THE FUNCTION OF NR3B AND NR4A ORPHAN NUCLEAR RECEPTORS IN OSTEOBLASTS

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ACADEMIC DISSERTATION

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To my dear husband and family

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ABSTRACT

Nuclear receptors comprise a large family of proteins that mediate the effects of small lipophilic molecules such as steroid and thyroid hormones. In addition, there are a group of nuclear receptors that lack identified natural ligands and are referred as orphan nuclear receptors. In this thesis, the function of two such orphan nuclear families has been studied. The NR3B family includes the receptors ERR α (NR3B1), ERR β (NR3B2) and ERR γ (NR3B3) and the NR4A family includes the receptors NGFI-B (NR4A1), Nurr1 (NR4A2) and Nor1 (NR4A3). NR3B receptors (ERRs) are constitutively active. They are closely related to estrogen receptors but unable to bind natural estrogens as their ligand. However, ERRs bind other ligands, including 4-hydroxytamoxifen and diethylstilbestrol, which function as their inverse agonists inhibiting their activity. NR3B receptors regulate cellular energy balance and carcinogenesis. In addition, it has been suggested that NR3B receptors play a role in bone homeostasis. NR4A receptors are true orphan receptors as their ligandbinding pockets (LBPs) are tightly packed with bulky, hydrophobic side chains, which makes them incapable of binding ligands. NR4A receptors have an important role in the central nervous system in which Nurr1 regulates the differentiation of dopaminergic neurons. However, NR4A receptors are also expressed in peripheral tissues including the bone.

The purpose of this thesis work was to study the signaling and function of NR3B and NR4A orphan nuclear receptors specifically in osteoblasts. The aim was to identify (I) new signaling pathways that regulate the transcriptional activity of NR3B and NR4A receptors, (II) new ligands for the NR3B family, (III) to investigate how NR3B and NR4A orphan nuclear receptors affect the Wnt signaling pathway and finally (IV) to analyze the role of ERR α in osteoblastic differentiation of mesenchymal stem cells (MSCs).

NR4A receptors were found to be regulated by NR3B receptors as ERR α and ERR γ inhibited the transcriptional activity of NR4A receptors in U2-OS cells. Another signaling pathway that was found to repress the activity of NR4A receptors in osteoblasts was the Wnt/ β -catenin signaling pathway. β -catenin repressed the transcriptional activities of Nurr1, NGFI-B, and Nor1. On the other hand, NR3B receptors were found to be repressed by NR4A receptors as NGFI-B and Nor1 repressed the transcriptional activity of ERR γ in HeLa cells.

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The phytoestrogen equol was identified as a new agonist for ERR γ and ERR β in PC-3, U2-OS, and SaOS-2 cells. Equol increased the transcriptional activity of ERR γ by increasing the interaction between ERR γ and the co-activator GRIP-1 and by inducing a conformational change in the LBP of ERR γ . We also showed that ERR γ could mediate some of the potentially beneficial health effects of equol as the growth inhibitory effect of equol on PC-3 prostate cancer cells was decreased by blocking ERR γ expression by siRNA.

The Wnt signaling pathway is important for the differentiation and function of osteoblasts. Both the NR3B and also the NR4A receptors were found to repress the transcriptional activity mediated by β -catenin in U2-OS cells. Nurr1 was also able to repress the β -catenin induced expression of Axin2 mRNA in MC3T3-E1 cells.

The MSCs isolated from the bone marrow of 8-12 week old male ERR α knockout (KO) mice showed diminished proliferation, osteoblastic differentiation and expression of the bone marker genes osteocalcin and bone sialoprotein (*BSP*) compared to the cells isolated from their wild-type littermates. The overexpression of ERR α in osteoblastic MC3T3-E1 cell line increased their mineralization and the expression of BSP, Runx2 and alkaline phosphatase mRNAs. *BSP* was shown to be a direct target gene for ERR α and ERR γ as the *BSP* promoter was activated in HeLa cells when transfected with ERR α or ERR γ together with PGC-1 α . The adipogenic differentiation of ERR α KO MSCs was also decreased and they expressed less adipogenic markers PPAR γ and aP2.

As a conclusion, the studies described in this thesis demonstrated that the transcriptional activity of NR3B and NR4A receptors can be regulated by other orphan nuclear receptors and signaling pathways in osteoblasts. NR3B receptors can also be regulated by ligands and a new agonist, equol, was identified for ERR β and ERR γ . New roles for NR3B and NR4A were also identified as they were shown to converge with the Wnt signaling pathway in osteoblasts, ERR γ was shown to mediate the growth inhibitory effect of equol in prostate cancer cells, and ERR α was shown to regulate positively MSC proliferation, osteoblastic differentiation and adipogenic differentiation.

ORIGINAL PUBLICATIONS

The thesis is based on following original articles that are referred to in this text by their Roman numerals.

- I. Lammi J, Rajalin AM, Huppunen J, Aarnisalo P (2007) Cross-talk between the NR3B and NR4A families of orphan nuclear receptors. Biochem Biophys Res Commun 359: 391-397
- II. Hirvonen J*, Rajalin AM*, Wohlfahrt G, Adlercreutz H, Wähälä K, Aarnisalo P (2011) Transcriptional activity of estrogen-related receptor γ (ERRγ) is stimulated by the phytoestrogen equal. J Steroid Biochem Mol Biol 123:46-57 *Equal contribution
- III. Rajalin AM, Aarnisalo P (2011) Cross-talk between NR4A orphan nuclear receptors and β-catenin signaling pathway in osteoblasts. Arch Biochem Biophys 509:44-51
- IV. Rajalin AM, Pollock H, Aarnisalo P (2010) ERRα regulates osteoblastic and adipogenic differentiation of mouse bone marrow mesenchymal stem cells. Biochem Biophys Res Commun 396: 477-482

In addition to the above studies, some unpublished data are presented.

Original publication I was included in the thesis "Orphan nuclear receptor subfamily NR4A – their interplay with other nuclear receptors and functions in osteoblasts" by Dr. Johanna Lammi. The manuscript of the article II was included in the thesis "Transcriptional regulation by the orphan nuclear receptor $ERR\gamma$ " by Dr. Johanna Hirvonen.

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ABBREVIATIONS

AF	activation function
ALP	alkaline phosphatase
AP-1	activator protein-1
AR	androgen receptor
BALP	bone-specific alkaline phosphatase
BMD	bone mineral density
BMP	bone morphogenetic protein
BSP	bone sialoprotein
CAR	constitutive androstane receptor
Chſβ	core-binding factor β
C/EBP	CCAAT/enhancer-binding protein
Coll I	collagen type I
CTE	C-terminal extension
DAX-1	dosage-sensitive sex reversal-adrenal hypoplasia congenita critical region on
DAA-1	the X chromosome, gene 1
DBD	DNA-binding domain
DBD DES	diethylstilbestrol
DES Dsh	Dishevelled
EMSA	electrophoretic mobility shift assay
ER	estrogen receptor
ERE	estrogen response element
ERK	
ERR	extracellular signal-regulated kinase
ERRE	estrogen-related receptor
	estrogen-related receptor response element
ESR	estrogen receptor (gene)
ESRRA	estrogen-related receptor alpha (gene)
ESRRB	estrogen-related receptor beta (gene)
ESRRG	estrogen-related receptor gamma (gene)
FGF FSH	fibroblast growth factor
FSH FXR	follicle-stimulating hormone
FZD	farnesoid X receptor frizzled
GR	glucocorticoid receptor
GRIP1	glucocorticoid receptor-interacting protein 1
GSK3β	glycogen synthase kinase 3 β
НАТ	
HDAC	histone acetyltransferase histone deacetylase
HRE	•
KO	hormone response element knockout
LBD	ligand-binding domain
LBD LBP	ligand-binding pocket
Lbr	
LRP	lymphoid enhancer-binding factor low density lipoprotein receptor-related protein
LXP	liver X receptor
MAPK	mitogen-activated protein kinase
MAPK M-CSF	•
IVI-CSF	macrophage colony-stimulating factor

MEK	MAPK and ERK kinase
MSC	mesenchymal stem cell
NBRE	NGFI-B responsive element
NFATc1	nuclear factor of activated T cell c1
NF-κB	nuclear factor-KB
NGFI-B	nerve growth factor inducible-B
Nor1	neuron-derived orphan receptor 1
NR	nuclear receptor
NTD	amino-terminal domain
Nurr1	Nur-related factor 1
NurRE	Nur-responsive element
OCN	osteocalcin
4-OHT	4-hydroxytamoxifen
OPG	osteoprotegerin
OPN	osteopontin
Osx	osterix
PGC-1	peroxisome proliferator-activated receptor γ coactivator-1
PI3K	phosphatidylinositol 3-kinase
PPAR	peroxisome proliferator-activated receptor
PTH	parathyroid hormone
PTHrP	parathyroid hormone-related peptide
PXR	pregnane X receptor
RANK	receptor activator of nuclear factor-κB
RANKL	receptor activator of nuclear factor-κB ligand
RAR	retinoic acid receptor
RIP140	receptor-interacting protein 140
Runx2	runt-related transcription factor 2
RXR	retinoid x receptor
S.D.	standard deviation
SHP	small heterodimer partner
SIBLING	small integrin-binding ligand N-linked glycoprotein
SMRT	silencing mediator of retinoid and thyroid hormone receptors
Sox	SRY-related HMG-box
SRC	steroid receptor co-activator
Tcf	T cell factor
TGF-β	transforming growth factor β
TNSALP	tissue-nonspecific alkaline phosphatase
TR	thyroid hormone receptor
TRAF6	tumor necrosis factor receptor-associated factor 6
VDR	vitamin D receptor

REVIEW OF THE LITERATURE

1. NUCLEAR RECEPTORS

1.1 The nuclear receptor superfamily

All living organisms, from simple prokaryotic cells such as bacteria to complex eukaryotic systems such as mammals, are composed of cells. These cells have to be able to communicate with each other and with the prevailing environment they are in to be able to function properly. The communication is mediated mainly by different types of molecular signals and cellular receptors that interpret those signals. Four types of receptors are found on the surface of eukaryotic cells: G protein-coupled receptors, ion-channel receptors, tyrosine kinase-linked receptors, and receptors with intrinsic enzymatic activity (Lodish et al. 2000). Receptors are embedded in the cell membrane where they convert the extracellular signals that are transmitted in the form of specific ion and protein ligands into one or more intracellular signals that alter the behaviour of the target cell. In addition to the cell surface, receptors can also be located inside a cell. Nuclear receptors (NRs) are transcription factors that are essential for many physiological processes including embryonic development and differentiation, metabolism, and cell proliferation and death. They are located in the cytosol and in the nucleus, and therefore their ligands have to be lipophilic to be able to reach them (Alberts et al. 1994, Gronemeyer et al. 2004, Mangelsdorf et al. 1995).

There are 48 identified NR genes in the human genome. The NR superfamily consists of receptors that bind steroid hormones, such as the estrogen receptors (ERs), the androgen receptor (AR) and the glucocorticoid receptor (GR), and receptors that bind non-steroidal ligands, such as the thyroid hormone receptors (TRs), the vitamin D receptor (VDR), and the retinoic acid receptors (RARs). Some NRs, such as the constitutive androstane receptor (CAR), the pregnane X receptor (PXR), and the peroxisome proliferator-activated receptors (PPARs) bind multiple structurally diverse ligands. Typically, these are naturally occurring metabolites of nutrients (Bain *et al.* 2007, Benoit *et al.* 2004, Gronemeyer *et al.* 2004, Noy 2007).

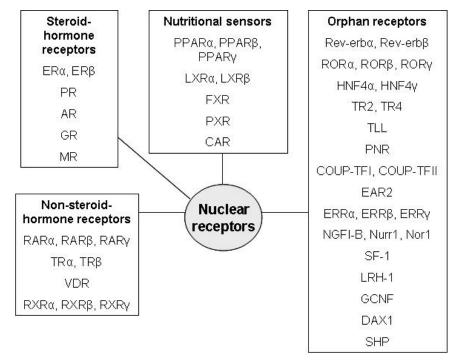


Fig. 1. Human nuclear receptors

In addition to the traditional NRs with known physiological ligands, there are many NRs that were discovered by their structural similarities to the classical NRs and which lacked ligand at the time they were discovered (Giguère 1999). For some of these, physiological ligands have since been found. For retinoid X receptors (RXRs) the recognized ligand was 9-cis-retinoic acid (Heyman et al. 1992, Levin et al. 1992). RXRs participate in a wide range of hormone response systems by associating with other NRs and forming non-permissive or permissive heterodimers. Non-permissive heterodimers are formed, *inter alia*, with RARs, TRs and VDR and can be activated only by the partner's ligand. Permissive heterodimers that can be activated by both RXR's and partner's ligand are formed, inter alia, with PPARs and liver X receptors (LXRs) (Germain et al. 2006). PPARs, LXRs, farnesoid X receptor (FXR), PXR and CAR are a group of NRs that were described as orphans when first identified but are now known to have large ligand-binding pockets (LBPs) that make them less discriminating and capable of binding several different ligands. As previously mentioned, the ligands that are bound are typically naturally occurring metabolites of nutrients and other compounds. Therefore, it has been suggested that these receptors function as nutritional and metabolic sensors (Benoit et al. 2004). PPARs bind for example fatty acids (Göttlicher et al. 1992) and eicosanoids (Forman et al. 1995, Yu et al. 1995), and PPARy binds selectively thiazolidinediones (Forman et al. 1995, Lehmann et al. 1995). LXR has been shown to bind different

oxidized derivatives of cholesterol (Janowski *et al.* 1996, Janowski *et al.* 1999). FXR binds bile acids (Makishima *et al.* 1999, Parks *et al.* 1999, Wang *et al.* 1999) and PXR binds C21 steroids pregnanes and several compounds used as drugs, including dexamethasone (Kliewer *et al.* 1998) and hyperforin (Moore *et al.* 2000).

1.2 The structure of nuclear receptors

Nuclear receptors have a characteristic, modular structure, which includes the aminoterminal domain (NTD), a central and highly conserved DNA-binding domain (DBD) and a carboxyl-terminal ligand-binding domain (LBD) which binds the ligand. A schematic representation of the NR structure is shown in figure 2.

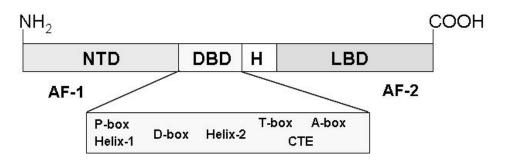


Fig. 2. The schematic layout of the nuclear receptor structure. NRs are composed of an amino-terminal domain (NTD), which contains an activation function 1 (AF-1), DNAbinding domain (DBD), a hinge region (H) and a ligand-binding domain (LBD) that contains an activation function 2 (AF-2). The highly conserved DBD folds into two zinc finger motifs and two α -helices. The residues that are critical for the sequence-specific DNA binding are located in helix 1 and are defined as P-box. The residues of the D-box are located in the C-terminal zinc finger and make up the dimer interface. The C-terminal extension (CTE) contains T-box and A-box that function in receptor DNA binding and heterodimerization (adapted from Bain *et al.* 2007).

1.2.1 The DNA-binding domain

The centrally located DBD docks the NR to specific DNA sequences known as hormone response elements (HREs). The highly conserved DBD folds into two zinc finger motifs, on which each zinc atom is co-ordinated by four cysteine residues. The atoms are necessary to retain stable domain structure (Bain *et al.* 2007, Ribeiro *et al.* 1995). The zinc fingers are common for the whole family, with the exception of SHP (small heterodimer partner) and DAX-1 (dosage-sensitive sex reversal-adrenal hypoplasia congenita critical

region on the X chromosome, gene 1), each of which lack a DBD and do not associate directly with DNA (Gronemeyer *et al.* 2004, Noy *et al.* 2007). Two α -helices extend from the base of the zinc fingers. The first helix (helix 1) contains a region called P-box that interacts with DNA and is responsible for the sequence specificity of the binding. The C-terminal zinc finger contains the D-box, which is involved in dimerization (Aranda and Pascual 2001, Bain *et al.* 2007, Ribeiro *et al.* 1995). The second α -helix (helix 2) contributes to the stabilization of the overall protein structure. After the zinc fingers DBD continues as a C-terminal extension (CTE) that contains the T- and A-boxes, which contribute to the sequence specificity, DNA binding and heterodimerization (Aranda and Pasqual 2001, Bain *et al.* 2007).

1.2.2 The ligand-binding domain

The DBD is linked via a small and flexible hinge region to the C-terminal half of the NR that harbors the LBD. The LBD is a multifunctional domain that mediates ligand binding, homo- and heterodimerization, interaction with heat shock proteins, nuclear localization and ligand-dependent transactivation functions (Aranda and Pasqual 2001, Giguère 1999, Ribeiro *et al.* 1995). The LBD contains 10-13 α -helices (typically 12 numbered H1-H12), several β -turns and connecting loops of varying size arranged into a three-layered "sandwich"-like structure (Benoit *et al.* 2004, Moras and Gronemeyer 1998). The overall architecture of LBD is well conserved among the family members but still different enough to ensure selective ligand recognition. Eleven of the helices form a LBP, whereas C-terminal helix 12 forms a movable lid over the entrance of the pocket (Gronemeyer *et al.* 2004, Moras and Gronemeyer 1998, Noy 2007). Helix 12 also contains residues that are crucial for the function of activation function 2 (AF-2), a highly conserved hydrophobic motif required for co-activator recruitment and ligand-dependent transactivation (Bain *et al.* 2007, Giguère 1999).

1.2.3 The amino-terminal domain

The NTD, which is sometimes referred as an A/B region is the most variable domain both in length and in sequence among the NR family members. The lack of homology may be critical in explaining the different transcriptional responses of closely related NRs binding to similar response elements. The NTD contains the activation function 1 (AF-1) region that can function as a ligand-independent transcriptional activator or work in synergy with AF-2. The NTD can interact with co-activators and other transcription factors and is involved in both the activation and repression of NR target genes. The NTD can also be post-translationally modified by phosphorylation and sumoylation, which can result in changes in intracellular localization, turnover and protein-protein interactions of the NR (Bain *et al.* 2007, Giguère 1999, Lavery and McEwan 2005, Ribeiro *et al.* 1995).

1.3 The function of nuclear receptors as transcription factors

NRs regulate transcription by binding to specific DNA sequences, HREs, in regulatory segments of their target genes as monomers, homodimers or heterodimers (Giguère 1999, Sonoda *et al.* 2008). HREs can locate on proximal promoter regions upstream of the target gene but also on distal enhancer regions (Deblois and Giguère 2008, Kininis and Kraus 2008). A typical HRE consists of two hexa-nucleotide motifs of AGGTCA or its close variants, separated by a gap of several nucleotides and is possibly preceded by a 5′-flanking A/T-rich sequence. The half-core motifs and 5′-flanking A/T-rich sequence are recognized by the first zinc finger and the CTE. Binding specificity of different NRs is largely achieved by spacing three to five nucleotides in between the elements and by the orientation of the two half sites that can be configured as a direct-repeat, inverted-repeat or everted-repeat (Giguère 1999, Sonoda *et al.* 2008).

The ability of some NRs to bind ligand was acquired during evolution as the ancestral NR was an orphan (Escriva *et al.* 1997). In the absence of a ligand, NRs are either present in the cytoplasm in a complex with heat shock proteins and immunophilin chaperones or in the nucleus constitutively bound to their HREs, where they form a repressive complex with co-repressors and histone deacetylases (HDACs). The HDACs generate a condensed chromatin structure over the target promoter that results in gene repression (Gronemeyer *et al.* 2004, Perissi and Rosenfeld 2005, Sonoda *et al.* 2008). NRs can bind a broad range of different ligands such as glucocorticoids, androgens, mineralocorticoids, progestins, estrogens, thyroid hormones, vitamin D and retinoic acid. The lipophilic ligands travel in the circulation bound to the plasma proteins. After dissociating from the proteins, ligands enter the cell by passive diffusion or by using specific transport processes (Ribeiro *et al.* 1995, Visser *et al.* 2008). NRs can also bind

ligands that are intracellularly originated as metabolic products (Aranda and Pasqual 2001).

When the ligand reaches its receptor it binds to the LBP in the LBD and induces a conformational change. In the case of an activating agonistic ligand, helix 12 is stabilized against the surface of the LBD, which disrupts a repressive hydrophobic groove. The intact repressive hydrophobic groove binds co-repressors which contain a corepressor nuclear-receptor box, and its disruption causes their release. Instead, a new hydrophobic cleft is formed that allows co-activator recruitment by AF-2. The coactivators, such as the steroid receptor co-activator (SRC) family, typically contain a helical LxxLL motif (where L is leucine and x is any amino acid) and interact with histone acetyltransferases (HATs), chromatin remodeling proteins and the general transcriptional activation machinery to allow initiation of transcription (Bain et al. 2007, Gronemeyer et al. 2004, Renaud and Moras 2000). However, there are many exceptions to this model. For example, ligand-dependent nuclear-receptor corepressor (LCoR) and receptorinteracting protein 140 (RIP140) can bind to NRs in a ligand-dependent fashion and compete with co-activators by displacing them. Some co-factors, such as the SWI/SNF chromatin remodeling complexes, can function either as repressors or as activators depending on the context. The ability of co-activators and repressors to associate in different complexes allows a temporal- and tissue-specific modulation of target gene transcription (Perissi and Rosenfeld 2005). In contrast to an agonistic ligand, an antagonist inhibits co-activator binding by sterically blocking the ability of helix 12 to approach the core LBD structure or by inducing helix 12 to bind within the hydrophobic cleft thus unproductively mimicking a co-activator (Bain et al. 2007). However, helix 12 has more than two positions (on and off). It can adopt several intermediary positions, which enables the design of ligands with different degrees of agonism and antagonism (Gronemeyer et al. 2004). With some NRs such as estrogen-related receptors (ERRs), the AF-2 domain is fixed in an active conformation in the absence of ligand, which results in constitutive receptor activation. In these cases, the transcriptional activity of the NR is regulated by nuclear availability of the receptor or its co-activators, by signal-induced receptor modifications such as phosphorylation or acetylation, or by interactions with other transcription factors. However, the transcriptional activity of constitutively active NRs can also be modified by ligands that repress or increase their activity by, for example,

inhibiting or enhancing co-activator binding, respectively (Benoit et al. 2004, Sonoda et al. 2008).

NRs can also regulate cellular functions via direct interactions with other transcription factors. A classic example of such regulation is mutual transrepression of the GR and NF- κ B (nuclear factor- κ) (Gronemeyer *et al.* 2004). In addition, many so-called non-genomic effects have been associated with NRs. These effects are often very rapid and do not need mRNA or protein synthesis to be mediated. An example of such an effect is the regulation of endothelial nitric oxide synthase activity in endothelial cells by estrogen. Steroids have been shown to interact with non-NRs such as ion channels and G protein-coupled receptors at the plasma membrane. Moreover, potentially relevant membrane-bound steroid receptors have been identified for at least ER α , ER β , progesterone receptor, and AR (Gronemeyer *et al.* 2004, Wierman 2007).

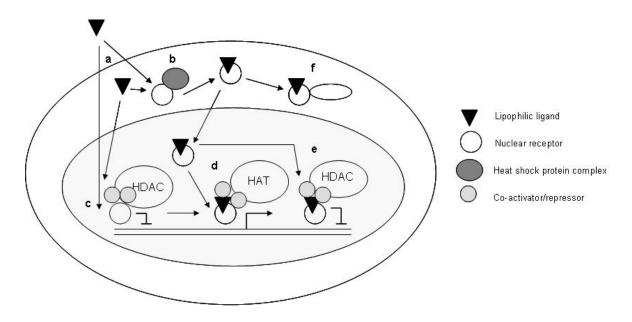


Fig. 3. The function of nuclear receptors. NRs can bind small lipophilic ligands and products of cellular metabolism (a). In the absence of ligand, NRs are present in the cytoplasm in a complex with heat shock proteins (b) or in the nucleus constitutively bound to their HREs, forming a repressive complex with co-repressors and HDACs (c). Ligand binding induces a conformational change that results in either recruitment of co-activators and HATs (agonist) (d) or co-repressors and HDACs (antagonist) (e). NRs can also regulate cellular functions by other mechanisms, for instance, by interacting directly with other transcription factors and repressing or increasing their function (f).

2. ORPHAN NUCLEAR RECEPTORS

Orphan NRs are defined as receptors that lack an identified natural ligand. Some of the NRs, such as PPARs and RXRs, were first identified as orphan receptors but were recategorized after having been shown to bind ligands. However, many receptors still remain in the diverse group of orphan receptors (Benoit *et al.* 2006). ERRs were the first orphan receptors to be discovered (Giguère *et al.* 1988). ERRs are constitutively active in the absence of any ligand (Kallen *et al.* 2004). Their LBDs are still capable of binding ligands, although most of the recognized synthetic ligands inhibit their constitutive activity and therefore function as their inverse agonists. There are also orphan NRs such as hepatocyte nuclear factor 4 (HNF-4) that bind structural ligands, which are unable to leave the receptor once bound and constitute part of the receptor itself (Benoit *et al.* 2006). The members of the NGFI-B receptor family are true orphan NRs incapable of ligand binding because of their small LBP (Wang *et al.* 2003). Although the transcriptional activity of these receptors can not be regulated by ligands, their function is modulated at the level of their expression or by post-translational mechanisms, which will be discussed in more detail in chapter 2.2.1.

2.1 The NR3B orphan nuclear receptor family

The NR3B orphan NR family comprises three members: ERR α (NR3B1), ERR β (NR3B2) and ERR γ (NR3B3). ERR α was the first orphan NR ever discovered. Its gene (*ESRRA*) was indentified in the search for genes that encode proteins related to ER α and it was accordingly named estrogen-related receptor. The gene that encodes ERR β (*ESRRB*) was identified by using the ERR α cDNA as the probe (Giguère *et al.* 1988). The last member of the family, ERR γ (*ESRRG*), was finally identified a decade later (Eudy *et al.* 1998, Heard *et al.* 2000, Hong *et al.* 1999).

2.1.1 The structure of the NR3B family

ERR receptors share the typical NR structure with domains necessary for ligand and DNA binding and a nonconserved NTD. The different members of the ERR family show considerable homology in their amino acid sequence. The NTD is the most variable

domain whereas the DBDs of ERR β and ERR γ show 91% similarity compared to ERR α . The LBD of ERR α is 65% and 63% identical to those of ERR β and ERR γ , respectively (Fig. 4). In addition to the three main isoforms (ERR α 1, ERR β 2, ERR γ 2), several splice variants of ERRs have been identified. Human ERR β has a short-form that is the human ortholog of mouse ERR β and lacks 67 amino acids from its C-terminus. hERR β 2- Δ 10 lacks exon 10 and encodes a different C-terminal end (Zhou *et al.* 2006). ERR γ 1 is 23 amino acids smaller than ERR γ 2 from the NTD and lacks the functional AF-1 domain that is present in the larger isoform (Heard *et al.* 2000). Although the subject remains poorly known, the different variants could have independent functions in cells (Bombail *et al.* 2010, Tremblay and Giguère 2007). The crystal structures of ERR α (Kallen *et al.* 2004) and ERR γ (Greschik *et al.* 2002) have been solved and they show that the receptors are in their active conformation in the absence of any ligand.

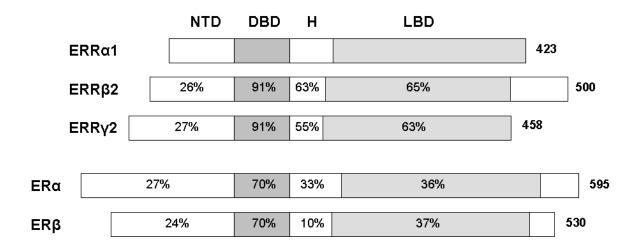


Fig. 4. The amino acid sequence identity between human estrogen-related receptors and estrogen receptors. The percentages represent the similarity of ERR β and ERR γ proteins and the related ER α and ER β proteins when compared to ERR α . The length of each protein is also shown. The figure is adapted from Ariazi and Jordan (2006) and Tremblay and Giguère (2007).

2.1.2 The DNA and ligand binding of NR3B receptors

ERRs bind DNA by recognizing an ERR response element (ERRE), which contains the nucleotides 5'-TNAAGGTCA-3'. ERRs can bind to the ERRE as a monomer, a homodimer or a heterodimeric complex that is composed of two distinct ERR isoforms (Barry *et al.* 2006, Johnston *et al.* 1997, Sladek *et al.* 1997). The ERRE sequence can be

recognized and also bound by steroidogenic factor-1 (Wilson *et al.* 1993a). ERRs can bind *in vitro* to the same hormone response element as the ERs (ERE) (Johnston *et al.* 1997, Vanacker *et al.* 1999, Zhang and Teng 2000) but the physiological significance of the ERE binding remains to be determined.

ERRs and ERs share considerable amino acid identity between their respective LBDs (Fig. 4) though none of the ERR family members bind natural estrogens. Although most of the amino acids that line the LBP are identical between ER α and ERR γ , a few differences lead to a smaller ERR γ LBP volume. The most significant of these differences is ERR γ F435, which corresponds to ER α L525. F435 partially fills the ligand binding cavity and prevents ERRy from binding to the estrogen ligands (Wang et al. 2006a). ERRs can still bind several other chemical compounds. The transcriptional activity of all three ERR isoforms is inhibited by the potent synthetic estrogen analog diethylstilbestrol (DES) and its close relatives hexoestrol and dienestrol (Coward et al. 2001, Tremblay et al. 2001b). A selective estrogen receptor modulator 4hydroxytamoxifen (4-OHT) acts as an inverse agonist for ERR β and ERR γ (Coward *et al.* 2001, Tremblay et al. 2001a). Due to the small volume of the ERRy LBP, the receptor has to undergo a large conformational change to be able to bind DES or 4-OHT. Binding of the ligands results in a rotation of F435, which induces the displacement of the AF-2 helix to a position that interferes with the recruitment of co-activators (Greschik et al. 2004, Wang et al. 2006a). Bisphenol A, which is an ubiquitous environmental contaminant with estrogenic activity, can bind to ERR γ . Bisphenol A does not affect the transcriptional activity of ERRy but it can prevent 4-OHT from binding to the LBP (Takayanagi et al. 2006). ERRa has been found to bind two organochlorine pesticides, toxaphene and chlordane, and a specific synthetic ligand XCT790, which inhibit its activity (Busch et al. 2004, Willy et al. 2004, Yang and Chen 1999). In addition, there are several synthetic agonists that ERR receptors bind. Phenolic acyl hydrazones GSK4716 and DY131 act as selective ERR β and ERR γ agonists that increase their transcriptional activity (Yu and Forman 2005, Zuercher *et al.* 2005). The crystal structure of ERR γ with the agonist GSK4716 was solved and it shows that binding of GSK4716 forces a rotation of E275 and R316 that allows access of the ligand to an additional pocket, which was previously shielded. This increases the volume of the combined pocket so that it can accommodate an acyl hydrazone ligand without requiring displacement of the AF-2 helix. GSK4716 induces a small increase in protein stability in an active conformation, which could partly

explain the agonistic effect (Wang *et al.* 2006a). The isoflavones genistein, daidzein, and biochanin A, and the flavone 6,3',4'-trihydroxyflavone can also bind to ERRs and act as their agonists (Suetsugi *et al.* 2003).

Table 1. The specificity of selected ERR ligands. Ligands can either increase (\uparrow) or decrease (\downarrow) the transcriptional activity of the ERRs. Some of the ERR ligands bind specifically to the designated ERR isoforms but have no effect (-) on others.

	ERRα	ERRβ	ERRγ
4-OHT	-	\downarrow	\downarrow
DES	\downarrow	\downarrow	\downarrow
XCT790	\downarrow	-	-
GSK4716	-	↑ (1
daidzein	1	↑	1

2.1.3 The function of NR3B family as transcriptional regulators

The LBD of the ERR receptors contains a conserved AF-2 motif that is in an active configuration when in the absence of any ligand (Greschik *et al.* 2002, Kallen *et al.* 2004, Kallen *et al.* 2007, Wang *et al.* 2006a). Therefore, ERRs interact with co-activators in a ligand-independent manner. Because the transcriptional activity of ERRs is mostly dependent on the configuration of co-factor binding, their potencies as transcriptional activators vary according to the cell type and the promoter in question, the overall effect being either negative or positive.

ERRs bind numerous co-regulatory proteins that they share with other NRs. The transcriptional activity of ERRs is greatly enhanced by peroxisome proliferatoractivated receptor γ coactivator-1 α and β (PGC-1 α and PGC-1 β) (Huss *et al.* 2002, Kamei *et al.* 2003, Schreiber *et al.* 2003). Moreover, members of the steroid receptor co-activator family, which include SRC-1 (NcoA1), SRC-2 (NcoA2, GRIP1, TIF2) and SRC-3 (NcoA3, AIB1, ACTR, RAC3, TRAM-1) bind to ERRs and function as their co-activators (Hong *et al.* 1999, Xie *et al.* 1999, Zhang and Teng 2000). RIP140 can either repress or increase the transcriptional activity of ERRs depending on the target sequence on the promoter (Castet *et al.* 2006). Co-repressors of ERRs include PROX1 (prospero-related homeobox 1) (Albers *et al.* 2005, Charest-Marcotte *et al.* 2010) and SMRT (silencing mediator of retinoid and thyroid hormone receptors) (Wang *et al.* 2006a). The coregulatory protein interactions can be altered by ligand binding. For example, 4-OHT blocks AF-2 co-activator binding by changing receptor conformation as described in previous chapter. The transcriptional activity of ERRs can also be modulated by other transcription factors, such as SHP which represses their transcriptional activity (Sanyal *et al.* 2002), and by post-translational modifications. The NTDs of ERR α and ERR γ contain a functional phosphorylation-dependent sumoylation motif. In the case of ERR α , the phosphorylation of serine 19 is required for the sumoylation at lysine 14, and both the phosphorylation and the sumoylation decrease the transcriptional activity of ERR α (Tremblay *et al.* 2008, Vu *et al.* 2007). Dimerization can also affect the transcriptional activity of ERRs. For instance, homodimerization increases whereas heterodimerization with ERR α decreases the transcriptional activity of ERR γ (Huppunen and Aarnisalo 2004). ERR α dimers can interact with PGC-1 α on DNA whereas monomers can not (Barry and Giguère 2005).

2.1.4 The biological function of the NR3B family

ERRs are ubiquitously expressed in mouse and human. All of the ERR isoforms are expressed in the heart and kidney. ERR α is also highly expressed in many other tissues such as the intestine, skeletal muscle, brain and brown adipose tissue. ERR γ is most highly expressed in the brain and in the spinal cord (Bookout *et al.* 2005). ERR β is mostly expressed during embryonic development (Luo *et al.* 1997, Mitsunaga *et al.* 2004). After birth it is expressed in the eye with lower concentrations in thyroid, testis and parts of the brain (Bookout *et al.* 2005). NR3B receptors have been shown to regulate many biological processes, including energy metabolism, embryonic development and carcinogenesis.

2.1.4.1 The function of ERR α and ERR γ in energy homeostasis

ERR α (*Esrra*) knockout (KO) mice are viable and fertile and they do not have any gross anatomical alterations. However, they have reduced body weight and peripheral fat deposits and they are resistant to high-fat diet-induced obesity (Luo *et al.* 2003). The lean phenotype of ERR α KO mice can, in part, be explained by lipid malabsorption exhibited by ERR α KO pups (Carrier *et al.* 2004). ERR α KO mice show altered expression and altered regulation of several enzymes and proteins involved in energy metabolism (Huss et al. 2004, Luo et al. 2003, Rangwala et al. 2007). ERRa KO mice are also unable to maintain body temperature when exposed to cold because of decreased mitochondrial mass and oxidative capacity in their brown adipocytes (Villena *et al.* 2007). ERR α has been shown to have an important role as a regulator of energy metabolism, mitochondrial biogenesis and oxidative phosphorylation in numerous additional studies (Giguère 2008) and therefore the mild phenotype of ERR α KO mice is quite surprising. However, this could be explained by compensation by the other two ERR isoforms. In fact, in the ERR a KO heart, the expressions of ERR γ and PGC-1 α are increased, which suggests a compensatory mechanism (Dufour et al. 2007). ERRa is a plausible candidate for metabolic diseases due the important role it has in energy metabolism. Nonetheless, in genetic studies no association between the variants of ERR α encoding gene ESRRA and type 2 diabetes or obesity was found in caucasian Danish population (Larsen et al. 2007). *ESRRA23* is a polymorphic 23-base pair sequence located at position -682 in the 5'flanking region of the ESRRA. It can be found in one to four copies in human chromosomes with higher number of repeats leading to higher expression of ERRa. In Japanese individuals the longer 2.3 genotype of ESRRA23 was linked to a higher body mass index (BMI) when compared to the shorter 2.2 genotype (Kamei et al. 2005). In addition, in mice ERR α was found to be essential for the ATP synthesis and therefore for bioenergetic and functional adaptation of the heart subjected to hemodynamic stressors known to cause heart failure (Huss *et al.* 2007). In humans, the expressions of ERR α and its target genes are decreased in the hearts of cardiomyopathy and end-stage heart failure patients (Karamanlidis et al. 2010, Sihag et al. 2009).

At birth, the heart undergoes a metabolic switch from a predominant dependence on carbohydrates to a greater dependence on postnatal oxidative metabolism. Disruption of the ERR γ encoding gene *Esrrg* from mice (ERR γ KO mice) blocks this switch which results in lactatemia, electrocardiographic abnormalities and death during the first week of life (Alaynick *et al.* 2007). ERR γ regulates the expression of key ion homeostatic genes, including a voltage-gated potassium channel *Kcne2*, in heart, stomach and kidney, which leads to elevated serum potassium, reductions in gastric acid production markers, and cardiac arrhythmia in ERR γ KO mice. A correlation between specific *ESRRG* single-nucleotide polymorphism genotypes and altered blood pressure has also been reported in humans (Alaynick *et al.* 2010). ERR γ also functions in skeletal

muscle in which it is induced by exercise and it positively regulates mitochondrial activity and oxidative capacity (Rangwala *et al.* 2010).

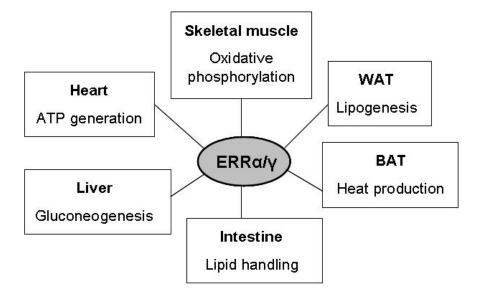


Fig. 5. The metabolic functions of ERR α and/or ERR γ in different tissues.

2.1.4.2 The function of ERR β in embryonic development

ERR β has been shown to sustain embryonic stem cell self-renewal and pluripotency by regulating the expression of *Oct4* and *Nanog* genes (van den Berg *et al.* 2008, Zhang *et al.* 2008). ERR β also functions in concert with Oct4 and Sox2 to mediate reprogramming of mouse embryonic fibroblasts to induced pluripotent stem cells with many of the characteristics of embryonic stem cells (Feng *et al.* 2009). ERR β is also essential for normal placental formation as ERR β (*Esrrb*) KO mice die in utero at 10.5 days post coitum due to impaired placental formation (Luo *et al.* 1997). The complement of placental defects with wild-type tetraploid embryos has demonstrated that ERR β KO embryos have a diminished number of primordial germ cells in their gonads. Despite the defects in primordial germ cell number, the adult ERR β KO mice are fertile. However, they show behavioural abnormalities with, *inter alia*, circling behaviour and head-tossing (Mitsunaga *et al.* 2004).

2.1.4.3 The function of NR3B receptors in carcinogenesis

ERRs are expressed in many cancer tissues. These include tumors of the breast (Ariazi *et al.* 2002, Deblois *et al.* 2009, Lu *et al.* 2001, Suzuki *et al.* 2004), prostate (Cheung *et al.* 2005, Fujimura *et al.* 2007, Fujimura *et al.* 2010, Yu *et al.* 2008), ovary (Sun *et al.* 2005), and the endometrium (Gao *et al.* 2006, Watanabe *et al.* 2006). The expression of ERR α and ERR γ correlate with unfavourable and favourable biomarkers, respectively, in human breast cancer (Ariazi *et al.* 2002). It has been suggested that ERR α functions as a determinant of heterogeneity in breast cancer (Deblois *et al.* 2009) and ERR γ mediates tamoxifen resistance in invasive lobular breast cancer cells (Riggins *et al.* 2008). The elevated expression of ERR α has been shown to correlate with poor survival in prostate (Fujimura *et al.* 2007) and ovarian (Sun *et al.* 2005) cancers. On the other hand, ERR β and ERR γ suppress growth of prostate cancer cells (Yu *et al.* 2007, Yu *et al.* 2008). In endometrial invasion whereas ERR γ negatively correlates with nodal metastasis (Gao *et al.* 2006).

2.2 The NR4A orphan nuclear receptor family

The NR4A subfamily of NRs comprises three members: NGFI-B (NR4A1, Nur77, TR3), Nurr1 (NR4A2, NOT), and Nor1 (NR4A3, MINOR, TEC). *NGFI-B* (nerve growth factor inducible-B) was the first member of the subfamily identified as a gene induced by serum in mouse fibroblast cells (Hazel *et al.* 1988) and by the nerve growth factor in the rat pheochromocytoma cell line PC12 (Milbrandt 1988). *Nor1* (neuron-derived orphan receptor 1) was cloned from forebrain neural cells that were undergoing apoptosis (Ohkura *et al.* 1994) and finally Nurr1 (Nur-related factor 1) was characterized as a brain-specific transcription factor in dopaminergic neurons (Law *et al.* 1992).

2.2.1 The structure and transcriptional regulation by the NR4A family

The structures of NR4A receptors are very similar to each other. Therefore, it has been suggested that the members of the family have evolved from a common ancestral gene (Martínez-González and Badimon 2005, Maxwell and Muscat 2005). The NTD containing

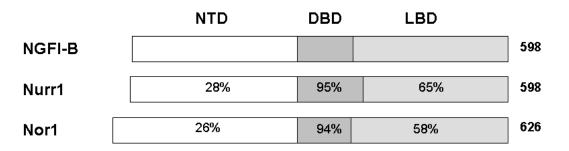


Fig. 6. The schematic representation of the NR4A1 receptor structure. The percentages represent the similarity of Nurr1 and Nor1 amino-terminal domain (NTD), DNA-binding domain (DBD) and ligand-binding domain (LBD) when compared to NGFI-B. The length of each protein is also shown.

the AF-1 is the most variable domain. The NTD of NGFI-B shows 28% amino acid homogeneity with Nurr1 and 26% with Nor1 (Fig. 6) (Martínez-González and Badimon 2005). The AF-1 of NR4A receptors is exceptionally potent and mediates the transactivation, cell specificity and co-factor recruitment of these receptors (Maira *et al.* 2003, Wansa *et al.* 2002, Wansa *et al.* 2003). DBD is well conserved with over 90% homology. It interacts with the consensus response element NGFI-B responsive element (NBRE) AAAGGTCA as monomers and with the palindromic Nur-responsive element (NurRE) TGATATTTX₆AAATGCCA comprising two inverted NBRE sequences spaced by 6 bp as homodimers and heterodimers (Fig. 7) (Maira *et al.* 1999, Philips *et al.* 1997, Wilson *et al.* 1991). NGFI-B and Nurr1 can form heterodimers with retinoic X receptor (RXR) though Nor1 can not. As heterodimers with RXR, Nurr1 and NGFI-B mediate transactivation in response to the RXR ligands through the DR-5 element. The DR-5 element comprises two direct repeats of the consensus NR binding motif separated by five nucleotides (Fig. 7) (Aarnisalo *et al.* 2002, Perlmann and Jansson 1995, Zetterström *et al.* 1996a).

The NR4A receptors are incapable of binding ligands to their LBPs. The structure of the Nurr1 LBD has been determined by X-ray crystallography and it revealed that the LBP is tightly packed with bulky, hydrophobic amino acid side chains (Wang *et al.* 2003) that are conserved throughout the NR4A subfamily (Flaig *et al.* 2005, Wang *et al.* 2003). Moreover, the hydrophobic co-activator binding cleft typical of NRs is filled with polar side chains, which makes it incapable of binding co-regulators (Wang *et al.* 2003). However, there is a hydrophobic patch between helices 11 and 12 that potentially interacts with co-factors and modulates transcriptional activity (Codina *et al.* 2004, Flaig

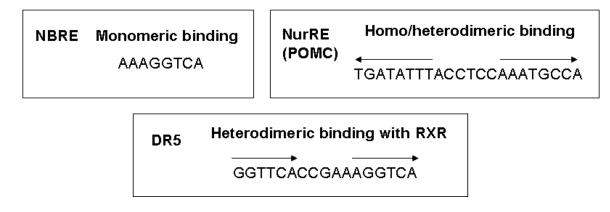


Fig. 7. NR4A receptors can bind DNA as monomers (NBRE), by forming homodimers or heterodimers with other NR4A receptors (NurRE on the pro-opiomelanocortin promoter), or by forming heterodimers with RXR (DR5).

et al. 2005). This patch has been reported to bind, for example, co-repressors SMRT and NCoR (nuclear receptor co-repressor) (Codina *et al.* 2004). In addition, NR4A family has been reported to bind SRC-1, SRC-2, p300 and PCAF (p300/CBP-associated factor) co-regulators through their AF-1 and NTD (Wansa *et al.* 2002). Despite the fact that NR4A receptors do not bind ligands to their LBP, there are compounds that target regions outside of the LBP that regulate receptor/co-factor interactions and receptor functions (Shi 2007). One of these compounds is 6-mercaptopurine, which is a widely used antineoplastic and anti-inflammatory drug that activates Nurr1 (Ordentlich *et al.* 2003) and Nor1 (Wansa *et al.* 2003) through their AF-1 domains. Moreover, other agonists have been described for Nurr1 but their mechanisms of action are still unknown (Dubois *et al.* 2006, Hintermann *et al.* 2007). 1,1-bis(3-indolyl)-1-(*p*-anisyl)methane activates NGFI-B through the LBD (Chintharlapalli *et al.* 2005) and prostaglandin A2 functions as a transactivator of Nor1 by a mechanism that is dependent of both LBD and AF-1 (Kagaya *et al.* 2005).

An important mechanism for regulating the function of NR4A receptors is mediated through the alterations of their protein expression. The NR4A family functions as immediate-early genes and their expression is induced rapidly in response to a range of signals, such as parathyroid hormone (PTH) (Pirih *et al.* 2003, Pirih *et al.* 2005, Tetradis *et al.* 2001a, Tetradis *et al.* 2001b), typical and atypical antipsychotic drugs such as raclopride and olanzapine (Maheux *et al.* 2005), vascular endothelial growth factor (Liu *et al.* 2003) and inflammatory cytokines (Pei *et al.* 2005). Furthermore, physical stimuli such as stress, magnetic fields, mechanical agitation and membrane depolarization can induce their expression (Bandoh *et al.* 1997, Hazel *et al.* 1991, Honkaniemi *et al.* 1994, Katagiri *et al.* 1997, Miyakoshi *et al.* 1998). Protein kinase A (Kovalovsky *et al.* 2002, Pirih *et al.* 2003, Song *et al.* 2001, Tetradis *et al.* 2001a, Tetradis *et al.* 2001b), Ca²⁺/calmodulin dependent kinase II (Kovalovsky *et al.* 2002), protein kinase C, phosphatidylinositol 3-kinase (PI3K) (Lammi and Aarnisalo 2008, Song *et al.* 2001), NF- κ B (Pei *et al.* 2005), and mitogen-activated protein kinase pathways (MAPK) (Kovalovsky *et al.* 2002, Lammi and Aarnisalo 2008) have been reported to be involved in the regulation of the NR4A expression.

In addition to the regulation of expression, extracellular stimuli can also influence the NR4A post-translational modifications. For instance NGFI-B can be phosphorylated by several kinases, including the PI3K/Akt and MEK1/2-ERK1/2 MAP kinase pathways. Phosphorylation by PI3K/Akt pathway has been shown to antagonize the DNA binding of NGFI-B and to increase its translocation from the nucleus to the cytoplasm (Cunningham *et al.* 2006, Masuyama *et al.* 2001, Pekarsky *et al.* 2001). Phosphorylation by MEK1/2-ERK1/2 MAP kinase pathway regulates NGFI-B's nuclear export and translocation to mitochondria (Jacobs *et al.* 2004, Wang *et al.* 2009a). Nurr1 has been shown to be sumoylated by PIAS γ , which leads to the repression of the transcriptional activity of Nurr1 (Galleguillos *et al.* 2004).

In addition, cross-talk with other signaling pathways has been shown to regulate the transcriptional activity of Nurr1. GR interacts with NR4A receptors and represses their NurRE-dependent transcription (Martens *et al.* 2005). DAX-1 interacts with NGFI-B and thereby represses its transcriptional activity by competing with the co-activator SRC-1 for binding (Song *et al.* 2004).

2.2.2 The biological function of the NR4A family

NR4A receptors play an important role in the central nervous system. Nonetheless, recently, it has become clear that they also function in peripheral tissues and regulate processes such as those of the immune system, energy metabolism, the hypothalamic-pituitary-adrenal axis, and carcinogenesis.

2.2.2.1 The function of NR4A receptors in the central nervous system

Nurr1 is predominantly expressed in the central nervous system with high levels of expression at sites such as the substantia nigra, cerebellum, olfactory bulb, hypothalamus, neocortex and ventral tegmental area (Zetterström et al. 1996b). Nurr1 is essential for the development and survival of dopaminergic neurons. Dopamine neurons localize at the substantia nigra and ventral tegmental area where they regulate movement and affective behaviour. Mutations in Nurrl gene have been associated with Parkinson's disease, a condition in which dopamine neurons are degenerated (Le et al. 2003). Nurr1 KO mice fail to generate midbrain dopaminergic neurons, are hypoactive and die within two days after birth (Zetterström et al. 1997). Furthermore, heterozygous Nurr1 (Nurr1 +/-) mice have lower levels of dopamine in the midbrain, prefrontal cortex, and nucleus accumbens, and increased locomotor activity in response to mild stress (Eells et al. 2002). Nurr1 +/mice also show decreased ethanol preference and wheel running, which associates Nurr1 with excessive reward-seeking behaviour typical for addiction (Werme et al. 2003). The other two members of the NR4A family are also expressed in the brain (Zetterström et al. 1996a, Zetterström et al. 1996b). NGFI-B KO mice are hyperactive and have disturbances in both basal and haloperidol-induced dopamine turnover, which suggests a role for NGFI-B in dopamine clearance (Gilbert et al. 2006). Nor1 has been associated with the modulation of food intake and energy balance as the underexpression of Nor1 in mice suppresses their food intake and body weight (Nonogaki et al. 2009). Norl KO mice also show impaired postnatal axonal growth and region-specific cell death in the hippocampus that are associated with lasting changes in hippocampal excitability and increased susceptibility to chemically induced seizures (Pönniö and Conneely 2004).

2.2.2.2 The function of NR4A receptors in peripheral tissues

NR4A receptors have been shown to play an important role in the cells of the immune system. For instance, they function in T cell receptor-mediated apoptosis during which immature thymocytes and mature T cells that express self-reactive T cell receptors are deleted by apoptosis to eliminate self-reactive and potentially autoimmune lymphocytes. NGFI-B and Nor1 are induced to a high level during T cell receptor-mediated apoptosis in immature thymocytes and T cell hybridomas (Cheng *et al.* 1997, Liu *et al.* 1994,

Woronicz *et al.* 1994) and the blocking of NGFI-B expression or function by antisense or dominant negative NGFI-B inhibits T cell receptor mediated apoptosis (Calnan *et al.* 1995, Liu *et al.* 1994, Woronicz *et al.* 1994, Zhou *et al.* 1996). On the other hand, Nurr1 is strongly expressed in the peripheral blood T cells of multiple sclerosis patients (Satoh *et al.* 2005) in which it regulates the expression of interleukin-17 and interferon- γ , two key cytokines suggested to work in the multiple sclerosis pathogenesis (Doi *et al.* 2008).

In contrast to the apoptotic effects in T cells and thymocytes, the members of the NR4A family are able to mediate prosurvival effects in other tissues. In the endothelium, for example, Nor1 mediates the prosurvival effects of hypoxia-inducible factor 1 (Martorell *et al.* 2009) and in vascular smooth muscle cells Nor1 promotes proliferation (Nomiyama *et al.* 2006).

NR4A receptors regulate many aspects of energy metabolism and expenditure. NR4A receptors are involved in hepatic glucose metabolism. They are induced in the liver by different physiological stimuli, including glucagon stimulation and fasting (Oita et al. 2009, Pei et al. 2006). Adenovirus-mediated overexpression of NGFI-B in the mouse liver activates multiple genes involved in gluconeogenesis and stimulates hepatic glucose production (Pei et al. 2006). In skeletal muscle, the NR4A receptors are induced by β -adrenergic signaling (Pearen *et al.* 2008) and endurance exercise (Mahoney et al. 2005). NR4A receptors promote glucose utilization as NGFI-B KO mice have reduced expression of genes involved in skeletal muscle glucose and glycogen metabolism (Chao et al. 2007). NGFI-B KO mice also have an increased susceptibility to diet-induced obesity and insulin resistance in skeletal muscle and liver (Chao et al. 2009). NR4A receptors also participate in lipid metabolism. NGFI-B promotes lipolysis in muscle (Maxwell et al. 2005), decreases hepatic triglyceride content and modulates plasma lipoprotein profiles by increasing plasma low density lipoprotein cholesterol and by decreasing high density lipoprotein cholesterol (Pols et al. 2008). In addition, NR4A receptors may participate in adipogenic differentiation (Chao et al. 2008, Fumoto et al. 2007) and central regulation of energy homeostasis (Nonogaki et al. 2009).

NR4A receptors also function in many other peripheral tissues. They are overexpressed in atherosclerotic lesions obtained from patients with coronary artery disease (Arkenbout *et al.* 2002, Martínez-Gonzaléz *et al.* 2003, Nomiyama *et al.* 2006) and they inhibit macrophage activation and foam-cell formation and differentiation that suggests a protective role in atherogenesis (Bonta *et al.* 2006). The NR4A family has been

linked in the regulation of gene expression in the hypothalamic-pituitary-adrenal axis that is related to inflammation and steroidogenesis. Their expression is rapidly induced by corticotropin releasing hormone (Parkes *et al.* 1993, Philips *et al.* 1997) and adrenocorticotropic hormone (Enyeart *et al.* 1996), and their target genes include proopiomelanocortin (Murphy and Conneely 1997, Philips *et al.* 1997), 21-hydroxylase (Wilson *et al.* 1993b), and 20 α -hydroxysteroid dehydrogenase (Stocco *et al.* 2000). However, there is normal basal regulation of the hypothalamic-pituitary-adrenal axis and normal steroidogenesis in *NGFI-B* KO mice possibly due to the compensatory effects of related proteins (Crawford *et al.* 1995).

Finally, the NR4A receptor family has been linked to carcinogenesis. The dominating cytoplasmic expression of Nurr1 over nuclear Nurr1 correlates with an advanced pathological stage and an invasive growth pattern in bladder cancer patients. *In vitro*, silencing of endogenous Nurr1 by siRNA reduced the migration of bladder cancer cells (Inamoto *et al.* 2010). Chromosomal translocations that create chimeric fusions of full Nor1 protein fused with the amino-terminal domains of EWS (Ewing sarcoma breakpoint region 1 protein) (Clark *et al.* 1996, Labelle *et al.* 1999), TCF12 (Transcription factor 12) (Sjögren *et al.* 2000), TAF2N (TATA box binding protein (TBP)-associated factor, RNA polymerase II, N) (Attwool *et al.* 1999, Panagopoulos *et al.* 1999, Sjögren *et al.* 1999) or TFG (TRK-fused gene) (Hisaoka *et al.* 2004) proteins have been linked to extraskeletal myxoid chondrosarcoma.

3. THE BONE AND OSTEOBLASTS

In vertebrates, skeletal bone has various physiological roles. Bone functions in locomotion, protection and support of soft tissues but it is also a hematopoietic and endocrine organ and regulates calcium homeostasis (Imai *et al.* 2009, Lee *et al.* 2007, Tortora and Grabowski 2000).

3.1 The structure of bone

Bone is composed mainly of extracellular matrix, which contains both organic and inorganic substances. The inorganic component accounts for 65% of the bone's weight and contains minerals. Calcium and phosphate exist in bone in the form of hydroxyapatite $(3Ca_3(PO_4)_2 \cdot Ca(OH)_2)$. The skeleton contains about 99% of the body's calcium, 90% of its phosphate, 50% of its magnesium and 33% of its sodium. The organic matrix consists mainly of collagen (90-95%) whereas the rest is made of proteoglycans, glycoproteins, sialoproteins and a small amount of lipid (Brook and Marshall 2001).

Bones are composed of two different types of bone tissue: cortical (compact) and trabecular (cancellous, spongy) bone. The rigid cortical bone, which constitutes about 80% of the skeleton, forms the external layer of all bones and provides protection and support to resist stress produced by weight and movement. Cortical bone tissue is arranged in units called osteons or Haversian systems. Blood and lymphatic vessels and nerves penetrate the cortical bone through central Haversian canals and perforating Volkmann's canals. The hard, calcified matrix is arranged in ringlike concentric lamellae which are arranged around the central canals. Between the lamellae small spaces called lacunae that contain osteocytes can be found. Radiating in all directions from the lacunae are tiny channels called canaliculi, which are filled with extracellular fluid and which connect lacunae with one another and with the central canals. The areas between osteons contain interstitial lamellae comprising fragments of older osteons, which have been partially destroyed during bone remodeling or growth. In contrast to cortical bone, trabecular bone does not contain true osteons. Instead it contains lamellae that are arranged in an irregular lattice of thin columns of bone called trabeculae. The space between the trabeculae of certain bones is filled with red bone marrow, which produces blood cells. Trabecular bone is light and it tends to be located at sites where bone is not heavily stressed or where stress

is applied from many directions. Trabecular bone constitutes about 20% of bone and makes up most of the bone tissue of short, flat, and irregular shaped bones such as the sternum. Moreover, the epiphyses and a narrow rim around the medullary cavity of the diaphysis of long bones contain trabecular bone (Tortora and Grabowski 2000).

3.2 The different cell types of bone

There are several types of cells in bone. The cells that are specific for bone are preosteoblasts, osteoblasts, osteocytes, and osteoclasts. Preosteoblasts differentiate from the mesenchymal stem cells (MSCs) of the bone marrow. Preosteoblasts in turn can differentiate into osteoblasts, which are bone forming cells that synthesize and secrete collagen fibers and other organic components to the bone matrix. Osteoblasts, preosteoblasts and MSCs are discussed in more detail in next chapter. Osteocytes are mature bone cells that are derived from osteoblasts that have been embedded in the extracellular matrix. Osteocytes do not secrete matrix materials but maintain the metabolic activities of bone tissue such as the exchange of nutrients and waste products with the blood. They make contact with the neighbouring cells and nearby blood supply by means of cytoplasmic processes, which lie in canaliculi. Osteoclasts are large cells that are derived from the fusion of several monocytes, which are concentrated in the endosteum. The side of the cell that makes contact with the bone surface is composed of a ruffled border, by which osteoclast releases lysosomal enzymes and acids that digest the protein and mineral components of the underlying bone (Brook and Marshall 2001, Tortora and Grabowski 2000).

There are two major modes of bone formation, intramembranous and endochondral ossification, which both involve the transformation of a preexisting mesenchymal tissue into bone tissue. Flat bones of the skull are formed by a process of intramembranous ossification by which MSCs first proliferate and condense and then differentiate directly into the bone matrix secreting osteoblasts. In endochondral ossification MSCs first form a hyaline cartilage model by differentiating into chondroblasts and chondrocytes. Cells that surround the cartilage model subsequently start to differentiate into osteoblasts and to form bone matrix and eventually the cartilage model is completely replaced by bone (Gilbert 2000, Tortora and Grabowski 2000).

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3.3 The osteoblasts

3.3.1 The osteoblastic differentiation of mesenchymal stem cells

Adult stem cells are undifferentiated cells that include MSCs, which can differentiate into multiple cell lineages such as osteoblasts, adipocytes and chondrocytes. In addition to MSCs, adult stem cells also include hematopoietic stem cells that differentiate into blood cells and osteoclasts, and neural stem cells that differentiate into neural cells (Jeong and Mangelsdorf 2009, Liu *et al.* 2009b).

The differentiation process of MSCs is controlled by specific signals and transcription factors. The key transcription factor for osteoblastic differentiation is Runt related transcription factor 2 (Runx2, Cbfa1). Runx2 KO mice have a complete lack of ossification due to maturational arrest of osteoblasts (Komori et al. 1997, Otto et al. 1997). In human, Runx2 haploinsufficiency causes the autosomal dominant bone disorder cleidocranial dysplasia, which is characterized by defective bone formation (Lee et al. 1997, Mundlos et al. 1997). Runx2 expression is initiated in the mesenchymal condensations of the developing skeleton (Ducy et al. 1997). Runx2 binds to and activates the promoters of several osteoblastic genes, which results in the commitment and establishment of osteoblastic phenotype. These genes include type I collagen (Coll I) (Ducy et al. 1997, Kern et al. 2001), osteopontin (OPN) (Ducy et al. 1997, Sato et al. 1998), and osteocalcin (OCN) (Ducy et al. 1997). On the other hand, Runx2 inhibits the terminal differentiation of osteoblasts as mice overexpressing Runx2 have an increased number of immature osteoblasts but a decreased number of mature osteoblasts and osteocytes, which results in osteopenia with multiple fractures (Liu et al. 2001). In addition, Runx2 regulates the differentiation of hypertrophic chondrocytes as Runx2 KO mice have delayed chondrocyte maturation (Inada et al. 1999).

The expression and function of Runx2 is regulated by several factors, which include growth factors such as bone morphogenetic proteins (BMPs) and fibroblast growth factors (FGFs) and hormones such as PTH. The binding of BMP-2 to its receptor activates Smads, which can interact with Runx2 and enhance its transcriptional activity (Hanai *et al.* 1999, Lee *et al.* 2000). Mice that express dominant negative form of BMP receptor IB in their osteoblasts have reduced bone growth and formation, which indicates an important role for BMPs in osteoblast differentiation (Zhao *et al.* 2002). FGF-2 increases the

phosphorylation of Runx2 improving its transcriptional activity (Xiao *et al.* 2002). Intermittent PTH treatment increases the expression and activity of Runx2 (Krishnan *et al.* 2003). In addition to Smads, numerous other interacting proteins have been reported to regulate the function of Runx2. Runx2 requires the interaction with a co-transcription factor Cbf β (Core-binding factor β) for the efficient association with DNA and transcriptional activity. Cbf β is therefore needed for skeletal development (Yoshida *et al.* 2002). Runx2 also binds proteins such as CCAAT/enhancer-binding protein β (C/EBP β) (Gutierrez *et al.* 2002), and co-activators such as retinoblastoma protein (Thomas *et al.* 2001), TAZ (Transcriptional co-activator with PDZ-binding motif) (Cui *et al.* 2003), and p204 (Liu *et al.* 2005), which all enhance its transcriptional activity. Other transcription factors and co-regulators, including PPAR γ (Jeon *et al.* 2003) and Stat1 (signal transducer and activator of transcription 1) (Kim *et al.* 2003), reduce the transcriptional activity of Runx2.

Osterix (Osx) is another osteoblast specific transcription factor that is important for the osteoblastic differentiation. It functions downstream of Runx2 as *Osx* KO mice show a lack of osteoblasts and have defective bone formation in spite of normal Runx2 expression (Nakashima *et al.* 2002). Very little is known about factors that regulate Osx. BMP-2 up-regulates Osx expression during osteoblast differentiation (Nakashima *et al.* 2002). Nuclear factor of activated T cells c1 (NFATc1) binds Osx and activates Osx-dependent *Coll I* promoter activity (Koga *et al.* 2005) and p53 has been shown to negatively regulate Osx expression (Wang *et al.* 2006b).

The canonical Wnt signaling pathway is an important factor in the control of bone formation and bone mass and will be discussed in detail under the heading 3.3.1.1.

In vitro, the bone nodule formation can be divided into three stages: (I) proliferation, (II) extracellular matrix development and maturation, and (III) mineralization. Although an extensive diversity in the expression of osteoblastic marker genes exists, some guidelines have been developed. In general, the expression of alkaline phosphatase (ALP) increases during the extracellular matrix development and decreases again when mineralization is well progressed. OPN peaks prior to bone sialoprotein (BSP) and OCN, which are expressed by differentiated mineralizing osteoblasts (Aubin 2001).

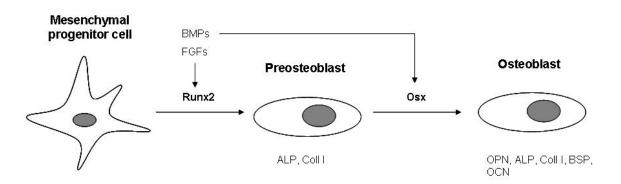


Fig. 8. Osteoblast progenitors in mesenchymal condensations of endochondral and membranous skeletal elements differentiate first into preosteoblasts because of the function of Runx2. Preosteoblasts express low levels of type I collagen (Coll I) and alkaline phosphatase (ALP). To become fully committed osteoblasts, preosteoblasts require the function of Osx. Mature osteoblasts start to secrete osteoblastic markers, including Coll I, ALP, osteopontin (OPN), bone sialoprotein (BSP) and osteocalcin (OCN) into the extracellular matrix and are therefore responsible for the formation of highly mineralized bone matrix.

3.3.1.1 The Wnt signaling pathway

Whats are a family of 19 secreted glycoproteins that control many important biological processes such as embryogenesis and tumorigenesis. Whits bind to a membrane receptor complex composed of a Frizzled (FZD) G protein-coupled receptor and a low-density lipoprotein receptor-related protein 5 or 6 (LRP5/6) on the cell surface. What can activate three different intracellular signaling cascades: the canonical Wnt/ β -catenin pathway, the Wnt/Ca^{2+} pathway and the Wnt/planar polarity pathway. The most comprehensively characterized of these is the canonical Wnt/β-catenin pathway. In the absence of Wnt ligands, a degradation complex of glycogen synthase kinase 3 (GSK3), casein kinase 1a, Axin2 and adenomatous polyposis coli is formed that promotes the phosphorylation of β catenin, which leads to the ubiquitylation and degradation of β -catenin. When Wnt ligands are present, they bind to their receptors. This activates the cytoplasmic mediators, Dishevelled (Dsh) phophoproteins, which inhibit the β -catenin degradation complex and thereby block the degradation of β -catenin. The stabilized β -catenin protein accumulates within the nucleus, where it binds lymphoid enhancer-binding factor (Lef)/T cell factors (Tcf), displaces co-repressors and recruits transcriptional co-activators to stimulate the expression of specific target genes such as *c-myc* and *cyclin D1*. However, canonical Wntsignaling can also repress gene expression by mechanisms that are less understood (Angers and Moon 2009, Bodine 2008, Bodine and Komm 2006, Cadigan and Liu 2006, Kahler and Westendorf 2003, Westendorf *et al.* 2004).

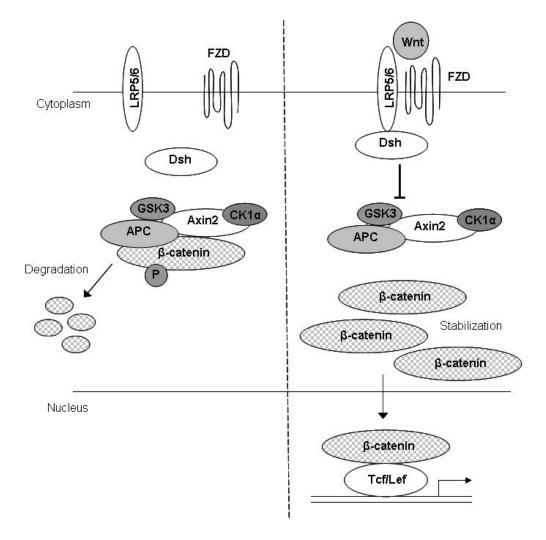


Fig. 9. The function of canonical Wnt signaling pathway. In the absence of Wnt ligands (left), a degradation complex of glycogen synthase kinase 3 (GSK3), casein kinase 1 α (CK1 α), Axin2 and adenomatous polyposis coli (APC) is formed that promotes the phosphorylation of β -catenin, which leads to the ubiquitylation and degradation of β -catenin. When Wnt ligands are present (right), they bind to their receptors that constitute of Frizzled (FZD) and LRP5/6 proteins, which activates the cytoplasmic mediator Dishevelled (Dsh). Dsh inhibits the β -catenin degradation complex, and thereby blocks the degradation of β -catenin. The stabilized β -catenin protein accumulates and translocates into the nucleus where it binds lymphoid-enhancer binding factor (Lef)/T cell factors (Tcf) and stimulates expression of specific target genes.

Wnt/ β -catenin signaling pathway is essential for skeletal development and homeostasis. In human, different LRP5 mutations correlate with high or low bone mass (Boyden *et al.* 2002, Gong *et al.* 2001, Little *et al.* 2002). When β -catenin is deleted early

in the embryonic development in the limb and the head mesenchyme, the loss of β -catenin results in an early osteoblast differentiation that leads to the absence of mature osteoblasts (Hill *et al.* 2005). Canonical Wnt signaling is also required for osteoblast proliferation. *LRP5* KO mice have low bone mass due to decreased osteoblast proliferation and function (Kato *et al.* 2002). The *in vitro* effects of Wnt signaling on osteogenic differentiation are controversial. In mouse, the canonical Wnt signaling pathway seems to promote the osteoblastic differentiation of MSCs (Gaur *et al.* 2005, Gong *et al.* 2001). On the other hand, in the preosteoblastic mouse MC3T3-E1 cell line the Wnt signaling pathway has been found to both increase (Gaur *et al.* 2005) and decrease osteoblastic differentiation (Kahler *et al.* 2006, Shi *et al.* 2007). In human MSCs, both stimulatory (Gregory *et al.* 2005) and inhibitory (Boland *et al.* 2004, de Boer *et al.* 2004, Liu *et al.* 2009a) effects have been reported for Wnt signaling pathway.

3.3.1.2 The pluripotency of mesenchymal stem cells

MSCs are pluripotent and can give rise to the cells of different mesodermal cell lineages including osteoblasts, chondrocytes and adipocytes. In addition, they have endodermic and ectodermic differentiation potential although the *in vivo* results are still controversial (Uccelli *et al.* 2008). Of these osteoblastic and adipogenic differentiation especially seem to be in balance as the decrease in bone volume found in osteoporosis, immobilization, or ovariectomy is accompanied by an increase in bone marrow adipose tissue (Ahdjoudj *et al.* 2002, Justesen *et al.* 2001, Martin and Zissimos 1991).

PPARγ is the master regulator of adipogenesis and its forced expression is sufficient to induce adipogenesis in fibroblasts (Tontonoz *et al.* 1994). The temporal expression of C/EBP family also plays a central part in adipogenic differentiation. The cascade starts with early induction of C/EBPβ and δ that leads to the induction of C/EBPα and PPARγ, which activate adipocytic gene transcription (Rosen and MacDougald 2006). In part, the adipocytic differentiation process is controlled by the same factors that control osteoblastic differentiation. For example, Wnt signaling decreases adipogenesis by inhibiting PPARγ and C/EBPα function and by maintaining preadipocytes therefore in an undifferentiated state (Ross *et al.* 2000). BMP-4 commits MSCs to the adipocytic lineage (Tang *et al.* 2004) and BMP-2 can cooperate with PPARγ and C/EBPα to increase adipogenic differentiation (Fux *et al.* 2004, Sottile and Seuwen 2000).

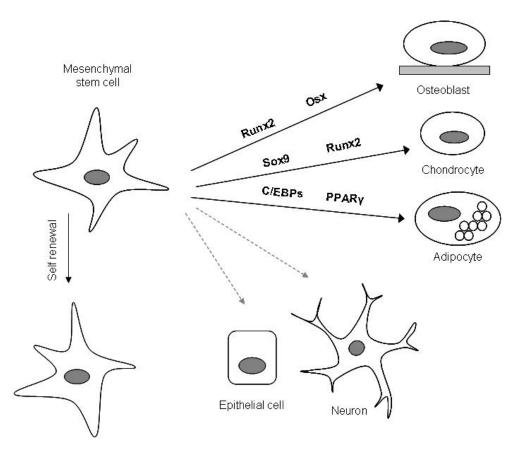


Fig. 10. The mesenchymal stem cells (MSCs) are capable of self renewal. They can also differentiate towards mesodermal lineages, which include osteoblasts, chondrocytes and adipocytes. Osteoblastic differentiation is dependent on the transcription factors Runx2 and Osx. Sox9 and later Runx2 are needed for chondrocyte differentiation, and C/EBPs and PPAR γ are obligatory for adipocytic differentiation. The ability of MSCs to differentiate into non-mesodermal lineages *in vivo* is still under debate with controversial results.

MSCs are of interest in regenerative medicine because of their capacity for self-renewal, for their ability to differentiate and because they are relatively easily isolated from a small aspirate of bone marrow (Giordano *et al.* 2007, Mishra *et al.* 2009). MSCs have been used to treat severe osteogenesis imperfecta, which results in increased total bone mineral content associated with an increased growth velocity and fewer fractures (Horwitz *et al.* 1999). MSCs support the growth of hematopoietic progenitors *in vitro* (Robinson *et al.* 2006, Wagner *et al.* 2007) and cancer patients treated with systemic infusion of MSCs with peripheral-blood progenitor cells after high-dose chemotherapy had rapid hematopoietic recovery (Koc *et al.* 2000). MSCs also have immunosuppressive effects and they have been used to effectively prevent graft-versus-host disease (Le Blanc *et al.* 2008). However, in leukemia patients, MSCs might also impair

the therapeutic graft-versus-leukemia effect as a higher incidence of relapses was seen in these patients (Ning *et al.* 2008). The ability of MSCs to migrate to the sites of inflammation, injury and solid tumors, makes them promising as a gene delivery mechanism in gene therapy (Giordano *et al.* 2007, Mishra *et al.* 2009). However, there are several concerns about their safety. It has been proposed that MSCs could be a source of carcinoma-associated fibroblasts (Mishra *et al.* 2009) and could promote tumor growth and metastasis (Djouad *et al.* 2003, Karnoub *et al.* 2007). In other studies, MSCs had suppressing effects on tumor growth (Cousin *et al.* 2009, Khakoo *et al.* 2006). Culturing MSCs *in vitro* makes them susceptible to cytogenic abnormalities. Differentiation of the MSCs into tumor cells after *in vivo* administration has been shown to occur in rodents (Tolar *et al.* 2007). However, it has been demontrated that human MSCs can be safely cultured *in vitro* (Bernardo *et al.* 2007). Hitherto there have been no reports of *in vitro* cultured MSC formed tumors in humans (Tikkanen *et al.* 2010).

3.3.2 The function of osteoblasts

Osteoblasts control most of the functions of bone. They are responsible for bone formation, extracellular matrix mineralization, osteoclast differentiation, and thereby indirectly for bone resorption.

3.3.2.1 Osteoblasts form bone

Osteoblasts synthesize the organic constituents of bone. Most of the organic matrix is highly cross-linked Coll I. Collagen is constituted by three polypeptide α -chains that form a triple-helix structure. Osteoblasts synthesize and secrete collagens in the form of soluble procollagens. During the secretion, propeptides are enzymatically cleaved, which triggers spontaneous self-assembly of collagen molecules into fibrils. Fibrils arrange into complex three-dimensional concentric weaves whose structures are stabilized by several post-translational modifications that allow intermolecular and interfibrillar crosslinks to take place (Blair *et al.* 2002, Viguet-Carrin *et al.* 2006). Collagen plays a substantial role in the toughness of bone and mutations in the genes that encode the α 1 or α 2 chains of Coll I have been associated with osteogenesis imperfecta (Marini *et al.* 2007).

Mineral is generated within the dense collagen matrix. Osteoblasts regulate the matrix mineralization by releasing small, membrane-bound matrix vesicles that contain concentrated calcium and phosphate which may lead to the first CaPO₄ deposits. Initiation of hydroxyapatite crystal formation is facilitated by the activity of phosphatases, such as ALP, which are enriched in the matrix vesicle membranes. The preformed hydroxyapatite crystals are released into the extravesicular fluid, which normally contains homeostatically maintained levels of calcium and PO_4 that are sufficient to support continued nucleation of new hydroxyapatite crystals on preformed hydroxyapatite templates (Anderson 2003).

ALP is ubiquitously found in plants and animals. In human, four ALP isoenzymes are encoded by four genes. One of the genes is expressed in all cells, but especially highly in bone, liver, and kidney, and is designated tissue-nonspecific ALP (*TNSALP*). It is essential for skeletal mineralization as its product hydrolyzes inorganic pyrophosphate, which is an inhibitor of hydroxyapatite formation. In humans, deficiency of the *TNSALP* gene leads to hypophosphatasia with skeletal hypomineralization, that leads to rickets and osteomalacia (Whyte 2010). *TNSALP* KO mice show skeletal hypomineralization that mimicks a severe form of hypophosphatasia (Narisawa *et al.* 1997). Osteoblasts isolated from these mice differentiate normally, but are unable to initiate matrix mineralization *in vitro* (Wennberg *et al.* 2000). Bone-specific ALP (BALP), which is an isoform of the TNSALP isoenzyme, is used as a biochemical marker for bone formation. BALP is a relatively specific marker of osteogenesis and elevated levels occur in conditions such as Paget's disease, bone cancer, and osteomalacia (Coleman *et al.* 2008).

Other matrix proteins that are secreted by osteoblasts include BSP, OPN, and OCN. BSP and OPN are both members of the SIBLING (small integrin-binding ligand N-linked glycoprotein) family (Fisher *et al.* 2001). OPN is expressed in osteoblasts and osteocytes, but also in kidney and epithelial linings, and is secreted in bodily fluids including milk, blood, and urine. *OPN* is upregulated at sites of inflammation and tissue remodeling. The expression of BSP is more restricted as it is mostly produced in cells associated with mineralized tissues and especially highly in osteoblasts. SIBLINGs mediate cell migration, adhesion and survival through interactions with cell surface receptors such as integrins and extracellular matrix constituents including collagen and hydroxyapatite (Ganss *et al.* 1999, Lund *et al.* 2009). BSP enhances osteoblast

differentiation and matrix mineralization in vitro (Gordon et al. 2007), and the BSPcollagen interaction has been shown to promote hydroxyapatite formation (Baht et al. 2008). On the other hand, OPN inhibits hydroxyapatite formation (Boskey et al. 1993, Hunter et al. 1994). BSP KO mouse fetuses and young adults exhibit shorter and hypomineralized bones. Adult BSP KO mice display a high trabecular bone mass despite reduced bone formation rate due to impaired bone resorption (Malaval et al. 2008). OPN KO mice show normal development and bone structure (Rittling et al. 1998). The OPN deficiency still increases bone fragility possibly due to increased matrix heterogeneity (Thurner et al. 2010). In human, elevated serum OPN levels have been shown to be associated with a higher risk of osteoporosis in menopausal women (Chang et al. 2010). BSP and OPN are also expressed at pathological sites of mineralization such as microcalcifications in the breast, and they have been suggested to play a role in bone metastasis (Bellahcène and Castronovo 1995, Bellahcène and Castronovo 1997). Indeed, BSP and OPN expressions have been associated with bone metastasis and/or reduced survival in patients with breast (Bellahcène et al. 1996, Rudland et al. 2002), lung (Donati et al. 2005, Papotti et al. 2006), and prostate cancer (Forootan et al. 2006, Waltregny et al. 1998).

OCN is the most abundant noncollagenous protein produced by osteoblasts and it is a terminal marker of osteoblastic differentiation. It has been suggested to OCN has an inhibitory role during bone formation as *OCN* KO mice show increased bone formation (Ducy *et al.* 1996). OCN has a high affinity for mineral ions and hydroxyapatite (Hauschka and Wians 1989) but its exact role in matrix mineralization is not known as there are contradictory results on the subject (Boskey *et al.* 1998, Murshed *et al.* 2004). OCN can also be found in the circulation. Both osteolysis and osteogenesis release OCN into the serum and therefore OCN levels might reflect the overall bone metabolism instead of just osteogenesis (Coleman *et al.* 2008).

After completion of bone formation approximately 50 to 70% of osteoblasts undergo apoptosis whereas the reminder become either osteocytes or inert bone lining cells. Flattened bone-lining cells are thought to be quiescent osteoblasts found in the endosteum. They may regulate the flux of mineral ions into and out of bone extracellular fluid and retain the ability to redifferentiate into functional osteoblasts upon exposure to stimulus such as PTH or to a mechanical force (Clarke 2008, Dobnig and Turner 1995). Osteocytes have been long thought to be rather inactive cells, but new information about

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their function has emerged. Osteocytes, for example, regulate bone mass by expressing high levels of sclerostin, which has been shown to be a negative regulator of bone formation in human (Balemans *et al.* 2001, Brunkow *et al.* 2001). Another protein that is produced in large quantities in osteocytes is FGF-23. FGF-23 is a key regulator of phosphorus and vitamin D metabolism, and its excess production can cause hypophosphatemic diseases that are characterized by impaired renal phosphate reabsorption and osteomalacia (Wesseling-Perry 2010).

3.3.2.2 Osteoblasts regulate osteoclastogenesis

Another important function for osteoblasts is the regulation of osteoclastic differentiation. Osteoblasts regulate osteoclastogenesis mainly by expressing macrophage colonystimulating factor (M-CSF) and receptor activator of nuclear factor-κB ligand (RANKL). RANKL binds to RANK receptor on osteoclast precursors, which results in the recruitment of TRAF6 and activation of downstream molecules including NF-KB. Ultimately NFATc1 is induced and activated, which initiates the transcription of osteoclastic genes and differentiation. In addition to osteoclastogenesis, RANKL stimulates osteoclast activation and inhibits their apoptosis (Asagiri and Takayanagi 2007, Kearns et al. 2008). RANKL mutations have been shown to be associated with osteopetrosis in both mice (Kong et al. 1999) and humans (Sobacchi et al. 2007). Moreover, *op/op* mice that lack functional M-CSF have osteopetrosis because of a severe deficiency of mature osteoclasts (Yoshida et al. 1990). M-CSF expression by osteoblastic stromal cells is required for osteoclastogenesis, but M-CSF per se can not complete this process. M-CSF binds to its receptor c-Fms on osteoclast precursor cells and regulates their proliferation and survival (Asagiri and Takayanagi 2007, Boyce and Xing 2008, Kearns et al. 2008). Furthermore, osteoprotegerin (OPG) is an important regulator of osteoclastogenesis. It is a decoy receptor that binds to RANKL and therefore prevents its interaction with RANK (Boyce and Xing 2008). OPG KO mice develop early onset severe osteoporosis (Bucay et al. 1998). In human, the mutations in the OPG gene are associated with juvenile Paget's disease (Whyte et al. 2002) and idiopathic hyperphosphatasia (Cundy et al. 2002). There is a tight regulation of RANKL, OPG and M-CSF expressions in osteoblasts, in which many external factors such as growth factors, hormones, cytokines and drugs take part.

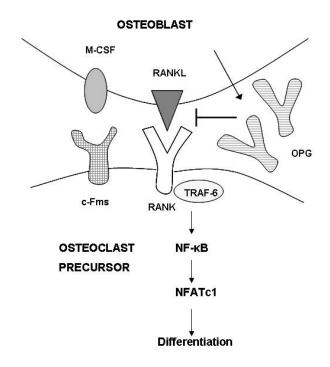


Fig. 11. A simplified model of how osteoblasts regulate osteoclast differentiation. Osteoblasts express RANKL that can bind to its receptor RANK, which is located on the surface of the osteoclast precursor. Binding induces a signaling cascade with TRAF-6, NF- κ B, and NFATc1 and leads to the activation of osteoclastic genes and osteoclastogenesis. Osteoblasts also secrete OPG, which is a decoy receptor for RANKL and inhibits RANKL/RANK-binding. In addition, osteoblasts express M-CSF that binds to its receptor c-Fms on osteoclast precursor cells and enhances their proliferation, survival and osteoclastic differentiation.

3.4 Skeletal homeostasis

Bone is a dynamic tissue that is constantly being renewed in a process called bone remodeling, which is necessary to maintain calcium homeostasis and to remove and prevent the accumulation of aged or weakened bone. Bone remodeling occurs in a sequential manner (Fig. 12). Bone surface is activated by unknown signals that attract osteoclast precursor cells from the circulation (activation phase). These cells fuse and form multinucleated cells that adhere to the bone surface, differentiate into mature osteoclasts in response to signals mediated by osteoblasts, and start bone resorption (resorption phase). The degraded bone proteins and matrix minerals enter the osteoclast by endocytosis. They cross the cell in vesicles, and undergo exocytosis on the opposite side of the cell, from where the products diffuse into the nearby blood capillaries. When osteoclasts finish resorbing, they die by apoptosis, which is followed by the recruitment of

mononuclear cells, which prepare the bone surface for bone formation, and preosteoblasts (reversal phase). Preosteoblasts differentiate into functional osteoblasts and fill the cavity with a collagenous matrix that is finally mineralized (formation phase). Bone resorption is a much faster process than bone formation. It takes approximately three months to rebuild the equivalent mass of bone that was resorbed in two to three weeks (Hadjidakis and Androulakis 2006, Henriksen *et al.* 2009, Kearns *et al.* 2008, Tortora and Grabowski 2000).

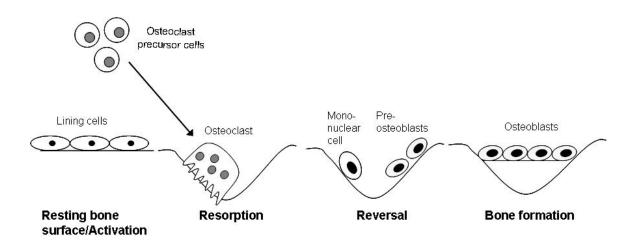


Fig. 12. Bone remodeling occurs in sequential phases. During the activation phase osteoclast precursors are recruited and activated to form multinucleated osteoclasts, which start bone resorption. During the reversal phase mononuclear cells and preosteoblasts are recruited onto the bone surface. In the formation phase preosteoblasts differentiate into functional osteoblasts and fill the cavity with new bone.

The control of bone metabolism is a complex and still largely unknown process. The purpose of having a tight control is to keep the two processes of bone resorption and formation in balance. It is regulated by endocrine, paracrine and autocrine actions of diverse hormones, cytokines and growth factors that in concert with numerous transcription factors act on osteoblast and osteoclast differentiation and function. This regulation will be discussed next emphasizing its effect on bone formation.

3.4.1 The regulation of bone formation and homeostasis

The rate of bone formation is determined by the number and function of osteoblasts. The cell number is regulated partly by those factors that regulate osteoblastic differentiation of

MSCs and pre-osteoblasts already discussed (heading 3.3.1). Many of these factors, including the Wnt signaling pathway (Westendorf *et al.* 2004) and FGFs (Fakhry *et al.* 2005, Valta *et al.* 2006) also enhance the proliferation of preosteoblasts and osteoblasts adding to the increase in osteoblast number.

Estrogens evidently play a critical role in the maintenance of bone homeostasis as exemplified by postmenopausal osteoporosis. The complex effects of estrogen and other nuclear receptors will be discussed in more detail under the next heading. However, decreased bone volume can also be detected in late premenopausal women with normal circulating estrogen levels. Instead, increased bone resorption is associated with elevated follicle-stimulating hormone (FSH) levels (Ebeling et al. 1996). FSH has been found to have direct effects on bone as it stimulates osteoclast formation and function via its G protein-coupled receptor FSHR (Sun et al. 2006). The early perimenopausal rise in FSH levels in women is attributed to a decrease in inhibin B secretion (Klein et al. 1996, Welt et al. 1999). Inhibin A and inhibin B are heterodimeric proteins that belong to the transforming growth factor β (TGF- β) superfamily and are able to suppress FSH secretion. The function of inhibins is antagonized by the related homodimeric peptides activin A and activin B that belong to the same TGF- β superfamily (Nicks et al. 2010). Both activins and inhibins have been shown to regulate osteoblastogenesis, osteoclastogenesis and bone mass. Activins have been described as being pro-osteoclastogenic but there are reports of both negative and positive effects on osteoblast differentiation (Nicks et al. 2009). Inhibins have been shown to repress the differentiation of osteoblasts and osteoclasts (Gaddy-Kurten et al. 2002). However, the effect of inhibins seems to be biphasic as continuous Inhibin A exposure *in vivo* has been described to have an anabolic effect on osteoblasts (Perrien et al. 2007).

Another biphasic and important regulator of bone mass is PTH. PTH, parathyroid hormone-related peptide (PTHrP) and vitamin D are the main calciumregulating hormones that regulate bone cell differentiation and mineral transport at multiple points. PTH increases distal tubular calcium re-absorption and increases the production of the active form of vitamin D. Continuous administration of PTH increases osteoclast differentiation, activation and consequently bone resorption by stimulating RANKL and inhibiting OPG expression in osteoblasts. Nonetheless, intermittent PTH treatment has an anabolic effect on bone as it increases osteoblast proliferation and differentiation and inhibits osteoblast apoptosis. PTHrP shares amino acid homology with PTH and binds the same G protein-coupled receptors (Datta and Abou-Samara 2009, Goltzman 2010). *PTHrP* KO mice show widespread abnormalities in endochondral bone development with decreased chondrocyte proliferation, premature chondrocyte maturation and accelerated bone formation (Karaplis *et al.* 1994). PTHrP has also been reported to increase osteoblast proliferation (Du *et al.* 2000).

Mechanical stimulus is another regulator of bone mass. Increased mechanical loads stimulate bone formation and suppress resorption, whereas unloading has the opposite effect. The exact mechanisms remain unknown but calcium channels, Wnt/ β -catenin signaling, integrins, prostaglandin E2, and nitric oxide are some of the proposed mediators (Harada and Rodan 2003, Papachristou *et al.* 2009).

The central nervous system can also regulate bone formation. In mice, factors such as neuropeptides cocaine- and amphetamine-regulated transcript (CART) and neuromedin U (NMU) have been shown to associate with low bone mass with increased bone resorption (Elefteriou *et al.* 2005) and high bone mass with increased bone formation (Sato *et al.* 2007), respectively. The most studied of the centrally affecting factors is leptin. Leptin is a hormone produced by adipose cells that binds to its receptor in the hypothalamus and suppresses appetite and increases energy expenditure (Hamrick and Ferrari 2008, Kawai *et al.* 2009, Takeda 2008). *Ob/ob* mice that lack functional leptin and leptin-receptor deficient *db/db* mice have a high bone mass despite hypogonadism and hypercortisolism (Ducy *et al.* 2000). The suggested mechanism for this phenomenon involves leptin binding to its receptor in the hypothalamus and stimulating the release of noradrenaline from the sympathetic nerve fibers that project into the bone. Noradrenaline in turn is thought to inhibit bone formation by binding to β 2-adrenergic receptors on osteoblasts (Ducy *et al.* 2000, Hamrick and Ferrari 2008).

3.4.1.1 The influence of nuclear receptors on bone and osteoblasts

Many NRs regulate bone and osteoblast function. Most important of these are perhaps VDR, GR, AR and ERs, which will be discussed in more detail.

Vitamin D has long been known as a potent stimulant of calcium absorption. Vitamin D deficiency leads to rickets in children and osteomalacia and osteoporosis in adults. VDR mutations that cause complete loss of function of the receptor lead to bone growth abnormalities (Imai *et al.* 2009). *VDR* KO mice have reduced bone mineral density (BMD) (Yoshizawa *et al.* 1997) but increased bone volume. This phenotype can be corrected by the administration of calcium and phosphate supplements (Amling *et al.* 1999) and therefore vitamin D seems to regulate bone mass mainly by controlling the systemic calcium-phosphate metabolism. Despite this, there is increasing evidence showing that VDR is capable of regulating bone cells directly during bone metabolism (Anderson and Atkins 2008). VDR has been found to inhibit osteoblast differentiation and mineralization *in vitro* (Shi *et al.* 2007, Sooy *et al.* 2005). VDR also induces the expression of RANKL by chondrocytes and osteoblasts, which increases osteoclastogenesis (Kitazawa *et al.* 2003, Masuyama *et al.* 2006, Takeda *et al.* 1999).

Glucocorticoids increase bone resorption and decrease bone formation, which leads to decreased bone mass and osteoporosis as manifested by prolonged steroid therapy and Cushing's syndrome (Imai *et al.* 2009). Glucocorticoids have complex effects on bone and although extensively studied, consensus has yet to be achieved. Glucocorticoids have been shown to induce accelerated apoptosis in osteoblasts (Weinstein *et al.* 1998). However, they increase the ability of osteoprogenitors to form mineralized bone nodules *in vitro* (Jaiswal *et al.* 1997) and dexamethasone, a synthetic glucocorticoid, is commonly used to induce osteoblastic differentiation in MSC cultures.

The bones of males have higher mineral density and a lower risk of osteoporosis and fracture than those of females. This is thought to be due to the anabolic effects of androgenic hormones (Imai *et al.* 2009). Testosterone and other androgens act through AR. Indeed, patients suffering from complete androgen insensitivity syndrome due to a mutation in AR have decreased BMD (Bertelloni *et al.* 1998). *Ar* KO male mice have osteopenia with increased trabecular and cortical bone resorption and formation (Kawano *et al.* 2003). It is still somewhat controversial, which cells in bone are the targets of androgen-AR signaling and whether the effect is systemic or direct (Imai *et al.* 2009).

It has been long known that the decline in circulating estrogen in menopausal women triggers high bone turnover and a decrease in BMD. Ovariectomy induces similar bone defects in experimental animals. This suggests that estrogens and ERs have bone-protective effects (Frenkel *et al.* 2010, Imai *et al.* 2009). Estrogens have both direct and indirect effects on bone. For instance, immune cells participate indirectly in conducting the proskeletal effects of estrogen (Lorenzo *et al.* 2008). In humans and mice, cortical bone expresses mainly ER α but little or no ER β , whereas trabecular bone contains both receptors (Bord *et al.* 2001, Mödder *et al.* 2004). Despite the clear anti-resorptive and

anabolic effect of estrogen in humans, ER α (Esr1) KO female and male mice exhibit increased trabecular bone volume with a decreased number of osteoclasts. This could be explained by the increased testosterone concentration in these mice (Lindberg et al. 2001, Parikka et al. 2005, Sims et al. 2002). Results from studies on cortical bone are conflicting with reports of both increased (Lindberg et al. 2001) and decreased (Sims et al. 2002) cortical BMD in ER α KO mice. Deletion of *Esr2* (the gene that encodes ER β) in male mice has no impact on their skeleton. In female mice, $ER\beta$ seems to have a repressive effect on bone as a deletion of Esr2 increases cortical bone mass at the age of 3 months (Windahl et al. 1999) and protects them from age-related bone loss as aged animals have an increased trabecular and cortical bone mass at the age of one year (Windahl et al. 2001). ER α /ER β double KO male mice show similar but milder bone phenotype than ER α KO mice but females have decreased trabecular bone mass (Sims et al. 2002). Although estrogens have been reported to promote osteoblast commitment (Okazaki et al. 2002, Dang et al. 2002) and to prevent apoptosis of MSCs and osteoblasts (Almeida et al. 2007, Zhou et al. 2001), in postmenopausal women, both bone resorption and bone formation have been found to be increased (Garnero et al. 1996). However, this can be explained by osteoblast-osteoclast coupling mechanisms. Accordingly, an acute estrogen deficiency of three weeks is associated with a fall in markers of bone formation in both men (Falahati-Nini et al. 2000) and women (Charatcharoenwitthaya et al. 2007). It also appears that the effects of estrogen on osteoblast differentiation and function may be stage and cell type specific and can vary greatly between individuals (Leskelä et al. 2006). Estrogen has been shown to stimulate osteoblastic differentiation in some studies (Qu et al. 1998, Waters et al. 2001) but not to have any effect or to inhibit differentiation in others (Keeting et al. 1991, Robinson et al. 1997). Estrogen inhibits osteoclastic differentiation, inter alia, by increasing OPG (Hofbauer et al. 1999) and decreasing RANKL (Eghbali-Fatourechi et al. 2003) production by osteoblastic cells. Estrogen also induces apoptosis in osteoclasts by activating the expression of the Fas ligand. Female mice with osteoclast specific ablation of *Esr1* have low trabecular bone mass, which suggests that the osteoprotective effects of estrogen are partly mediated by osteoclastic ER α in trabecular bone (Nakamura *et al.* 2007). All of these results show that estrogen can function on multiple levels and has both direct and indirect effects on different compartments and cell types of bone, but also reflects the difficulty and complexity of bone research.

Table 2. Summary of the bone phenotypes of different ER KO mice (adapted from Vico and Vanacker 2010). ER KO mice manifest different phenotypes in their trabecular and cortical bone with either increased (\uparrow), decreased (\downarrow), or unaffected (-) bone mass. Some putative effects are still under debate as there are conflicting results (\uparrow/\downarrow).

Genotype	Female		Male	
	Trabecular	Cortical	Trabecular	Cortical
ΕRα ΚΟ	1	\uparrow/\downarrow	1	\downarrow
ΕRβ ΚΟ	↑ (one year)	\uparrow (3 months)	-	-
ΕRα/ΕRβ ΚΟ	\downarrow	\downarrow	1	\downarrow

In addition to the classical NRs, many orphan NRs regulate the function of bone and osteoblasts. These include NR3B and NR4A families, which will be discussed next.

3.4.1.1.1 The NR3B family in bone and mesenchymal stem cell differentiation

There are several published studies that address the role of NR3B family in bone and osteoblast differentiation. ERR α is expressed in several human and mouse osteoblastic cell lines that include TE85 and SaOS (Bonnelye *et al.* 1997b). ERR α is also expressed in the ossification zones of the mouse embryo during the onset of bone formation (Bonnelye *et al.* 1997a). In bone the expression of ERR α is not only restricted to osteoblasts as MSCs, chondrocytes, mature osteocytes and osteoclasts all express ERR α (Bonnelye and Aubin 2002a). ERR β is not expressed in osteoblastic cell lines SaOs, TE85 or primary human osteoblasts (Bonnelye *et al.* 1997b). ERR γ is expressed in osteoblastic cell line MC3T3-E1 and in primary mouse osteoblasts but very modestly (Jeong *et al.* 2009).

ERRs regulate several bone-related genes. One of these is *OPN*, which is regulated by ERR α in a cell context dependent manner. The expression of *OPN* is upregulated by ERR α in HeLa cells but repressed in ROS17/2.8 cells (Vanacker *et al.* 1998, Zirngibl *et al.* 2008). ERR α also regulates lactofferin (Yang *et al.* 1996), aromatase (Yang *et al.* 1998), and endothelial nitric oxide synthase (Sumi and Ignarro 2003) expression. ERR α is expressed during osteoblast differentiation and it has a positive effect on bone formation *in vitro* in rat calvarial osteoblasts (Bonnelye *et al.* 2001). However, recently there has been some controversy on the subject. Delhon *et al.* showed that ERR α KO mice have slightly increased femoral cancellous BMD and that the absence of ERR α in human MSCs increases their BMP-2 induced osteoblastic differentiation (Delhon et al. 2009). Another independent ERR α KO mouse model was shown to be resistant to bone loss induced by age or estrogen deficiency. However, the younger 14 week old female ERRa KO mice had significantly lower trabecular bone volume and trabecular number, which is in contradiction with that found in the ERR α KO mouse model of Delhon *et al.* (Teyssier et al. 2009). In the same study MSCs obtained from the female mice had increased osteoblastic differentiation, which can explain the resistance to estrogen deficiency but not the lower trabecular bone volume in normal state. Wei and colleagues reported osteopetrosis in ERRa KO mice that was mostly explained by decreased bone resorption due to a diminished number of osteoclasts. Osteoblast surface and number were also increased although OCN levels were not significantly altered (Wei et al. 2010). Delhon et al. and Teyssier et al. also studied osteoclast number and function in their ERR α KO models but did not see any significant differences to the wild-type mice (Delhon et al. 2009, Teyssier et al. 2009). Laflamme and others discovered an association between a frequent regulatory variant of ESRRA and BMD. French-Canadian premenopausal women who carried the long ESRRA genotype, which increases the expression of ERRa, had a 3.9% higher lumbar spine BMD than those who carried the short ESRRA genotype (Laflamme et al. 2005). A similar study was performed in another population of premenopausal women and no correlation between ESRRA variants and bone density was detected (Giroux *et al.* 2008). All of these studies show that ERR α plays a role in bone metabolism, but the mechanism could be more complex than first anticipated and may involve different cell types of bone.

A silent variant of *ESRRG* has been associated with multiple bone measurements, which could indicate that ERR γ plays a role in bone cell biology (Elfassihi *et al.* 2010). ERR γ expression is increased by BMP-2 in primary osteoblasts, C2C12 and MC3T3-E1 cells and ERR γ physically interacts with Runx2 and represses its transcriptional activity. Intramuscular overexpression of adenoviral ERR γ in mice did not affect intramuscular bone formation by itself *in vivo* but it inhibited BMP-2-induced ectopic bone formation (Jeong *et al.* 2009).

NR3B receptors have been shown to affect other differentiation routes of MSCs. ERR α appears to function in adipogenesis as the underexpression of ERR α inhibits adipogenesis of 3T3-L1 and human MSCs (Delhon *et al.* 2009, Ijichi *et al.* 2007). On the other hand, there is also a study that shows that the underexpression of ERR α increases

adipogenesis in rat calvarial osteoblasts (Bonnelye *et al.* 2002b). The expression of ERR γ increases in mouse mesenchyme-derived cells under the adipogenic differentiation conditions and in the brown and white adipose tissue of mice fed a high-fat diet. ERR γ knockdown by siRNA resulted in down-regulation of adipogenic marker gene expression that implies that ERR γ positively regulates the adipocyte differentiation (Kubo *et al.* 2009). ERR α is also expressed in fetal and adult rat chondrocytes in growth plate and articular cartilage. The overexpression of ERR α in chondrocytic C5.18 cell cultures increases the expression of Sox9 (SRY-related HMG-box 9), which is a master gene in cartilage formation. Reduced expression of ERR α by antisense oligonucleotides led to an inhibition of cartilage formation that was associated with decreased Sox9 and Indian hedgehog expression (Bonnelye *et al.* 2007).

3.4.1.1.2 The NR4A family in bone and mesenchymal stem cell differentiation

The NR4A family members are expressed in bone and osteoblasts. Their expression is induced in osteoblasts by PTH (Pirih *et al.* 2003, Pirih *et al.* 2005, Tetradis *et al.* 2001a, Tetradis *et al.* 2001b) and FGF-8b (Lammi and Aarnisalo 2008). FGF-8b stimulates the proliferation of MC3T3-E1 cells, which is at least partly mediated by Nurr1 and NGFI-B (Lammi and Aarnisalo 2008). NR4A receptors have been shown to regulate some bone related genes. They transactivate the *OPN* promoter directly which increases OPN expression in osteoblastic cells (Lammi *et al.* 2004). Nurr1 also regulates the expression of the *OCN* gene by directly binding to its promoter (Pirih *et al.* 2004). Intermittent PTH administration to mice induces NR4A expression in calvaria, long bones and kidney. Intermittent PTH also increases the expression of OPN and OCN mRNAs in osteoblasts (Pirih *et al.* 2005). Nurr1 is also involved in osteoblast differentiation as Nurr1 siRNA decreases OCN and Coll I A1 expression and ALP activity in MC3T3-E1 cells. The expression of osteoblastic markers is also reduced in calvarial osteoblasts derived from *Nurr1* KO mice (Lee *et al.* 2006).

It has been suggested that NR4A receptors influence adipogenic differentiation. The expression of these receptors is rapidly induced in response to adipogenic cocktail used to induce differentiation in 3T3-L1 preadipocytes (Au *et al.* 2008, Chao *et al.* 2008, Fu *et al.* 2005, Fumoto *et al.* 2007). The role of NR4A receptors in adipogenic differentiation is still controversial with reports of both negative and positive

effects in addition to the absence of effects (Au *et al.* 2008, Chao *et al.* 2008, Fumoto *et al.* 2007). Nurr1 is also thought to have a protective function in cartilage homeostasis as Nurr1 selectively represses the expression of matrix metalloproteinases during inflammation. Matrix metalloproteinases digest components of the extracellular matrix, which leads to the degradation of cartilage, tendon and bone (Mix *et al.* 2007).

3.4.2 Osteoporosis and other bone related diseases

Osteoporosis is a major health problem that affects approximately 400 000 people in Finland. It has been estimated that 30 000 to 40 000 bone fractures are associated with osteoporosis every year (Duodecim 2007). Osteoporosis is characterized by the loss of bone mass and strength due to an imbalance between bone resorption and formation that leads to an increased risk of fractures. Osteoporosis is a heterogenous disease caused by complex interactions among local and systemic regulators of bone cell function (Canalis 2010, Raisz 2005). Many factors, including age, sex, diet, physical activity, medication use, positive family history and menopausal status, influence the risk of osteoporosis. To date, at least 15 genes (VDR, ESR1, ESR2, LRP5, LRP4, SOST, GRP177, OPG, RANK, RANKL, COLL I A1, OPN, ITGA1, OSX, and SOX6) have been assigned as osteoporosis susceptibility genes and over 30 genes have been identified as promising candidates. These susceptibility and candidate genes are clustered in three biological pathways of which the first one is the estrogen pathway (Li et al. 2010). As discussed before, estrogen and its receptors obviously play a critical part in the development of osteoporosis in women (Raisz 2005) and also in men (Falahati-Nini et al. 2000, Khosla et al. 2008). The other two gene clusters include the Wnt/β-catenin and the RANKL/RANK/OPG pathways (Li et al. 2010).

The primary treatment for osteoporosis are bisphosphonates. Bisphosphonates include alendronate, risedronate, and etidronate, which are stable analogues of pyrophosphate and they have strong affinity for hydroxyapatite. Bisphosphonates decrease bone turnover and enhance bone mass by inhibiting the function and recruitment of osteoclasts and by increasing their apoptosis. Estrogen replacement therapy prevents bone loss in postmenopausal osteoporosis. However, the hormone replacement therapy is not suitable for all patients as it increases the risk of uterine and breast cancer, stroke, thrombotic events, and cardiovascular diseases. On the

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other hand, a selective estrogen receptor modulator raloxifene lacks most of these undesirable side effects and has been approved for the prevention and treatment of postmenopausal osteoporosis. Raloxifene, which acts on bone as estrogen, diminishes the differentiation and activity of osteoclasts while it maintains the function of osteoblasts, which reduces the occurrence of vertebral fracture. Calcitonin is a peptide produced by thyroid, that inhibits osteoclast activity and therefore bone resorption. It is not as efficient as bisphosphonates in inhibiting bone loss but it has an analgesic effect on bone pain not shared by other antiresorptive therapies. Teriparatide (1-34 PTH) is a synthetic PTH analog and is the only accepted anabolic medication available for osteoporosis. The teriparatide treatment is expensive but effective in increasing the BMD, in improving bone microstructure, and in decreasing fracture incidence by stimulating new bone formation by osteoblasts. Teriparatide is approved to treat severe osteoporosis for a maximum of 18 months (Duodecim 2007, Gass and Dawson-Hughes 2006, Migliaccio *et al.* 2007).

Bone is quite a rare place for a primary tumor to occur. In Finland, 50 to 60 cases of malignant primary tumors are found per year, which constitutes only 1/80 of all malignant tumors. The most common primary bone malignancies are myeloma, osteosarcoma, chondrosarcoma, and Ewing sarcoma (Mäkelä 2001). Whereas the incidence of chondrosarcoma and myeloma peaks in adults, osteosarcoma and Ewing sarcoma mainly occur in pediatric patients and young adults and usually develop in the extremities or in the pelvis (Mäkelä 2001, Heare *et al.* 2009).

Instead of primary tumors, cancer metastases commonly develop in the skeleton. For example, breast and prostate cancers preferentially metastase in the bone. The bone microenvironment is highly favourable for tumor invasion and growth. To facilitate the interactions of tumor and bone cells, the bone metastasizing tumor cells often mimic the bone cells. For example, metastatic breast cancer cells have been shown to express BSP and Runx2 (Barnes *et al.* 2003). Physical properties of the bone matrix, such as low oxygen content and acidic pH, promote tumor growth. There are two types of bone metastases, osteoblastic and osteolytic lesions, which result from the imbalance between bone formation and resorption. Osteoblastic lesions are a characteristic of prostate cancer. In osteolytic lesions, tumor cells secrete factors that stimulate osteoclast function. This, in turn, helps the release of growth factors such as TGF- β and insulin-like growth factors I and II that are immobilized within the bone matrix, which favours tumor growth. In

osteoblastic lesions, tumor cells secrete pro-osteoblastic factors, including Wnt, BMPs and endothelin-1 that stimulate various steps in osteoblast proliferation, differentiation and mineralization. Activated osteoblasts in turn secrete growth factors, such as TGF- β , BMPs and vascular endothelial growth factor, which favor tumor cell survival and proliferation. However, bone lesions are often mixed and show both osteoblastic and osteoclastic elements. Bone metastases lead to many skeletal complications, such as bone pain, hypercalcemia and fractures, which increase morbidity and diminish quality of life (Kingsley *et al.* 2007, Mundy 2002, Virk and Lieberman 2007).

AIMS OF THE STUDY

The members of the orphan NR families NR3B and NR4A are expressed in osteoblasts. However, the regulation of their transcriptional activity and function in osteoblasts is largely unknown. Therefore, the aim of this study was to address the signaling and function of NR3B and NR4A receptors in osteoblasts with the following specific aims:

- To identify new signaling pathways able to regulate the transcriptional activity of NR3B and NR4A receptors in osteoblasts
- To identify possible new ligands for NR3B receptors
- To study how NR3B and NR4A orphan nuclear receptors affect Wnt signaling pathway in osteoblasts
- To analyze the role of ERRα in osteoblastic differentiation of mesenchymal stem cells

MATERIALS AND METHODS

Short descriptions of the materials and methods are presented here. For more detailed descriptions, the reader is referred to the original publications.

 Table 3. The methods used in original publications.

Method	Original publication
1. Plasmid construction and recombinant DNA technology	I, II, III, IV
2. Site-directed mutagenesis	I, II, III, IV
3. Cell culture and reporter gene assays	I, II, III, IV
4. Electrophoretic mobility shift assay (EMSA)	Ι
5. SDS-PAGE and immunoblotting	II, III
6. Partial proteolysis assay	II
7. Cell growth assay	II
8. Molecular modeling	II
9. Primary mesenchymal stem cell isolation and osteoblastic and adipogenic differentiation	IV
10. Primary osteoblast isolation and culture	IV
11. ³ H-thymidine incorporation	IV
12. Alizarin red S and Oil Red O stainings	IV
13. RNA extraction and RT-PCR	II, III, IV
14. Statistical analysis	II, III, IV

1. Plasmid construction and recombinant DNA technology

Expression vectors, reporter constructs, and probes were prepared using standard recombinant DNA techniques. The luciferase reporter constructs NBRE₃tk-LUC, MH100tk-LUC and ERRE₃tk-LUC, and the pCMX- β gal, pCMX-PL1, and pCMX-Gal4 vectors were provided by Dr. Ronald M. Evans (Howard Hughes Medical Institute, The Salk Institute for Biological Studies, La Jolla, CA). The expression vectors for pCMX-Nurr1, pCMX-NGFI-B, pCMX-Nor1, pCMX-Gal4-Nurr1 NTD, pCMX-Gal4-Nurr1 LBD, pCMX-Nurr1\Delta1-84, pCMX-Nurr1D589A, pCMX-Nurr1\Delta1-84/D589A, and pCMX-Nurr1

DN were gifts from Dr. Thomas Perlmann (Ludwig Institute for Cancer Research, Sweden). pCMX-ERR α , pCMX-ERR β , and pCMX-ERR γ were provided by Dr. Vincent Giguère (McGill University Health Center, Canada). pM-GRIP1(563-1121) was a gift from Dr. Jorma Palvimo (University of Kuopio, Finland) and pCI-Gal4-RIP140 from Dr. Malcolm Parker (Imperial College London, UK). pCDNA3-hPGC-1 α was received from Dr. Anastasia Kralli (Scripps Research Institute, La Jolla, CA) and pCMX-Flag-ERR α from Dr. Toren Finkel (NHLB, NIH, Bethesda, MD). The pGL3-OT reporter and the expression vector for S33Y β -catenin (pCl-neo- β -catenin-S33Y) were gifts from Dr. Bert Vogelstein (The John Hopkins Oncology Center, Baltimore, MD) and the -927 BSP-LUC reporter from Dr. Yorimasa Ogata (Nihon University School of Dentistry at Matsudo, Chiba, Japan). The expression vector for VP16-S33A- β -catenin (pCS2+/ β S33A-VP16) was provided by Dr. Edward P. Gelmann (Lombardi Cancer Center, Washington, DC).

2. Site-directed mutagenesis

Mutant plasmids were created by using the QuickChange[®] Site-Directed Mutagenesis kit (Stratagene) according to the manufacturer's instructions. The nucleotide sequences of the mutants were confirmed by sequencing.

3. Cell culture and reporter gene assays

All cells were received from the American Type Culture Collection (ATCC). U2-OS, SaOS-2 and 293T cells were maintained in DMEM supplemented with penicillin (25 U/ml), streptomycin (25 U/ml), 10% FBS (v/v) and L-glutamine. HeLa cells were maintained in DMEM supplemented with penicillin (25 U/ml), streptomycin (25 U/ml), 10% FBS (v/v), and non-essential amino acids. PC-3 cells were maintained in F-12 medium supplemented with penicillin (25 U/ml), streptomycin (25 U/ml), and 10% FBS (v/v). MC3T3-E1 subclone 14 cells were maintained in α -MEM supplemented with penicillin (50 U/ml), streptomycin (50 U/ml) and 10% FBS (v/v), and the osteogenic differentiation was induced by adding 50 µg/ml ascorbic acid and 10 mM sodium β -glycerophosphate to the medium.

For reporter assays the cells were seeded on 12-well plates (5 x 10^4 or 6 x 10^4 cells/well) and 24 h later were transfected with FuGENE (Roche Molecular

Biochemicals), FuGENE HD (Roche Molecular Biochemicals) or Lipofectamine 2000 (Invitrogen) according to manufacturer's recommendations with 300 ng of the luciferase reporter plasmid, 100 ng of the pCMX- β gal internal control plasmid, and 50 ng of the expression vectors or empty vector. When indicated, at 20 h after the transfection the cells received fresh medium containing either 2% charcoal-stripped FBS and different hormones, synthetic ligands and phytoestrogens or 10% FBS and LiCl. 24 h later, the cells were harvested, lysed, and assayed for luciferase and β -galactosidase activities. Transfections were performed in triplicate dishes and repeated two to six times.

4. Electrophoretic mobility shift assay (EMSA)

Proteins were produced by coupled *in vitro* transcription and translation in reticulocyte lysates (TNT[®] Quick Coupled Transcription/Translation Systems, Promega) and incubated with ³²P-labeled double-stranded oligonucleotide probes (ERRE, NBRE, OPN S1). The protein-DNA complexes were resolved by electrophoresis on 4% non-denaturing polyacrylamide gel, after which the gel was dried for autoradiography.

5. SDS-PAGE and immunoblotting

PC-3 and U2-OS cells and were transfected on 6-well plates with 2 μ g and 1.5 μ g of expression or empty vectors, respectively, using FuGENE or Lipofectamine 2000 transfection reagents. When indicated, the cells were treated with vehicle (DMSO), equol, GSK4716 or 4-OHT 20 h after transfection. The cells were harvested 48 h after transfection and protein samples were prepared in Laemmli sample buffer. Proteins were resolved by electrophoresis on a 10% polyacrylamide gel under denaturing conditions. Proteins were then transferred onto Hybond enhanced chemiluminescence nitrocellulose membrane (Amersham Biosciences). Detections of specific proteins were carried out by using the following antibodies: anti-ERR γ antibody (1 μ g/ml, Perseus Proteomics Inc.), Lamin B C-20 antibody (0.2 μ g/ml, Santa Cruz Biotechnology), and β -catenin antibody 9562 (1:2000, Cell Signaling). The immunocomplexes were visualized by using horseradish peroxidase-conjugated secondary antibodies and ECL Western blotting detection reagents (Amersham Biosciences).

6. Partial proteolysis assay

Flag-ERR γ was produced by coupled *in vitro* transcription and translation (TNT[®] Quick Coupled Transcription/Translation Systems, Promega). [³⁵S]methionine-labeled translation mixture was incubated with equol, enterodiol or 4-OHT and digested by trypsin (30 µg/ml or 50 µg/ml). The digestion products were resolved on SDS-PAGE and the radioactive peptides were visualized by autoradiography.

7. Cell growth assay

PC-3 cells were plated on 12-well plates (4.5 x 10^4 cells/well) and 24 h later were transfected with 300 ng of pCMX-FLAG-ERR γ or empty pCMX-FLAG vector using the FuGENE HD reagent. Five hours later, the cells received fresh medium containing 10% charcoal-stripped FBS supplemented with DMSO (vehicle), equol, or GSK4716 when indicated. At 5 h and 72 h post transfection, cells were trypsinized and the cell numbers counted by a Coulter[®] Particle Counter (Beckman Coulter).

For siRNA experiments, PC-3 cells were plated on 12-well plates (6 x 10^4 cells/well). Subsequently, at 24 h after plating the cells were transfected with 30 pmoles of siRNA duplexes targeted for human ERR γ or non-targeting Luciferase GL2 control siRNA (Qiagen) using the Lipofectamine 2000 reagent. Four hours later, the cells received fresh medium that contained 10% charcoal-stripped FBS supplemented with DMSO or equol. At 4 h and 72 h post transfection, the cells were trypsinized and the cell numbers counted by a Cedex XS semi-automated cell counter (Roche Innovatis AG).

8. Molecular modeling

The binding of equol in the ERR γ ligand-binding pocket was studied by generating a computer model of ERR γ LBD in a complex with equol. Geometric analysis and superposition of ERR γ X-ray structures were performed with Maestro 7.0 (Schrödinger, LLC: Portland, OR).

9. Primary mesenchymal stem cell isolation and osteoblastic and adipogenic differentiation

The ERR α KO mice, in which the *Esrra* gene locus was targeted to delete ERR α amino acids 28-89, were obtained from Amgen Inc. All animals were housed in the animal facility of the University of Helsinki. Male ERR α KO mice (n=3) aged between 8 – 12 weeks and their wild-type littermates (n=3) were euthanized by carbon dioxide followed by cervical dislocation, after which primary mesenchymal stem cells were isolated from their bone marrow. The diaphysis of tibiae and femuri were flushed with α -MEM and the cells were collected by centrifugation. The cells were counted in 2% acetic acid and plated 1 x 10⁶ cells/cm² in α -MEM containing 10% FCS (v/v), penicillin (50 U/ml) and streptomycin (50 µg/ml). Six days later, the cells were trypsinized and seeded on six-well plates (5 x 10³ cells/cm²) and the media was supplemented with 10 mM sodium β -glycerophosphate, 10 nM dexamethasone and 50 µg/ml ascorbic acid to initiate osteoblastic differentiation. To initiate adipogenic differentiation, the cells were seeded on six-well plates (2 x 10⁴ cells/cm²) and the media were supplemented with 5 µg/ml insulin, 1 µM rosiglitazone and 1 µM dexamethasone.

10. Primary osteoblast isolation and culture

Primary mouse osteoblasts were sequentially digested with collagenase from the tibiae and the femuri of 8-12 week old ERR α KO male mice and their wild-type littermates. Cells from the digestions 2-6 were collected and cultured in α -MEM supplemented with 15% FCS (v/v), 10 nM dexamethasone, penicillin (200 U/ml), streptomycin (200 µg/ml), and amphotericin B (2.5 µg/ml) until confluent. For proliferation assays, the cells were replated (2.5 x 10³ cells/cm²).

11. ³H-thymidine incorporation

Cell proliferation was studied using mouse mesenchymal stem cells and osteoblasts after 3 and 5 days in culture. After a 6 hour 1 μ Ci [³H]thymidine pulse the cells were rinsed with ice cold PBS and 5% TCA. The cells were lysed in 0.3 M NaOH and incorporated radioactivity was measured using Wallac 1409 Liquid Scintillation Counter

(PerkinElmer). The proliferation experiments were performed three times in triplicate dishes.

12. Alizarin red S and Oil Red O stainings

Mineralized bone nodules were detected by Alizarin red S staining and lipid accumulation by Oil Red O staining. In Alizarin red S staining, the cultures were washed with PBS, fixed with 3% PFA-PBS, and washed again with PBS and sterile water. The cells were covered with 2% Alizarin red S solution (pH 4.0) for 3 min. The Oil Red O staining was performed by washing the cells with PBS, fixing with 10% formaldehyde, and finally by staining with a filtered 0.3% Oil Red O solution in 60% isopropanol for one hour. After staining the cells were washed extensively and left to dry.

13. RNA extraction and RT-PCR

The PC-3 cells, primary mesenchymal stem cells and osteoblasts, and MC3T3-E1 cells were harvested and RNA samples collected in Trizol (Invitrogen) for RNA extraction. Total RNA was isolated according to the manufacturer's protocol. 1 µg of RNA was used for cDNA synthesis with Superscript II (Invitrogen). Quantitative real-time PCR was performed with LightCycler 480 instrument (Roche Applied Science) and SYBR Green I (Roche Applied Science) according to manufacturer's recommendations. The RT-PCR reactions were performed in duplicate for at least three independent experiments. The results were normalized to G3PDH or TBP and the resulting values were compared with the basal level (=1) and computed as fold inductions. Alternatively, the PCRs were performed with Taq DNA polymerase (GE Healthcare) and the products fractioned on 1% agarose gel.

14. Statistical analysis

All experiments with calculated statistical significances were performed at least three times. The statistical significance of the differences between two groups were assessed by the two-tailed Student's t test, unless the reference group was standardized to a constant value (=1) with no variability. In this case, a one-sample t test was used. When several t

tests were performed, the *p*-values were corrected by the Bonferroni correction. Multiple groups were compared by one-way ANOVA followed by Scheffe's post hoc test to determine the significant differences among groups. A *p*-value of <0.05 was considered to represent a statistically significant difference. All the statistical analyses were performed by using SPSS software (version 15.0).

RESULTS AND DISCUSSION

1. The transcriptional activity of the NR4A family can be regulated by cross-talk with other nuclear receptors and transcription factors in osteoblasts (I, III)

The LBP of NR4A receptors is tightly packed with bulky, hydrophobic amino acid side chains (Wang *et al.* 2003) and thus it is incapable of binding ligands. Therefore it is important to know which other mechanisms are used to regulate the transcriptional activity of NR4A receptors. The activity of NR4A receptors can be regulated by modifying their expression and post-translational status but also by cross-talk with other signaling pathways (Aarnisalo *et al.* 2002, Martens *et al.* 2005, Song *et al.* 2004). Our goal was to identify new signaling pathways that could potentially regulate NR4A receptors in osteoblasts.

1.1 NR3B orphan nuclear receptors repress the transcriptional activity of Nurr1

NR3B and NR4A receptors are co-expressed in many tissues such as the central nervous system and bone (Bonnelye *et al.* 1997a, Bookout *et al.* 2005, Tetradis *et al.* 2001a, Zetterström *et al.* 1996b). To study if ERR receptors can regulate the transcriptional activity of NR4A family, we performed reporter assays in U2-OS osteosarcoma cells. The cells were transfected with the expression plasmids for Nurr1, NGFI-B and Nor1 alone or in combination with ERR γ plasmid along with the NBRE₃tk-LUC or OPN-LUC reporters. NBRE₃tk-LUC has three NBRE binding sites and *OPN* has been described as a target gene for NR4A receptors (Lammi *et al.* 2004). ERR γ had only a small repressive effect on the transcriptional activity of NGFI-B and Nor1 but it abolished the activity mediated by Nurr1. ERR α was also able to repress Nurr1, whereas ERR β had no apparent effect.

1.1.1 The DNA-binding domains of ERR γ and Nurr1 are essential for the repressive effect of ERR γ on Nurr1 transcriptional activity

Next we studied the structural requirements needed for the repressive effect of ERR γ on Nurr1. Mutant plasmids were created in which Nurr1 LBD and NTD were fused to the Gal4 DNA-binding domain (Gal4-Nurr1 LBD and Gal4-Nurr1 NTD, respectively). ERR γ

failed to inhibit the transcriptional activity of these mutant receptors lacking DBD. However, ERR γ was capable of inhibiting a Nurr1 deletion mutant that lacked AF-1 but contained DBD and LBD (Nurr1 Δ NTD) and a mutant that contained the DBD and NTD but lacked LBD (Nurr1 Δ LBD). These results suggest that the repressive effect of ERR γ is dependent upon Nurr1 DBD, but not upon either LBD or NTD.

Construct	NTD	DBD	LBD
pCMX-Nurr1	Х	Х	Х
Gal4-Nurr1 LBD	-	-	Х
Gal4-Nurr1 NTD	X	-	-
Nurr1 ∆NTD	-	X	X
Nurr1 ΔLBD	X	Х	-
ERR $\gamma \Delta NTD$	-	X	X
ERRy LBD	-	-	X
Gal4-ERRγLBD	-	-	X

Table 4. Representation of the functional domains present (x) or absent (-) in different Nurr1 and ERR γ expression constructs.

To study which ERR domains were required for the repression of Nurr1, ERR γ mutants were created. ERR γ mutant that lacked most of the NTD (ERR $\gamma \Delta$ NTD) was still able to repress Nurr1, whereas the ERR γ LBD construct that lacked the entire NTD and DBD failed to repress Nurr1. The lack of inhibition was not due to the altered expression or reduced nuclear localization as the expression level was similar to that of the wild-type ERR γ and as Gal4-ERR γ LBD that contains a nuclear localization signal failed to repress Nurr1. Therefore, the repressive effect of ERR γ on Nurr1 is dependent on ERR γ DBD. This was confirmed by introducing point mutations in ERR γ DBD. ERR γ C125G and ERR γ R176A in which the mutations are located in the first zinc finger and A-box, respectively, failed to repress Nurr1-mediated OPN-LUC activation.

As DBDs of both Nurr1 and ERR γ were determined to be crucial for the repressive effect, we then studied whether the repression involved competition of DNA binding by EMSA. DNA binding was studied by using the NBRE element and the S1 element of the *OPN* promoter as the probe. *In vitro* translated ERR α and ERR γ proteins bound to these elements very weakly and were unable to prevent Nurr1 protein from binding. This subject was also studied indirectly in a reporter assay. U2-OS cells were transfected with NBRE₃tk-LUC reporter and a dominant negative Nurr1 (Nurr1 DN) variant in which the *Drosophila* repressor protein Engrailed is fused with the DBD of Nurr1. Nurr1 DN had been reported to inhibit transactivation of the NR4A receptors (Castro *et al.* 2001) and accordingly in our study it inhibited the basal NBRE₃tk-LUC reporter activity. ERR γ did not diminish the repressive effect of Nurr1 DN, which indicates that it does not directly compete with Nurr1 DN for the DNA binding. This supports the result of the EMSA binding experiments.

1.1.2 The dimerization interface of ERR γ is needed for the repression of Nurr1

Most NRs form homo- or heterodimers. NR4A receptors form heterodimers with RXR (Perlmann and Jansson 1995, Zetterström et al. 1996a) that can either inhibit or stimulate the transactivation mediated by NGFI-B and Nurr1 (Aarnisalo et al. 2002, Perlmann and Jansson 1995). Therefore, we studied if dimerization could be involved in the repressive effect of ERRy on Nurr1 transcriptional activity. We introduced mutations to the I-box of ERR γ , a domain mediating receptor dimerization (Aarnisalo *et al.* 2002, Huppunen *et al.* 2004). ERRy ML(394,395)AA, R390A, and L398A were not able to repress Nurr1 mediated transactivation, which implies that the dimerization interface of ERR γ is important for the repressive effect. The heterodimerization between NR3B and NR4A receptors was studied by using a mammalian two-hybrid assay for which Nurr1 LBD was fused to the yeast Gal4 DNA-binding domain and ERRy LBD was fused to the herpes simplex virus VP16 activation domain. MH100tk-LUC that is driven by four Gal4-binding sites was used as a reporter. VP16-ERRy LBD was not able to stimulate transactivation by Gal4-Nurr1 LBD which indicates that the receptors do not interact. We could not detect any dimers between full length Nurr1 and ERRy proteins in either the EMSA or the coimmunoprecipitation experiments. Therefore, the repression does not involve heterodimerization between Nurr1 and ERRy. Instead I-boxes might have auxiliary roles in the repression perhaps by stabilizing the receptor conformation or by mediating interaction with other proteins.

Co-activators play an important role in NR transactivation. NR4A and NR3B families have been found to bind to the same co-activators (Hong *et al.* 1999, Wansa *et al.* 2002, Xie *et al.* 1999) and therefore competition for these factors could be one mechanism

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by which receptors exert effects on each other's transcriptional activities. Many of the coactivators interact with the AF-2 and to address the potential role of the co-activator competition in repression, the repressive effect of ERR γ AF-2 mutant E429A was studied. ERR γ E429A was able to repress Nurr1 as effectively as the wild-type ERR γ in U2-OS cells and therefore the repression does not involve competition for co-activators that interact with the ERR γ AF-2. However, co-activators can also bind to other NR domains. An example of this is PGC-1 α which does not require AF-2 in order to co-activate ERR γ (Huppunen *et al.* 2004). PGC-1 α has been reported to enhance both NR3B and NR4A mediated transactivation (Huppunen *et al.* 2004, Nervina *et al.* 2006). In our experimental conditions, PGC-1 α was not found to co-activate Nurr1 but rather to repress it. Thus, competition for PGC-1 α can not explain the repression mediated by ERR γ on Nurr1.

1.2 Wnt signaling pathway represses the transcriptional activity of NR4A receptors in osteoblasts

Recently, a regulatory circuit between Nurr1 and the Wnt signaling pathway was found. The transcriptional activity of Nurr1 was enhanced by different Wnt signaling cascade activating factors, including β -catenin, lithium chloride (LiCl) and Wnt1 in 293F cells (Kitagawa *et al.* 2007). Both the Wnt/ β -catenin signaling pathway and NR4A receptors function in the bone. Therefore, we studied if the proteins influence each other in osteoblasts. U2-OS cells were transfected with NBRE₃tk-LUC reporter and the expression vectors for Nurr1, NGFI-B and Nor1 with or without S33Y β -catenin, which is a constitutively active form of β -catenin. Surprisingly, the transcriptional activation induced by all of the NR4A family members was repressed by S33Y β -catenin. This finding was contrary to the results reported by Kitagawa et al. (2007) from 293F cells. To confirm the differential regulation of Nurr1 signaling, we transfected 293T cells with NBRE₃tk-LUC reporter and the expression vector for Nurr1 and S33Y β-catenin. Indeed, as Kitagawa et al. reported, S33Y β -catenin had a small but significant increasing effect on the transcriptional activity of Nurr1 in 293T cells. However, in HeLa cells the transfection of S33Y β -catenin with Nurr1 repressed the transcriptional activity of Nurr1 as in the U2-OS cell line. Therefore, Wnt signaling pathway can have both activating and inhibiting effects on the transcriptional activity of NR4A receptors depending on the cell type. In U2-OS cells, the repressive effect of S33Y β-catenin on Nurr1 induced NBRE-activation was

dose-dependent. Moreover, 20 mM LiCl modestly repressed Nurr1 mediated transactivation. LiCl is evidently quite an inefficient inducer of β -catenin signaling in U2-OS cells as it produced a very small activation of the pGL3-OT reporter compared to the overexpressed β -catenin itself, which could explain the modest repression of Nurr1. S33Y β -catenin also repressed the transcriptional activation induced by Nurr1 on OPN-LUC reporter.

1.2.1 The repressive effect of β -catenin on Nurr1 transactivity involves the ligand-binding domain of Nurr1

We studid which protein domains are important for NR4A family to be able to be repressed by β -catenin. Therefore, U2-OS cells were co-transfected with expression vectors Gal4-Nurr1 LBD and Gal4-Nurr1 NTD with or without S33Y β -catenin. S33Y β -catenin failed to repress the transactivation induced by Gal4-Nurr1 NTD but did repress the transcriptional activity of Gal4-Nurr1 LBD. Nurr1 LBD is therefore needed for the repression. The importance of AF-1 and AF-2 domains was studied on OPN-LUC reporter with Nurr1 AF-1 (Nurr1 Δ 1-84) and AF-2 (Nurr1D589A) mutants, which lack functional activation functions but are still able to activate OPN-LUC. The Nurr1 AF-1 and AF-2 mutants induced transactivation on the OPN-LUC reporter, which S33Y β -catenin significantly repressed. Therefore AF-1 and AF-2 domains seem to be irrelevant for β -catenin mediated NR4A-repression.

1.2.2 The repressive effect of β -catenin on Nurr1 transactivity is not dependent on direct interaction between the proteins, nor alterations in Nurr1 DNA binding or expression

Kitagawa and colleagues reported that Nurr1 interacts with β -catenin and Lef1 in 293F cells at a site that was mapped to amino acids 363-598 where LBD and AF-2 are situated (Kitagawa *et al.* 2007). In addition, other NRs modulate Wnt signaling pathway by direct interactions and, for example, AR, RAR, VDR, RXR, PPAR, ER, GR and TR interact with β -catenin (Easwaran *et al.* 1999, Guigon *et al.* 2008, Kouzmenko *et al.* 2004, Liu *et al.* 2006, Pálmer *et al.* 2001, Truica *et al.* 2000, Xiao *et al.* 2003). We could not detect an interaction between β -catenin and Nurr1 or NGFI-B in mammalian one- and two-hybrid experiments or in the co-immunoprecipitation experiments in U2-OS cells. In the two-

hybrid experiments VP16-S33A- β -catenin failed to induce the activity of Gal4-Nurr1 LBD, Gal4-Nurr1 NTD or Gal4-NGFI-B LBD expression plasmids on MH100tk-LUC reporter. In one-hybrid experiments full length pCMX-Nurr1 and pCMX-NGFI-B plasmids were transfected in U2-OS cells alone or with VP16-S33A- β -catenin along with the NBRE₃tk-LUC reporter. Again, VP16-S33A- β -catenin did not stimulate Nurr1 and NGFI-B activities. In co-immunoprecipitation assays overexpressed Flag-tagged Nurr1 protein was immunoprecipitated from the U2-OS cells but no specific binding between Nurr1 and β -catenin was detected. Co-immunoprecipitation experiments were also conducted by precipitating endogenous or overexpressed β -catenin protein but again no specific binding between β -catenin and Nurr1 was detected. Therefore, we were not able to show that the repressive effect of NR4A family on β -catenin would be dependent on direct interaction between the proteins in U2-OS cells.

We also studied whether β -catenin affects DNA binding of the NR4A receptors. Nurr1 DN and S33Y β -catenin expression plasmids were co-transfected in U2-OS cells. S33Y β -catenin could not abolish the repressive effect of Nurr1 DN on the basal NBRE₃tk-LUC reporter activity, which implies that β -catenin does not interfere with the ability of Nurr1 to bind DNA.

Recently, it was shown that the colonic carcinogen deoxycholic acid increases the expression of NGFI-B in colon cancer cells. The mechanism involved stabilization of β -catenin, which formed a complex with the activator protein-1 (AP-1) thas was capable of binding to the AP-1 sites on the *NGFI-B* gene promoter (Wu *et al.* 2011). We did not detect any alteration in the amount of Nurr1 mRNA in U2-OS cells transfected with S33Y β -catenin. Furthermore, the expected result of an increase in protein expression would be its enhanced function rather than the repression observed in our experiments.

In conclusion, we identified two new pathways, NR3B orphan NRs and Wnt signaling pathway, which repress the transcriptional activity of NR4A receptors in osteoblasts. The repressive effect of ERR γ on Nurr1 is dependent on Nurr1 and ERR γ DBDs, but does not involve competition for DNA binding. The repression also involves intact dimerization interfaces but no heterodimerization or competition for co-activator binding. β -catenin repressed transcriptional activation mediated by all of the NR4A receptors by a mechanism dependent on the LBD. As the Wnt signaling pathway has an activating effect on Nurr1 transcriptional activity in 293F (Kitagawa *et al.* 2007) and 293T

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cells, it seems that the Wnt signaling pathway can function both as an activator and a repressor of Nurr1 transcriptional activity according to the prevailing cellular circumstances and therefore forms an interesting regulatory mechanism for Nurr1. This is also true for other NRs. For most of the NRs, including AR, RARs, VDR and ERs, Wnt/βcatenin signaling functions as a stimulator of their transcriptional activity (Mulholland et al. 2005). However, AR can also be inhibited by the Wnt signaling pathway as AR binds Tcf4 through its DNA-binding domain, which decreases its transcriptional activity (Amir et al. 2003). Wnt signaling represses or activates ER activity according to the dominating cellular Tcf factors. When ERs directly interact with Tcf1, the effect on the promoter is synergistic, when ERs interact with Tcf4, the effect is antagonistic (El-Tanani et al. 2001). The exact mechanisms of both ERRy and β -catenin repression on NR4A receptors still remain to be solved. The biological significance of the repression should also be further studied in natural NR4A target genes. Both ERR γ and β -catenin are highly expressed in the central nervous system and Wnt/β-catenin has been shown to regulate dopaminergic differentiation (Cajánek et al. 2009) where Nurr1 also has an essential role. Kitagawa and others showed that Nurr1, β -catenin and Lef1 can associate on the same DNA elements and regulate each other's co-factor recruitment in SK-N-MC neuroblastoma cells. In addition, Nurr1 inhibited the nuclear accumulation of β -catenin in these cells (Kitagawa et al. 2007). Therefore, it is of potential interest to study further how these pathways converge in neural tissue.

2. The transcriptional activity of NR3B family can be regulated by ligands and crosstalk with other nuclear receptors (I, II)

2.1. Identification of the phytoestrogen equol as an ERR γ and ERR β ligand

NR3B receptors constitute another family of orphan NRs for which a natural ligand has not been found. However, it was shown that certain isoflavones can bind to ERRs and act as their agonists (Suetsugi *et al.* 2003). Furthermore, phenolic acyl hydrazones GSK4716 and DY131 function as selective ERR β and ERR γ agonists (Yu and Forman 2005, Zuercher *et al.* 2005). Certain flavonoids were reported to inhibit transcriptional activity of ERR γ by suppressing the interaction between ERR γ and co-activator PGC-1 α (Huang *et al.* 2010, Wang *et al.* 2009b). Therefore, we wanted to study how phytoestrogens affect the transcriptional activity of ERR γ . The subject was studied in U2-OS, SaOS-2 and PC-3 cells, where ERR γ is transcriptionally active (Huppunen *et al.* 2004 and our unpublished results). In accordance with earlier reports, DES and 4-OHT efficiently inhibited the transcriptional activity of ERR γ in PC-3 cells (Coward *et al.* 2001, Tremblay *et al.* 2001b) and GSK4716 increased the activity by a maximum of 3-fold. Estradiol had no effect on the transcriptional activity of ERR γ as previously reported (Giguère *et al.* 1988, Yang *et al.* 1996).

PC-3, U2-OS and SaOS-2 cells were transfected with Gal4-ERR γ LBD expression vector along with MH100tk-LUC reporter and treated with genistein, daidzein, equol, enterodiol, and enterolactone to study the effects of phytoestrogens on ERR γ . The only substance that influenced the activity of ERR γ was equol, which had agonistic potential. Equol increased the transcriptional activity of ERR γ in a dose-dependent manner in PC-3 cells transfected with the ERRE₃tk-LUC reporter driven by three ERRE binding sites. The maximum stimulation was approximately 2-fold at the concentration of 20 μ M.

The effect of equol on ERR γ seemed to be selective as equol did not increase the activity of ERR α or ERR β above the level of control vector (PL1) in PC-3 or SaOS-2 cells. Equol increased the basal activity of the ERRE₃tk-LUC reporter, which is most likely due to the endogenous ERR γ present in PC-3 and SaOS-2 cells. ERR α and ERR β showed no transcriptional activity in PC-3 or SaOS-2 cells and equol might have a different effect in a situation in which these receptors would be more active. Therefore the ERR expression vectors were transfected in PC-3 cells together with PGC-1 α that has been shown to stimulate the activity of these receptors (Huss *et al.* 2002). Equol stimulated the activity induced by ERR β and ERR γ together with PGC-1 α . Equol was not able to significantly increase the activity induced by ERR α and PGC-1 α . These results suggest that equol is selective for ERR γ and ERR β as has been reported for GSK4716 (Zuercher *et al.* 2005).

2.1.1 Equol increases ERRy co-activator binding

Some phytoestrogens have been shown to inhibit the activity induced by ERRs and PGC- 1α by decreasing the interaction between the proteins. The phytoestrogens that have this effect fall into three categories, flavones, flavonols and flavanones. On the other hand, isoflavones genistein and daidzein have either no effect at all or a small stimulating effect on the transcriptional activity of ERRy and PGC-1a (Huang et al. 2010). Equal falls into the category of isoflavone, which is in accordance with its ability to increase the transcriptional activity of ERR β /ERR γ and PGC-1 α . ERRs have also been shown to bind other co-factors. For example, ERRy has been reported to interact with GRIP1 (Hong et al. 1999), which functions as a co-activator. Moreover, ERRy interacts with RIP140, which in many cases functions as a transrepressor (Castet et al. 2006, Wang et al. 2006a). A mammalian two hybrid experiment was performed to study whether equol enhances the interaction between ERRyLBD and GRIP1 or RIP140. PC-3 cells were co-transfected with the expression vectors for Gal4-GRIP1 or Gal4-RIP140 and VP16-ERRY LBD along with the MH100tk-Luc reporter. Equol enhanced the interaction between ERRyLBD and GRIP1 but had no effect on the interaction between ERRyLBD and RIP140. Therefore, equal was found to increase the transcriptional activity of ERR γ at least partly by increasing the co-activator binding of ERR γ . On the other hand, the effect of equol was not due to an effect on ERRy protein stability as equol and GSK4716 did not influence the expression level of ERRy protein in PC-3 cells. In contrast, 4-OHT treatment slightly increased ERR γ expression.

2.1.2 Equol binds to the ERRy ligand-binding pocket

Next we studied the binding of equol to the ERR γ LBP. Equol decreased the inhibitory effect of 4-OHT on the transcriptional activity of ERR γ in a dose-dependent manner. On the other hand, 4-OHT decreased the stimulatory effect of equol. These results suggest that equol and 4-OHT compete for binding to the LBP. Equol also induced a conformational change in the ERR γ LBD in an assembly assay described by Pissios *et al.* (2000), where helix 1 of the LBD is fused to the yeast Gal4 DNA-binding domain and helices 3-12 are fused to herpes simplex virus VP16 activation domain. The interaction of H1 and H3-12 is measured as the activation of a MH100tk-LUC reporter gene driven by Gal4-binding sites. This interaction has been reported to be influenced by ligand binding, co-repressors, and other signals that modulate the transcriptional activity of LBD (Huppunen *et al.* 2004, Pissios *et al.* 2000, Wang *et al.* 2003). Equol, GSK4716, DES and 4-OHT increased the interaction thus indicating that these ligands induce a conformational change in the ERR γ LBD. In contrast, estradiol and enterodiol had no effect. In partial proteolysis assay, *in vitro* translated ERR γ or ERR γ LBD proteins were treated with

vehicle, equol, enterodiol and 4-OHT and then with trypsin. Trypsin digested vehicle or enterodiol treated proteins completely whereas equol and 4-OHT treated proteins were able to resist digestion. The binding mode of equal to the ERR γ LBP was studied by molecular modeling and compared to the models in which ERRy was bound to 4-OHT, DES and GSK4716. The apo-ERRy structure could not adopt the equol molecule. Nevertheless, GSK4716 binds to an enlarged cavity at which H12 is in its agonistic conformation. This structure allowed equol binding which correlates well with the agonistic effects of equol observed in experiments. The binding mode was further studied by introducing point mutations in the LBP of ERR γ and by studying the effects of different ligands on these mutants in reporter assays. PC-3 cells were transfected with Gal4-ERRy LBD expression vector and its mutated variants along with the MH100tk-LUC reporter and subsequently treated with equol, GSK4716, 4-OHT and DES. A272, which is in close proximity with all four ligands, was mutated into a larger phenylalanine with the intention to block the cavity. Indeed, Gal4-ERRy LBD A272F did not significantly respond to any of the tested ligands. Next F435 was mutated to a smaller leucine to create more space in the binding pocket. Mutating F435 did not affect the inhibitory effect of 4-OHT but changed DES into a weak agonist. This finding is in accordance with an earlier study in which the antagonistic effect of DES on ERR γ was shown to involve a change in the conformation of F435, which then leads to a displacement of H12 (Greschik et al. 2002). Equol and GSK4716 remained as agonists and the stimulatory effect of equol was slightly enhanced by the F435L mutation. V313W and Y326W mutations abolished the inhibitory effects of DES and 4-OHT on ERRy and decreased the agonistic effect of GSK4716. However, equol remained as an agonist which suggests that equol binds to the ERRy LBP in a slightly different manner than the other ligands studied.

Based on these experiments we identified equol as a new ERR γ ligand. More than that, we showed that in addition to the previously identified synthetic ligands GSK4716 and DY131, there are natural compounds that can function as ERR γ agonists. The equol concentration that was needed to stimulate ERR γ activity was fairly high (5 μ M). However, plasma concentrations of phytoestrogens in soya-consuming populations can reach levels as high as 1 μ M (Adlercreutz *et al.* 1993, Bloedon *et al.* 2002). Furthermore, phytoestrogens have been shown to concentrate in prostate fluid and tissue where they can reach concentrations up to 10-fold those of serum (Gardner *et al.* 2009, Hedlund *et al.* 2005). In addition, modulation of the transcriptional activity of NRs in transient transactivation assays often requires ligand concentrations that exceed those required *in vivo*. Therefore, the concentrations needed to stimulate ERR γ in our experiments may well be possible to attain in humans. What should be further studied is the effect of equol on ERR γ target genes. We analyzed the mRNA expression of previously reported ERR γ target genes (*ESRRA*, *PGC-1A*, *PGC-1B*, *p21*, *p27*, *PDK2*, *PDK4*, *GR*, *PLK2*, *MAOB*, and *APOD*) (Park *et al.* 2007, Wang *et al.* 2008, Wang *et al.* 2010a, Wang *et al.* 2010b, Xie *et al.* 2009, Yu *et al.* 2007, Zhang *et al.* 2006) in GSK4716 or ERR γ siRNA treated PC-3 cells by RT-PCR. None of these genes were induced by GSK4716 or repressed by ERR γ siRNA. We were thus unable to study the role of equol as an ERR γ agonist by analyzing its effect on these previously suggested ERR γ target genes.

2.2 Orphan nuclear receptor NGFI-B represses the transcriptional activity of ERRy

In addition to ligands, ERR receptors can also be regulated by other NRs. For example, ERs have been shown to inhibit the transcriptional activity of ERRs on monoamine oxidase B promoter (Zhang *et al.* 2006). SHP interacts with ERR receptors and inhibits the transcriptional activity of ERR γ (Sanyal *et al.* 2002). As already discussed, NR3B and NR4A receptors are co-expressed in many tissues and therefore we studied if NR4A receptors can regulate ERR function. HeLa cells were transfected with the expression vector for ERR γ along with the ERRE₃tk-LUC reporter. Co-expression of NGFI-B efficiently repressed the activity induced by ERR γ . Nor1 had a modest repressive effect on ERR γ whereas Nurr1 had no effect. The repressive effect of NGFI-B was dose-dependent and NGFI-B totally abolished the activity of ERR γ when NGFI-B and ERR γ were transfected in equal amounts. The repressive effect of NGFI-B was dependent on the DBD, as NGFI-B DBD mutant C252G was not able to repress ERR γ . The repression also involved dimerization interfaces as NGFI-B I-box mutant NGFI-B GKL(522-524)AAA repressed ERR γ less efficiently than the wild-type vector. However, the exact mechanism and the biological relevance of this phenomenon remains to be solved

In conclusion, we identified two new mechanisms capable of regulating the function of ERR γ in osteoblasts. Of these, equol had a positive effect on the transcriptional activity of ERR γ whereas NR4A receptors had a negative effect.

3. NR4A and NR3B families repress the transcriptional activity of Wnt signaling pathway in osteoblasts (III)

3.1 NR4A receptors repress the transcriptional activity mediated by β-catenin

Both β -catenin and the NR4A family are expressed in osteoblasts (Lammi *et al.* 2004, Monaghan *et al.* 2001). β -catenin is essential for skeletal development and maintenance and thus it is important to know which factors regulate the function of the Wnt signaling pathway.

To study if NR4A receptors regulate β -catenin mediated transcriptional activity, U2-OS cells were transfected with pGL3-OT reporter that contains three binding sites for Tcf4, a constitutively active S33Y β -catenin and either Nurr1, NGFI-B or Nor1 expression vectors. S33Y β -catenin induced a very high activation on the pGL3-OT reporter that all members of the NR4A family significantly repressed. LiCl is a known inhibitor of GSK3 β (Klein and Melton 1996, Stambolic *et al.* 1996) and it increases the amount of active nuclear β -catenin. 10 mM LiCl treatment was able to induce pGL3-OT reporter and Nurr1 also repressed this induction. The effect of Nurr1 on S33Y β -catenin induced pGL3-OT activity was dose-dependent.

Nurr1 and NGFI-B mutants were used to study the structural requirements of the NR4A receptors needed for β -catenin repression. Nurr1 Δ 1-84 that lacks AF-1 (AF1 mut), Nurr1 D589A that lacks a functional AF-2 (AF2 mut), and a Nurr1 mutant Δ 1-84/D589A in which the function of both activation functions is abolished (AF1/AF2 mut) were transfected to U2-OS cells together with S33Y β -catenin and pGL3-OT reporter. All the mutants were able to repress the S33Y β -catenin induced pGL3-OT activity at the same level as the Nurr1 wild-type. Therefore, AF-1 and AF-2 domains are not needed for the repression of β -catenin. The NGFI-B I-box mutant NGFI-B GKL(522-524)AAA was expressed in U2-OS cells to study if dimerization is involved in the repression. NGFI-B dimerization mutant was still capable of repressing the S33Y β -catenin induced pGL3-OT activation. Therefore homo- or heterodimerization of the NR4A receptors with themselves or with, for example, RXR receptors, does not influence the repressive effect of NR4A receptors on β -catenin. This is in agreement with the notion that Nor1, which does not bind RXR (Zetterström *et al.* 1996a) is also capable of repressing β -catenin. The role of DBD was studied by a NGFI-B DBD mutant C252G. Interestingly, NGFI-B C252G could not repress the β -catenin mediated pGL3-OT activation, which implies that an intact DNA-binding domain is needed for the repression. Similar results were obtained with Nurr1 DNA-binding mutant C283G.

To investigate if the repression also occurs on the level of β -catenin target genes, the expression of Axin2 mRNA was studied. Axin2 is a negative regulator of the Wnt signaling pathway, as it promotes the phosphorylation and degradation of β -catenin, and a known Wnt/ β -catenin/Tcf target gene (Jho *et al.* 2002). The expression of Axin2 is stimulated by canonical Wnt signaling in many different cell types, including the preosteoblastic MC3T3-E1 cell line (Reinhold and Naski 2007). We noted an increase in Axin2 mRNA in S33Y β -catenin transfected MC3T3-E1 cells. When the cells were cotransfected with Nurr1, the expression of Axin2 mRNA decreased by 40%. Therefore Nurr1 is capable of repressing the mRNA expression of β -catenin target genes.

NR4A receptors are immediate early genes whose expression is strongly and rapidly induced by various stimuli that include PTH (Pirih *et al.* 2003, Tetradis *et al.* 2001a, Tetradis *et al.* 2001b) and FGF-8b (Lammi and Aarnisalo 2008). PTH has also been reported to modulate the canonical Wnt signaling pathway (Kulkarni *et al.* 2005). Moreover, FGFs and the Wnt pathway intertwine as FGF signaling antagonizes Wnt-induced transcription (Ambrosetti *et al.* 2008). NR4A receptors thus potentially serve as a link between these signaling pathways in osteoblasts. Wnt signaling is also an important determinant of the osteoblastic and adipogenic differentiation of MSCs (Hill *et al.* 2005, Ross *et al.* 2000). The NR4A family has also been reported to be induced during adipogenic differentiation (Au *et al.* 2008, Chao *et al.* 2008, Fu *et al.* 2005, Fumoto *et al.* 2007) and Nurr1 increases osteoblast differentiation (Lee *et al.* 2006). Therefore, it would be interesting to study if the pathways are linked in these processes.

3.2 NR3B receptors repress the transcriptional activity mediated by β -catenin

In addition to NR4A receptors, NR3B receptors are also expressed in several of the same tissues and cells that express β -catenin. Therefore we studied whether NR3B receptors influence Wnt signaling pathway. U2-OS cells were transfected with expression plasmids for S33Y β -catenin, ERR α and ERR γ along with the pGL3-OT reporter plasmid. ERR γ inhibited S33Y β -catenin mediated activity efficiently, whereas the inhibition elicited by ERR α was more modest (Fig. 13A). The ERR γ DBD mutant ERR γ C125G was used to

study if the DNA binding was needed for the repression. ERR γ C125G was not able to repress S33Y β -catenin mediated transactivation (Fig. 13B). The result is similar to that obtained with NR4A receptors, which implies that orphan NRs could use the same mechanisms to repress β -catenin. As already discussed, PGC-1 α is an important co-activator of the ERR receptors. When U2-OS cells were transfected with PGC-1 α along with the expression vector for S33Y β -catenin and pGL3-OT reporter, PGC-1 α had a repressive effect on S33Y β -catenin mediated activity. PGC-1 α was also able to increase the repressive effect of ERR γ (Fig. 13C). On the other hand, the repressive effect of ERR γ on β -catenin was abolished by 4-OHT treatment (Fig. 13D). This finding and also the

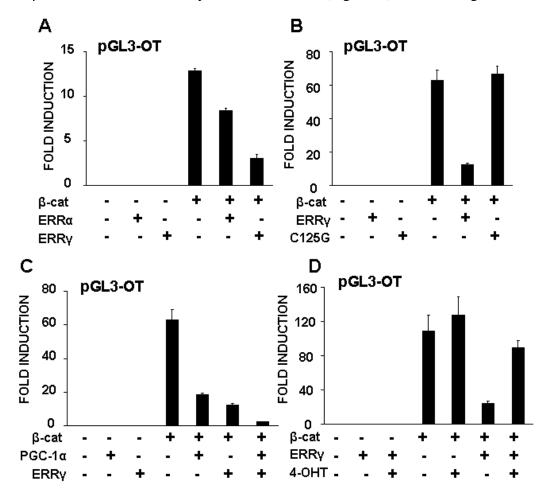


Fig. 13. U2-OS cells were transfected with the pGL3-OT reporter (300 ng) along with the expression plasmids (a total of 50 ng) for β -catenin S33Y, ERR α and ERR γ (A); β -catenin S33Y, ERR γ and ERR γ C125G (B); or β -catenin S33Y, PGC-1 α and ERR γ (C) as indicated. (D) U2-OS cells were transfected with the pGL3-OT reporter along with the expression plasmids for β -catenin S33Y and ERR γ and subsequently treated with 1 μ M 4-OHT for 24 h as indicated. The experiments were performed in triplicate dishes and repeated at least twice with essentially identical results. The mean \pm S.D. of one representative experiment is shown.

dependence of the repressive effect on DBD are in accordance with a mechanism by which ERR γ represses the transcriptional activity of Nurr1 (Lammi *et al.* 2004). Therefore, NR3B receptors could have a repressive mechanism dependent on their DBD and LBD that they use to repress NR4A receptors, Wnt signaling and possibly also other signaling pathways.

Very recently, a study that reported a cross-talk between ERR α and Wnt signaling pathway was published. Wnt signaling pathway and ERR α potentiated each other's transcriptional activity in SKBR3 and MDA-MB-436 breast cancer cells. In addition, both ERR α and β -catenin were involved in the migration of breast cancer cells by inducing the expression of Wnt11 (Dwyer *et al.* 2010). In U2-OS cells, ERR α and ERR γ had an inhibitory effect on Wnt/ β -catenin signaling pathway. Therefore, ERRs seem to have both negative and positive effects on Wnt signaling depending on the cell type.

In conclusion, NR4A and NR3B receptors were discovered to repress the function of the Wnt signaling pathway in osteoblasts. As Wnt signaling pathway has an important role in many biological processes and tissues in which NR4A and NR3B receptors also function, this repressive effect is of potential importance. In addition, by regulating the Wnt signaling pathway, NR3B and NR4A receptors may be involved in the pathogenesis of different Wnt signaling pathway related diseases. The biological relevance and mechanisms of the regulation should be further examined by, for example, exploring the repression on β -catenin/Tcf target gene promoters and by studying if the function of Wnt signaling pathway and the processes it regulates are altered in NR3B and NR4A KO mice.

4. NR3B family participates in the growth of osteoblasts and prostate cancer cells and in the differentiation of mesenchymal stem cells (II, IV)

4.1. NR3B receptors regulate the growth of osteoblasts and prostate cancer cells

NR3B receptors have been shown to regulate the proliferation and growth of cells with both positive and negative effects in different cell types (Ijichi et al. 2011, Yu et al. 2008). Therefore, we studied the effect of NR3B receptors on the proliferation and growth of osteoblasts, MSCs and prostate cancer cells.

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4.1.1 ERRα increases the proliferation of osteoblasts and mesenchymal stem cells

Blocking the expression of ERR α diminishes the proliferation of rat calvarial osteoblasts dose-dependently (Bonnelye *et al.* 2001). To investigate further the impact of ERR α on proliferation, we studied the proliferation of osteoblasts and MSCs isolated from ERR α KO and wild-type mice by the ³H-thymidine incorporation method on days 3 and 5 of the proliferation phase. ERR α KO MSCs proliferated significantly less than the cells derived from wild-type littermates on both days. ERR α KO osteoblasts also proliferated less but the results did not reach statistical significance. The results were ascertained by cell cycle analysis, which showed that on day 5 there were 14% fewer MSCs and 45% fewer osteoblasts in the S-phase in the ERR α KO cultures. Our results are consistent with the earlier results from rat calvarial osteoblasts and the MSCs derived from another ERR α KO line (Bonnelye *et al.* 2001, Teyssier *et al.* 2009). In contrast, Delhon and colleagues did not detect any difference in the proliferation of ERR α deficient mouse calvarial osteoblasts (Delhon *et al.* 2009). ERR α has also been linked to the regulation of tumor growth and proliferation of breast cancer cells (Deblois *et al.* 2009). The function of ERR α in cell proliferation in different cell types should therefore be further studied.

4.1.2 ERRy and equol decrease the growth of prostate cancer cells

ERR γ regulates the proliferation of cancer cells in, *inter alia*, breast (Ijichi *et al.* 2011) and prostate cancer (Cheung *et al.* 2005). In prostate cancer cells ERR γ has a negative effect on their proliferation (Cheung *et al.* 2005). Equol has also been shown to decrease the growth of prostate cancer cells *in vitro* (Magee *et al.* 2006, Mitchell *et al.* 2000). Therefore, we examined whether equol was able to enhance further the growth inhibitory effect of ERR γ . PC-3 cells were transfected with the expression vector for ERR γ and treated with equol. Treatment of the mock-transfected cells with equol reduced the cell number 72 h post transfection. The number of cells was further decreased when the cells were transfected with ERR γ . We transfected the cells with siRNA targeted for ERR γ to study if the growth-inhibitory effect of equol in mock-transfected cells was mediated by the endogenous ERR γ . ERR γ siRNA reduced the expression of endogenous ERR γ mRNA to about 50% and abolished the growth-inhibitory effect of equol. GSK4716 also reduced the number of ERR γ transfected PC-3 cells. These results indicate that ERR γ is involved in mediating the antiproliferative effects of equol. Reciprocally, equol enhances the antiproliferative effects of ERR γ . The ability to produce equol and high serum equol levels have been associated with a reduced prostate cancer risk (Yuan *et al.* 2007) and ERR γ has been indicated as a marker of favourable prognosis in prostate cancer (Fujimura *et al.* 2010). Therefore, the function of ERR γ and equol in prostate cancer cells is potentially of clinical importance and should be further studied by exploring the mechanisms behind the growth inhibition and by investigating if the effect is also obtained *in vivo*. Furthermore, it would be interesting to study if ERR γ also participates in mediating equol effects in ERR γ expressing cells and tissues other than the prostate.

4.2 ERR α regulates the osteoblastic and adipogenic differentiation of mesenchymal stem cells

It has been suggested that ERR α plays a role in bone formation. ERR α has been shown to increase osteoblastic differentiation *in vitro* in rat calvarial osteoblasts (Bonnelye *et al.* 2001). Recently, conflicting results have been obtained. ERR α KO mice were shown to have slightly increased cancellous BMD and primary osteoblasts isolated from these mice showed increased differentiation *in vitro* (Delhon *et al.* 2009). Therefore the effects of ERR α on osteoblastic differentiation and function need more clarification. Osteoblasts and adipocytes differentiate from the same multipotent precursor cells, MSCs. On this account, we also studied the influence of ERR α on adipogenic differentiation.

4.2.1 ERRα increases the osteoblastic differentiation of mesenchymal stem cells

MSCs were isolated from the bone marrow of 8-12 week old ERR α KO male mice and their wild-type littermates. After 6 days in culture the cells were counted, equal numbers were replated and osteogenic differentiation was induced by Na- β -glycerophosphate, dexamethasone and ascorbic acid. ERR α KO mesenchymal cultures had decreased mineralization compared to the wild-type cells on day 20 of differentiation when detected by Alizarin red S staining. The expression of osteoblastic maker genes was determined on days 20 and 25 by RT-PCR to analyze the possible mechanism of ERR α in osteoblast differentiation. The ERR α KO cultures had significantly diminished expression of BSP and OCN mRNA, which might well explain the difference seen in mineralization. The

expression of OPN and ALP was also decreased in every experiment performed but these differences were not statistically significant. The expression of Runx2 was relatively similar in both wild-type and KO cultures. We also studied ERR α mRNA expression and found it to be fairly constant throughout the differentiation process (Rajalin *et al.* unpublished results).

To study how the overexpression of ERR α affects mineralization in preosteoblastic MC3T3-E1 cell line, we transiently transfected cells with empty (pCMX-Flag) or ERR α (pCMX-Flag-ERR α) expression vectors. The overexpression of ERR α increased the mineralization of MC3T3-E1-cells as determined by Alizarin red S staining. Overexpression of ERR α also increased the expression of BSP, Runx2 and ALP mRNAs. The expressions of OPN and OCN were not significantly altered.

The disparity between our results and the results reported by Delhon et al. (2009) may be due to the different mouse models, cells used in the experiments and also other differences between the experimental conditions. Delhon and colleagues differentiated mouse calvarial cells in contrast to our MSCs and used BMP-2 in the osteogenic medium. The expression of osteoblastic markers BSP and OCN was also analyzed at a rather early time point (10 d) by Delhon and colleagues compared to our study (20d and 25d). In the study by Teyssier and others MSCs isolated from the ERRa KO female mice had increased osteoblastic differentiation capacity when compared to wild-type cells (Teyssier et al. 2009). Again, there were many experimental differences between our studies. Teyssier and others did not use dexamethasone in the osteogenic medium and plated cells isolated from the bone marrow directly in differentiation cultures, whereas we started our differentiation cultures only after expanding MSCs first in an initiation culture. Cell density is a major determinant of the mineralization capacity (Jaiswal et al. 1997). Therefore, alterations in factors that affect cell density, such as the number of MSCs in the bone marrow and cell adherence, can affect mineralization in the experimental setting of Teyssier et al (2009). Indeed, Wei et al. (2010) reported a decrease in the number of bone marrow cells in ERR α KO mice compared to ERR α heterozygous controls. There is also a potential gender-dependent effect of ERRa, which might affect the results. As ERR α has been reported to impinge on the estrogen signaling pathway (Bonnelye et al. 2002b), the gender-dependent effects of ERRα are of interest. In addition, the *in vitro* results reported by Teyssier and colleagues do not explain the decreased bone

volume fraction and diminished trabecular number observed in their female mice at the age of 14 weeks (Teyssier *et al.* 2009).

4.2.2 Bone sialoprotein is a target gene for ERR α and ERR γ

As the expression of BSP mRNA was altered in ERR α KO MSCs and also ERR α overexpressing MC3T3-E1 cultures, we next investigated whether the NR3B family can directly control the BSP gene promoter. Because MC3T3-E1 cells did not transfect efficiently enough for reporter assays, we decided to use human cervical cancer HeLa cells in which the ERR family is transcriptionally active (Lu et al. 2001). HeLa cells were cotransfected with the expression plasmids for ERR α , ERR β or ERR γ and PGC-1 α when indicated along with the human BSP-LUC reporter. ERRa and ERRy together with PGC- 1α activated BSP-LUC reporter efficiently. ERR β could not activate BSP-LUC reporter. To study the regulation of BSP promoter by ERR α further, point mutations were introduced into the ERRa expression vector in order to abolish ERRa DNA-binding (C99G) or to disrupt AF-2 (E413A). Although the expression level of both mutants was comparable to that of the wild-type ERR α , both mutations abolished the transactivation of BSP-LUC. Therefore, the regulation of BSP seems to depend upon ERRa DNA-binding and transcriptional activity. The reporter assays together with the mRNA expression analysis show that BSP is a target gene for ERR α . In a study by Bonnelye and colleagues the expression of BSP was inhibited in cultures deficient of ERR α and increased in cultures that overexpressed ERR α (Bonnelye *et al.* 2001). In addition to ERR α , ERR γ stimulated BSP-LUC activity when co-transfected with the co-activator PGC-1a. Interestingly, the activation of the BSP-LUC reporter by ERR γ and PGC-1 α was not responsive to 1 µM 4-OHT treatment (Fig. 14A) whereas 4-OHT was able to abolish ERRy driven transactivity on ERRE₃tk-luc reporter (Fig. 14B). In contrast to our results, ERRy was shown to repress Runx2-dependent BSP promoter activation in a recent report (Jeong et al. 2009). Therefore, ERRs may play different roles in BSP regulation depending on the stage of osteoblastic differentiation. BSP is also expressed in breast and prostate cancer cells in which it possibly plays a major role in mineral deposition and preferred bone homing (Ganss *et al.* 1999). ERR α and ERR γ are expressed in many cancer cell lines and ERRa functions as a prognostic marker of breast and endometrial cancer (Ariazi et al.

2002, Deblois *et al.* 2009). Therefore the relationship between ERRs and BSP should be further studied in cancer cells.

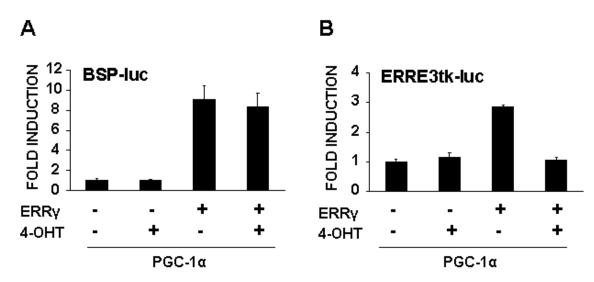


Fig. 14. HeLa cells were transfected with 300 ng of the BSP-LUC (A) or ERRE₃tk-luc (B) reporter along with the expression plasmids for PGC-1 α (25 ng) and pCMX-ERR γ (25 ng) as indicated. After 24 h the cells were treated with vehicle (EtOH) or 1 μ M 4-OHT for another 24 h. The experiments were performed in triplicate dishes and repeated three times with essentially identical results. The mean \pm S.D. of one representative experiment is shown.

4.2.3 ERRα increases the adipogenic differentiation of mesenchymal stem cells

To study whether ERR α can affect adipogenic differentiation of MSCs, we induced wildtype and ERR α KO MSCs towards the adipocytic differentiation with a cocktail that contained insulin, dexamethasone and rosiglitazone. After 14 days we stained the cultures with Oil Red O to detect lipids. ERR α KO cultures had diminished numbers of adipocytes compared to the wild-type cultures. In addition, the mRNA expression of adipogenic markers aP2 and PPAR γ showed a statistically significant decrease in the ERR α KO cultures on day 7. Therefore, according to our results ERR α has a positive effect on adipogenic differentiation. In line with our result ERR α siRNA was reported to inhibit adipogenesis and overexpression of ERR α by stable transfection up-regulated adipogenic marker genes and promoted triglyceride accumulation during the adipogenic differentiation in 3T3-L1 cells (Ijichi *et al.* 2007). Recently, it was also found that an inverse agonist of ERR α , XCT-790, reduced the expression of PPAR γ and aP2, lowered triglyceride content and decreased the size of lipid droplets in a dose-dependent manner in 3T3-L1 cells (Nie and Wong 2009). Silencing ERR α in human MSCs has been shown to result in decreased adipogenic differentiation and adipocytic marker gene expression (Delhon *et al.* 2009). ERR α KO mice also have reduced fat mass and they are resistant to high-fat diet-induced obesity due to derangements in white adipocyte lipid metabolism (Luo *et al.* 2003) and in lipid absorption from the intestine (Carrier *et al.* 2004). In contrast, silencing ERR α by the antisense method increased the differentiation of rat calvarial osteoblasts into adipocytes (Bonnelye *et al.* 2002b). This potentially stems from the use of cells that are more committed to the osteoblastic lineage.

In conclusion, ERR α controls the differentiation of mouse MSCs by increasing both the adipogenic and osteoblastic differentiation. There are also opposing results about the role of ERR α in osteoblastogenesis, which could indicate that ERR α has cell type-, differentiation stage- and gender-dependent effects that need more clarification. Moreover, the identification of *BSP* as a new target gene for ERR α and ERR γ suggests a new mechanism for their bone related effects. ERR α could thus function in normal bone homeostasis and participate in the pathology of bone related diseases, such as osteoporosis by regulating osteoblast proliferation and differentiation.

CONCLUSIONS

- The activity of NR4A receptors is regulated by NR3B receptors and Wnt signaling pathway in osteoblasts. ERRα, ERRγ and β-catenin repress the transcriptional activity of NR4A receptors in U2-OS cells.
- The phytoestrogen equol was identified as a new agonist for ERRγ in PC-3, U2-OS and SaOS-2 cells. ERRγ increases the growth inhibitory effect of equol on PC-3 cells and could therefore mediate some of the beneficial health effects of equol.
- The activity of NR3B receptor ERRγ is regulated by NR4A receptors as NGFI-B and Nor1 repress its transcriptional activity in HeLa cells.
- NR3B and NR4A receptors regulate the canonical Wnt signaling pathway as they repress the transcriptional activity mediated by β-catenin in U2-OS cells.
- ERRα increases the proliferation of mesenchymal stem cells and osteoblasts. ERRα enhances osteoblastic differentiation and increases the expression of bone sialoprotein in mouse mesenchymal stem cells and MC3T3-E1 preosteoblastic cell line. Bone sialoprotein was identified as a direct target gene for ERRα and ERRγ. ERRα also increases adipogenic differentiation of mesenchymal stem cells

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