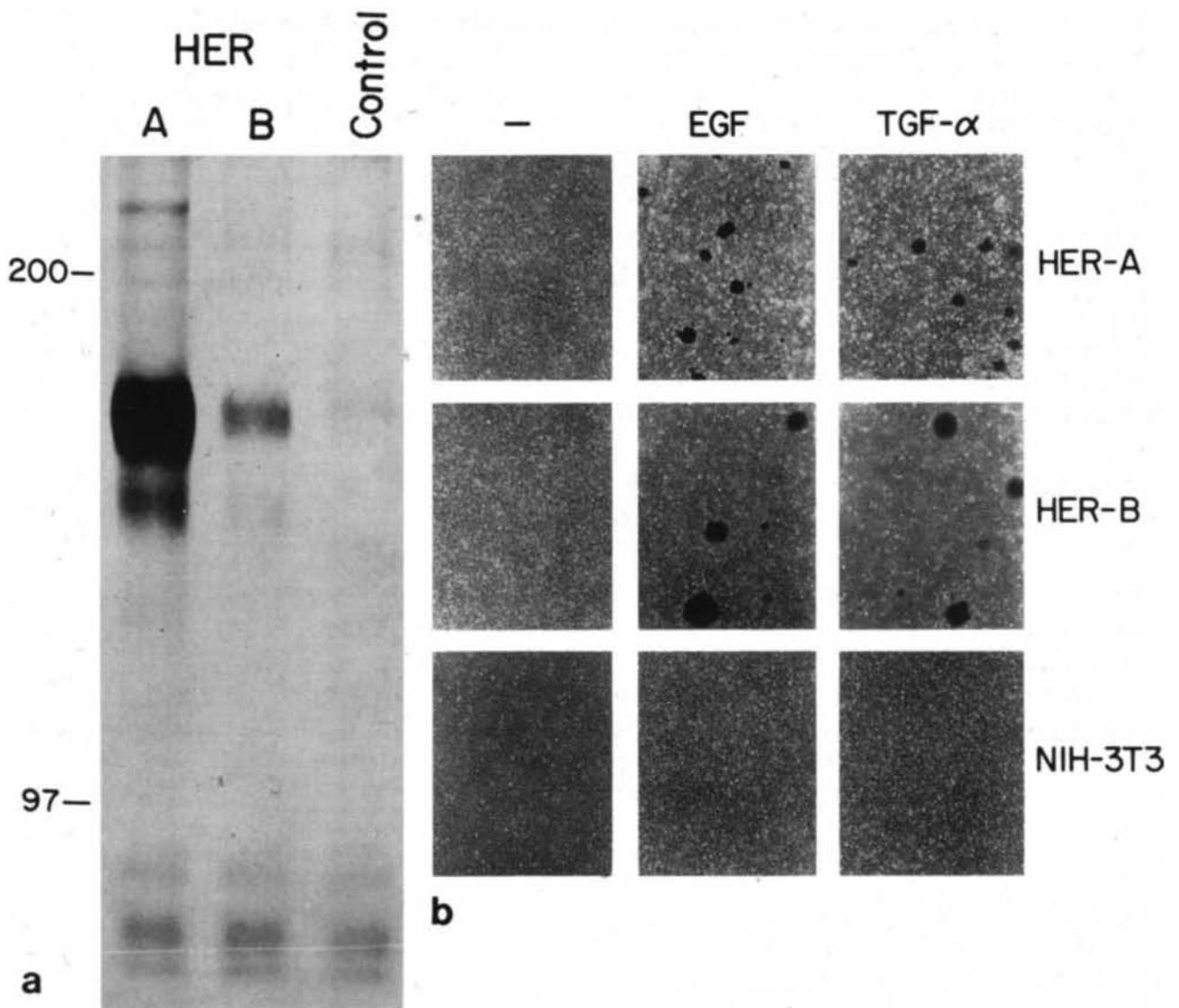


Fig. 6a,b. Cell transformation by EGF receptor overexpression. NIH-3T3 cell lines HER-A and HER-B overexpressing the hu-

man EGF receptor (a) were stimulating with EGF or TGF- α and tested for their ability to grow in soft agar (b)

factor (FGF), basic FGF, and their specific RTKs. Thus, autocrine receptor activation represents yet another scenario of subversion of normal growth control. For mammary and ovarian carcinoma, extensive studies have demonstrated a direct correlation between the extent of overexpression of p185^{HER2/neu} and a patient's prognosis, a result which strongly suggests a critical role for this EGF receptor-like RTK in tumor progression and perhaps even tumor initiation [Slamon et al. 1989] (Fig. 5). This possibility is further supported by efficient induction of mammary carcinoma in mice by an activated *neu* gene product [Muller et al. 1988] and transformation of NIH-3T3 cells by overexpression of un-

altered p185^{HER2/neu} [Hudziak et al. 1987]. Analogous experiments with the EGF receptor indicated that autocrine stimulation of the overexpressed receptor was essential to achieve a transforming effect [Di Fiore et al. 1987; Velu et al. 1987; Riedel et al. 1988] (Fig. 6).

On the basis of these findings, strategies involving antireceptor antibodies were designed for the treatment of mammary and ovarian carcinoma. Monoclonal antibodies, such as the anti-HER2/*neu* antibody 4D5, are able to interfere with autocrine activation of the receptor, which results in inhibition of tumor cell growth in tissue culture and nude mouse models (Ullrich et al., unpublished).

In principle, every receptor with PTK activity has oncogenic potential. One can anticipate that many more types of activating mutations, as well as specific instances of RTK overexpression, will be detected in animal and human tumors. The molecular identification and characterization of these mutants will not only provide important insights into fundamental mechanisms underlying receptor activation and normal growth control, but may also enhance our understanding of oncogenesis and open new avenues for diagnosis and therapy.

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