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## **Molecular pathology of hereditary cerebral hemorrhage with amyloidosis-Dutch type**

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# Chapter 1

## Introduction

## Introduction

Hereditary cerebral hemorrhage with amyloidosis-Dutch type (HCHWA-D) is an autosomal dominant hereditary disease caused by a missense mutation on chromosome 21 in the amyloid precursor protein (APP), resulting in a glutamine for glutamic acid substitution (NP\_000475.1:p.Glu693Gln, known as APP E693Q) (1). HCHWA-D patients suffer predominantly from hemorrhagic strokes, infarcts, and vascular dementia (2). The so-called APP “Dutch” mutation, originally described in families from small coastal villages in the Netherlands, is characterized by a severe Cerebral Amyloid Angiopathy (CAA) pathology.

The term CAA pathology is first used by Mandybur in 1975 (3) and is defined by the progressive accumulation of amyloid beta ( $A\beta$ ) in the cerebrovasculature, resulting in acellular thickening of the vessel wall (4). CAA pathology is a risk factor for lobar intracerebral hemorrhages (ICH) (5) and for ischemic cerebral infarction (6). Because it disrupts the delicate cerebral vascular homeostasis, it can have both hemorrhagic and/or ischemic consequences (7).

HCHWA-D has been first described as the familial occurrence of ICH (8) but associated with the cerebrovascular pathology of Alzheimer’s disease (AD) only twenty-four years later (9). Shortly after, the Dutch mutation is identified as the first missense mutation associated with the AD phenotype (1), due to the shared pathological brain  $A\beta$  deposition. In AD  $A\beta$  is aggregating in parenchymal plaques but CAA is also found in 80 to 90% of AD cases from autopsy series (10–17). Therefore the vasculotropic Dutch- $A\beta$  peptide has been extensively studied to unravel the etiology of AD cerebrovascular pathology (references in this chapter).

$A\beta$  is a 4kDa peptide resulting from APP cleavage by processing enzymes ( $\alpha$ - and  $\beta$ -secretases cleaving the N-terminal peptide and  $\gamma$ -secretases cutting the C-terminal). Although  $\alpha$ -secretase cleavage results in a benign pathway,  $A\beta$  peptides produced by  $\beta$ -secretase cleavages can aggregate and form different  $A\beta$  species ranging from monomers to fibrils. The Dutch mutation is located near the  $\alpha$ -secretase cleavage site of APP, and is thought to affect the APP processing (18). The  $A\beta$  peptide with the Dutch mutation is also known as  $A\beta$  E22Q, as the modification occurs in position 22 (when using  $A\beta$  peptide amino acid numbering). Depending on which cleavage site is used, different  $A\beta$  peptides are formed. Most studied isoforms are  $A\beta$  (1-40) (or  $A\beta$ 40, 40 amino acids) and  $A\beta$  (1-42) (or  $A\beta$ 42, 42 amino acids) but many N-terminal and C-terminal truncated peptides coexists in HCHWA-D (19), adding complexity to the aggregation process of the peptides.

## Clinicopathology of HCHWA-D

White matter lesions (recognized as white matter hyperintensities [WMHs] in magnetic resonance imaging [MRI] scans) are the earliest radiological manifestations in pre-symptomatic mutation carriers (detectable in standard 1.5 Tesla [T] scan). Although more subtle, the grey matter is also affected by cortical thinning in relatively young mutation carriers (mean age 46 years) when compared at 3T MRI to a control group (20). Cortical microinfarcts detected at high resolution 7T MRI are also more prevalent in pre-symptomatic patients than in controls (21). WMHs are located in subcortical areas, and tend to be more severe in the occipital lobe (22). Other radiological manifestations such as microbleeds, intracerebral hemorrhages, superficial siderosis, convexity subarachnoid hemorrhages and microinfarcts, have a higher prevalence in symptomatic patients.

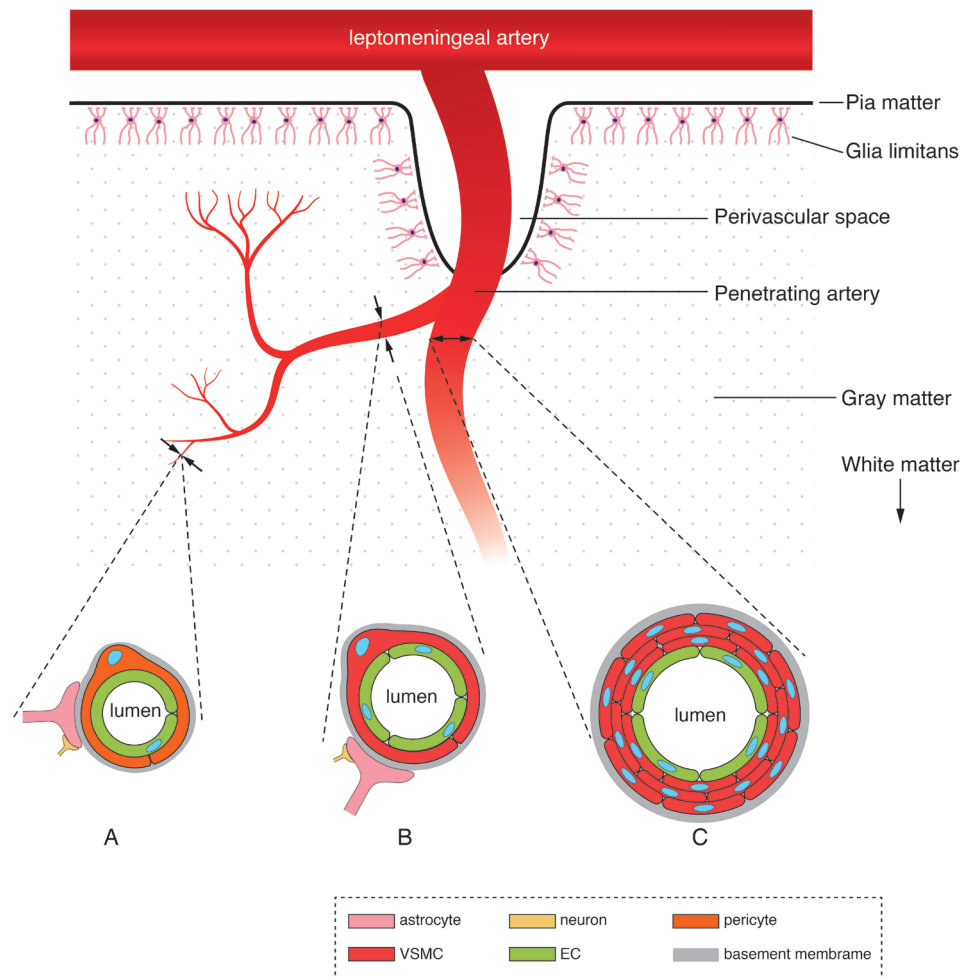
Strokes in HCHWA-D are mostly hemorrhagic but ischemic strokes can also occur. The hemorrhages mostly involve temporal and occipital lobes and occur predominantly in the deeper cortical layers and in subcortical white matter (2) but can be present in the cerebral cortex as well and tend to spare the frontal lobes (23). According to the latest clinical data, the first stroke (mean age onset  $54 \pm 8$  years,  $n=58$ ) is fatal in only 14% of the cases (against two- third of patients 23 years ago; (2)) and the majority of hemorrhages (35%) are located in the occipital lobe followed by the parietal lobe (21%) (24). The mean number of strokes is 3 (range 0-10 strokes) and the mean survival after the first stroke is 10 years (range 0-28 years). Epilepsy occurs in about half of the patients who have suffered from one or more strokes (25). Cognitive decline can precede the onset of hemorrhagic strokes (22) although in a recent study, cognitives abnormalities are not detected in presymptomatic mutation carriers ( $n=12$ , (21)). Cognitive decline frequently occurs in a stepwise fashion between stroke episodes (26,27).

## Neuropathological features of HCHWA-D

CAA pathology in HCHWA-D is widespread and invariably affects cerebral and cerebellar meningeal arteries and cerebrocortical arterioles with a higher severity occipitally (23). The amyloid angiopathy is believed to progress from the leptomeninges towards the neocortex and in most severe cases subcortical white matter and capillaries are involved (vessels anatomy in **Figure 1**). Subcortical white matter shows areas of demyelination, axonal loss, and gliosis (leukoencephalopathy). Tau pathology (one of the neuropathological hallmarks of AD) in HCHWA-D is rare and not associated with dementia (28).

$A\beta$  protein deposition starts at the abluminal basement membrane of vascular smooth muscle cells (VSMCs; grade 1 CAA, **Figure 2A**). At later

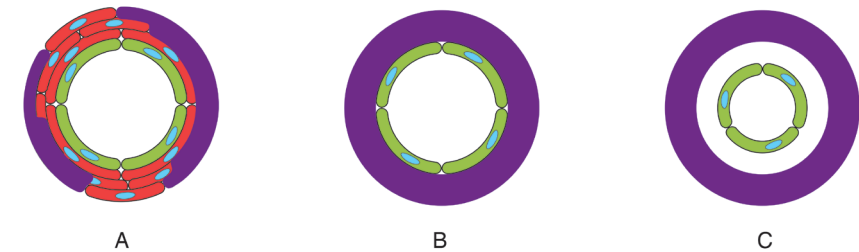
stages, amyloid fibrils are observed between VSMCs and in heavily affected vessels, VSMCs are completely displaced by the amyloid (grade 2 CAA, **Figure 2B**). With CAA progression, additional radial layers of A $\beta$  (one or two) around a layer of homogeneous A $\beta$  develop in cerebrocortical arterioles at the level of cortical layers II–III of severe cases (absent in leptomeninges and cerebellum) (23,29). Vessels with radial A $\beta$  are associated with degenerating neurites, reactive astrocytes and activated microglia [30, Maatschieman p227].



**Figure 1:** Illustration of the cortical brain vessels anatomy and details of the vascular components in (A) a capillary at the neurovascular unit (NVU), (B) an arteriole and (C) a penetrating artery.

Non-fibrillar A $\beta$  clouds and fine diffuse plaques in the parenchyma tend to disappear with age and suggests a clearance of non-fibrillar parenchymal A $\beta$  by glial cells in early stage of the disease (23,31). Indeed, although non-activated glial cells (astrocytes and microglia) are bearing cytoplasmic A $\beta$  granules, activated glial cells in fibrillar deposits (parenchymal or perivascular associated with CAA) are devoid of A $\beta$  granules. This suggests that glial response to fibrillar A $\beta$  is not clearly linked with A $\beta$  removal (32). Consequently, in contrast to parenchymal A $\beta$ , CAA severity defined by CAA load and vessel wall thickening tends to intensify with age, even though it might differ considerably between patients of comparable age (28).

Further, disease progression in HCHWA-D is also associated with secondary microvascular degenerations or CAA-associated microvasculopathies such as vascular fibrosis (or hyalinization), microaneurysms, macrophage infiltration, “vessel-within-vessel” configurations (grade 3 CAA in **Figure 2C**), calcifications and vascular thrombi (33). CAA-associated microvasculopathies correlate with the number of cerebrovascular lesions (CAA-associated hemorrhages and/or infarcts; (34)) and with dementia diagnosis (28).



**Figure 2:** Illustration of CAA severity grading (based on Vonsattel & Greenberg hemorrhage risk scale 1 to 3,(106)). (A) Grade 1 CAA. Start of amyloid deposits (purple colour). (B) Grade 2 CAA. The media of this cortical vessel is fully replaced by amyloid and the wall is thickened. (C) Grade 3 CAA. Example of secondary microvasculopathies classified as grade 3, here a cracking of the vessel wall that creates a “vessel-within-vessel” appearance.

A $\beta$ -associated proteins found in vascular deposits are investigated in HCHWA-D. Similarly to findings in AD, Amyloid P-component and Apolipoprotein E (ApoE) are identified in vascular and parenchymal A $\beta$  (35–37). Particularly, APP and CystatinC immunoreactivity are strongly associated with CAA in HCHWA-D (38,39). Inflammatory proteins are not investigated in HCHWA-D brains except for the presence of complement proteins in amorphous plaques (40) and the association of molecular chaperone proteins with CAA (HspB8, Hsp20 and Hsp27), which could

mediate inflammatory reactions (41). The occurrence of other proteins could also vary depending on the type of material used (cryosections vs formalin-fixed and antibodies specificities). As such the presence of heparan sulfate proteoglycans found by van Horssen (42) but not by van Duinen (43),  $\alpha$ 1-antichymotrypsin found by Timmers (35), but not by Rozenmuller (40) and low-density lipoprotein receptor-related protein-1 (LRP-1) found by Wilhelmus (44), but not by Deane (45) are a matter of debate.

One characteristic feature in HCHWA-D is the presence extracellular matrix (ECM) parenchymal coarse deposits presenting a strong immunoreactivity for several ECM components (HSPG, laminin, collagen type 3 and 4), clustering around thick-walled A $\beta$  vessels, but not associated with A $\beta$  plaques. Collagen type 1 and 3 and fibronectin are associated with strongly A $\beta$ -laden arterioles (43). Interestingly, lysyl oxidase (LOX) and tissue transglutaminase (tTG), which are enzymes cross-linking ECM-proteins, are associated with angiopathic vessels in HCHWA-D (46,47). Laminin, fibronectin, HSPG, and collagen are substrate for these enzymes whose reaction might participate in CAA formation.

### Pathomechanisms of HCHWA-D

*In vitro* studies in human cerebrovascular cells have largely demonstrated a higher toxicity of the synthetic A $\beta$  Dutch peptide compared to the wild type peptide (48–54). More precisely, with the Dutch mutation, a charged residue is substituted with an uncharged residue that results in higher oligomer stability favorizing the formation of these non-fibrillar toxic assemblies (55–58). Moreover, Dutch amyloid seeds, have prion-like effect on WT A $\beta$  and are thus harmful and irreversible (59).

Amyloid deposits in HCHWA-D are a mixture of wild type and Dutch variant (60,61). Whereas CAA in general is mostly composed of A $\beta$ 40 and to a less extent of A $\beta$ 42, it is hypothesized that the Dutch mutated A $\beta$ 42 might seed and trigger the CAA formation. Indeed, both Dutch-mutated A $\beta$ 40 and wild type A $\beta$ 40 are present in isolated vessels from brain tissue, but only the Dutch-mutated A $\beta$ 42, and not the wild-type A $\beta$ 42 is detected (19). Moreover, histological studies with C-terminal specific antibodies have shown that A $\beta$ 42 precedes A $\beta$ 40 deposition in cortical arterioles (23). In addition, electronic microscopy identified non-fibrillar A $\beta$ 42 as the first species deposited in the basement membrane of capillaries (62).

The vascular pathogenicity of the Dutch mutation is also influenced by an increase in the A $\beta$ 40:A $\beta$ 42 ratio (63), as demonstrated in transgenic mice overexpressing in neurons the human APP gene with the E693Q mutation (64). This mouse model, called APP Dutch model, develops an extensive CAA pathology (around 22-25 months) composed of A $\beta$ 40 predominantly with few diffuse A $\beta$ 42 parenchymal plaques similar to the neuropathology

of HCHWA-D. Increase in A $\beta$ 42 concentration by crossing with a PS45 transgenic line (familial AD-causing PS1 mutations) resulted in abundant parenchymal plaque formation at a young age, with limited CAA pathology (64).

So far, no risk factors have been linked with the clinical symptoms of HCHWA-D. In particular, the ApoE genotype (influence on CAA pathology described in the next section) and the polymorphism in the Presenilin (PS) 1 gene, both highly impacting A $\beta$  transport and processing, have been investigated and did not show any significant association with the disease phenotype (65,66). Only gender may modulate the phenotypic expression of the mutation, indeed the mortality rate is respectively significantly higher for female but lower for individuals with a maternal transmission (67). Nevertheless the reason is unidentified and a recent study on a smaller cohort did not confirm the gender association with the mortality rate (24).

The Dutch mutation can also alter other mechanisms having influence on A $\beta$  accumulation and clearance from interstitial cerebral fluid. It is suggested from *in vitro* studies that the mutation could enhance the resistance to proteolytic degradation (68,69) thereby reducing the A $\beta$  turnover rate, while A $\beta$  production rate seemed unaffected (70–73). Furthermore, altered affinity changes due to the Dutch mutation affects A $\beta$  transport across the blood-brain-barrier (74). One explanation could be a lower affinity for LRP1 which could affect the LRP-mediated brain capillary clearance (45).

Pathomechanisms such as alteration in vessel wall integrity (VSMCs disappearance), activation of perivascular cell (astrogliosis and microgliosis) and disturbances in peripheral drainage (basement membrane thickening), although more severe in HCHWA-D, are shared features of all CAA pathologies (75–78).

### CAA pathology: sporadic CAA (sCAA) and AD with CAA

CAA pathology is frequent in normal ageing, may be asymptomatic in mild cases (79), but is an important cause of spontaneous lobar ICH (80). When taken at any level of severity, in population-based (>85 years) and community-based (median age 88.5) studies, neuropathological evidence of CAA are recorded in respectively 69.6% and 78.9% of autopsied cases (81,82). Earlier studies have related that CAA pathology is related to cognitive impairment and dementia in ageing (83). It is in addition recently proposed that besides being more prevalent among AD patients, CAA might induces an independent cognitive contribution to AD dementia (81,84).

CAA pathology in AD with CAA or in sCAA are intermingled disorders closely resembling at pathological investigation when solely regarding at A $\beta$  vascular deposition (29). A distinction is made in subjects which rely both on the clinical diagnosis of dementia and on the definite neuropathologic

examination (tau pathology seen as neurofibrillary tangles) presence is a hallmark in AD). Both in AD with CAA and in sCAA, subjects can present an hemorrhagic phenotype which is related to CAA severity. Indeed, in AD with CAA, CAA pathology is predominantly mild to moderate but cases with the higher frequency of hemorrhages had also a more severe CAA (85). Likewise, in sCAA cases presenting lobar ICH, CAA pathology severity is, in general higher (86,87).

Besides ageing, which is the strongest known clinical risk factor for developing CAA pathology (88), certain genetic risk factors have been identified. As in AD, ApoE genotype is strongly associated with CAA pathology and has influence on the pathophysiology of CAA (89–91). ApoE  $\epsilon$ 2 and ApoE  $\epsilon$ 4 are related to more severe CAA but only ApoE  $\epsilon$ 4 is linked with capillary involvement (92,93). Carriers of ApoE  $\epsilon$ 2 risk are more at risk for CAA-related hemorrhages (87,91,94). Other non-ApoE gene polymorphisms have been compared in a meta-analysis and the strongest association with CAA pathology are found for the transforming growth factor  $\beta$ 1 gene (TGF $\beta$ 1), the translocase of outer mitochondrial membrane 40 gene (TOMM40) and the complement component receptor 1 gene (CR1) (95).

Interestingly, TGF $\beta$ 1 expression modulates the CAA phenotype. In transgenic mice, both astrocytic or neuronal overexpression of TGF $\beta$ 1 resulted in cerebral angiopathy due to an increase in vascular fibrosis (96,97). Moreover, co-overexpression of TGF $\beta$ 1 and APP in mice resulted in a reduction in parenchymal A $\beta$  plaque load with CAA increase (98). Multiple studies have shown a role for TGF $\beta$ 1 in promoting APP and A $\beta$  production by astrocytes *in vitro* (99–102) but also *in vivo* with increased endogenous APP and A $\beta$  levels in TGF $\beta$ 1-astrocytic mouse model (102). However, whether these animal models actually accumulate murine A $\beta$  is likely mouse strain-dependant (103). In VSMCs, TGF $\beta$ 1 associated to ApoE4 protein strongly increased the amount of cellular A $\beta$  (104) and enhances A $\beta$  internalization in a dose-dependent manner [30, Prior & Urmoneit p255].

Two different CAA grading methods, both based on A $\beta$  staining, are primarily referred to in neuropathological studies. A first semi-quantitative approach is ranking CAA mostly based on its spreading from leptomeninges to intracortical area (105). A second approach focused on the vessel wall morphology of individual vessel, is assessing a scale ranging from 1 to 3 for hemorrhage risk (106), as illustrated in **Figure 2**. More recently, two similar approaches have been proposed for CAA pathologic assessment (16,107) in an attempt to find a consensus on a single method to assess CAA severity.

### HCHWA-D: a model to study biomarkers & therapy for CAA pathology

Totally reliable and noninvasive diagnostic tests of CAA pathology as well as anti-CAA therapy do not exist. Therefore HCHWA-D, as an accepted monogenetic model of CAA pathology, is useful to develop biomarkers (either radiologic imaging or molecular signature) and to find new therapeutic targets.

Neuroimaging biomarkers of CAA pathology at MRI are developed in symptomatic (after first clinically assessed stroke) and pre-symptomatic HCHWA-D patients. In particular, the current diagnostic Boston criteria (based on the pattern of hemorrhagic lesions and superficial siderosis to assess probable CAA during life) have been evaluated and its sensitivity was improved by the inclusion of microbleed counts (108). Lately, two studies identified early imaging biomarkers (before cognitive symptoms and ICH) for CAA pathology diagnosis by inclusion of presymptomatic carriers. In the first study, WMHs and microinfarcts which are ischaemic manifestations of CAA have been detected with high field (3T) and ultra-high field (7T) MRI (21). In the second study measuring regional cerebral blood flow (by Blood-Oxygen-Level Dependent functional MRI or BOLD fMRI), an altered vascular reactivity to visual stimulation in occipital lobe was detected in pre-symptomatic mutation carriers (109). More recently, a striped cortex appearance on 7T MRI (visualized as hypointense lines perpendicular to the pial surface) solely detected in 40% of symptomatic patients (n=15) has for that reason been described as a neuroimaging marker of advanced CAA pathology (110).

Fluid biomarkers, in particular A $\beta$ , sAPP and Tau (total tau, and phosphorylated tau) protein levels in plasma and cerebrospinal fluid (CSF) are the most common studied biomarkers in amyloid beta related pathologies. In HCHWA-D, A $\beta$ 42 level in plasma are decreased (111) although no difference are perceived in sCAA (112). In CSF, pronounced decreased levels of A $\beta$ 40 and A $\beta$ 42 are measured in HCHWA-D pre-symptomatic mutation carriers (113) and less pronounced but consistent decreased levels are found in sCAA (114,115).

Lastly, other AD specific biomarkers have been tested in an HCHWA-D western Australian family. Pulpil flash response, which is linked to cholinergic deficit in AD, is reduced in mutation carriers and deserves further investigation (116). In the same study, mutation carriers tested with positron emission tomography imaging with Pittsburgh compound B (PiB-PET) showed a higher compound retention, although below the standard threshold for amyloid positivity in AD.

So far, the above mentioned biomarkers can estimate CAA pathology but none of them can precisely determine its severity, nor predict hemorrhagic

risk, nor assess with certainty the efficiency of a therapy. More specific biomarkers are highly needed in clinical trials of A $\beta$  disease-modifying therapies (117). Although no therapy exist against CAA, besides focusing on amyloid removal therapies uniquely, alternative paths targeting aggravating factors of CAA pathology could help slowing down the CAA build up and delay the onset of symptoms.

### Scope and outline of this thesis

The general aim of this thesis is to disentangle the molecular pathogenesis behind CAA formation in HCHWA-D. Since no proven therapeutic treatment exists to prevent or even delay the CAA pathology, understanding the underlying pathomechanisms in HCHWA-D is important and may lead to identification of potential therapeutic targets.

**Chapter 2** review the literature on HCHWA-D pathogenesis, combining neuropathological and *in vitro* findings and focusing in particular on the role of ECM in HCHWA-D.

Former research in CAA field indicates the existence of factors able to influence A $\beta$  to accumulate predominantly in vessels rather than in brain parenchyma, such as TGF $\beta$ . Identification of aggravating factors of CAA pathology that can interact with currently approved drugs is one area of investigation and therefore we explored in **Chapter 3** TGF $\beta$  pathway activation in HCHWA-D compared to sCAA.

In order to interpret imaging findings and better evaluate the disease progression **chapter 4 & 5** are dedicated to calcifications in HCHWA-D, a specific CAA-associated microvasculopathy. **Chapter 4** is a histopathological study assessing the histological correlate of a recently discovered MRI radiologic finding in HCHWA-D. **Chapter 5** is exploring the pathomechanisms leading to these abnormalities and tries to assess the relationship of these changes and the TGF $\beta$  findings from chapter 3.

**Chapter 6** is an exploratory transcriptomic study to identify major deregulated pathways in HCHWA-D and broaden our comprehension of molecular pathogenesis.

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