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## **The evolving genetic and pathophysiological spectrum of migraine**

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# 1.0

**General introduction  
& scope of the thesis**

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## 1.1. Migraine

Migraine is an episodic neurovascular disorder that is characterized by attacks of severe, unilateral, pulsatile headache that is often accompanied by nausea, vomiting, photo- and/or phonophobia. Typical migraine attacks last a few hours to several days.<sup>1</sup> Migraine can start at any age, but the age at onset usually is before the age of 50 years. The peak age at onset is between 10 to 12 years of age for males and between age 14 to 16 for females.<sup>2</sup> Migraine is a very common disease that is more prevalent in women than in men. The one-year overall prevalence of migraine in Western countries is around 11%; with 6-8% in men and 15-18% in women.<sup>3-6</sup> The median attack frequency is 1.5 per month. Approximately ten percent of migraineurs have weekly attacks.<sup>6</sup> The World Health Organisation (WHO) rates severe migraine among the most disabling chronic disorders.<sup>7</sup>

## 1.2. Migraine with and without aura

Migraine can be subdivided in migraine without aura (MO) and migraine with aura (MA), based on the absence or presence of an aura phase preceding the headache phase (Table 1). About one-third of the migraine patients experience an aura. The aura phase generally lasts 20-60 minutes and includes mostly visual symptoms, but symptoms can also be sensory or speech related.<sup>8</sup>

Currently no reliable biological markers are available for the diagnosis of migraine. Therefore, the diagnosis depends on the patient's symptom description, using the Diagnostic and Classification Criteria of the International Headache Society.<sup>1</sup> Patients are characterised by the recurrence of their migraine attacks (Table 1).<sup>1</sup> To classify as an MO patient, the patient needs to have had at least five MO attacks. An MA patient has had at least two MA attacks. Current treatment options for migraine are far from optimal and effective in only about half of the patients.<sup>9</sup>

**Table 1.** *International headache criteria for migraine without and migraine with aura*<sup>1</sup>

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### **Migraine without aura**

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- A. At least five attacks fulfilling criteria B-D
  - B. Headache attacks lasting 4 to 72 hours (untreated or unsuccessfully treated)
  - C. Headache has at least two of the following characteristics:
    - 1. Unilateral location
    - 2. Pulsating quality
    - 3. Moderate or severe pain intensity
    - 4. Aggravation by or causing avoidance of routine physical activity (e.g., walking or climbing stairs)
  - D. During headache at least one of the following;
    - 1. Nausea and/or vomiting
    - 2. Photophobia and phonophobia
  - E. Not attributed to another disorder
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**Migraine with aura**

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- A. At least two attacks fulfilling criteria B-D
  - B. Aura consisting of at least one of the following, but no motor weakness:
    - 1. Fully reversible visual symptoms including positive features (e.g., flickering lights, spots, or lines) and/or negative features (i.e., loss of vision)
    - 2. Fully reversible sensory symptoms including positive features (i.e., pins and needles) and/or negative features (i.e. numbness)
    - 3. Fully reversible dysphasic speech disturbance
  - D. Headache fulfilling criteria B-D for migraine without aura begins during the aura or follows aura within 60 minutes
  - E. Not attributed to another disorder
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**1.3. Migraine is a genetic disorder**

Migraine has a strong genetic component. Many patients have first-degree relatives who also suffer from migraine.<sup>10</sup> Population-based family studies showed that the familial risk of migraine is increased.<sup>11,12</sup> First-degree relatives of probands with MO have an almost 2-fold increased risk to also suffer from this disorder, but had only 1.4 times the risk of MA, compared with the general population. Instead, first-degree relatives of probands with MA had a nearly 4-fold increased risk for MA, but no increased risk for MO.<sup>11</sup> Studies of mono- and dizygotic twin pairs are the classical method to investigate the relative importance of genetic and environmental factors. Migraine concordance rates are between 1.5 and 2 times higher in monozygotic twins than in dizygotic twins for both MO and MA<sup>13,14</sup>, indicating that genetic factors are important in migraine susceptibility. A large population-based twin study comprising of some thirty thousand twin pairs revealed that genetic and environmental factors had an almost equally large contribution.<sup>15</sup> Shared environmental factors seemed to play a minor role as shown by studies comparing twins that were raised together or apart.<sup>16,17</sup>

**1.4. Hemiplegic migraine**

An often-used approach to find genes for complex genetic disorders is to study monogenic subtypes of these disorders. A monogenic subtype of migraine with aura exists and is called familial hemiplegic migraine (FHM). FHM is characterized by transient hemiparesis during the aura phase (Table 2)<sup>1</sup>, which may last from several minutes to several hours or even days. FHM patients have at least one additional first-degree family member that has identical hemiplegic migraine attacks.<sup>1</sup> FHM can be associated with additional neurological features, including cerebellar dysfunction, epilepsy and mental retardation.<sup>18-20</sup>

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A sporadic form of hemiplegic migraine does exist and is called sporadic hemiplegic migraine (SHM). These patients do not have affected family members.<sup>1</sup> The estimated population prevalence for SHM is similar to that of FHM; approximately 0.01%. The clinical symptoms of SHM patients are identical to those of FHM.<sup>21</sup> It is unknown whether FHM and SHM share biological pathways and genetic factors.

**Table 2.** *International Headache Society Criteria for Familial Hemiplegic Migraine<sup>1</sup>*

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### **Familial hemiplegic migraine**

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- A. At least two attacks fulfilling criteria B and C
  - B. Aura consisting of fully reversible motor weakness and at least one of the following;
    - 1. Fully reversible visual symptoms including positive features (e.g., flickering lights, spots, or lines) and/or negative features (i.e., loss of vision)
    - 2. Fully reversible sensory symptoms including positive features (i.e. pins and needles) and/or negative features (i.e., numbness)
    - 3. Fully reversible dysphasic speech disturbance
  - C. At least two of the following:
    - 1. At least one aura symptoms develops gradually over  $\geq 5$  minutes, and/or different aura symptoms occur in succession over  $\geq 5$  minutes
    - 2. Each symptom lasts  $\geq 5$  and  $\leq 24$  hours
    - 3. Headache fulfilling criteria B-D for migraine without aura begins during the aura or follows aura within 60 minutes
  - D. At least on first-or second-degree relative has had attacks fulfilling these criteria A-E
  - E. Not attributed to another disorder
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### **1.5. Hemiplegic migraine as a model for common migraine**

A considerable proportion of the FHM and SHM patients also has attacks of common migraine with or without aura, not associated with hemiparesis.<sup>22,18,23</sup> Furthermore, the main clinical symptoms of the headache and aura phase are similar in HM and common migraine.<sup>24</sup> Therefore, FHM is believed to be part of the migraine spectrum and is considered a suitable model to study the pathophysiology of common migraine. Thus, genes and pathways involved in HM can be considered candidate genes and pathways for the common forms of migraine.

### **1.6. Hemiplegic migraine genes**

So far, three genes have been identified in families with FHM. The first FHM gene identified is *CACNA1A* (FHM1) that is located on chromosome 19p13.<sup>25</sup> *CACNA1A* encodes the  $\alpha 1$  subunit of neuronal  $\text{Ca}_v2.1$  (P/Q-type) voltage-gated calcium channels that are widely expressed throughout the central nervous system (CNS)<sup>26</sup> and the neuromuscular junction.<sup>27</sup> FHM1 mutations are

associated with a broad spectrum of clinical features besides hemiplegic migraine.<sup>18</sup> Cerebellar ataxia<sup>28-31</sup> and epilepsy, both during severe FHM attacks<sup>32</sup> or independent of FHM attacks<sup>33,34</sup>, are not uncommon. FHM1 mutations are also identified in some sporadic patients with hemiplegic migraine.<sup>35</sup>

Mutations in the *CACNA1A* gene can also cause episodic ataxia type-2 (EA2)<sup>25</sup> and spinocerebellar ataxia type-6 (SCA6).<sup>36</sup> EA2 is characterized by recurrent episodes of ataxia often associated with vertigo and migrainous headache and can be triggered by exercise, fatigue, and stress.<sup>37</sup> Whereas FHM1 is mainly caused by missense mutations, EA2 is mostly caused by nonsense, frameshift, splice site, and sometimes missense mutations.<sup>38</sup> SCA6 resulting in late onset ataxia is characterized by atrophy of cerebellar Purkinje cells. SCA6 is a polyglutamine disorder caused by small extensions of a CAG repeat that is located in the 3'-end of the *CACNA1A* gene.

The second FHM gene, *ATP1A2* (FHM2), is located on chromosome 1q23.<sup>39</sup> It encodes the  $\alpha 2$  subunit of sodium-potassium pumps. Most of the *ATP1A2* mutations are associated with pure FHM without additional clinical symptoms.<sup>39-42</sup> However, over the years, a number of FHM2 mutations have been reported that are associated with FHM and cerebellar problems<sup>43</sup>, childhood convulsions (BFIC)<sup>19</sup>, and epilepsy.<sup>41</sup> Interestingly, certain *ATP1A2* mutations were shown to be associated with non-hemiplegic migraine phenotypes, such as basilar migraine<sup>44</sup> and even common migraine.<sup>45</sup> A specific *ATP1A2* mutation was identified in a family with atypical alternating hemiplegia of childhood (AHC)<sup>46,47</sup>, a rare brain disorder that is characterized by hemiplegia, quadriplegia and other paroxysmal phenomena, including choreoathetotic movements and nystagmus. Age at onset in AHC is typically before 18 months (but later in the AHC family with the *ATP1A2* mutation) and symptom cessation often occurs after falling asleep.<sup>48</sup>

The most recently identified FHM gene is the *SCN1A* (FHM3) gene, which is located on chromosome 2q24<sup>49</sup> and encodes the  $\alpha 1$  subunit of neuronal voltage-gated  $\text{Na}_v 1.1$  sodium channels. *SCN1A* is a well-known epilepsy gene with over 150 truncating and missense mutations that are associated with childhood epilepsy (i.e., severe myoclonic epilepsy of infancy (SMEI) or generalized epilepsy with febrile seizures (GEFS+)).<sup>50,51</sup> The fact that not all FHM families are linked to one of the three known FHM loci implies that there are additional FHM genes to be identified.

### 1.7. Monogenic and complex disorders in which migraine is prevalent

Over the past years, several biological pathways have been suggested to play a role in migraine pathophysiology. Most prevailing hypotheses suggest that migraine has a vascular, a neuronal or inflammatory origin. Interestingly, migraine patients have an increased risk (comorbidity) for several diseases in which these pathways also play a role.

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### *Vascular pathway*

A vascular component in the etiology of migraine has been debated for many years<sup>52,53</sup> and several vascular disorders show an increased prevalence of migraine. A clear example of a monogenetic vascular disorder in which migraine can be considered part of the clinical spectrum is the autosomal dominant disorder Cerebral Autosomal Dominant Arteriopathy with Subcortical Infarcts and Leukoencephalopathy (CADASIL).<sup>54</sup> CADASIL is caused by mutations in the *NOTCH3* gene, which encodes the Notch3 receptor that plays a key role in vascular smooth muscle cell function in small arteries and arterioles of the brain.<sup>55</sup> Up to one-third of CADASIL patients suffer from migraine with aura, where migraine often is the presenting clinical symptom.<sup>56</sup> Another example of a vascular monogenic disorder in which migraine is highly prevalent is Hereditary Vascular Retinopathy (HVR).<sup>57</sup> HVR is primarily characterized by progressive blindness due to vascular retinopathy and can be associated with a wide range of systemic and cerebral symptoms, including cerebral infarcts and white matter hyperintensities, vascular dementia, liver and kidney dysfunction, Raynaud's phenomenon, and migraine. Two additional North American families with similar symptoms were reported<sup>58,59</sup>, which like the Dutch HVR family were linked to the same 3p21.1-p21.3 region.<sup>60</sup> A family-based genetic association analysis between the 3p21 locus and migraine and Raynaud's phenomenon showed that the HVR locus gives a higher susceptibility for migraine and Raynaud's phenomenon in the Dutch HVR family.<sup>61</sup> Furthermore, also non-genetic vasculopathies, such as ischemic stroke and ischemic heart disease can be comorbid with migraine.<sup>62,63</sup>

### *Neuronal pathway*

Especially genetic studies in monogenic FHM showed evidence for involvement of neuronal hyperexcitability pathways in migraine.<sup>64,65</sup> Two other common brain disorders in which neuronal hyperexcitability pathways seem to play a role are epilepsy and depression. The shared neuronal hyperexcitability pathway, may well explain why both epilepsy and depression are bi-directionally comorbid with migraine.<sup>66,67</sup> The association between migraine and epilepsy is particularly evident for FHM. Epilepsy often observed in carriers of FHM gene mutations, and as mentioned earlier, the FHM3 *SCN1A* gene is also a well-known epilepsy gene. Moreover, six percent of patients with common migraine have epilepsy<sup>68</sup> and patients with epilepsy have a 2.4 times increased risk to also suffer from migraine.<sup>69</sup> Migraineurs also have increased risk for major depression; population-based odds ratios (ORs) range from 2.0 to 5.8, with strongest associations for MA.<sup>70</sup> Patients with depression have a 2.8-3.4 times increased risk for migraine.<sup>71</sup> The bi-directional comorbidity for these disorders suggests that epilepsy and depression have, at least in part, a shared etiology with migraine. This is strengthened by the fact that anti-epileptic and antidepressant drugs are effective in migraine patients.<sup>72</sup>

### *Inflammatory pathway*

During the headache phase of a migraine attack several vasoactive neuropeptides are released in the brain. It is hypothesized that these neuropeptides can cause neurogenic inflammation.<sup>73,74</sup> An example of an inflammatory disorder in which migraine is prevalent is systemic lupus erythematosus (SLE). SLE is a relapse-remitting autoimmune disorder that may affect multiple organs including the brain. About 40% of SLE patients have migraine, mostly migraine with aura.<sup>75</sup> Studying the genetics and molecular pathways of the disorders that are comorbid with migraine may provide valuable insights in molecular mechanisms involved in migraine.

### **1.8. Migraine mechanisms**

Although it was previously thought that migraine either had a vascular or a neurogenic origin, the current view is that migraine has a neurovascular origin (for review see Goadsby 2007).<sup>76</sup> Headache is not merely the consequence of painful vasodilatation, but is due to the activation of the trigeminovascular system (TGVS) that consists of meningeal and superficial cortical blood vessels that are innervated by the trigeminal nerve. The TGVS projects to the trigeminal nucleus caudalis in the brainstem, which transfers abnormal pain signals to higher order central nervous system centers giving rise to the headache. It is now well accepted that the migraine aura is not due to reactive vasoconstriction, but is neurally derived and most likely caused by the human equivalent of the cortical spreading depression (CSD) of Leao.<sup>77,78</sup> In experimental animals, CSD is characterized by a short-lasting, intense wave of neuronal and glial cell depolarization that starts in the occipital (visual) cortex and spreads slowly to frontal regions of the cortex at a rate of approximately 2-5 mm/min and that is accompanied by massive fluxes of ions ( $\text{Ca}^{2+}$ ,  $\text{Na}^+$ , and  $\text{K}^+$ ) followed by a longer-lasting inhibition of spontaneous and evoked neuronal activity (for review see Somjen 2002).<sup>79</sup> The electrophysiological changes are associated with changes in cerebral blood flow (CBF). There is a considerable body of clinical evidence that CSD is the likely basis of the migraine aura. Visual aura symptoms in humans<sup>80-82</sup> typically spread from the centre of the visual field to the periphery with a propagation rate comparable to CSD evoked in experimental animals. Positive (e.g. scintillations, paraesthesia's) and negative (e.g. scotomata, paresis) phenomena of the migraine aura can be explained by the initial transient hyperexcitation front of CSD followed by neuronal depression. Most importantly, however, functional neuroimaging studies in humans using blood-oxygen level dependent (BOLD) signals have convincingly demonstrated that CBF changes that occur during a migraine aura are very similar to those observed in experimental animals during CSD.<sup>83</sup>



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Animal studies have shown that CSD can activate the TGVS, and thus might trigger headache mechanisms.<sup>84</sup> However, the connection between CSD and headache in patients remains an open question.<sup>85,86</sup> For instance, it would not explain how the headache phase is triggered in the majority of migraine patients that never experience an aura. Also, the fact that ketamine treatment can reduce aura symptoms but fails to prevent the headache<sup>87</sup> would argue against a key role of CSD in triggering the headache. Although one can hypothesize that spreading depression may occur in these patients in clinically silent subcortical areas of the brain without propagating to the visual cortex<sup>5,88</sup>, this has never been demonstrated.

### **1.9. Functional consequences of FHM mutations**

#### *Functional effects of FHM1 mutations on $Ca_v2.1$ $Ca^{2+}$ channels*

Electrophysiological methods have been used to study the effect of FHM1 mutations on calcium channel functioning. Multiple aspects of the calcium channel are of importance for its function: expression of the channel, localization on the cell membrane, conductance of the channel, voltage-dependence of opening, closing and reopening, and duration of the open state. For electrophysiological studies of FHM1 mutations, heterologous expression systems (without endogenous expression of  $Ca_v2.1-\alpha_{1A}$ ) were transfected with recombinant  $Ca_v2.1$  channel components. Calcium channel parameters were measured using whole cell or single channel electrophysiology to assess the consequence of FHM1 mutations on the cellular level (i.e., the combined effect of all  $Ca_v2.1$  channels at the plasma membrane) or on the single channel, respectively (for review see Pietrobon 2007). At the single channel level, FHM1 mutations open at more negative voltages and have an enhanced channel open probability, compared to wild-type channels.<sup>90-92</sup> This *gain-of-function* consequence FHM1 mutations results in increased neuronal  $Ca^{2+}$  influx, which would predict increased neurotransmission. At the whole cell level, however, neurons from  $Ca_v2.1-\alpha_{1A}$  knockout mice<sup>93,94</sup> that were transfected with either wild-type or mutant  $Ca_v2.1-\alpha_{1A}$  cDNA constructs, all seem to indicate a *loss-of-function* effect of FHM1 mutations.<sup>90-92,96</sup> Hippocampal neurons derived from  $Ca_v2.1-\alpha_{1A}$  knockout mice, that were transfected with wild-type or mutant  $Ca_v2.1-\alpha_{1A}$  cDNA constructs revealed a reduced neurotransmitter release and a decreased contribution of P/Q-type channels controlling neurotransmitter release.<sup>95,96</sup>

#### *Functional effects of FHM2 mutations on Na,K ATPases*

The functional consequences of *ATP1A2* mutations have been investigated by using various in vitro assays. The cell survival assay is a frequently used functional test that gives an indication of disease causality of *ATP1A2* mutations.  $Na^+,K^+$ -ATPase activity is necessary for cell survival. In the cell survival assay, endogenous sodium potassium pumps are inactivated by application of the drug ouabain to HeLa cells that express either wild-type or mutant  $\alpha 2$   $Na^+,K^+$ -ATPase cDNAs that are made insensitive to ouabain.<sup>97</sup> The assay tests whether transfected wild-type

or mutant  $\alpha 2$  Na<sup>+</sup>,K<sup>+</sup>-ATPase cDNAs are able to rescue cell survival. Several *ATP1A2* mutations are tested using this cell survival assay and many showed mutations that have an effect on cell survival. For a few *ATP1A2* mutations, Segall and colleagues studied additional parameters, such as catalytic turnover, extracellular K<sup>+</sup> affinity and Na<sup>+</sup>,K<sup>+</sup> ATPase kinetics.<sup>98,99</sup> These studies showed that certain mutations, such as FHM2 mutation T345A, that were fully functional in the cell survival assay, could show an effect on other parameters.

#### *Functional effects of FHM3 mutations on sodium channels*

Similar to functional studies for FHM1 mutations, electrophysiological methods were used to determine the functional effect of the first FHM3 mutation. FHM3 mutation p.Gln1489Lys was cloned into the highly homologous heart-specific *SCN5A* cDNA due to apparent cloning difficulties with the brain-specific *SCN1A* cDNA. Wild-type or mutant *SCN5A* cDNA was transfected into human tsA201 cells.<sup>49</sup> Electrophysiological measurements (whole cell recordings) revealed a 2-4-fold accelerated recovery from fast inactivation for mutant Na<sub>v</sub>1.5 sodium channels compared to wild-type<sup>49</sup>, indicating increased firing capacity of the mutant neuron.

### **1.10. Common pathway and increased neurotransmission**

The three FHM genes fit in a common neuronal pathway. Mutations in all three FHM genes affect the transport of ions and lead to increased levels of glutamate and K<sup>+</sup> ions in the synaptic cleft. This may lead to an increased susceptibility for CSD.<sup>79</sup> Increased susceptibility for CSD could well explain the aura phase of migraine attacks. Another gene that would perfectly fit this neuronal pathway is the *SLC1A3* gene, encoding EAAT1 the excitatory amino acid transporter type 1. EAAT1 is involved in glutamate removal from the synaptic cleft.<sup>100,101</sup> Mutations in EAAT1 could, like the known FHM mutations, affect the glutamate levels in the synaptic cleft.

Several additional observations point at a potentially pivotal role of enhanced brain glutamate levels in the triggering of migraine attacks. For instance, (i) glutamate receptor antagonists may have acute anti-migraine activity<sup>102</sup>; (ii) noxious dural stimulation, as an experimental animal model for acute migraine, increases glutamate release from trigeminal ganglion neurons<sup>103</sup>; (iii) plasma<sup>104</sup> and cerebrospinal fluid<sup>105</sup> levels of glutamate are increased in migraineurs with and without aura in between attacks, further rising during attacks.

### **1.11. Migraine mouse models**

#### *Natural mouse mutants*

Different natural mouse mutants with mutations in the *Cacna1a* gene exist, such as *Tottering*, *Leaner*, *Rolling Nagoya* and *Rocker*.<sup>106-109</sup> Missense *Cacna1a* mutations are present in the *Tottering*, *Rolling Nagoya* and *Rocker* mutants (i.e., P601L, R1262G and T1310K, respectively).<sup>106,110,111</sup>

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The *Leaner* mutant has a rather complex *Cacna1a* mutation leading to exon skipping and the inclusion of intronic sequences in the aberrantly spliced *Cacna1a* gene.<sup>112</sup> These natural mouse mutants all exhibit some degree of ataxia, and except for *Rocker*, several seizure types are also present. Furthermore, dyskinesia and dystonia are part of the phenotype of *Tottering* and *Leaner*, respectively.<sup>113,107</sup>

### *Transgenic mouse models*

*Cacna1a*-deficient knock-out mice ( $\alpha_{1A}^{-/-}$ ) that do not express  $Ca_v2.1$   $Ca^{2+}$  channels initially appear healthy. However, at approximately 10 days after birth, these mice develop a rapidly progressive neurological deficit with specific characteristics of ataxia and dystonia, and after 3-4 weeks after birth they die.<sup>93,94</sup> These knock-out mice are perhaps not very useful to study migraine for several reasons: i) whereas neurotransmission in the NMJ in heterozygous seems unaffected<sup>114</sup>, the homozygous mice have a lethal phenotype very different from migraine, ii) the knockout mutation is a *loss-of-function* mutation, unlike FHM1 mutations that are considered *gain-of-function mutations*.<sup>89</sup> Therefore, it seems more appropriate to study migraine pathophysiology using knock-in migraine mouse models that carry human pathogenic FHM1 mutations.

Two transgenic knock-in (KI) mouse models harbouring either the R192Q or the S218L FHM1 mutation were generated by introducing the respective mutation into the orthologous *Cacna1a* gene by homologous recombination.<sup>115,116</sup> These mutations were previously identified in FHM1 patients.<sup>25,117</sup> Whereas the R192Q mutation causes a relatively mild form of FHM, the S218L mutation is associated with a more severe form of FHM with additional neurological features (i.e., cerebellar ataxia, epilepsy and brain edema after mild head trauma). Interestingly, S218L KI mice show a complex phenotype that is very similar to that observed in S218L patients, whereas R192Q KI mice show no overt phenotype. These migraine mice models are considered valuable models to study migraine pathophysiology.

### 1.12. Scope and outline of the thesis

Identification and characterization of migraine susceptibility genes and pathways that are involved in the disease mechanisms are very important for understanding the pathophysiology of migraine. It may also give new insights that can be useful for drug development and treatment of migraine. Studies in this thesis focus on genetic factors and molecular pathways involved in FHM, SHM, other monogenic diseases in which migraine is prevalent, as well as the common forms of migraine. As HM is considered a suitable model for the common forms of migraine, the identification of mutations in FHM genes and investigating their functional consequences is also relevant to increase insights in the genetic and molecular background of the common forms of migraine. At the start of the thesis, three FHM genes had been identified: *CACNA1A*, *ATP1A2* and *SCN1A*.

In **Chapter 2**, several mutations in the three known FHM genes are presented with a functional characterisation using cellular assays or electrophysiological studies in cell systems. The mutations are associated with a broad spectrum of clinical symptoms, ranging from FHM and epilepsy to atypical AHC.

In **Chapter 3**, the involvement of the FHM genes in 39 sporadic patients with HM is studied. Although SHM patients are clinical indistinguishable from FHM patients, it has not been extensively studied whether FHM genes may play a major role in this form of hemiplegic migraine. The mutation scan resulted in the identification of several novel DNA variants. For all variants, functional studies were performed.

**Chapter 4** describes the involvement of the excitatory amino acid transporter EAAT1 in EA2 patients that were negative for mutations in the *CACNA1A* gene. EAAT1 fits the same cortical glutamate-related pathway of the three known FHM gene products. Previously, a mutation in this gene had been identified in a patient with a particularly severe clinical phenotype that included episodic ataxia and hemiplegic attacks. A novel EAAT1 mutation is identified in a EA2 patient and associated clinical and functional characteristics are described.

Previously, a Dutch family with a vascular monogenic disorder; Hereditary Vascular Retinopathy (HVR), was together with two additional North American families with similar symptoms linked to chromosome 3p21. In **Chapter 5.1**, the *TREX1* gene is identified as the causative gene in these three families. Retinal Vasculopathy with Cerebral Leukodystrophy (RVCL) is the novel name for this vascular disorder with autosomal dominant inheritance, that is characterized by progressive blindness due to vascular retinopathy that can be associated with a wide range

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of clinical symptoms, including migraine. *TREX1* mutations are also identified in several other vascular and immune-related disorders, including Systemic Lupus Erythematosis (SLE). **Chapter 5.2** describes the first *TREX1* mutation in a patient with *neuropsychiatric* SLE (NPSLE).

The rapid development of high-throughput genotyping during the last years made genome-wide association studies (GWAS) a feasible and attractive method to identify genetic factors for genetically complex disorders, such as migraine. Large clinic-based migraine cohorts from various European headache clinics (**Chapter 6.1**) and population-based cohorts from the Dutch Icelandic (DICE) consortium (**Chapter 6.2**) were used for these GWA studies. The most significantly associated SNP in the clinic-based migraine GWAS was tested in several independent MA and MO replication cohorts encompassing a total amount of over 3,000 migraine patients. For the population-based study first a GWAS was performed in a large genetically isolated population from the south of the Netherlands (ERF) that was followed by meta-analysis of GWAS data from five additional cohorts.

The identification of FHM genes gave the opportunity to generate transgenic mouse models. Two *Cacna1a* knock-in migraine mouse models with specific FHM1 mutations (i.e. S218L and R192Q) were generated. These knock-in mice are considered useful tools to study migraine. In **Chapter 7**, we study the RNA expression profiles of cerebellum and occipital cortex of FHM1 knock-in mice under basal (i.e. un-triggered) conditions, to investigate whether and to which extent neurobiological differences in these migraine mice were regulated at the gene expression level.

**Chapter 8** provides a general discussion of the thesis, reviewing the results and discussing future possibilities for research in migraine genetics.

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