

# **Pathogenic role of (S)IgA in IgA nephropathy** Oortwijn, B.D.

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**General Introduction** 

С Η P Т E R 

## Clinical presentation of IgA nephropathy

Primary IgA nephropathy (IgAN) is the most common form of primary glomerulonephritis. The disease shows a broad spectrum of clinical presentations, leading to progressive renal failure in a substantial proportion of patients. The hallmark of this disease is deposition of IgA1 in the glomerular mesangium (1-3). In the glomeruli of patients with IgAN mostly high molecular weight IgA1 is detected, sometimes together with IgM and/or C3 (4,5). After renal transplantation recurrent mesangial IgA deposition is observed in 50 % of the patients (6). Case reports have shown that IgA deposits disappear after transplantation of a kidney with IgA deposits into a non-IgAN patient (7). These results strongly suggest that IgAN is not only a disease of the kidney, but also dependent on systemic factors.

Interestingly, patients with IgAN often present macroscopic hematuria following upper respiratory tract infections. Mucosal immune challenge leads to an increased production of IgA in the systemic compartment, probably based on the migration of B cells (the mucosa-bone marrow axis) (8). This mucosa-bone marrow traffic has been confirmed by challenging healthy individuals intranasally with the neoantigen cholera toxin subunit B (CTB) (9). In patients with IgAN a mucosal IgA hyporesponse to mucosal immunization with this neoantigen was observed (9).

Since differences in circulating IgA together with IgA binding to mesangial cells have been proposed to play an important role in the pathogenesis of IgA nephropathy, detailed analysis of circulating IgA and its interactions with cellular receptors is important.

#### Histopathology of IgA nephropathy

The most common histological lesion seen in renal biopsies from patients with IgAN are focal or diffuse mesangial proliferative glomerulonephritis (10). The initial phase of IgAN is characterized by increase in mesangial matrix but no segmental sclerosis. Focal proliferative lesions comprise the largest subgroup of IgA nephropathy. The histologic changes range from focal and segmental mesangial proliferative glomerulonephritis to focal glomerulonephritis with segmental endocapillary cell proliferation, with or without crescent formation. Associated with these variable expressions of glomerular pathology are variable degrees of tubular atrophy, interstitial comprised fibrosis. and interstitial inflammation of lymphocytes. monocytes/macrophages, and plasma cells. The number of macrophages in the glomeruli correlates with the presence of crescents and proteinuria (11). Furthermore, more monocytes and T-cells were found in biopsies of patients with active disease as compared to those without disease activity (12).

Immunohistochemistry has revealed that IgA deposits mainly consist of the IgA1 subclass (13,14), and commonly occur with co-deposits of C3, IgG, and, less common, IgM (15). The predominance of IgA1 deposits and the specific hinge region of IgA1 with potential O-linked glycosylation sites have initiated a directed search for alterations in glycosylation. Indeed, in the eluate of renal deposits, a specific reduction of O-linked glactosylation has been observed (16,17). Furthermore, with size fractionation of eluted proteins from kidney sections, it was shown that deposited

IgA is mostly high molecular weight of nature (18). Additional evidence for the deposition of high molecular weight IgA was obtained from immunohistochemical analysis of renal tissue (14,19,20).

# **Composition of IgA**

IgA is the most abundant class of immunoglobulin synthesized in humans, with 66 mg of IgA/kg of body weight produced daily compared to 34 mg of IgG and 8 mg of IgM. The half life of IgA in the circulation is 6 days. Almost all circulating IgA (2 mg/ml) is produced in the bone marrow and the liver is involved in the catabolism of the circulating IgA. Only negligible amounts (1 mg/ kg bodyweight/ day) of the total IgA produced in the bone marrow, spleen and lymph nodes (20 mg/ kg bodyweight/ day) reach the external secretions (21). The other part of the IgA (46 mg/ kg bodyweight/ day) is produced at the mucosal sites and is secreted efficiently as secretory IgA (SIgA).

#### General composition

Human IgA exists as two isotypes, IgA1 and IgA2, with IgA2 having two allotypic variants: IgA2m(1) and IgA2m(2). The human IgA subclasses differ at 14 amino acid (aa) positions in the  $\alpha$ -chain sequence.  $\alpha$ -Chains have three constant region domains C $\alpha$ 1 to C $\alpha$ 3 (Figure 1A). IgA2 of the A2m(2) allotype differs from A2m(1) and IgA1 in 6 positions; 2 in C $\alpha$ 1 and 4 in C $\alpha$ 3. The C $\alpha$ 3 domain is the same for IgA1 and IgA2m(1). The C $\alpha$ 2 domain is the same for both A2 allotypes and differs from IgA1.

A major difference between IgA1 and IgA2 occurs in the hinge region. IgA2 molecules lack a 13-aa segment found in the hinge region of IgA1 molecules, which contain 5 potential O-linked carbohydrate sites.

#### Serum IgA

Human IgA in serum exists with an IgA1: IgA2 ratio of about 9:1 (22,23) and is found in different molecular forms: monomeric IgA (mIgA), composed of two heavy and two light chains; dimeric IgA (dIgA), consists of two IgA molecules linked with a joining (J-) chain. Finally, in serum also additional high molecular weight forms of IgA can be recognized, generally described as polymeric IgA (pIgA). The composition of human serum polymeric IgA is diverse and may include CD89/IgA complexes, IgA immune complexes and IgA-fibronectin complexes (24). In humans, circulating IgA primarily consists of monomeric IgA (mIgA), and only 10-20% of the IgA is found in high molecular weight IgA (dIgA and pIgA) forms. In contrast, in rodents IgA is mostly present in a high molecular weight form (25).

#### Secretory IgA

Secretory IgA (SIgA) is the major immunoglobulin responsible for protecting the mucosal surfaces. To generate SIgA, dimeric IgA with the attached J-chain is produced in plasma cells close to the epithelium. The epithelial cells express on the basolateral side the polymeric Ig receptor (pIgR) that binds to dIgA; this complex is translocated through the epithelial cell (transcytosis). During transcytosis the extra-

cellular part of the pIgR, the secretory component (SC), is covalently linked to dIgA. At the mucosal surface the secretory component is cleaved from the pIgR and secretory IgA is secreted. Besides the presence of SIgA in the mucosa, low levels (10  $\mu$ g/ ml) of SIgA can be detected in serum (Figure 1B) (26,27).



Figure 1: proposed domain structure of human monomeric IgA

A) The  $\alpha$  heavy chain contains 3 constant domains  $C\alpha 1$ ,  $C\alpha 2$  and  $C\alpha 3$  and 1 variable domain VH. The light chain contains 1 constant domain CL and 1 variable domain VL. Positions of disulfide bonds (S), N- (N) and O-(O) linked glycosylation sites are indicated. (adapted from (30)). B) Pathway of plgR through an epithelial cell (adapted from (104))

#### Glycosylation of serum IgA

Glycans contribute 6 to 7 % of the total molecular mass of IgA1 and 8 to 10% of the total mass of IgA2 proteins. The higher carbohydrate content in IgA2 proteins is the result of additional N-linked oligosaccharide side chains (28). Human IgA1 contains two conserved N-glycosylation sites in each  $\alpha$ -chain (Asn263 and Asn459), while the IgA2 subclass contains an additional two (IgA2m(1)) or three (IgA2m(2)) conserved N-glycans (29). The number, the type and the terminal sugar residues vary between proteins of IgA subclasses but also within one subclass (Figure 2) (30). Serum IgA contains complex type N-linked carbohydrate moieties. Biantennary structures accounted for 86 % of the N-linked glycans on IgA whereas 14 % of the oligosaccharides were multiantennary or extended (31).

IgA1 is one of the few serum proteins and unique among circulating immunoglobulins in having O-glycosylation as well as N-glycosylation sites. These O-glycosylation sites are restricted to the hinge region of IgA1, which contains four to five short chains. The O-glycans are relatively simple sugars in which N-acetylgalactosamine (GalNAc) is O-linked to a serine or threonine residue. The glycan is completed with a terminal galactose (Gal) with or without additional sialic acid residues (NeuNAc) (Figure 2).

#### **Glycosylation of SlgA**

The glycosylation of SIgA is different compared to that of serum IgA in several aspects (Figure 2). Modelling of SIgA suggests that the N-glycans on the heavy chain can be masked by the SC (32). This may also result in a different exposure of the O-glycans. Moreover, specific analysis of the glycosylation of the IgA heavy chain present in SIgA, demonstrated different N-glycan structures compared to that of serum IgA. Specifically, terminal GlcNAc residues are present on the majority of the N-glycans of SIgA (32). The O-glycans on the hinge region of the heavy chain of SIgA1 presented a wide range of glycan structures, of which the major part is now characterized (32). Finally, also SC itself is heavily glycosylated.

The J chain (16 kDa) contains a single carbohydrate side chain linked to asparagine. This N-linked glycan is approximately 8 % of the molecular mass of J chain. This chain consists of fucose, mannose, galactose, N-acetylglucosamine and sialic acid. The N-glycan appears to be critical to polymer formation between J chain and IgA monomer subunits (Figure 2) (33).

Free secretory component (SC) was isolated from mucosal secretions as well as associated with SIgA. SC (70 kDa) consists of five immunoglobulin-like domains with approximately 22 % of the total molecular mass of SC contributed by carbohy-drates. The 5 to 7 site chains contain N-acetylglucosamine, fucose, mannose, galactose and sialic acid, N-glycosidic linked to the protein backbone (Figure 2) (34).



### Effector functions of IgA

IgA plays an important role in providing protection at mucosal surfaces. Passive protection by SIgA, secreted by the mucosal immune system, plays a central role in the protection of mucosal surfaces in general. Mechanisms of protection by SIgA at mucosal surfaces are: inhibition of adherence (SIgA appears to surround a microbe and other particulate antigens with a hydrophilic shell that repels attachment to a mucosal surface), agglutination, mucus trapping (SIgA diffuses freely through mucus (35)), neutralization of enzymes and toxins, and interaction with innate antimicrobial factors. On the other site there is increasing evidence that serum IgA is able to trigger effector functions that have the potential to destroy micro-organ-

isms, including: interaction with the complement pathway (although the level of activation differs between isotypes), interaction with Fc receptors on leukocytes, and epithelial cells (Figure 3).



# Figure 3: Biological consequences of the interaction of IgA with various cell types (adapted from (30)).

Cells of the myeloid lineage (neutrophils, eosinophils, monocytes, and macrophages) express CD89 through which these cells can be activated by IgA. B cells produce IgA, whereas T cells are important for the regulation of the IgA production. The interaction of IgA with Natural Killer (NK) cells may be mediated by lectin-like receptors for carbohydrate determinants. Epithelial cells transport dIgA to the apical surface where it release SIgA. Hepatocytes are important in the clearance of IgA from the circulation.

#### Complement activation

The complement system is a key component of our innate immune system and is comprised of a complex of at least 30 proteins and regulators. The liver is the main source of complement synthesis. The complement molecules constitute approximately 5 % of the total serum proteins. Three principle pathways are involved in complement activation, the classical pathway, the alternative pathway and the lectin pathway, each with their own recognition mechanism. These pathways converge at the central component of the complement system, C3. The final common pathway leads to the formation of a protein complex on a complement-activating surface, named the membrane attack complex (MAC) (Figure 4). IgA can activate complement via the alternative pathway and the lectin pathway (36,37). The lectin pathway can be activated via the recognition molecules mannose-binding lectin (MBL), H-ficolin and L-ficolin. IgA can interact with MBL and thereby activate the lectin pathway as demonstrated by activation and deposition of C4 (37), whereas for the ficolins no IgA binding data are available yet.

## IgA receptors

Different IgA receptors are described in literature (Table 1). These receptors belong to two major families of receptors, namely the Ig superfamily and the lectin family. The known receptors for IgA in the Ig superfamily are the  $Fc\alpha RI$  (CD89), the  $Fc\alpha/\mu R$  and the polymeric Ig receptor. The polymeric Ig receptor is present on epithelial cells and is important for the transcytosis of IgA to the mucosal surfaces (38). The known receptors for IgA in the lectin family are the asialoglycoprotein receptor (ASGPR) and the mannose receptor. The ASGPR is present on hepatocytes and is important for clearance of IgA (39). The ligand specificity for ASGPR is terminal galactose. The other IgA receptor in the lectin family, the mannose receptor, is present on dendritic cells and macrophages, and can bind and internalize SIgA without inducing maturation in dendritic cells (40). This binding of SIgA to the mannose receptor is sugar dependent and can be blocked with mannose, fucose and N-acetylglucosamine.



#### <u>FcαRI (CD89)</u>

FcαRI (CD89) is an IgA receptor, which is constitutively expressed on polymorphonuclear leukocytes (PMN), monocytes, eosinophils, and selected macrophages (41). CD89 is also expressed on Kupffer cells in the liver. It was suggested that CD89 on Kupffer cells provides a second line of defence in mucosal immunity (42). Initially it has been suggested that CD89 might be an IgA receptor at the surface of mesangial cells (43), however it is now widely accepted that CD89 is not expressed by mesangial cells (44-47). CD89 consists of two extracellular Ig-like domains with potential N- and O-linked glycosylation sites, followed by a stretch of hydrophobic

amino acids representing the predicted transmembrane domain, with a positively charged arginine which is essential for association of CD89 with the FcR  $\gamma$ -chain homodimer-signalling subunit (48), and a short cytoplasmic tail devoid of recognition signalling motifs (Figure 5). The protein core of CD89 has a predicted molecular mass of 30 kDa with differential glycosylation at six potential N-linked sites, and the probability of additional O-glycosylation contributing to the variable size observed for the mature receptor, 55-75 kDa on monocytes and neutrophils, 70-100 kDa on eosinophils. The site of interaction between CD89 and IgA was identified in the first extracellular domain of CD89 (49,50) and in the C $\alpha$ 2/C $\alpha$ 3 junction of IgA (51,52).

CD89 participates in different aspects in host defence. CD89 induces phagocytosis of IgA complexed antigens (53), initiates antibody-dependent cellular cytotoxity (54) and CD89 is important for the clearance of IgA from the circulation (48). Upon activation, a soluble form of CD89 is released from the surface of monocytes and monocytic cell lines (55). These soluble CD89 molecules circulate in a complex, covalently linked with IgA, in the high molecular weight fractions of serum IgA (56). Binding studies with different molecular forms of IgA have shown that pIgA binds better to CD89 than mIgA (54,57,58). Furthermore one study suggested that SIgA can only interact with CD89 if MAC-1 (CD11b/ CD18) is present (59).

To study the role of the IgA-CD89 interaction mouse models were used. Although CD89 is described on human myeloid cells, no murine homolog has yet been defined. Therefore transgenic mouse models have been created, including a model in which the CD11b promoter was used (60). In this model human CD89 was highly expressed on macrophages/ monocytes. These transgenic mice develop spontaneously massive mesangial IgA deposits after 12 weeks, suggesting a role for CD89 in IgA nephropathy (60).

	Receptor	Ligand	Cellular distribution
lg		plgA>	
family	FcαRI (CD89)	mlgA	Myeloid cells
	Fcα/μR	lgA∕ lgM	B cells, Macrophages, Mesangial cells
	plgR	dlgA	Epithelial cells
C-type	ASGPR	IgA	Hepatocytes
lectins	Mannose receptor (CD205)	SIgA	Macrophages, Dendritic cells
	Transferrin receptor (CD71)	lgA1	Mesangial cells

# Table 1: Receptors with IgA binding capacities

#### Fcα/µR

The Fc $\alpha/\mu$ R, located on chromosome 1, is a newly identified receptor for IgA. Transcription of the receptor is demonstrated in several tissues including thymus, spleen (B cells and macrophages, but not on granulocytes, T cells or NK cells), liver, kidney, small and large intestines, testis and placenta (61,62). Furthermore, transcription of the Fc $\alpha/\mu$ R was described on mesangial cells and was upregulated after stimulation of mesangial cells with IL-1 (63).

The Fc $\alpha/\mu$ R is a type 1 transmembrane protein with a 32-aa leader sequence, a

423-aa extracellular domain, a 20-aa transmembrane domain and a 60-aa cytoplasmic region. The extracellular domain has four potential sites for NH<sub>2</sub>-linked glycosylation (61), leading to a mature protein of 60- 70 kDa. In the extracellular domain of the receptor cysteine residues are identified and it is flanked by the consensus sequence for immunoglobulin-like domains, indicating that this molecule is a member of the immunoglobulin super family. The Fca/µR shows no significant homology with other proteins. However, in the immunoglobulin like domain there is a motif that is conserved in the first immunoglobulin like domain of the polymeric Ig receptor (Figure 5) (61).

The Fc $\alpha/\mu$ R mediates endocytosis of immune complex composed of Staphylococcus aureus and IgM anti-S. aureus antibody by primary B lymphocytes (61). The underlying mechanism of this internalization is not yet known. However, experiments with Fc $\alpha/\mu$ R mutants suggest that the di-leucine motif is important in this process (61). Furthermore, the Fc $\alpha/\mu$ R acquires the ability to bind IgM and IgA antibodies after stimulation of B cells.



**Figure 5: structure of Fc** $\alpha$ / $\mu$ **R and of CD89 with the**  $\gamma$ **-chain.** The extracellular, membrane and cytoplasmic domains of the Fc $\alpha$ / $\mu$ R and CD89 as well as the  $\gamma$ -chain with its signalling motifs are depicted.

#### IgA receptors and mesangial cells

The binding of high molecular weight IgA is better to mesangial cells than that of monomeric IgA. However the specific mechanism for the binding and retention of IgA1 remains uncertain. Several findings point to an IgA-specific receptor(s) on mesangial cells (41,64). However none of the known IgA receptors (CD89, ASGPR, pIgR) is expressed on mesangial cells (45,47). Two other receptors have recently emerged as candidate receptors for binding IgA; CD71 (transferrin receptor) and the Fc $\alpha/\mu$ R (63,65,66). CD71 expression is enhanced in the glomeruli of IgA nephropathy patients and co-localizes with IgA1 deposits. Mesangial cells bind both IgA sub-

classes, whereas CD71 binds only IgA1, suggesting involvement of an additional receptor. Theoretically, it may be the Fc $\alpha/\mu$ R that can be transcribed by mesangial cells in vitro (63). In contrast, another group found that polymeric IgA1 from IgA nephropathy patients induces macrophage migration inhibitory factor (MIF) and TNF- $\alpha$  in mesangial cells. This induction is probably through an unidentified IgA receptor, as shown by failure to suppress IgA-induced MIF synthesis by blocking IgA receptors with specific antibodies or various ligands to IgA receptors (67).

#### IgA in IgA nephropathy

Several studies using lectin interactions (Table 2) and fluorophore-assisted carbohydrate electrophoresis (FACE) focused on the analysis of IgA glycosylation, showing aberrant O-glycosylation in circulating IgA from IgAN patients, resulting in increased Tn antigen (GalNAc $\beta$ 1-Ser/Thr) residues (68-71). This undergalactosylated IgA1 may lead to recognition by IgG antibodies and generation of circulating IgG-IgA1 complexes (72). Furthermore, altered interaction with mesangial cells has been described (73). This aberrantly O-glycosylated IgA is suggested to be dependent on a hampered function of the  $\beta$ 1-3 galactosyltransferase (74). Furthermore, it is suggested that downregulation of the  $\beta$ 1-3 galactosyltransferase chaperone (Cosmc) is important for the aberrant O-glycosylation in patients with IgAN (75).

Table 2: Reactivit	y of lectins	used for a	analysis d	of IgA	glycos	ylation
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Name	Abbreviation	Sugar specificity
Artocarpus integrifolia	Jacalin	Galβ1-3GalNAc
Helix aspersa	HAA	GalNAc
Vicia villosa	VV	GalNAc
Helix pomatia	HPO	GalNAc
Erythrina crystagalli	ECL	Galβ1-4GlcNAc
Ricinus communis	RCA	βGal
Sambucus nigra	SNA	NeuNAc
Peanut agglutinin	PNA	Galβ1-3GalNAc

Levels of plasma IgA1 are elevated in about half of the patients with IgAN (76-78), which appears to be the result of an increased production of this isotype by the bone marrow (79-82) and by a low elimination rate by the liver. Mucosal plgA plasma cell numbers are normal or even reduced in IgAN (83,84), whereas plgA antibody levels in mucosal secretions are not elevated and are sometimes lower than controls (9). Furthermore, systemic antigen challenge results in increased titers of circulating plgA1 antibodies (85,86) with normal levels in mucosal secretions (87).

# IgA and mesangial cells

Functional studies with purified IgA from IgAN patients showed that IgA from IgAN patients binds better to mesangial cells than IgA healthy individuals (73),

although this is still controversial (88). The binding of polymeric and aggregated IgA to mesangial cells was stronger as compared to monomeric IgA. Moreover, polymeric IgA with the highest net negative charge is superior in binding to mesangial cells (73). In IgAN circulating aberrantly glycosylated IgA1 has been described. To mimic this IgA, IgA1 was purified with Jacalin and in vitro degalactosylated. The removal of galactose residues from IgA1 isolated with Jacalin increases binding to mesangial cells in vitro (89).

The activation of mesangial cells by IgA1 immune complexes is considered the initiating event in the pathogenesis of IgA nephropathy. Mesangial cell activation was observed in vitro in many instances (90-93). Exposure of mesangial cells to IgA is capable of initiating a proinflammatory cascade involving mesangial cell secretion of IL-1 $\beta$ , TNF- $\alpha$ , IL-6, TGF- $\beta$  and MIF and the release of the chemokines MCP-1 (CCL2), IL-8, and IP-10 (91,94-97). After stimulation of mesangial cells with degalactosylated IgA the production of these factors is higher as compared to control IgA. In vivo, urinary IL-6 (98), the tubular and interstitial expression of intercellular adhesion molecule type 1 (99), and the intrarenal expression of proinflammatory cytokines and chemokines (100) correlated with renal injury and may have prognostic value.

IgA is also capable of altering mesangial cell-matrix interactions by modulating integrin expression, and this could have an important role in remodeling of the mesangium following glomerular injury (101). There is also evidence that activation of mesangial cells by co-deposited IgG could synergistically contribute to the development of a proinflammatory mesangial cell phenotype and thereby influence the degree of glomerular injury (102). It is not yet clear which specific physicochemical properties of mesangial IgA affect mesangial cell activation; however, there is some in vitro evidence that undergalactosylated IgA glycoforms from patients with IgAN reduce proliferation, increase nitric oxide synthesis and the rate of apoptosis, and enhance integrin synthesis in cultured mesangial cells (101,103). This, together with the overrepresentation of aberrantly glycosylated IgA1 in mesangial IgA, suggests that IgA1 O-glycosylation plays a role in both the deposition of IgA and the subsequent injury.

#### Scope of this thesis

For a better understanding of the role of IgA and mesangial cells in IgA nephropathy, we focused on different questions in the course of the disease. In chapter 2 and 3 we focused on the possible receptor mechanisms underlying mesangial IgA deposition. Therefore we studied the interaction of IgA with CD89 in different binding assays. We showed a similar association to CD89 for monomeric and polymeric IgA (chapter 2). CD89 is described not to be present on mesangial cells, whereas the recently identified  $Fc\alpha/\mu R$  is suggested to be expressed by mesangial cells. To investigate the role of the  $Fc\alpha/\mu R$  in IgA nephropathy we produced fusion proteins of this receptor and used these fusion proteins for IgA binding studies (chapter 3).

Because it is suggested that IgAN is not only a disease of the kidney, but also dependent on systemic factors we investigated in chapter 4 to chapter 8 which changes in IgA lead to the deposition of IgA in the glomeruli. Therefore, we investi-

gated in chapter 4 the activation of the lectin pathway of complement via IgA in glomeruli of IgAN patients. We show that activation of the lectin pathway of complement in the glomeruli of patients with IgAN is associated with more severe renal disease. In chapter 5 we isolated IgA from patients and controls and separated this IgA in monomeric and polymeric IgA. With these IgA preparations we investigated the differences between monomeric and polymeric IgA between patients and controls including the interaction with lectins and mesangial cells. In this study we observed clear differences between monomeric and polymeric IgA for lectin and mesangial cell interactions, but there were no differences between patients and controls. However, the concentration of SIgA in the polymeric IgA preparations was significantly higher in patients as compared to controls. This suggests that only a minor part of the IgA from patients might be different from controls. Finally, we demonstrated that SIgA is able to bind stronger to mesangial cells than serum IgA, and that SIgA is present in glomerular IgA deposits (chapter 6). To confirm the presence of SIgA in the glomerular IgA deposits we studied the presence of SIgA in biopsies from IgAN patients. We showed in chapter 7 that in 15 % of the cases SIgA is detectable in the glomerular IgA deposits. Finally, chapter 8 summarizes the studies described in this thesis and discusses the relevance of these new findings.

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