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Novel Functions of ErbB4 and NRG-1 in Development and Cancer

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To my family

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Novel functions of ErbB4 and NRG-1 in development and cancer

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ABSTRACT

Cells communicate, or signal, with each other constantly to ensure proper functioning of tissues and organs. Cell signaling is often performed by interplay of receptors and ligands that bind these receptors. ErbB receptors (epidermal growth factor receptors, EGFR, HER) bind extracellular growth factors and transduce these signals inside of cells. ErbB dysfunction promotes carcinogenesis, and also results in numerous defects during normal development. This study focused on the functions of one member of the ErbB receptor family, ErbB4, and growth factor, neuregulin-1 (NRG-1), that can bind and activate ErbB4.

This study aimed to find novel functions of ErbB4 and NRG-1. Hypoxia, or deficiency of oxygen, is common in cancer and ischemic conditions. One of the key findings of the work was the identification and characterization of a cross-talk between ErbB4 and Hypoxia-inducible factor 1 α (HIF-1 α), the central mediator of hypoxia signaling. ErbB4 activation by NRG-1 was found to increase HIF-1 α activity. Interestingly, this regulation occurred in reciprocal manner as HIF-1 α was also able to increase protein levels of NRG-1 and ErbB4. Moreover, expression of NRG-1 and ErbB4 was associated with HIF activity *in vivo* in human clinical samples and in mice. Reduction of functional ErbB4 in developing zebrafish embryos resulted in defects in development of the skeletal muscles. To study ErbB4 functions in pathological situation in humans, clinical samples of serous ovarian carcinoma were analyzed using tissue microarrays and real-time RT-PCR. A specific isoform of ErbB4, CYT-1, was associated with poor survival in serous ovarian cancer and increased anchorage independent growth of ovarian cancer cells *in vitro*.

These observations demonstrate that ErbB4 and NRG-1 are essential regulators of cellular response to hypoxia, of development, and of ovarian carcinogenesis.

Ilkka Paatero

ErbB4- ja NRG-1 signaloinnin merkitys syövässä ja yksilönkehityksen aikana

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TIIVISTELMÄ

Elimistön solut viestivät keskenään normaalin kehityksen ja aikuisten kudosten normaalin toiminnan aikana. Tämä viestintä varmistaa solujen ympäristöönsä soveltuvan toiminnan. Soluviestintää välittävät reseptorit ja niihin sitoutuvat ligandit. ErbB (epidermaalisen kasvutekijän reseptorit, EGFR, HER) reseptorit sitovat solunulkoisia kasvutekijöitä, ja välittävät viestin solun sisälle. Monissa syövässä ErbB reseptorien toiminnan säätely on häiriintynyt. Tämä tutkimus keskittyi erään ErbB reseptorin, ErbB4:n, ja sen ligandin NRG-1:n toimintaan.

Tutkimuksen päämääränä oli löytää uusia ErbB4:n ja NRG-1:n säätelemiä prosesseja ja niiden toimintamekanismeja. Hapenpuutetta, hypoksiaa, esiintyy monissa syövässä ja iskeemisissä tautitiloissa. Tutkimuksessa löytyi yhteys ErbB4:n välittämän viestinnän ja keskeisen hapen vähyyden viestijän (hypoksian indusoima tekijä 1α , HIF- 1α) välillä. NRG-1 ja ErbB4 lisäsivät HIF- 1α :n määrää ja aktiivisuutta. Tämä vuorovaikutus oli molemminpuolista, sillä myös HIF- 1α :n aktiivisuus johti lisääntyneeseen NRG-1- ja ErbB4-määrään. Lisäksi lisääntynyt HIF-aktiivisuus oli yhteydessä lisääntyneeseen ErbB4:n ja NRG-1:n määrään kliinisissä näytteissä ja hiirimalleissa. ErbB4:n toiminnan estäminen seeparakalan alkioissa johti luurankoli hasten kehityksen häiriöihin. ErbB4:n toiminnan tutkimiseksi ihmisissä analysoitiin seröösien munasarjasyövän potilasnäytteitä kudossiruja sekä reaaliaikaista RT-PCR:ää käyttäen. ErbB4:n erityisen CYT-1 isomuodon ilmentyminen oli yhteydessä huonoon ennusteeseen seröösissä munasarjasyövässä sekä lisäsi munasarjasyöpäsolujen kasvua in vitro.

Tutkimuksessa tehdyt havainnot viittaavat siihen, että NRG-1 ja ErbB4 ovat tärkeitä säätelijöitä solujen reagoimisessa hapenpuutteeseen, kudosten kehittymisessä sekä seröösissä munasarjasyövässä.

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ABBREVIATIONS

ADAM17	a disintegrin and metalloproteinase domain 17
Akt	v-akt murine thymoma viral oncogene homolog
AP-1	activator protein 1
ATP	adenosine triphosphate
BTC	betacellulin
CAIX	carbonic anhydrase IX
Cbl	cas-br-m murine ecotropic retroviral transforming sequence homolog
cDNA	complementary DNA
Cre	cyclization recombinase
CYT	cytoplasmic
DAG	diacylglycerol
DMOG	dimethylloxalyl glycine
DNA	deoxyribonucleic acid
dpf	days post-fertilization
ECD	extracellular domain
EGF	epidermal growth factor
EGFR	epidermal growth factor receptor
EPO	erythropoietin
ErbB	v-erb-a erythroblastic leukemia viral oncogene homolog
Erk	extracellular signal regulated kinase
FAM	6-carboxyfluorescein
Gb	gigabase
GDP	guanosine diphosphate
GLUT-1	glucose transporter 1
Grb2	growth factor receptor-bound protein 2
GST	glutathione-S-transferase
GTP	guanosine triphosphate
HAF	hypoxia associated factor
HB-EGF	heparin-binding epidermal growth factor-like growth factor
HER	human epidermal growth factor receptor
HIF	hypoxia-inducible factor
hpf	hours post-fertilization
HSP90	heat-shock protein 90
ICD	intracellular domain
IP3	inositol 1,3,5 trisphosphate
JM	juxtamembrane
KD	kinase domain
MAPK	mitogen activated protein kinase
Mb	megabase
Mek	mitogen activated protein kinase kinase
MMTV	mouse mammary tumor virus

MO	morpholino
Morphant	morpholino treated embryo
mRNA	messenger RNA
mTor	mammalian target of rapamycin
Myl2	myosin, light chain 2, regulatory, cardiac, slow
n	number of samples
NRG	neuregulin
p	statistical probability
PAX8	paired box gene 8
PCR	polymerase chain reaction
PHD	prolyl 4-hydroxylase
PI3K	phosphoinositol-3 kinase
PIP2	phosphatidylinositol 4,5-diphosphate
PIP3	phosphatidylinositol 3,4,5-trisphosphate
PKC	protein kinase C
PLA	in situ proximity ligation assay
PLC	phospholipase C
PMA	phorbol 13-myristate 12-acetate
ppm	parts per million
PTP	protein tyrosine phosphatase
RACK1	receptor of activated protein kinase C
Raf	v-RAF murine viral oncogene homolog
Ras	ras rat sarcoma viral oncogene homolog
RIP	regulated intramembraneous proteolysis
RNA	ribonucleic acid
RT	room temperature
RT-PCR	reverse transcriptase polymerase chain reaction
RTK	receptor tyrosine kinase
SH2	src homology 2
SH3	src homology 3
Shc	shc transforming protein
siRNA	small-interfering RNA
SNP	single nucleotide polymorphism
Sos	son of sevenless (<i>Drosophila</i>) homolog
SP-1	transcription factor Sp-1
STAT	signal transducer and activator of transcription
TACE	tumor necrosis factor-alpha converting enzyme
TAMRA	tetramethylrhodamine
TGF- α	transforming growth factor α
TM	transmembrane domain
VHL	von Hippel-Lindau tumor suppressor
WAP	whey acidic protein
Xmrk	Xiphophorus melanoma receptor kinase

LIST OF ORIGINAL PUBLICATIONS

The thesis is based on following original publications, which are referred to in the text by the Roman numerals I-V

- I Paatero I, Jokilammi A, Heikkinen PT, Iljin K, Kallioniemi OP, Jones FE, Jaakkola PM, Elenius K. 2012. Interaction with ErbB4 promotes hypoxia-inducible factor-1 α signaling. *J. Biol. Chem.* 287(13):9659-71.
- II Paatero I, Seagroves TN, Johnson RS and Elenius K. 2013. Hypoxia-inducible factor-1 α induces ErbB4 signaling in the differentiating mammary gland. Manuscript.
- III Iivanainen E, Paatero I, Heikkinen SM, Junttila TT, Cao R, Klint P, Jaakkola PM, Cao Y, Elenius K. 2007. Intra- and extracellular signaling by endothelial neuregulin-1. *Exp. Cell Res.* 313: 2896-909.
- IV Paatero I, Lassus H, Junttila TT, Kaskinen M, Bützow R, Elenius K. 2013. CYT-1 isoform of ErbB4 is an independent prognostic factor in serous ovarian cancer and selectively promotes ovarian cancer cell growth in vitro. *Gynecol, Oncol.* in press, electronic publication 9.1.2013.
- V Paatero I, Veikkolainen V, Pelliniemi LJ, Elenius K. 2013. ErbB4a is required for skeletal muscle development in zebrafish. Manuscript.

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1 INTRODUCTION

Cells communicate with each other constantly. The purpose of this communication, or cell signaling, is to guide cells to respond properly to their context and physiological state to maintain homeostasis or a developmental program. Most prominently cell signaling is perhaps illustrated during development, where clumps of undifferentiated cells differentiate into a variety of different cell types and form beautiful and ordered structures such as the eye or contracting heart (Gilbert 2006; Wolpert 2007). In many diseases, such as cancer, cell signaling is dysregulated resulting in loss of tissue homeostasis and structure (Hanahan and Weinberg 2000; Hanahan and Weinberg 2011).

One of the mechanisms by which cells communicate is by production of soluble growth factors, or ligands, and their specific target molecules, receptors, within the recipient cells. As their name implies, growth factors regulate cellular growth, but they do also regulate many other cellular processes such as metabolism, cell survival and cell migration. Growth factor signaling regulates both development and disease, and it is of significant importance in medicine and developmental biology.

ErbB receptors are receptors for epidermal growth factor like ligands. The focus of this thesis lies in the elucidation of diverse functions of one of the ErbB receptors, ErbB4, and its ligand NRG-1, in both development and disease.

2 REVIEW OF THE LITERATURE

Protein tyrosine kinases are proteins that phosphorylate other proteins on the tyrosine residues. Although the human genome encodes over 90 tyrosine kinases, they are involved in virtually all cellular and developmental processes (Blume-Jensen and Hunter 2001). A subset of the family, receptor tyrosine kinases (RTK), is located on the cell plasma membrane. Their primary function is to bind secreted or membrane-bound growth factors and transduce this information inside the recipient cell (Lemmon and Schlessinger 2010).

2.1 ErbB receptors and ligands

Originally ErbB receptors were discovered as genes homologous to avian erythroblastosis virus oncogene in chicken (Vennstrom and Bishop 1982) and later in human (Jansson et al. 1983) genome. The name of gene family ErbB, *v-erb-a erythroblastic leukemia viral oncogene homolog*, also originates from these discoveries. ErbB receptors are also often called epidermal growth factor receptors (EGFR) after first discovered member EGFR (ErbB1) that binds epidermal growth factor (EGF).

ErbB receptors are transmembrane RTKs with several ligands. They are expressed in all multicellular, metazoan, organisms. The number of receptors and ligands differs between different species (Table 1). Mammals have four different ErbB genes (*ERBB1*, *ERBB2*, *ERBB3* and *ERBB4*) and have at least 11 epidermal-growth factor like ligands that bind ErbB receptors (Stein and Staros 2000; Stein and Staros 2006).

Table 1. Number of predicted ErbB genes and their ligands in selected animal species according to (Stein and Staros 2000; Stein and Staros 2006).

Species	Receptors	Ligands
<i>Caenorhabditis elegans</i> (soil nematode)	1	1
<i>Drosophila melanogaster</i> (fruit fly)	1	5
<i>Danio rerio</i> (zebrafish)	6 (7)	14
<i>Xenopus tropicalis</i> (african clawed-frog)	4	14
<i>Gallus gallus</i> (chicken)	4	11
<i>Mus musculus</i> (mouse)	4	11
<i>Homo sapiens</i> (man)	4	11

The ligands bind ErbB receptors selectively although no high-affinity ligand for ErbB2 has been found (Table 2). Ligands can be divided into four groups based on their capability to directly bind ErbB receptors. The first group can activate only ErbB1. Ligands that belong to this group are amphiregulin (Shoyab et al. 1988), epidermal growth factor (EGF) (Cohen 1962), epigen (Strachan et al. 2001) and transforming growth factor α (TGF- α) (Derynck et al. 1984). The second group consists of ligands that bind ErbB1 and ErbB4. Betacellulin (Sasada et al. 1993), epiregulin (Toyoda et al. 1995) and heparin-binding epidermal growth factor-like growth factor (HB-EGF) (Higashiyama et al. 1991) belong to this group. The third group of ligands can bind both ErbB3 and ErbB4. NRG-1 and NRG-2 form this group, although NRG-2 can also be produced as several isoforms of which alpha type isoforms bind and activate only ErbB3 (Hobbs et al. 2002). The fourth group consists of ligands that bind only ErbB4 and NRG-3 (Zhang et al. 1997) and NRG-4 (Harari et al. 1999) belong to this group. Interestingly, ErbB4 also recruits different signaling proteins depending on which ligand activates the receptors (Sweeney et al. 2000).

Table 2. Binding specificities of human ErbB ligands to human ErbB receptors (Linggi and Carpenter 2006).

	ErbB1	ErbB2	ErbB3	ErbB4
Amphiregulin	X			
EGF	X			
Epigen	X			
TGF- α	X			
Betacellulin	X			X
Epiregulin	X			X
HB-EGF	X			X
NRG-1			X	X
NRG-2			X	X
NRG-3				X
NRG-4				X

2.1.1 Structure & function

ErbB receptors have three distinct domains, which is also the common overall structure of other members of the RTK gene family (Lemmon and Schlessinger 2010). The receptors possess an extracellular domain (ECD), a transmembrane domain (TM) and an intracellular domain (ICD), each having distinct structural and functional properties (Holbro and Hynes 2004).

ECD is the ligand binding domain. The structure of ErbB1 (Garrett et al. 2002), ErbB3 (Cho and Leahy 2002), and ErbB4 (Bouyain et al. 2005) has both an open and a closed conformation, and it is predicted that a ligand can bind and stabilize the open conformation (Ferguson et al. 2003) (Figure 1). However, ErbB2 is constitutively in the open conformation and does not need a ligand to be activated (Garrett et al. 2003). Consistently, no direct activating high-affinity ligands have been found for ErbB2 (Holbro and Hynes 2004). Ligand

binding allows receptors to dimerize and form an active dimer, although the very details of this ligand-induced dimerization are not yet fully understood (Lemmon 2009).

TM domain is the domain that attaches the receptor into the hydrophobic plasma membrane. It composes of a single α helix that spans the membrane once. The α -helical structure contains hydrophobic residues which allow the protein to cross the lipid bilayer. Thus, the TM domain regulates the localization of the receptor (Lemmon and Schlessinger 2010). However, TM domain may also have an active role in ErbB receptor activation (Wides et al. 1990) and dimerization (Mendrola et al. 2002).

ICD possesses the catalytical kinase activity of the receptor. The kinase domain (KD) within the ICD catalyzes transfer of a phosphate group from ATP to a tyrosine residue of a substrate protein (Hubbard and Till 2000). At the non-activated state the autoinhibitory loop prevents the full activity of the KD. As a ligand binds to the receptor, the autoinhibitory loop is phosphorylated by another ErbB receptor in the dimer resulting in full activation of the receptor (Qiu et al. 2008). The KD of ErbB3 is often considered catalytically inactive (Yarden and Sliwkowski 2001; Holbro and Hynes 2004), although it has a low level of autophosphorylation activity (Shi et al. 2010). In addition to the KD the ICD has binding sites for many ErbB substrates and regulators (Schulze et al. 2005).

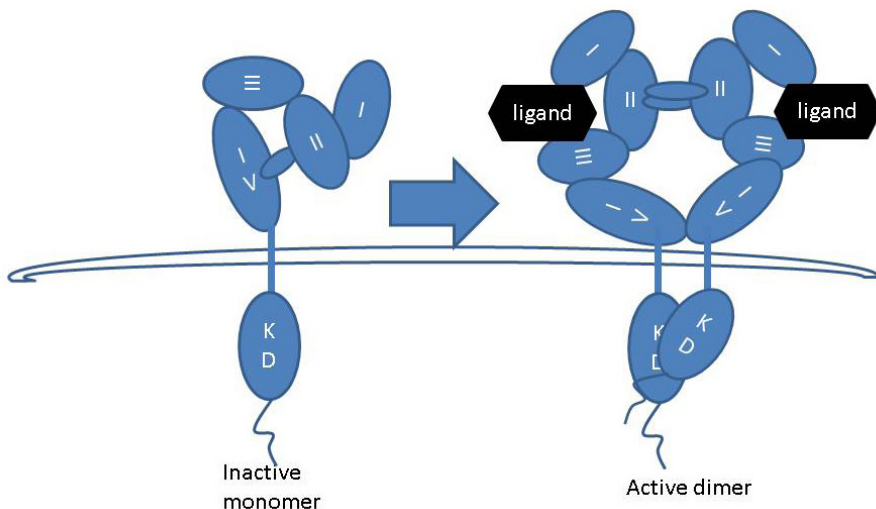


Figure 1. Schematic figure of the structure of the ErbB receptor. The ECD contains four distinct subdomains (roman numerals I-IV). Unoccupied, inactive receptor monomers adopt closed conformation. The ligand binds an open conformation allowing dimerization of two receptor monomers. Upon dimerization, the intracellular KDs transphosphorylate each other resulting in fully activated receptors (Lemmon 2009).

2.1.2 Signaling pathways

ErbB receptors can activate several intracellular signaling pathways such as *phosphoinositol-3 kinase* (PI3K), *phospholipase C γ* (PLC- γ), *signal transducer and activator of transcription*

(STAT) and *mitogen activated protein kinase* (MAPK) pathways (Holbro and Hynes 2004) (Figure 2). The kinase activity of the receptor results in tyrosine phosphorylation of the target proteins, which often leads to altered cellular functions or activities (Lemmon and Schlessinger 2010).

ErbB receptors can activate PI3K pathway by recruiting the regulatory p85 subunit of PI3K via binding to its SH2 domain (Skolnik et al. 1991). Direct binding sites of PI3K have been identified in ErbB4 and ErbB3 (Schulze et al. 2005). Binding of p85 enables activation of the catalytic subunit p110 of PI3K and increased conversion of phosphoinositol-2-phosphate (PIP2) to phosphoinositol-3-phosphate (PIP3). This in turn can activate the Akt/mTor pathway resulting in, depending on the context, increased cell survival and migration (Manning and Cantley 2007).

PLC- γ can also be activated by ErbB receptors (Margolis et al. 1990; Peles et al. 1991). Upon activation it is phosphorylated, which activates the PLC γ . PLC γ cleaves PIP2 to secondary messenger molecules inositol-trisphosphate (IP3) and diacylglycerol (DAG). These secondary messenger molecules activate Protein kinase C (PKC) and increase intracellular calcium levels among other events (Rhee 2001). Both of these signals regulate multiple cellular functions such as migration, cell survival and proliferation (Suh et al. 2008).

ErbB receptors can also activate members of the STAT molecular family. In humans there are seven STAT genes. The ErbB receptors differ in which STAT molecules they activate ErbB1 being capable of activating STAT1, STAT3, STAT5a and STAT5b (Olayioye et al. 1999), ErbB2 can activate STAT1 and 3 and ErbB4 can activate STAT5a and STAT5b (Olayioye et al. 1999). After phosphorylation, the STATs dimerize and translocate into the nucleus where they bind specific target sequences on DNA to regulate gene expression affecting cell growth and survival. Modulation of STAT signaling has potential as a target for cancer therapeutics (Yu and Jove 2004).

Classical mitogenic signaling pathway involving MAPKs can also be activated by all ErbB receptors (Olayioye et al. 2001). All ErbB receptors may bind shc transforming protein (Shc) or growth factor receptor-bound protein 2 (Grb2) adaptor protein (Schulze et al. 2005) to recruit guanine-nucleotide exchange factor Sos, which initiates signaling via MAPK pathway by “catalyzing” the exchange of GDP bound to Ras to GTP. GTP-binding Ras is in active form and interacts with RAF, which in turn phosphorylates MEK. MEK in turn phosphorylates Erk resulting in translocation of Erk into nucleus and activation of several transcription factors such as SP-1 and AP-1 (Mor and Philips 2006).

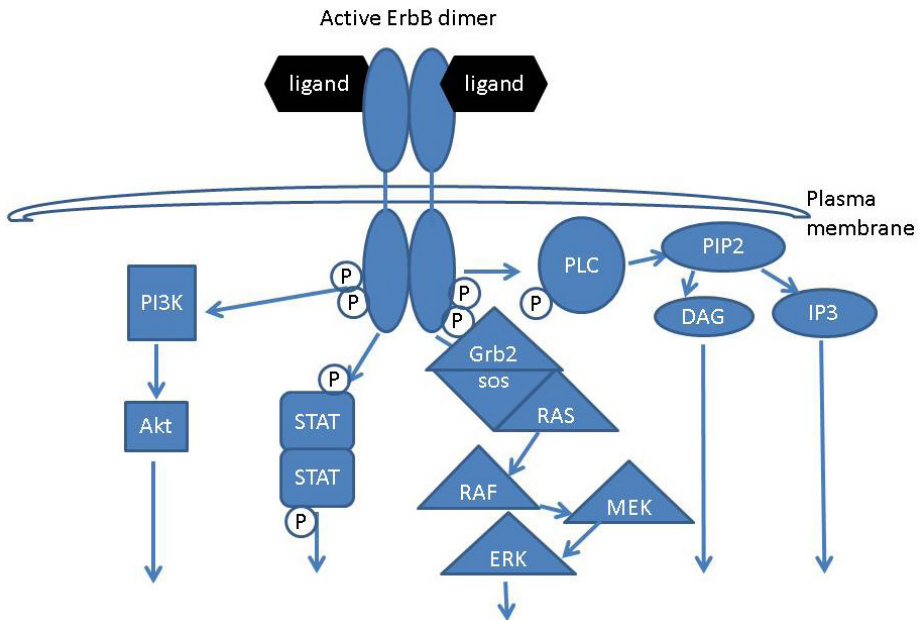


Figure 2. Schematic illustration of signaling cascades activated by the ErbB receptors. P, phosphorylated tyrosine residue.

2.1.3 Nuclear localization and regulated intramembrane proteolysis

All ErbB receptors have been detected in the cell nucleus in several studies (Marti et al. 1991; Xie and Hung 1994; Lin et al. 2001b; Ni et al. 2001; Offterdinger et al. 2002). The receptors may travel into the nucleus as intact full-length forms (ErbB1) or the ICD can be released from the membrane via intramembrane proteolysis (ErbB4). For ErbB2 and ErbB3 the mechanisms of nuclear translocation are not clearly understood but probably they use a similar route as ErbB1. All ErbB receptors have a tripartite nuclear localization signal, which allows their trafficking into the nucleus (Hsu and Hung 2007). The receptors may regulate gene expression in the nucleus. Mechanisms for nuclear translocation and functions for ErbB1 and ErbB4 have been studied in detail, and interestingly they seem to differ in their mechanisms and physiological roles (Figure 3).

ErbB1 is first endocytosed from the plasma membrane. After endocytosis, ErbB1 trafficks to the perinuclear area. Then, via interaction with importin b1, ErbB1 is translocated into the nucleoplasm (Lo et al. 2006), or via additional interaction with translocon sec61 first to the inner nuclear membrane and from there into the nucleoplasm (Wang et al. 2010). In the nucleus, full-length ErbB1 can act as a transcriptional co-activator (Lin et al. 2001a). As ErbB2 (Xie and Hung 1994), ErbB3 (Offterdinger et al. 2002) and also ErbB4 (Icli et al. 2012) have been detected in the nucleus as full-length receptors it is plausible that these full-length proteins may be transported via similar route to the nucleus as ErbB1.

ErbB4 ICD can also translocate into nucleus (Ni et al. 2001). The cleavage of the ICD of ErbB4 is enhanced by activation of receptor by a ligand (Ni et al. 2001). Activated receptor can then

be cleaved by tumor-necrosis factor α converting enzyme (TACE) generating a membrane-tethered fragment (m80) and a soluble extracellular fragment of ErbB4 (Elenius et al. 1997; Rio et al. 2000). This m80 fragment is subsequently cleaved by γ -secretase protease complex, which releases the ICD of ErbB4 into the cytosol (Ni et al. 2001). From cytosol the ICD can then translocate into the nucleus where it has been observed to regulate diverse processes such as mammary gland differentiation (Williams et al. 2004; Muraoka-Cook et al. 2006) and differentiation of astrocytes (Sardi et al. 2006).

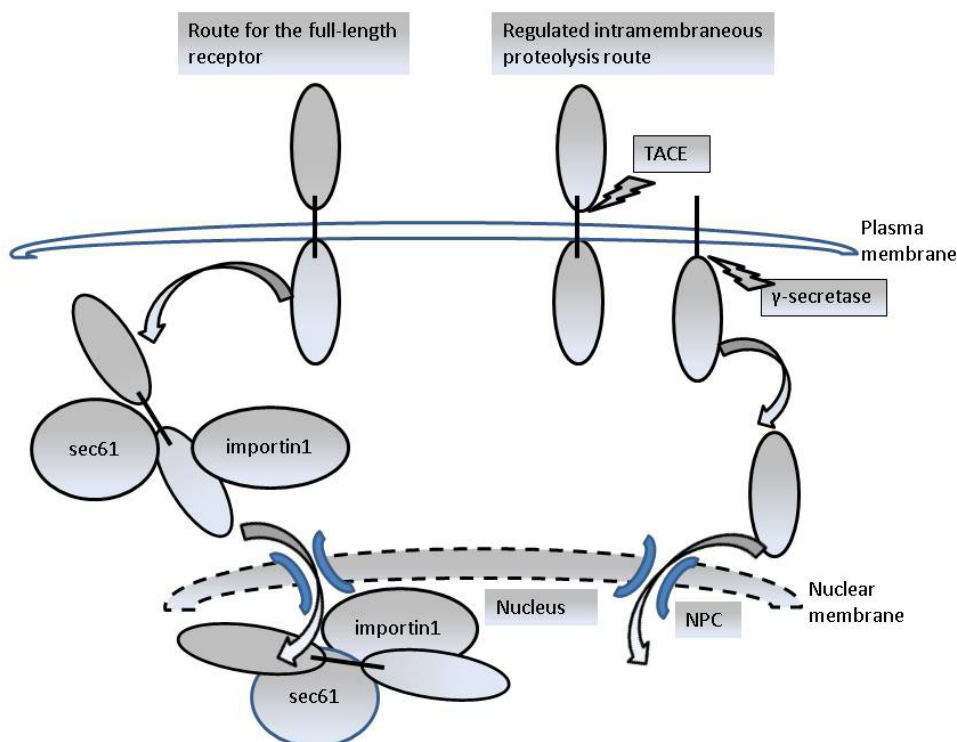


Figure 3: Nuclear transport routes of ErbB receptors. ErbB receptors can traffick to the nucleus either as full-length receptors or as proteolytically released soluble intracellular fragments. NPC=nuclear pore complex.

2.1.4 Negative regulation of ErbB receptors

As signaling of ErbB receptors is initiated by ligand binding or spontaneous activation (Linggi and Carpenter 2006), the signal also needs to be turned off. Three principal mechanisms negatively regulate signaling of ErbB receptors: internalization of the receptors by endocytosis, degradation of the receptors, and dephosphorylation of the receptors by tyrosine phosphatases (Fry et al. 2009).

During endocytosis, receptors are transferred from the cell membrane into intracellular vesicles. In the early endosomes, receptors may still be active and transmit signals (Miaczynska et al. 2004). In the late endosomes, the ligand dissociates from the receptor

and the unoccupied receptor may be translocated back to the cell surface or degraded in lysosomes (Miaczynska et al. 2004). ErbB1 seems to be most efficiently endocytosed (Baulida et al. 1996), although ErbB4 can also be effectively regulated by endocytosis (Sundvall et al. 2008).

Several ubiquitin ligases, that bind ErbB receptors and facilitate their ubiquitination, have been identified (Carraway 2010). Polyubiquitination of a protein typically targets it to degradation in the proteasomes (Pickart 2001), whereas monoubiquitination primarily affects receptor endocytosis and trafficking (Hicke and Dunn 2003). For example, cas-br-m murine ecotropic retroviral transforming sequence homolog (Cbl) binds activated ErbB1 and facilitates its ubiquitination and efficient internalization and degradation (Waterman et al. 1999) thus terminating the ligand-induced signaling.

Protein tyrosine phosphatases (PTP) are enzymes that remove phosphate moieties from phosphorylated tyrosine residues. Human genome harbors approximately 100 PTP genes as compared to approximately 90 tyrosine kinases. This suggests that similar complexity exists both in signal activation and signal attenuation mechanisms in phosphotyrosine signaling (Tonks 2006). Several PTPs have been associated with the regulation of ErbB signaling and affecting receptor endocytosis, receptor levels, and the extent of ErbB signaling (Tarcic et al. 2009; Monast et al. 2012).

2.1.5 ErbB receptors in embryonic development

Several knockout models for ErbB receptors have been generated. Generally, mice carrying homozygous deletion of any *ErbB* gene in all tissues die prematurely during embryonic development or during first three weeks of postnatal development (Gassmann et al. 1995; Miettinen et al. 1995; Sibilia and Wagner 1995; Threadgill et al. 1995). Some mouse strains carrying homozygous deletion of *ErbB1* are viable. However, the mechanisms behind this variation are not fully understood (Miettinen et al. 1995; Sibilia and Wagner 1995; Threadgill et al. 1995).

Consistent with the early observation that EGF is an agent that facilitates opening of eyelids in newborn mice (Cohen 1962), mice lacking functional *ErbB1* gene have defects in the opening of the eyelids (Miettinen et al. 1995; Threadgill et al. 1995). Mice with deleted *ErbB1* have defects in normal development of multiple tissues such as liver (Threadgill et al. 1995), kidney (Threadgill et al. 1995), lungs (Sibilia and Wagner 1995), and colon (Threadgill et al. 1995). Some *ErbB1*^{-/-} mice also have curly or wavy hair (Sibilia and Wagner 1995; Threadgill et al. 1995).

Deletion of the *ErbB2* gene in mice has revealed fundamental roles for *ErbB2* in cardiac and neuronal development. Mice deficient of functional *ErbB2* also die at embryonic day 10.5 due to poorly developed ventricular trabeculae (Lee et al. 1995; Erickson et al. 1997; Britsch et al. 1998; Chan et al. 2002). Mice lacking *ErbB2* have defects also in the development of the endocardial cushions, structures that later form the cardiac valves (Lee et al. 1995). During the neural development, the deletion of *ErbB2* affects development of Schwann cells

and myelination of the axons (Erickson et al. 1997; Woldeyesus et al. 1999; Garratt et al. 2000). Moreover, migration of neural crest cells and development of sympathetic nervous system is dependent on *ErbB2* (Britsch et al. 1998).

ErbB3 knock-outs have severe neuropathy involving defective development of Schwann cells and increased neuronal apoptosis (Riethmacher et al. 1997). Similarly to *ErbB2*-deficient mice, *ErbB3*-deficient mice have defects in the development of cardiac valves (Erickson et al. 1997; Qu et al. 2006) leading to heart dysfunction and embryonic lethality.

ErbB4-deficient mice have defects in the development of cardiac trabeculae, nervous system and the mammary gland. Function of ErbB4 during development is discussed in detail in chapter 3.2.2. Taken together, ErbB receptors are necessary for many aspects of normal development, and most striking phenotypes are perhaps observed in the cardiac and neural development.

2.1.6 ErbB receptors in disease

ErbB receptors have been associated with several malignancies, and they have an established role in tumorigenesis (Yarden and Sliwkowski 2001; Hynes and Lane 2005). ErbB receptors may turn oncogenic via several mechanisms such as somatic mutation, gene amplification or overexpression (Hynes and MacDonald 2009). For example, activation of *ERBB1* by somatic mutations has been observed in 19% of non-small cell lung cancers (Han et al. 2005) and *ERBB2* amplification has been reported even in 30% of breast cancers (Slamon et al. 1987). Indeed, ErbB1 and ErbB2 are useful therapeutic targets, and inhibition of ErbB1 in colorectal cancer (Cunningham et al. 2004) or ErbB2 in breast cancer (Slamon et al. 2001; Harris et al. 2011) has clinical anti-tumor activity and tens of thousands of patients are being treated with agents, such as therapeutic antibodies cetuximab and trastuzumab, interfering with ErbB signaling.

Although ErbB-modulating therapies are currently clinically used primarily to treat cancer, preclinical evidence suggests that ErbB-modulation could have therapeutic potential also for several other diseases, such as cardiac myopathia (Bersell et al. 2009), schizophrenia (Stefansson et al. 2002), and polycystic kidney disease (Richards et al. 1998; Wilson et al. 2006)

2.2 ErbB4

2.2.1 *ERBB4* gene and alternative splicing

The human *ERBB4* gene is located on chromosome 2 (2q33.3-q34) and covers about 1.2 Mb of genomic DNA. *ERBB4* cDNA was first cloned in 1993 (Plowman et al. 1993). *ERBB4* gene has 28 exons (Junttila et al. 2003) and at least six different isoforms are generated from *ERBB4* gene via alternative splicing. Variants of juxtamembrane regions (JM) are generated by alternative inclusion of exon 16 (JM-a) or exon 15 (JM-b) in the mature mRNA (Elenius

et al. 1997). Only JM-a isoform is able to undergo regulated intramembranous proteolysis (RIP) conducted by TACE and γ -secretase complex. The RIP process releases soluble ICD of ErbB4 into the cytosol and ICD can also translocate into the nucleus (Vecchi and Carpenter 1997; Ni et al. 2001). Consequently, JM-isoforms differ considerably in their biological functions (Veikkolainen et al. 2011b). Some evidence also exists that both exons 15 and 16 can be omitted (JM-c) or they can also both be present (JM-d) in the final mRNA product (Gilbertson et al. 2001).

Another variable region within the *ERBB4* mRNA is the cytoplasmic region (CYT), wherein exon 26 can be either included (CYT-1) or excluded (CYT-2) in the spliced mRNA product (Elenius et al. 1999; Junttila et al. 2003). Exon 26 encodes for binding sites for PI3K (Elenius et al. 1999) and for WW domain (Sundvall et al. 2008). These sites allow CYT-1 isoform to directly stimulate PI3K signaling and to bind additional WW domain-containing proteins such as Itch and WWOX (Sundvall et al. 2008).

Highest levels of *ERBB4* mRNA are observed in brain, kidney, salivary gland, trachea, thyroid gland, skeletal muscle and heart (Junttila et al. 2005). The different splice variants of *ERBB4* are expressed differently as exemplified by only JM-a being expressed in the kidney and JM-b being dominant in skeletal muscle (Junttila et al. 2005; Veikkolainen et al. 2011b). Cytoplasmic isoforms are both expressed in almost all tissues expressing ErbB4, although not necessarily in similar quantities (Junttila et al. 2005; Veikkolainen et al. 2011b).

2.2.2 ErbB4 in embryonic development

ErbB4 knock-out mice die at embryonic day 9.5 (Gassmann et al. 1995). Mice lacking *ErbB4* show decreased or absent trabeculation that results in defective functioning of the heart (Gassmann et al. 1995). In addition to the malformation of the heart, abnormal neural development is observed in the *ErbB4* deficient mice. *ErbB4* knock-outs that have been rescued for ErbB4 expression in the heart are viable suggesting that early mortality is due to cardiac defects (Tidcombe et al. 2003). These mice have abnormalities in the migration of neural crest cells, development of the nervous system and lung. Several studies have been conducted to analyze tissue-specific roles of ErbB4 using conditional tissue-specific deletions of *ErbB4*. Conditional knock-out mice generated by heart-specific (MyI2-Cre) deletions of *ErbB4* have reduced cardiomyocyte proliferation, absent trabeculae and these mice exhibit dilated cardiomyopathy (García-Rivello et al. 2005; Bersell et al. 2009).

Kidney-specific deletion of *ErbB4* (Pax8-Cre) results in defective polarization of tubular epithelial cells and increased size of the lumen of collecting ducts. Consistently, ErbB4 overexpression under the same promoter results in decreased lumen size and disorganized epithelial polarization (Veikkolainen et al. 2011a).

Mice with deletion of *ErbB4* (WAP-Cre) or expressing dominant-negative truncated form of *ErbB4* (MMTV-Cre) in the mammary gland show lactational failure indicating a critical role for ErbB4 in the development of the mammary gland (Jones et al. 1999; Long et al. 2003).

2.2.3 ErbB4 in disease

Expression of ErbB4 is altered in many cancers. ErbB4 has been reported to be underexpressed in meningioma (Laurendeau et al. 2009), renal cell carcinoma (Thomasson et al. 2004), thyroid cancer (Wiseman et al. 2008), pancreatic cancer (Graber et al. 1999; Thybusch-Bernhardt et al. 2001), glioma (Andersson et al. 2004) and in breast cancer (Srinivasan et al. 1998). On the other hand, has been reported to be overexpressed in breast cancer (Witton et al. 2003; Junttila et al. 2005), ovarian cancer (Steffensen et al. 2008), medulloblastoma (Gilbertson et al. 1997; Ferretti et al. 2006) and ependymoma (Gilbertson et al. 2002). At least a partial explanation for contradictory reports of ErbB4 expression in breast cancer may be provided by observation that ErbB4 expression is closely associated with estrogen receptor-positive subtype of breast cancer (Junttila et al. 2005), and that in earlier study (Srinivasan et al. 1998) the subtypes of breast cancers were not analyzed.

Expression of ErbB4 has also been shown to have prognostic significance. It has been associated with poor survival in breast cancer (Lodge et al. 2003), medulloblastoma (Gilbertson et al. 1997), gastric cancer (Shi et al. 2012) and colorectal cancer (Lee et al. 2002; Baiocchi et al. 2009). However, expression of ErbB4 has also been linked to favorable prognosis in breast cancer (Pawlowski et al. 2000; Witton et al. 2003; Junttila et al. 2005) and bladder cancer (Memon et al. 2004). Experimental models have also yielded contradictory results as ErbB4 has been suggested to function both as a tumor-promoting and as a tumor-suppressing factor (Naresh et al. 2006; Vidal et al. 2007; Das et al. 2010). This suggests that the role of ErbB4 in tumorigenesis is dependent on the tumor type.

Somatic mutations affecting *ERBB4* have been characterized in melanoma (Prickett et al. 2009; Dutton-Regester et al. 2012), lung cancer (Soung et al. 2006b; Ding et al. 2008), colon cancer (Soung et al. 2006b), gastric cancer (Soung et al. 2006b) and breast cancer (Soung et al. 2006b). At least some mutations affect signaling properties of ErbB4 (Prickett et al. 2009; Tvorogov et al. 2009) and it has been suggested that mutations of *ERBB4* play a role in tumorigenesis in these cancers (Soung et al. 2006b; Prickett et al. 2009). The malignant potential of ErbB4 remains controversial, and differs between cancer types. The reasons for these controversies remain to be elucidated.

ErbB4 has been linked with several neurological disorders. Clearest genetic evidence exist for schizophrenia wherein data from both mouse models (Stefansson et al. 2002) and human patients (Nicodemus et al. 2006; Silberberg et al. 2006; Greenwood et al. 2012) suggest that ErbB4 is associated with schizophrenia. Mice lacking one of the alleles of *ErbB4* or *Nrg1* show symptoms associated with schizophrenia in mice. In humans, single-nucleotide polymorphisms (SNP) of *ERBB4* (Nicodemus et al. 2006; Silberberg et al. 2006; Greenwood et al. 2012) and *NRG1* (Stefansson et al. 2002; Li et al. 2006; Munafo et al. 2006) loci have been statistically associated with likelihood of having schizophrenia.

ErbB4 deficient mice display defects in cardiac development (Gassmann et al. 1995; García-Rivello et al. 2005). Association of ErbB4 with heart failure has been observed also in humans, as hearts of patients suffering from heart failure have significantly reduced expression of

ErbB4 (Rohrbach et al. 2005). Preclinical evidence also implies potential for modulation of ErbB4 function in the treatment of myocardial infarction (Bersell et al. 2009).

2.3 Neuregulin-1

2.3.1 Neuregulin-1 gene and alternative splicing

The human *NRG1* gene is very large (1.4 Mb) and produces at least 15 different NRG-1 isoforms, which differ in their EGF-like domain (α or β), N-terminal ICD (type I,II or III) or being produced initially as soluble or membrane bound forms (NRG1 II β 3 is the only one produced as a soluble form) (Falls 2003). Membrane-bound forms can be released proteolytically by TACE (Horiuchi et al. 2005). Moreover, an intracellular fragment can be released into the cytosol by the γ -secretase complex (Bao et al. 2003) analogous to ErbB4. NRG-1 can bind its receptors both as soluble and membrane-bound forms and hence is capable of paracrine, autocrine and juxtacrine signaling (Falls 2003).

2.3.2 NRG-1 in embryonic development

Mice lacking *Nrg1* die early in their development around embryonic day 11.5 (Meyer and Birchmeier 1995). These mice have poorly developed ventricular trabeculae (Meyer and Birchmeier 1995) similar to *ErbB4*^{-/-} mice (Gassmann et al. 1995; García-Rivello et al. 2005). Deletion of *Nrg1* has revealed an important role for NRG-1 in the development of Schwann cells (Erickson et al. 1997; Britsch et al. 1998; Brinkmann et al. 2008), heart (Erickson et al. 1997; Britsch et al. 1998), muscle spindle (Hippenmeyer et al. 2002) and testis (Zhang et al. 2011). Besides these phenotypes, also various other defects of nervous system have been observed in the *Nrg1*-deficient mice (Meyer and Birchmeier 1995; Erickson et al. 1997; Liu et al. 1998; Wolpowitz et al. 2000). Interestingly, different NRG-1 isoforms have different roles during the development. For example, type I isoforms are important for development of the neural crest and type III isoforms for the development of Schwann cells (Meyer et al. 1997).

2.3.3 Neuregulin-1 in disease

NRG-1 has been associated with several diseases, such as schizophrenia (Stefansson et al. 2002; Li et al. 2006; Munafo et al. 2006). Mice carrying only one functional copy of *Nrg1* gene display schizophrenia-like phenotypes (Stefansson et al. 2002), resembling the phenotype of mice with *ErbB4* haploinsufficiency (Stefansson et al. 2002).

Consistent with the role of ErbB4 in proper functioning of the heart, also NRG-1 has been associated with heart dysfunction both in mice (Liu et al. 2005) and in humans. Indeed, promising results of using NRG-1 as a therapeutic agent in heart failure have been observed in both mice (Liu et al. 2006; Bersell et al. 2009) and in human clinical trials (Gao et al. 2010; Jabbour et al. 2011).

NRG-1 expression has been observed in many cancers including breast (Dunn et al. 2004), ovarian (Gilmour et al. 2002; Sheng et al. 2010), prostate (Leung et al. 1997; Memon et al. 2004), colorectal (Eschrich et al. 2005), pancreatic (Kolb et al. 2007) and thyroid cancer (Fluge et al. 2000). As with ErbB4, the prognostic role of NRG-1 varies between different cancer types and both associations with poor (Kolb et al. 2007; Sheng et al. 2010) and favorable (de Alava et al. 2007) prognosis have been observed.

2.4 Hypoxia-inducible factors

Hypoxia is defined as deficiency of oxygen. Hypoxic conditions are often encountered in pathological conditions such as malignant growth and ischemia. Hypoxia is also found in normal physiological milieu, for example of several cell types within cartilage. Cells sense hypoxia via distinct hypoxia sensing pathways. The key components of this pathway are hypoxia-inducible factors (HIF), which regulate the transcriptional response to hypoxia. HIF-1 α was cloned first (Wang et al. 1995), followed soon by HIF-2 α (EPAS-1) (Tian et al. 1997) and HIF-3 α (Gu et al. 1998). These HIF- α subunits dimerize with the HIF- β subunit also called aryl-hydrocarbon nuclear translocators (ARNT). HIF dimers can bind to DNA at specific hypoxia-response elements (Semenza and Wang 1992), and regulate transcription of specific target genes.

2.4.1 Oxygen-dependent and -independent regulation of HIFs

HIFs are regulated by multiple mechanisms. All HIF- α subunits are regulated by oxygen-dependent degradation, whereas the HIF- β subunit is not. The oxygen-dependent degradation of HIF- α subunit is initiated by post-translational prolyl 4-hydroxylation of the HIF- α subunit (Ivan et al. 2001; Jaakkola et al. 2001). In HIF-1 α , prolines 402 and 564 are hydroxylated in response to oxygen. This hydroxylation is mediated by three oxygen-sensitive prolyl 4-hydroxylases (PHDs) (Bruick and McKnight 2001; Epstein et al. 2001). These enzymes need molecular oxygen as a cofactor to function properly and therefore PHDs are fully active only in normal oxygen tension and are inhibited in hypoxic conditions. The hydroxylated proline residues of HIF-1 α are detected by von-Hippel Lindau protein (pVHL), which mediates ubiquitination and hence degradation of HIF-1 α by the proteasomes. In hypoxic conditions, when prolyl 4-hydroxylation does not occur, pVHL cannot bind and ubiquitinate HIF-1 α , ultimately leading into increased protein stability and accumulation of HIF-1 α protein in the cells (Pouyssegur et al. 2006). In addition to the regulation of the stability of HIF- α subunits, also transcriptional activity of HIF- α subunits is regulated in oxygen-dependent manner by another oxygen-dependent enzyme, factor inhibiting HIF-1 α (FIH-1) (Mahon et al. 2001). FIH-1 hydroxylates asparagine residue in the C-terminal transactivation domain of HIF- α subunits thus reducing transcriptional activity HIF- α subunits in normoxic conditions (Lando et al. 2002).

More recently, a few oxygen-independent mechanisms for the regulation of HIF-1 α protein stability have been described. These include stabilization of HIF-1 α by HSP90 to protect from

RACK1-dependent degradation (Liu et al. 2007) and degradation dependent of hypoxia-associated factor (HAF) (Koh et al. 2008). Also sumoylation (Bae et al. 2004; Berta et al. 2007; Carbia-Nagashima et al. 2007), acetylation (Jeong et al. 2002) and phosphorylation (Richard et al. 1999) of HIF-1 α have been described. Moreover, HIF-1 α may be regulated via classical signaling pathways such as PI3K (Laughner et al. 2001) and MAPK pathways (Richard et al. 1999). These examples imply that HIF-1 α is a subject to a complex regulatory machinery within the cell.

2.4.2 Hypoxia-inducible factors in embryonic development

HIFs are indispensable for normal development of mice. Deletion of *Hif1a* results in embryonic lethality and reduced angiogenesis (Iyer et al. 1998; Ryan et al. 1998). Conditional knock-out of *Hif1a* in mice has implicated a role for HIF-1 α also in development and homeostasis of lungs (Saini et al. 2008), heart (Huang et al. 2004), skeletal muscle (Mason et al. 2004), mammary glands (Seagroves et al. 2003) and brain (Tomita et al. 2003). Deletion of *Hif2a* results in embryonic lethality (Tian et al. 1998), altered metabolism (Scortegagna et al. 2003a), impaired development of the heart (Tian et al. 1998) and also in defective hematopoiesis (Scortegagna et al. 2003b). Mice deficient of *Hif3a* are, however, viable, although they exhibit developmental defects in the heart and lungs (Yamashita et al. 2008).

2.4.3 HIFs in disease

The link between increased anaerobic metabolism and cancer has been known for over 50 years (Warburg 1956). HIFs are key regulators of anaerobic metabolism, and indeed HIFs have been characterized as activators of multiple glycolytic enzymes (Semenza et al. 1994). Growth of new vessels, angiogenesis, represents another adaptation mechanism to hypoxia and it has been widely recognized as a highly important component of tumor biology (Folkman 1971). HIFs are important regulators of angiogenesis. Not surprisingly, HIFs are associated with several malignancies and HIF-1 α and HIF-2 α overexpression has been observed in numerous cancer types (Harris 2002; Pouyssegur et al. 2006).

Loss-of-function mutations in *VHL* gene have been linked to von Hippel-Lindau cancer syndrome (Latif et al. 1993) and Chuvash polycythemia (Ang et al. 2002a; Ang et al. 2002b). Similarly, gain-of-function mutations within *HIF2A* locus and loss-of-function mutations in *PHD2* locus have been linked to familial erythrocytosis (Percy et al. 2006; Percy et al. 2008a; Percy et al. 2008b). These observations imply that proper regulation of HIF activity is crucial for correct functioning of human body.

In ischemias of the heart and brain, the blood flow to tissue is suddenly blocked resulting in deficiency in oxygen and nutrients and ultimately to clinical strokes. As HIFs play fundamental roles in oxygen sensing and responses to hypoxia, they have also been implicated in the pathogenesis of ischemias. Interestingly, treatment of animals with HIF-activating compounds seems to reduce tissue damage elicited by ischemic conditions (Bergeron et al. 2000).

2.5 Zebrafish as an in vivo model to study ErbB4 signaling

2.5.1 Zebrafish as a model organism

Zebrafish has become a popular model vertebrate organism because it has several features that make it useful for research. Zebrafish are small vertebrates with a genome size comparable to humans, and the genome has been fully sequenced. Zebrafish lays eggs in large numbers, and they develop rapidly outside of the mother. This allows one to study developmental processes more easily than in mammals (Zon and Peterson 2005).

Many organ systems differ at the macroscopic level, but on microstructural, physiological and molecular level there is a great degree of conservation between zebrafish and mammals such as man and mouse (Zon and Peterson 2005).

Methodologically zebrafish is a highly utilizable and economic model for biomedical research (Zon and Peterson 2005). Several forward genetic screens have yielded mutations in hundreds or thousands of genes and Zebrafish Mutation Project (www.sanger.ac.uk/Projects/D_rerio/zmp/) which aims to mutate every zebrafish gene is currently in process and estimated to be completed in 2015. Moreover, targeted genome editing is achievable through the use of zinc-finger nucleases although homologous recombination techniques do not currently exist for the zebrafish (Doyon et al. 2008; Meng et al. 2008). Protein coding genes can also be easily targeted during early development by using morpholino antisense oligos, which can block translation or correct splicing of the mRNA (Nasevicius and Ekker 2000; Eisen and Smith 2008).

Hundreds of transgenic lines have been generated, which carry tissue-specific fluorescent reporters. These models are especially useful in zebrafish which is practically transparent during embryonic development and even almost transparent adult fish strains have been generated (White et al. 2008). Current transgenesis methods are robust and allow transient transgenic work with founder embryos without time-demanding breeding (Kwan et al. 2007). This allows rapid expression and testing of transgenes.

2.5.2 Biology of zebrafish

The zebrafish is a small fresh water fish that lives naturally in rivers of South East Asia. It is fairly easy to keep and breed in captivity. A single female can produce up to several hundred eggs per week. Lifespan of zebrafish is around 4 years and generation time 2-3 months. The development is rapid. The cleavage period is completed by 2.5 hours post fertilization (hpf), blastula stage by 5 hpf, gastrulation by 10 hpf and segmentation of the embryo is completed by 24 hpf (Figure 5) (Kimmel et al. 1995). The heart starts to beat and first muscle contractions occur one day post fertilization (dpf) and embryos are freely swimming and feeding at 5 dpf (Kimmel et al. 1995).



Figure 5. Development of zebrafish embryos at 2, 8, 24, 48 and 72 hours postfertilization (hpf). Embryos at 2 hpf are at cleavage stage, at 8 hpf at gastrulation stage, and at 24 hpf segmentation has been completed. Images have been taken with Zeiss StereoLumar stereomicroscope. Scale bar 0.5 mm.

Zebrafish are teleost (ray-finned) fish and they belong to cyprinid family (carps and minnows). The last common ancestor of teleost and tetrapods lived approximately 400-500 million years ago (Nüsslein-Volhard and Dahm 2002). The size of the zebrafish genome is 1.4 Gb and it consists of 25 autosomal chromosome pairs. It is currently estimated to carry 25,000 protein-coding genes. Zebrafish has no distinct sex chromosomes, but clear genetic component and association of distinct loci with sex determination have been reported (Anderson et al. 2012; Liew et al. 2012). In comparison, human genome is 3.2 Gb, has 23 autosomal chromosome pairs and two sex chromosomes and approximately 23,000 protein-coding genes. In teleosts, and also in the zebrafish, the genome has duplicated partially during the evolution and approximately 30% of genes have duplicated homologues in the zebrafish genome (Nüsslein-Volhard and Dahm 2002).

2.5.3 ErbB receptors in zebrafish

The ErbB family of receptor tyrosine kinase genes has expanded in teleosts and there are two homologues of *ERBB1* (*egfra* and *egfrb*), *ERBB3* (*erbb3a* and *erbb3b*) and *ERBB4* (*erbb4a* and *erbb4b*) in the zebrafish genome (Laisney et al. 2010). Also, some ErbB ligands have been duplicated including homologues of *HBEGF* (*hbegfa* and *hbegfb*) (Laisney et al. 2010) and *NRG2* (*nrg2a* and *nrg2b*) (Honjo et al. 2008).

Table 3. Summary of different phenotypes observed after perturbation of ErbB signaling in zebrafish.

Gene	Mutation / Morpholino	Phenotype	References
<i>egfra</i>	Morpholino	Blood circulation defect.	(Goishi et al. 2003)
<i>erbb2</i>	Mutation	Reduced heart trabeculation, Schwann cell migration and fin regeneration.	(Lyons et al. 2005; Rojas-Muñoz et al. 2009; Liu et al. 2010)
<i>erbb3b</i>	Mutation	Aberrant neural crest migration, pigmentation and fin regeneration.	(Budi et al. 2008; Hultman et al. 2009; Rojas-Muñoz et al. 2009)
<i>nrg1</i>	Mutation, morpholino	Reduced dorsal root ganglion neuron development, oligodendrocyte and neuron specification.	(Honjo et al. 2008; Wood et al. 2009)
<i>nrg2a</i>	Morpholino	Reduced dorsal root ganglion neuron development	(Honjo et al. 2008)
<i>hbegfb</i>	Morpholino	Cardiac defects	(Friedrichs et al. 2009)

The research on ErbB function in zebrafish models has had an emphasis on *erbb2* and *erbb3b* (also known as *picasso*) as loss-of-function mutations of these genes have been isolated (Lyons et al. 2005; Budi et al. 2008). Less work has been done on *egfr* and *erbb4*, although some results from a morpholino experiment to knock-down *egfra* have been published (Goishi et al. 2003). In zebrafish, ErbB receptors seem to be involved in similar developmental processes as in mouse, such as development of the heart and the neuronal system (Table 3). In addition to analysis of ErbB mutants and knock-down experiments, chemical genetic approaches have revealed roles for ErbB receptors in developmental angiogenesis (Tran et al. 2007) and heart valve formation (Scherz et al. 2008). Although tumorigenic potential of ErbB receptors in zebrafish has not been analyzed, in classical melanoma model of related fresh water fish *Xiphophorus* (Gordon 1927; Häussler 1928), an *EGFR* homologue (also called Xmrk) has been characterized as a powerful oncogene (Wittbrodt et al. 1989). In summary, the zebrafish model system seems to recapitulate many of the functions of ErbB receptors in mammals, and therefore can be considered a relevant and useful model system to study ErbB functions during development and disease.

3 AIMS OF THE STUDY

- Aim 1) To characterize novel interactions between the ErbB signaling system and HIF-1 α .
- Aim 2) To determine the biological significance of interactions between ErbB and hypoxia signaling pathways.
- Aim 3) To address the clinical significance and signaling mechanisms of ErbB4 in serous ovarian cancer.
- Aim 4) To generate a novel in vivo model to study the functions of ErbB4.

4 MATERIALS & METHODS

Materials and methods are described in detail in the original publications. Roman numbers I-V refer to original publication in which the given reagent/method was used.

4.1 Methods

Method	Used in
Affinity purification	I
Cell culture	I,II,III,IV
Cell fractionating	III
Co-immunoprecipitation	I
Confocal microscopy	I,II,V
Electron microscopy	V
Embryo culture	V
Glutathione-S-transferase (GST)-pull down	I
Hypoxia cabinet	I,III
Immunofluorescence	I,II,III,V
Immunohistochemistry	I,II,IV
In silico transcriptomics	I
In situ proximity ligation assay	I
In vitro transcription	V
In vitro translation	I
Ligand stimulations	I,II,III,IV
Luciferase assay	I,II
Microinjections	V
Molecular cloning	I,IV,V
Morpholino antisense oligos	V
Pharmacological modulations	I,II,III,IV,V
Primary cell isolation	III
Production of recombinant proteins in <i>E.coli</i>	I
Real-time RT-PCR	I,II,III,IV,V
Retroviral infection	I,IV
RNA extraction and synthesis of cDNA	I,II,III,IV,V
RNA interference with siRNAs	I,II
Soft agar growth assay	IV
Statistical analysis	I,II,III,IV,V
Stereo microscopy	V
Tissue microarray	IV
Transfections	I,II,IV
Transposon mediated transgenesis	V
Video imaging	V
Western blotting	I,II,III,IV,V

4.2 Plasmids

Name	Backbone	Purpose	Used in
β -casein-luc	pGL3	STAT5 activity reporter	II
ErbB4 JM-a CYT-2	pcDNA3.1-	Mammalian expression	I,II
ErbB4 JM-a CYT-2 HA	pcDNA3.1-	Mammalian expression	I,II
ErbB4 JM-b CYT-2	pcDNA3.1-	Mammalian expression	I,II
GST	pGEX-6P1	Bacterial expression	I
HIF1 α	pcDNA3	Mammalian expression	I,II
HIF1 α - Δ 1-174-6xhis	pcDNA3.1+	Mammalian expression	I
HIF1 α - Δ 1-343-6xhis	pcDNA3.1+	Mammalian expression	I
HIF1 α - Δ 1-529-6xhis	pcDNA3.1+	Mammalian expression	I
HIF1 α - Δ 1-631-6xhis	pcDNA3.1+	Mammalian expression	I
HIF1 α (P402A,P564G)	pcDNA3	Mammalian expression	I,II
HIF1 α -6xhis	pcDNA3.1+	Mammalian expression	I
HIF1 α -GST	pGEX-6P1	Bacterial expression	I
Hygro	pcDNA3.1+	Mammalian expression	I,II
ICD2	pcDNA3.1+	Mammalian expression	I,II
ICD2 Δ C	pcDNA3.1+	Mammalian expression	I
ICD2 Δ N	pcDNA3.1+	Mammalian expression	I
ICD2-GST	pGEX-6P1	Bacterial expression	I
Neo	pcDNA3.1-	Mammalian expression	I,II,
pBabe ErbB4 JM-a CYT-1	pBabe-puro	Mammalian retroviral expression	IV
pBabe ErbB4 JM-b CYT-2	pBabe-puro	Mammalian retroviral expression	I
pBabe-ErbB4 JM-a CYT-2	pBabe-puro	Mammalian retroviral expression	I,IV
pBABE-Puro	pBabe-puro	Mammalian retroviral expression	I,IV
pEGFP	pEGFP-N1	Mammalian expression	II
pPGK6-luc	pGL3	HIF activity reporter	I
pSV40-renilla	pRenilla	Control reporter	I
TK-renilla	pRenilla	Control reporter	I

4.3 Small interfering RNAs

Small interfering RNAs were synthesized as 21 nt double stranded (duplex) RNA. The duplexes were transfected into cells using Lipofectamine 2000 transfection reagent (Invitrogen) following recommendations of the manufacturer.

Name	Species	Company	Target sequence	Used
ErbB4 JM-a	Human	Eurogentec	gucaugacuaguggaccgtt	I
ErbB4 JM-b	Human	Eurogentec	guauugaagacugcaucggtt	I
ErbB4 total	Human	Eurogentec	acugagcucucucugactt	I
HIF1A#13	Human	Qiagen	aggaagaacuaugaacauaaa	II
HIF1A#5	Human	Qiagen	auggaaauauuucgcuuuu	II
Negative	Human	Qiagen	aattctccgaactgtcacgt	I,II
RACK1#1	Human	Qiagen	aucauguccgggaacugcggg	I
RACK1#5	Human	Qiagen	uaaacuucuagcgugugccuu	I

4.3 Primers and probes

Following real-time RT-PCR primers and probes were used in the studies. Numbered probes are from Universal Probelibrary (Roche), and other probes are standard hydrolyzation probes labeled with 6-carboxyfluorescein (FAM) and tetramethylrhodamine (TAMRA).

Target	Species	Left primer	Right primer	Probe	Used in
<i>BETA-ACTIN</i>	Human	atctggcaccacacctctacaat	ccgtcaccggagtcctca	tgaccagatcatgtttgagacctcaacac	II,IV
<i>EF-1α</i>	Human	ccccaggacacagagacttt	gccattcttgagatacca	#56	I
<i>EPO</i>	Human	tcccagacaccaaagta atttcta	ccctgccagacttctacgg	#58	I
<i>ERBB4 CYT-1</i>	Human	caacatcccacctcccctctatac	acactcctgttcagcagcaaa	tgaaattggacacagccctctcctcg	IV
<i>ERBB4 CYT-2</i>	Human	caacatcccacctcccctctatac	acactcctgttcagcagcaaa	aattgactcgaataggaaccagttgtataccgagat	IV
<i>ERBB4 JM-a</i>	Human	cccccattgccatccaaa	ccaattactccagctgcaatca	catggacgggcaattccactttacca	I,II,IV
<i>ERBB4 JM-b</i>	Human	cccccattgccatccaaa	ccaattactccagctgcaatca	ctcaagtattgaagactgcatcgccctgat	IV
<i>ERBB4 TOTAL</i>	Human	tcaagcattggataatccga	agtggctcattcacatactcatct	tatcacaaatgcaccaatggctcacc	II
<i>GLUT-1</i>	Human	gtggcatgtgcttcagtc	aagacagaaaccaggagcaca	aactgtgtggtccctcagctctcatct	I,II
<i>HIF-1α</i>	Human	gatagcaagacttctctcagtcg	tggctcatatcccataattc	#64	I
<i>PGK-1</i>	Human	tgcaaggccttgagag	tggatctgtctgcaact ttagc	#72	I
<i>VEGF-A</i>	Human	tctactctcaccatgccaaagt	tgatgattctgcctctctcc	ccaggctgcaccatggcaga	I
<i>cmcl2</i>	Zebrafish	caggagcccagaccaaca	agcagttttcccctcttg	#112	V
<i>erbb4a</i>	Zebrafish	aaaccgcaactgtcttcc	ccagaggaagatagtaaaactgg	#21	V
<i>erbb4b</i>	Zebrafish	atgtgcatcccctgcaact	cgtctgaaggctggcagct	#43	V
<i>myhc4</i>	Zebrafish	caagcagaagcagcgtga	gggtagcacaaaagccttcag	#82	V
<i>rp13a</i>	Zebrafish	gcgaccgattcaataagg	gaaagacgaccgaggtgaga	#147	V
<i>smyhc1</i>	Zebrafish	tgccaagaccatcagaaatg	cacaccaaagtgaattcgata	#52	V
<i>tpm1</i>	Zebrafish	gaacgccttgacagagc	ttccaactgaattagttcgtctct	#30	V

4.4 Cell lines

Cell line	Type	Species	Used in
MCF-7	Mammary adenocarcinoma cell	Human	I
T47D	Mammary adenocarcinoma cell	Human	II
COS-7	Fibroblast-like kidney cell	African green monkey	I
HEK-293	Embryonic kidney cell	Human	II
OVCAR-3	Ovarian carcinoma cell	Human	IV
SKOV-3	Ovarian carcinoma cell	Human	IV
HUVEC	Umbilical cord endothelial cell	Human	III
RCC4	Renal cell carcinoma	Human	I
MDA-MB-468	Mammary adenocarcinoma cell	Human	I,II

4.5 Reagents

Name	Target	Source	Used in
AG 1748	ErbB inhibition	Calbiochem	I,II,IV,V
CoCl ₂	PHD inhibition	Sigma Aldrich	I,II,III
DMOG	PHD inhibition	Cayman Chemicals	II
GSI IX	γ -secretase inhibition	Calbiochem	I,III
LY294002	PI3K inhibition	Calbiochem	I,IV
PMA	Inducer of NRG-1 cleavage	Calbiochem	II

4.6 Antibodies

Antigen	Name	Source	Type	Application	Used in
Akt	sc-1618	Santa Cruz	Goat polyclonal	WB	I,II,IV
Beta-actin	sc-1616	Santa Cruz	Goat polyclonal	WB	I,II,III,IV,V
ErbB1	sc-03	Santa Cruz	Rabbit polyclonal	WB	IV
ErbB2	sc-284	Santa Cruz	Rabbit polyclonal	WB	IV
ErbB3	sc-285	Santa Cruz	Rabbit polyclonal	WB	IV
ErbB4	sc-283	Santa Cruz	Rabbit polyclonal	WB, IHC, IF	I,II
ErbB4	e200	Abcam	Rabbit monoclonal momoclonalmonoclonal	WB, IF	I,II,IV,V
ErbB4	HFR-1	Abcam	Mouse monoclonal	IF,IHC, PLA	IV,IV,V
Erk	9102	CST	Rabbit polyclonal	WB	I,II,IV
GLUT-1	ab14683	Abcam	Rabbit polyclonal	IHC	I,II
GST		Santa Cruz	Goat polyclonal	WB	I
HA	3F10	Roche	Rat monoclonal	WB,IF	I,II
HIF-1 α	ab2185	Abcam	Rabbit polyclonal	WB,PLA	I,II
HIF-1 α	clone 54	BD	Mouse monoclonal	WB, IP	I,II,III
HIF-1 α	H1a67	Abcam	Mouse monoclonal	IHC, PLA	I
Lamin B	sc-6217	Santa Cruz	Goat polyclonal	WB	III
Muscle actin, fast type	F310	DSHB	Mouse monoclonal	WB, IF	V
Muscle, actin, slow type	F59	DSHB	Mouse monoclonal	WB, IF	V
NRG-1	F20	Santa cruz	Rabbit polyclonal	WB	III
p53	DO-1	Santa Cruz	Mouse monoclonal	WB	IV
phospho-Akt	9271	CST	Rabbit monoclonal	WB	I,II,IV
phospho-ErbB4	4757	CST	Rabbit monoclonal	WB	II,IV,V
phosphoErk	9101	CST	Rabbit monoclonal	WB	I,II,IV
RACK-1	ab62735	Abcam	Rabbit polyclonal	WB, PLA	I
Tropomyosin	CH1	DSHB	Mouse monoclonal	WB, IF	V

SC = Santa Cruz Biotechnology, CST = Cell Signaling Technology, DSHB = Developmental studies hybridoma bank, BD = Beckton-Dickinson Biosciences, WB = Western blotting, IF = immunofluorescence, IHC = immunohistochemistry, IP = immunoprecipitation, PLA = in situ proximity ligation assay.

4.7 Microinjected materials

Reagent	Type	Function	Used in
Control MO	Morpholino	Negative control	V
<i>erbb4a</i> MO	Morpholino	ErbB4a knock-down, prevents translation of ErbB4a mRNA.	V
<i>EGFP</i>	RNA	Negative control mRNA	V
<i>ERBB4-EGFP</i>	RNA	Rescue mRNA for <i>erbb4a</i> morpholino.	V
Tol2 transposon	RNA	Facilitate integration of transgenes into genome.	V
pDESTTol2A2-acta1- <i>EGFPpA</i>	DNA	Zebrafish muscle cell actin promoter driven muscle-cell specific expression of EGFP. Tol2 sites for genome integration by Tol2 transposase.	V
pDESTTol2A2-acta1- <i>ERBB4-P2A-EGFPpA</i>	DNA	Zebrafish muscle cell actin promoter driven muscle-cell specific expression of human ErbB4 (JM-a CYT-1) and co-expression of EGFP with self-cleaving P2A-sequence. Tol2 sites for genome integration by Tol2 transposase.	V
pDESTTol2A2- <i>βactin-EGFPpA</i>	DNA	Zebrafish beta-actin promoter driven expression of EGFP. Tol2 sites for genome integration by Tol2 transposase.	V
pDESTTol2A2- <i>βactin-ERBB4-P2A-EGFPpA</i>	DNA	Zebrafish beta-actin promoter driven expression of human ErbB4 (JM-a CYT-1) and co-expression of EGFP with self-cleaving P2A-sequence. Tol2 sites for genome integration by Tol2 transposase.	V

4.8 Zebrafish methods

4.8.1 Maintenance

Adult zebrafish were maintained at 26 °C in glass aquaria equipped with in-tank filters and aeration using standard procedures (Westerfield 2000). The system water was active charcoal filtered tap water and it was allowed to warm to 26°C overnight prior to addition to the aquaria. Fish were fed with flakes, frozen blood worms and live *Artemia nauplii* once or twice per day. Dried *Artemia* cysts were hatched at 26 °C (in medium containing 3% sea salt in system water) in inverted plastic bottles with vigorous aeration (Nüsslein-Volhard and Dahm 2002).

4.8.2 Breeding and embryo culture

Eggs were obtained by natural spawning by using self-made mesh-bottomed mating boxes to separate eggs from adult fish. The mating boxes were placed into the bottom of the fish aquaria in the afternoon. Zebrafish mate at the morning right after the lights have been

turned on, and hence the fertilized eggs could be collected from the mating boxes during the next morning. The eggs were collected by pouring the water from mating boxes into a tea strainer and washed several times with system water.

The fertilized eggs and developing embryos were cultured in E3-medium (5 mM NaCl, 0.17 mM KCl, 0.33 mM CaCl₂, 0.33 mM MgSO₄) at 28 °C (Nüsslein-Volhard and Dahm 2002). E3-medium was supplemented with methylene blue (100 ppm), penicillin and streptomycin to reduce microbial growth. When needed, pigmentation of embryos was inhibited by adding phenyl-thio-urea (0.2 mM) into the E3-medium.

4.8.3 Microinjection

Embryos at 1-8 cell stage were microinjected using Femtotip glass capillary needles (Eppendorf), Femtojet pressure system (Eppendorf) and Injectman2 micromanipulator attached to SteReoLumarV.12 stereomicroscope (Zeiss). A microscope glass slide was placed on a bacterial culture plate and embryos were aligned along the side of the slide. Excess water was aspirated and surface tension of water prevented the embryos from moving during the injections. Injection volume was calculated by injecting a small droplet into hydrocarbon oil (Sigma). The diameter of the droplet was measured and the volume calculated using following equation: $V = \frac{4}{3} \times \pi \times r^3$. Morpholinos, in vitro transcribed mRNAs and DNA constructs were injected into yolk (3 nl injection volume) near the animal pole of the embryo.

4.8.4 Immunofluorescence

Prior to fixation embryos were dechorionated by forceps or by incubation with 2 mg/ml pronase (Roche). Embryos were fixed with 4% paraformaldehyde in PBS overnight at 4 °C, or with 100% methanol for at least 20 min at -20 °C. Paraformaldehyde fixation was followed by permeabilization with methanol at -20 °C. To rehydrate the samples, they were placed for 5 min periods in 100%, 75%, 50%, 25% and 0% of methanol in PBST (0.1% Tween-20 in PBS). Embryos were blocked with 5% normal goat serum in PBST for 3 hours at +4°C. Primary antibodies were added to the solutions and samples were incubated overnight at 4 °C. Unbound antibodies were washed off with four washes with PBST (15 min, room temperature). Subsequently, Alexa -488 and Alexa 555 goat anti-mouse secondary antibodies were applied in 5% blocking solution, and incubated 3 hours at room temperature with nuclear stain DAPI. Unbound secondary antibodies were washed off with four 15 min washes with PBST at room temperature. Next, the embryos were cleared and mounted in 87% glycerol. Images were taken with LSM510 META confocal microscope (Zeiss) or with StereoLumar V.12 stereomicroscope (Zeiss).

4.8.5 RNA extraction

First, the embryos were collected into fresh microcentrifuge tubes. Medium was aspirated from the tubes and embryos were homogenized with a motorized pellet pestle (Sigma-

Aldrich) into 500 μ l of Trisure RNA extraction reagent (Bioline) supplemented with 2 μ g/ml glycogen (Roche) as an RNA carrier. Five hundred microliters of Trisure and 250 μ l of chloroform was added and samples were mixed thoroughly and incubated on ice for 15min. The samples were centrifuged at 12000 g for 15 min at 4 °C, and upper solution phase containing RNA was transferred into new tube. Equal volume of isopropanol was added, samples vortexed and centrifuged at 12000 g for 15 min at 4°C. The RNA was precipitated and supernatant discarded. The pellet was washed with 75% ice-cold ethanol, dried and resuspended in water. The protocol was used for sample sizes of 1-8 embryos resulting in total RNA yield of 1.2-2.4 μ g/embryo.

4.8.6 Touch-response assay and digital video motion analysis

The motility of zebrafish embryos was measured using a touch-response assay (Granato et al. 1996). Dechorionated 48 hpf embryos acclimated in room temperature for at least 15 min in E3-medium were used in the assay. The tail of the embryo was gently touched by using a plastic inoculation loop. This resulted in rapid escape-response, or burst-swim, of the embryo. To quantitate the response the assays were video recorded, and the length and average speed of the burst was analyzed by ImageJ and ParticleTracker plug-in (written by Fabrice Cordelieres, Institute Curie, Orsay, France; <http://rsb.info.nih.gov/ij/plugins/track/track.html>). Embryos that did not respond to touch at all were discarded and not used in statistical analyses.

5 RESULTS

5.1 *ErbB4* and *Hif1a*-deficient mice have similar phenotypes in lactating mammary gland (I)

During literary searches to find novel genes associated with ErbB4 function I observed that mice specifically deficient of *ErbB4* (Jones et al. 1999; Long et al. 2003) and *Hif1a* (Seagroves et al. 2003) in their mammary glands had highly similar phenotypes during lactation. In both mice, the lobuloalveoli were condensed and production of milk proteins was reduced, indicating that secretory differentiation of mammary gland epithelium was affected. These observations suggested that some kind of interplay between ErbB4 and HIF-1 α might exist.

5.2 ErbB4 and HIF-1 α target genes are co-expressed in humans (I)

To further study the potential interplay of ErbB4 and HIF-1 α an *in silico* gene expression analysis was carried out. *In silico* analysis (Kilpinen et al. 2008) of mRNA expression in 975 normal and 3577 cancer tissue samples revealed that expression of *ERBB4* and *NRG1* had clear positive association with expression of surrogate markers of HIF-1 α activity, erythropoietin (*EPO*), carbonic anhydrase IX (*CAIX*) and glucose transporter 1 (*GLUT1*) (I, Fig. 2, Table S1 and S2). This association was observed in both normal and malignant tissues. In normal tissue types, a statistically significant positive association was observed 32 tissue types and only one negative association was observed between *ERBB4* or *NRG1* and *EPO*, *GLUT1* or *CAIX* ($p < 0.001$). Similar situation was observed for malignant tissues where 37 positive and 2 negative statistically significant associations were found ($p < 0.001$). Statistically significant associations between the expression of *ERBB4* and *EPO* ($p = 0.002$), *CAIX* ($p = 0.003$) or *GLUT1* ($p < 0.001$) implied that these genes are indeed co-expressed in human tissues *in vivo*. Similarly, co-expression of *NRG1* and *EPO* ($p < 0.001$), *CAIX* ($p = 0.002$) or *GLUT1* ($p = 0.002$) was observed.

5.3 ErbB4 promotes HIF-1 α activity (I)

The similarity of phenotypes in *ErbB4* and *Hif1a*-deficient mice, and clear association of the expression of *ERBB4* with the expression of HIF-1 α target genes, supported a hypothesis that these two signaling pathways were connected. To address this hypothesis, series of *in vitro* experiments were carried out. Indeed, ErbB4 activity increased transcription of HIF-1 α target genes *EPO*, *GLUT1*, vascular endothelial growth factor A (*VEGF-A*) and phosphoglycerate kinase 1 (*PGK1*) (I, Fig 1B). Moreover, ErbB4 and *NRG-1* increased HIF-1 α transcriptional activity in luciferase reporter assays (I, Fig. 4A, B and G). Only JM-a isoforms of ErbB4 that are able to undergo γ -secretase mediated RIP, accumulated HIF-1 α protein and induced HIF-1 α activity (I, Fig. 4C and D). Moreover, treatment of cells with GSI IX, a γ

-secretase inhibitor, inhibited ErbB4-mediated HIF-1 α accumulation and HIF-activity (I, Fig. 4E and F).

5.4 Physical interaction between ErbB4 and HIF-1 α (I)

The observation that induction of HIF-1 α protein expression and transcriptional activity was dependent on the cleavage of ErbB4 raised the possibility that ErbB4 and HIF-1 α could directly interact in the nucleus. Indeed, physical interaction between ErbB4 and HIF-1 α was observed in co-immunoprecipitation (I, Fig. 5D and S4B), GST-pull down (I, Fig. 5F and G) and in situ proximity ligation (PLA) assays (I, Fig. 5B and C). GST pull down experiments using in vitro translated and bacterially expressed recombinant ErbB4 and HIF-1 α suggested that the physical interaction between ErbB4 and HIF-1 α was direct, and did not need any scaffold protein (I, Fig. S4A). GST-pull down analysis of in vitro translated deletion constructs of HIF-1 α and ErbB4 suggested that residues of 1-343 of HIF-1 α and residues 676-996 of ErbB4 were necessary for the physical interaction between HIF-1 α and ErbB4 (I, Fig. 4F and G). Moreover, using PLA assay, this interaction was observed in the nucleus of MCF-7 cells (I, Fig. 5B and C), where the colocalization of HIF-1 α and ErbB4 was also observed (I, Fig. 5A).

5.5 ErbB4 attenuates RACK1-mediated degradation of HIF-1 α (I)

To further characterize the role of ErbB4 in the regulation of HIF-1 α , the mechanism of accumulation of HIF-1 α by ErbB4 was investigated. Stimulation of cells with the ErbB4 ligand NRG-1 reduced HIF-1 α degradation as indicated by increased HIF-1 α protein levels after inhibition of protein synthesis by cycloheximide (I, Fig. 3E and F). Interestingly, this effect was neither dependent on prolyl 4-hydroxylation (I, Fig. 3G) nor the presence of pVHL (I, Fig. 3D). To find potential regulators of HIF-1 α stability, I performed a thorough literary screen. Indeed, RACK1 (GNB2L1) had been characterized as a protein that regulated proteasomal degradation of HIF-1 α in an oxygen-independent manner (Liu et al. 2007). As the deletion mapping of interaction between ErbB4 and HIF-1 α revealed a similar binding region for ErbB4 and RACK1 within the HIF-1 α protein (I, Fig. 5G and (Liu et al. 2007)), RACK1 represented a strong candidate for being involved in the ErbB4-mediated regulation of HIF-1 α . RNA interference of RACK1 increased basal level of HIF-1 α , and reduced the relative effect of NRG-1 in accumulating HIF-1 α (I, Fig. 6A). Moreover, stimulation of cells with NRG-1 led to reduced binding of HIF-1 α and RACK1 (I, Fig. 6B and C). Taken together, these results imply that ErbB4 stabilizes HIF-1 α by interfering with RACK1-HIF-1 α interaction and thus reduces ubiquitination and proteasomal degradation of HIF-1 α .

5.6 HIF-1 α promotes accumulation of ErbB4 protein (II)

To further assess the interplay of ErbB4 and HIF-1 α we turned our attention to the HIF-1 α deficient mice. Interestingly, mice deficient for HIF-1 α showed reduced ErbB4 expression

in their lactating mammary glands (II, Fig 1). RNA interference of HIF-1 α also resulted in reduced levels of ErbB4 in T47D breast cancer cells (II, Fig. 2B) and HEK293 human embryonic kidney cells (II, Fig. 3A). Consistently, increasing HIF-1 α levels by stabilization of HIF-1 α by hypoxia mimicking compounds cobalt chloride and dimethylxalyl glycine (DMOG), as well as, transfection of HIF-encoding plasmids, resulted in increased protein levels of ErbB4 (Fig. 2A, 2B and 3A). This mechanism was associated with reduced degradation of ErbB4, as after cobalt chloride treatment ErbB4 was degraded less rapidly after blocking protein synthesis by cycloheximide treatment (II, Fig 3D). Accumulation of ErbB4 also resulted in prolonged ErbB4 phosphorylation by NRG-1 and increased activity of ErbB4 to induce transcription from β -casein promoter construct in a luciferase assay (Fig. 4A and B).

5.7 ErbB4 and HIF-1 α interplay enhances differentiation of mammary epithelial cells (II)

An in vitro model of ErbB4-mediated mammary gland differentiation (3D matrigel cultures of MDA-MB-468 mammary adenocarcinoma cells (Tvorogov et al. 2009)) was used to study functional interplay of ErbB4 and HIF-1 α in vitro. In this model, the differentiation is seen by formation of organized ball-like structures called acini, whereas the undifferentiated cells form disorganized colonies (II, Fig 4C). In the studies, chemical induction of HIF-1 α (DMOG) increased ErbB4-mediated differentiation of MDA-MB-468 cells in vitro by 51% (II, Fig 4D). Consistently, targeting endogenous HIF-1 α by siRNAs inhibited ErbB4-mediated differentiation of MDA-MB-468 cells by 62% (II, Fig 4E).

5.8 HIF signaling regulates bidirectional signaling of the ErbB4 ligand NRG-1 (III)

As HIFs are main regulators of angiogenic responses both during development and disease (Pouyssegur et al. 2006), we analyzed the role and function of ErbB signaling in endothelial cells. In primary human vein endothelial cells isolated from umbilical cord (HUVEC), high-levels of NRG-1 was observed to be expressed in membrane bound form (III, Fig. 1A and B). ErbB1 and ErbB2 were expressed but ErbB3 and ErbB4 were not expressed in HUVECs (III, Fig. 3A and B). A soluble intracellular fragment of NRG-1 was generated in response to binding of ErbB4 ECD to membrane bound NRG-1. The ICD of NRG-1 was observed in the nucleus of endothelial cells (III, Fig. 2B and C). Interestingly, the mechanism of NRG-1 cleavage occurred in a similar manner to the regulated intramembranous proteolysis of ErbB4 and Notch. The membrane bound domain of NRG-1 was accumulated by γ -secretase inhibitor and the cleavage process was enhanced by phorbol 13-myristate 12-acetate (PMA) (III, Fig. 2A).

The hypoxia-mimick cobalt chloride and hypoxia increased NRG-1 protein level indicating potentiated NRG-1 signaling under these conditions (III, Fig. 2A and data not shown, respectively). The effect of bidirectional NRG-1 signaling was analyzed by measuring

chemotactic migration of endothelial cells. Interestingly, induction of NRG-1 ICD cleavage suppressed endothelial migration, and inhibition of ICD release by using γ -secretase inhibitor restored migration back to control level (III, Fig. 2D).

Consistent with the observation of absence of NRG receptors, addition of NRG-1 did not increase proliferation, migration or differentiation of HUVECs in vitro (III, Fig. 4 A-C). However, NRG-1 induced angiogenesis in vivo in the mouse corneal micropocket angiogenesis assay (III, Fig. 5) and in the chicken chorioallantoic membrane (CAM) assay (III, Fig. 7D). NRG-1 induced VEGF-A production of HACAT cells (III, Fig. 6) and VEGFR inhibition by SU1498 in CAM assay inhibited pro-angiogenic effect of NRG-1 (III, Fig. 7D). This indicated that NRG-1 induces angiogenesis in vivo by increasing VEGF-A production in paracrine manner.

5.9 The expression of CYT-1 isoform of ErbB4 is associated with poor prognosis in ovarian cancer (IV)

Functions of ErbB4 had been well studied in breast cancer, but only few studies on samples of ovarian cancer had been conducted and the role of ErbB4 in this disease was largely unknown. To analyze the potential role of ErbB4 in serous ovarian cancer, a tissue microarray analysis of ErbB4 protein (n=482) and real-time RT-PCR analysis of ErbB4 isoforms (n=198) were carried out. 90% of samples were detected positive for an intracellular epitope of ErbB4 protein by immunohistochemistry and strong expression was observed in 76% of cases (IV, Fig. 1 and Table 1). Total immunoreactivity of ErbB4 did not associate with any of the clinico-pathological markers used (IV, Fig. 1). Cytoplasmic expression of ErbB4 was associated with low grade and stage (IV, Table 1), but was not significantly associated with survival (p=0.11, data not shown).

When real-time RT-PCR analysis of the samples was conducted, it was observed that ErbB4 was expressed in 87% of samples (IV, Fig. 2B). Expression of JM-a isoform did not yield any significant associations and JM-b variants were not expressed in the sample material (IV, Fig. 2B). Interestingly, expression of the CYT-1 isoform was associated with poor survival of patients (p=0.0028, n=121), whereas expression of CYT-2 was not (IV, Fig. 2C). When the CYT-1:CYT-2 ratio was used in statistical analyses, an even stronger association with poor survival was observed (p<0.0001, n=113) (IV, Fig. 2C). Moreover, in multivariate analysis of survival performed by using Cox proportional hazards model, CYT-1 was identified as an independent prognostic indicator (IV, Hazard ratio 1.79, p= 0.021) in serous ovarian cancer.

5.10 ErbB4 CYT-1 promotes anchorage-independent growth of ovarian cancer cells in a PI3K dependent mechanism (IV)

To solve the apparent controversy between immunohistochemical and RT-PCR analysis of ErbB4 in serous ovarian cancer, a series of in vitro experiments were performed. ErbB4 variants were retrovirally introduced into naturally ErbB4-positive OVCAR-3 and ErbB4-negative SKOV-3 ovarian cancer cell lines (IV, Fig. 3B and C), and these cells were analyzed

in soft agar anchorage-independent growth assay to assess their transformed phenotype. ErbB4 JM-a CYT-1 isoform was able to increase growth of OVCAR-3 and SKOV-3 cells in soft agar, whereas JM-a CYT-2 variant was not (IV, Fig. 3D and E) suggesting that CYT-1 overexpression promoted transformation. CYT-1 isoforms possess a binding site for a subunit of PI3K and hence can directly activate PI3K, while CYT-2 isoforms cannot (Elenius et al. 1999). The signaling mechanism of the ErbB4 JM-a CYT-1 variant was pharmacologically analyzed by using chemical ErbB and PI3K inhibitors. Indeed, the increased growth in soft agar induced by CYT-1 was blocked by both ErbB kinase inhibitor and PI3K inhibitor (IV, Fig 4A). These results imply that ErbB4 JM-a CYT-1 can act as tumor growth promoting factor in ovarian cancer, and that this effect is dependent on ErbB kinase and PI3K activity.

5.11 Zebrafish model of ErbB4 signaling (V)

As expression of ErbB4 and HIF-1 α target genes was associated in many human tissues, I hypothesized that interplay of ErbB4 and HIF-1 α could be needed for development of several other tissues besides mammary gland. To explore the biology of ErbB4, I established a zebrafish model. Zebrafish genome harbors two *ERBB4* homologues, *erbb4a* and *erbb4b*. The *erbb4a* gene was the primary gene expressed during organogenesis, whereas *erbb4b* was mainly expressed during very early development (V, Fig 1A). Thus the further analyses were focused on *erbb4a*.

Activity of zebrafish ErbB4 was reduced by using the ErbB kinase inhibitor AG1478 (50% reduction in ErbB4 phosphorylation) and by blocking translation of ErbB4 protein by using anti-sense morpholino RNA interference oligos (99% reduction in ErbB4 protein expression) (V, Fig. 2A and 2E). Morpholino oligos were designed to block translation of mRNA into protein, an approach previously shown to be highly effective in the zebrafish model (Nasevicius and Ekker 2000).

Knock-down or pharmacological inhibition of the zebrafish homologue of *ERBB4*, caused defects in the developing skeletal and cardiac muscles. Slow-type muscle fibers were more condensed as, although they were thinner (V, Fig. 4A and B), fibers contained similar levels of slow-type myosin heavy chain protein as control fibers (V, Fig. 6C). Electron microscopic analysis of embryos revealed signs of myofibril degeneration in the *erbb4a* morphants (V, Fig. 5).

Zebrafish embryos exhibit an early escape response when touched gently on the tail already at day 2 of development (Naganawa and Hirata 2011), although actual swimming capability is achieved on day 5 of development when swim bladder inflates. To assess functional consequences of *erbb4a* knock-down, touch-response assays were performed. The speed and distance during early escape response was measured and quantified using video recordings. Interestingly, embryos treated with the ErbB kinase inhibitor or the *erbb4a* targeting morpholino showed both reduced average speed and distance of burst swimming (V, Fig. 2A-D). Swimming behavior of *erbb4a* morphants co-injected with *ERBB4* mRNA was

normal indicating that human *ERBB4* can functionally replace zebrafish *erbb4a*, and that defects associated with *erbb4a* morpholino injection were indeed caused by deficiency of *erbb4a* (V, Fig. 3A-D). Moreover, mosaic expression of human *ERBB4* under a muscle-specific promoter partially restored swimming ability of *erbb4a* morphants (V, Fig. 7B-D), indicating that *erbb4a* expression in the muscle cells was sufficient for restoring proper swimming ability.

6 DISCUSSION

6.1 Cross-talk between HIF-1 α and ErbB signaling pathways

ErbB4 was found to exhibit a close interplay with HIF-1 α . This interplay may function bidirectionally as ErbB4 can induce HIF-1 α , but HIF-1 α can also induce ErbB4 signaling. These observations suggest that ErbB4 and HIF may form a positive feed-back loop (Figure 6). In this type of a signaling pathway, the net outcome is a sharpened and intensified response of both pathways to activating stimulus (Alon 2007; Avraham and Yarden 2011). The conceptual model suggests that once the signaling loop is activated by an ErbB4 ligand or HIF-activation, the activation is more rapid, and intense and longer as compared to signaling without such a feed-back loop. Moreover, NRG-1 signaling may be induced by HIF-activation by cobalt chloride or hypoxia, in the endothelial cells. Hypoxia/HIF regulation of other ErbB4 ligands, such as HB-EGF (Xia et al. 2003; Munk et al. 2012) and NRG-2 (Munk et al. 2012), has also been described. These ligands may also potentially participate in the ErbB4-HIF cross-talk.

However, as HIF seems to reside both upstream and downstream of ErbB4 in the signaling networks, it is possible that both modes of signaling exist *in vivo*. To date several independent reports of either HIF regulation of the ErbB pathway or ErbB regulation of the HIF pathway exists (Zhong et al. 2000; Laughner et al. 2001; Munk et al. 2012). The full understanding of the effects of ErbB-HIF cross-talk in both pathways may require detailed kinetic and quantitative analysis of all involved proteins followed by mathematical modeling.

Currently it is not known if cross-talk of the ErbB and HIF pathways is a fundamental property of these pathways, or merely a fine tuning mechanism existing in mammals. In support of ErbB4-HIF cross-talk also in other organisms, knock-down of zebrafish homologue of HIF-1 α (HIF1ab) by HIF1ab targeting translation blocking morpholino oligos resulted in reduction of ErbB4 level and knock-down of ErbB4 resulted in reduced amount of HIF-1 α (Paatero et al, unpublished observations). These data imply that reciprocal regulation of ErbB4 and HIF-1 α may also exist in zebrafish.

As both ErbB receptor and HIF genes are co-expressed in almost all multicellular animals (Stein and Staros 2000; Srivastava et al. 2010; Rytönen et al. 2011), it is possible that the cross-talk between these signaling pathways has evolved early during evolution of the animals. Nematode *C. elegans* has only one ErbB receptor (*let-23*), one ErbB ligand (*lin-3*), and one HIF (*hif*) gene, suggesting that it would be a good candidate model for future research to elucidate the question of conservation of potential HIF-ErbB cross-talk across different phyla.

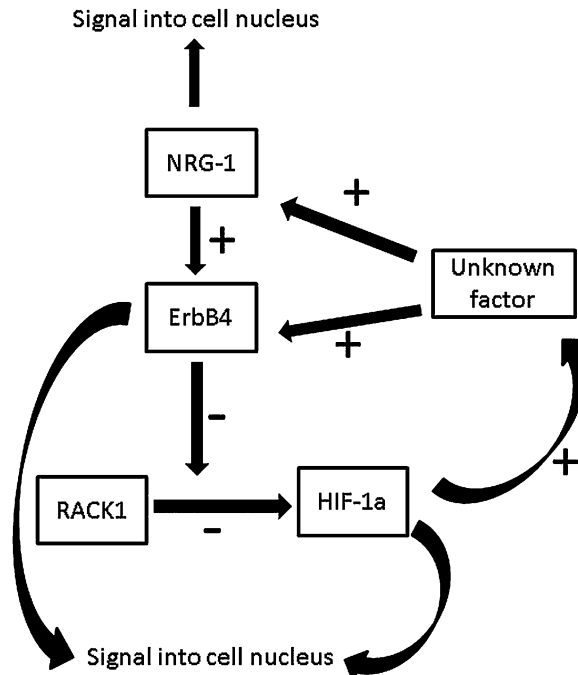


Figure 6. Schematic figure of ErbB4-HIF-1 α cross-talk. Arrow denotes for a functional interaction, plus sign (+) is for positive regulation and minus sign (-) for negative regulation.

6.2 Molecular insights into regulation of ErbB4 and HIF

My studies have uncovered the molecular mechanism by which ErbB4 regulates HIF-1 α . ErbB4 reduced proteasomal degradation of HIF-1 α in a process that was dependent on ErbB4 cleavage, proteasome function, kinase activity of ErbB4, binding of ErbB4 to HIF-1 α , and the presence of RACK1. On this basis I postulate that ErbB4 increased HIF-protein stability by interfering with binding of RACK1 to HIF-1 α . This mechanism is distinct from the earlier observation that the ErbB receptors are capable of activating HIF-1 α via the PI3K pathway (Zhong et al. 2000; Laughner et al. 2001) and most probably also via the MAPK pathway (Richard et al. 1999; Olayioye et al. 2001). These pathways, however, are generic signaling pathways activating numerous genes and proteins.

The molecular mechanism by which HIF-1 α regulates ErbB4 remains more elusive. ErbB4 protein degradation was reduced by induction of HIF-1 α but long over-night incubations were needed for this effect. This implies that some HIF-1 α regulated genes may be responsible for the reduced degradation of ErbB4. As HIF almost exclusively activates transcription of genes (Schödel et al. 2011), it seems plausible that this unknown factor is a HIF-1 α -induced repressor of ErbB4 degradation.

6.3 Bidirectional signaling of NRG-1 and ErbB4

Endothelial cells are a vital part of the organismal response to hypoxia, as HIFs induce production of many angiogenic factors. Therefore, we analyzed the role of ErbB signaling in endothelial cells. Interestingly, the ErbB4 ligand NRG-1 was expressed and processed by RIP in endothelial cells. In the process, soluble ICD was generated from NRG-1, and this ICD was capable of translocating into the nucleus. Interestingly, the generation of nuclear ICD reduced migration of endothelial cells, whereas paracrine signaling via the released soluble ectodomain of NRG-1 did not. These observations suggest that the generation of NRG-1 ICD produces a signal within the endothelial cell. In neurons, generation of NRG-1 ICD has been associated with neuronal survival (Bao et al. 2003).

In the RIP process active form of NRG-1 ECD is also released into the extracellular space. In vivo in the mouse corneal micropocket angiogenesis assay and in the chicken chorioallantoic membrane assay, NRG-1 ectodomain induced angiogenesis. Moreover, NRG-1 ectodomain induced VEGF-A production in the HACAT (III, Fig.6) and MCF-7 (I, Fig. 1B) cells indicating that endothelial NRG-1 may transmit angiogenic signals in paracrine manner. This suggests that RIP-mechanism may regulate both retrograde signaling of NRG-1 and also paracrine activation of NRG-1 receptors.

Interestingly, also other ErbB4 ligands BTC and HB-EGF have been observed to be processed by RIP. The BTC-ICD potentially transmits antiproliferative signals (Stoeck et al. 2010) whereas HB-EGF-ICD is associated with invasiveness of gastric cancer cells (Shimura et al. 2012). Similarly, bidirectional signaling mediated by RIP has been observed with for example Dll1/NOTCH (De Strooper et al. 1999; Six et al. 2003) and within the receptor tyrosine kinase family with Ephrins and their receptors (Tomita et al. 2006; Haapasalo and Kovacs 2011). Taken together, bidirectional signaling of membrane-bound ligands and their receptors is clearly a phenomenon extending beyond the RTK family and their ligands, and is potentially regulating many yet unidentified processes in development and disease.

6.4 Developmental implications of ErbB-HIF cross-talk

Analysis of normal tissues by in silico transcriptomics implied that ErbB-HIF co-regulation may also exist in normal tissues. Mammary gland specific deletion of *ErbB4* in mice showed reduced HIF signaling and mammary gland specific deletion of *Hif1a* reduced ErbB4 protein levels. This supports the hypothesis that ErbB4 and HIF pathways interact during normal development of the mammary gland. However, NRG-1/ErbB4 and HIF co-expression was identified also in several other tissues such as heart, muscle, pancreas, prostate and kidney, evoking hypothesis that co-regulation may occur also in these tissues. As knock-down of *erbb4a* in zebrafish embryos reduced *hif1ab* protein level (Paatero et al, unpublished data), it is plausible that ErbB4-HIF-1 α cross-talk occurs during development of other tissues besides the mammary gland.

6.5 Clinical implications of ErbB HIF regulation

The modulation of ErbB-HIF cross-talk could provide an opportunity to treat cancer. Both ErbB and HIF pathways are highly active in many solid tumors (Harris 2002; Holbro and Hynes 2004), implying that the cross-talk of these pathways might have a role in the biology of the tumors. The *in silico* transcriptomics analysis indicated that *ERBB4/NRG1* and HIF-1 α -regulated genes are co-expressed in many different cancer types. Moreover, ErbB4 overexpression in xenograft mouse tumor model increased HIF-signaling (Paatero et al, unpublished data). Several potential ways to inhibit ErbB-HIF cross-talk could be designed. Inhibition of ErbB receptors by kinase inhibitors and therapeutic antibodies already in use in the clinic could be used to reduce HIF-signaling in tumors. The interaction of ErbB4 and HIF-1 α could also be targeted, although inhibition of intracellular protein-protein interactions is currently technically challenging. Increasing ErbB activity by growth factor administration could increase HIF signaling and yield therapeutic effects for example in ischemic conditions.

6.6 Role of ErbB4 in biology of ovarian cancer

Despite of some earlier studies, the role of ErbB4 in the ovarian cancer has remained unclear. Increased total ErbB4 expression has been observed with increased stage of ovarian cancer (Gilmour et al. 2001; Steffensen et al. 2008; Pejovic et al. 2009). However no significant associations with survival have been found (Pejovic et al. 2009). Our analyses were focused on samples of serous ovarian cancer. Ovarian cancer can be divided into four subgroups and serous ovarian cancer comprises of about 40% of ovarian cancers (Kobel et al. 2008). Serous ovarian cancer originates from epithelial cells of fallopian tube (Bowtell 2010). Despite decades of research, the survival of patients with ovarian cancer has not prolonged since the 1970s (Vaughan et al. 2011).

Here I show that a specific isoform of ErbB4 CYT-1 was selectively associated with poor survival, and it increased the anchorage-independent growth of ovarian cancer cells. This indicates a role for a specific ErbB4 isoform in the biology of the serous ovarian cancer and may partially explain why significant correlations between total ErbB4 protein and survival in ovarian cancer had not been observed in earlier studies.

6.7 Targeting ErbB4 to treat ovarian cancer

My results support the idea that targeting of ErbB4 may provide a new approach to develop therapeutics for serous ovarian cancer. Targeting of other ErbB receptors such as ErbB1 and ErbB2 has shown a modest clinical effect in treatment of ovarian cancer (Gordon et al. 2006; Palayekar and Herzog 2007; Makhija et al. 2010). As ErbB receptors extensively heterodimerize and thus form a diverse signaling network (Yarden and Pines 2012), it may be necessary to block multiple, if not even all four, ErbB receptors to achieve a robust therapeutic response in the clinic. As ovarian cancer frequently harbors genetic lesions

activating signaling pathway components down-stream of the ErbB receptors (Network CGAR 2011), inhibiting these downstream targets, such as the PI3K-pathway, together with ErbB receptors may be necessary to achieve significant responses.

As CYT-1 and CYT-2 isoforms of ErbB4 demonstrated different role in serous ovarian cancer, it might be beneficial to selectively target the CYT-1 isoform. However, neither kinase inhibitors nor therapeutic antibodies can differentiate between the two ICDs. Therefore, more advanced approaches are needed to for selective targeting of CYT-1. Such potential methods would be RNA interference (Burnett et al. 2011), genetic inactivation of CYT-1 exon within the tumor by targeted nucleases (Kim et al. 2009) or homologous recombination (Russell and Hirata 1998), or by expressing CYT-1 targeting single-chain intracellular antibodies, intrabodies (Alvarez et al. 2000). However, all of these methodologies are still at the experimental stage.

6.8 Utilizing ErbB4 as a prognostic marker in ovarian cancer

Based on the results of this thesis, ErbB4 CYT-1 could be evaluated as a prognostic marker to predict the outcome of serous ovarian cancer. Both CYT-1 and the ratio of the expression levels of CYT-1 and CYT-2 were strongly associated with poor survival (IV, Fig. 2C). However, independent studies with additional patient cohorts are needed to confirm this association and to make it a clinically utilizable marker. As single markers often do not provide strong enough associations to make firm prognostic predictions (Zhang et al. 2007), the ErbB4 CYT-1, or CYT-1/CYT-2 ratio, could be combined with other molecular markers to strengthen the prognostic value and clinical usability. Currently, the prognostic significance of expression of any ErbB receptor in ovarian cancer is unclear, as many conflicting studies have been published (Lafky et al. 2008). This situation may be resolved by using larger patient cohorts and quantitative methods, such as real-time RT-PCR, in order to obtain robust statistical associations.

6.9 Modeling of ErbB4 signaling in zebrafish

To gain deeper insight into the role of ErbB4 during development, a zebrafish embryo model of ErbB4 signaling was developed. Treatment with morpholino antisense oligonucleotides or with an ErbB4 kinase inhibitor resulted in effective inhibition of ErbB4 function in the developing zebrafish embryos. Moreover, rescue experiments with human ErbB4 encoding mRNA and transgenes showed both specificity of the morpholino treatment and functional redundancy between human and zebrafish ErbB4.

Using the morpholino antisense oligonucleotides and the ErbB4 kinase inhibitor, ErbB4 (*erbb4a*) was found necessary for normal development of skeletal muscles in developing zebrafish embryos. In skeletal muscle specific conditional knockout mice deficient of both *ErbB2* and *ErbB4* (*HSA-Cre+/-;Erbb4^{fllox/fllox};Erbb2^{fllox/fllox}*) muscles have been reported to be normal and no strong muscle phenotype was reported (Escher et al. 2005), although some

defects in acetylcholine receptor recycling and signal transmission in the neuromuscular junction may occur (Schmidt et al. 2011). Nevertheless, these mice have significantly reduced body weight consistent with a defect in muscle growth (Escher et al. 2005). Heterozygous *ErbB4* null (*ErbB4*^{fllox/-}) mice also showed reduced body weight during post-natal period and homozygous nervous-system specific *ErbB4* null mice (*Nestin-CRE+/-; ErbB4*^{fllox/-}) reduced muscle strength and reduced physical activity (Golub et al. 2004). As these mice show multiple neurological defects (Stefansson et al. 2002; Golub et al. 2004), the direct effects on the muscle development are difficult to interpret from these studies.

Pathological relevance of the NRG-1/ErbB4 signaling in the human skeletal muscle is unclear. Both NRG-1 and ErbB4 are upregulated in the rat skeletal muscle after muscle denervation (Nicolino et al. 2009). Moreover, in a mouse model of muscular dystrophy (mdx mouse) NRG-1 injections ameliorate the muscular loss and dysfunction (Krag et al. 2004). Observations made with *erbb4a* morphant zebrafish suggest a critical role for ErbB4 in the development of skeletal muscles and imply that the therapeutic effect of NRG-1 in the mouse model of muscular dystrophy may be transduced via ErbB4.

When compared to results of a large zebrafish mutagenesis screen, *erbb4a* knock-down phenotype resembles the phenotype of mutants having reduced motility, reduced muscle striation, and heart defects (group A3) or mutants having reduced striation and muscle degeneration (group A4) (Granato et al. 1996). Genes affected in the mutant lines *slop*, *jam* and *slinky* in the A3 category have not been isolated. Mutations in the A4 category are located or linked to *dystrophin* (*dmd*, *sapje*) (Bassett et al. 2003), *laminin B2* (*lamb2*, *softy*) (Jacoby et al. 2009) or *titin* (*tttnb*, *runzel*) (Steffen et al. 2007) genes. These genes are all associated with different subtypes of muscular dystrophy in humans (Steffen et al. 2007; Lin 2012). Interestingly, ultrastructural analysis by electron microscopy have revealed that the *erbb4a* morphants have similar degenerative changes in sarcomeres as do embryos with *titin* mutation (Steffen et al. 2007).

Skeletal muscle differentiation and development has been well-characterized in zebrafish. Somitogenesis begins around 10 hpf and ends around 24 hpf, when all the embryonic somites have been formed (Kimmel et al. 1995). By 48 hpf the skeletal muscles have been innervated and are able to contract. Slow-type muscle cells develop earlier, and characteristic coiling behavior mediated by slow muscle contraction can be observed already at 24 hpf (Naganawa and Hirata 2011). Fast-type muscle cells develop later and burst swimming behavior characteristic to fast muscle cells can be first observed around 48 hpf (Naganawa and Hirata 2011). In the burst swim assays inhibition of ErbB4 either by morpholino oligos or with the kinase inhibitor reduced burst swimming speed and length, suggesting defects in functioning of fast-type muscle cells.

The zebrafish model of ErbB4 signaling could reveal other new phenotypes associated with ErbB4 function. As ErbB4 is strongly expressed in the brain of the zebrafish embryo, it seems plausible that future research will find neurological phenotypes of ErbB4-deficient embryos. The zebrafish model of ErbB4 signaling could also be used as a tool to functional

analysis of the increasing number of ErbB4 genetic variations and mutations associated with schizophrenia (Nicodemus et al. 2006; Silberberg et al. 2006; Greenwood et al. 2012) and cancer (Soung et al. 2006a; Ding et al. 2008; Prickett et al. 2009; Dutton-Regester et al. 2012).

7 CONCLUSIONS

In this study, functions of NRG-1 and ErbB4 were studied in vitro and in vivo. The following key conclusions can be made.

- 1) NRG-1/ErbB4 signaling stabilizes HIF-1 α and increases HIF-1 signaling.
- 2) Expression of NRG-1/ErbB4 is associated with increased HIF-1 activity in vivo in mice and in humans.
- 3) Reciprocally, HIF-1 activity can increase signaling via NRG-1/ErbB4 pathway by increasing NRG-1 and ErbB4 protein levels.
- 4) NRG-1 signal is transmitted both within the NRG-1 expressing endothelial cells as well as to adjacent cell expressing ErbB receptors in paracrine manner.
- 5) Expression of the specific ErbB4 isoform CYT-1 is associated with poor prognosis in serous ovarian cancer.
- 6) ErbB4 is needed for normal development of skeletal muscles in zebrafish embryos.

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Pipetin alla,
aukeaa tuntematon.
– uusi erämaa,
taas kutsuu kulkijaansa.

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