Screening for Familial \textit{APP} Mutations in Sporadic Cerebral Amyloid Angiopathy

Alessandro Biffi\textsuperscript{1,2,3}, Anna Plourde\textsuperscript{1,2,3}, Yiping Shen\textsuperscript{1}, Robert Onofrio\textsuperscript{3}, Eric E. Smith\textsuperscript{4}, Matthew Frosch\textsuperscript{5}, Claudia M. Prada\textsuperscript{5}, James Gusella\textsuperscript{1,3}, Steven M. Greenberg\textsuperscript{2}, Jonathan Rosand\textsuperscript{1,2,3,*}

\textsuperscript{1}Center for Human Genetic Research, Massachusetts General Hospital, Boston, Massachusetts, United States of America, \textsuperscript{2}Hemorrhagic Stroke Research Group, Massachusetts General Hospital, Boston, Massachusetts, United States of America, \textsuperscript{3}Program in Medical and Population Genetics, Broad Institute of MIT and Harvard, Cambridge, Massachusetts, United States of America, \textsuperscript{4}Department of Clinical Neurosciences, University of Calgary, Calgary, Alberta, Canada, \textsuperscript{5}Massachusetts General Hospital Institute for Neurodegenerative Disease, Massachusetts General Hospital, Boston, Massachusetts, United States of America

Abstract

\textbf{Background:} Advances in genetic technology have revealed that variation in the same gene can cause both rare familial and common sporadic forms of the same disease. Cerebral amyloid angiopathy (CAA), a common cause of symptomatic intracerebral hemorrhage (ICH) in the elderly, can also occur in families in an autosomal dominant pattern. The majority of affected families harbor mutations in the Beta amyloid Peptide (A\textbeta) coding region of the gene for amyloid precursor protein (\textit{APP}) or have duplications of chromosomal segments containing \textit{APP}.

\textbf{Methodology/Principal Findings:} A total of 58 subjects with a diagnosis of probable or definite CAA according to validated criteria were included in the present study. We sequenced the \textit{A\textbeta} coding region of \textit{APP} in 58 individuals and performed multiplex ligation-dependent probe amplification to determine \textit{APP} gene dosage in 60. No patient harbored a known or novel \textit{APP} mutation or gene duplication. The frequency of mutations investigated in the present study is estimated to range from 0% to 8% in individuals with probable CAA in the general population, based on the ascertained sample size.

\textbf{Conclusions/Significance:} We found no evidence that variants at loci associated with familial CAA play a role in sporadic CAA. Based on our findings, these rare highly-penetrant mutations are unlikely to be seen in sporadic CAA patients. Therefore, our results do not support systematic genetic screening of CAA patients who lack a strong family history of hemorrhage or dementia.


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* E-mail: jrosand@partners.org

Introduction

Recent advances in genetic technology have clarified that variation in the same gene can cause both familial (usually more severe and/or earlier onset) and sporadic forms of the same disease. For example, rare highly penetrant sequence variants in several genes (\textit{HNF4A}, \textit{GCK}, \textit{TCF1}/\textit{HNF1A}, \textit{TCP2}/\textit{HNF1B}) invariably cause a monogenic disorder known as maturity-onset diabetes of the young (MODY), while common less penetrant variants in the same genes are risk factors for multifactorial type 2 diabetes. [1] Similarly, rare and common sequence variants within the \textit{ABCC8} gene have been associated with monogenic disorders (congenital hyperinsulinism of infancy), as well as sporadic type 2 diabetes. [2,3]

The effect of more common variants is generally much less potent than that of rare variants, and as a result, for example, not all carriers of \textit{ABCC8} variants develop diabetes. However, clustering of common and rare disease-causing variants in a single gene provides additional insight into pathophysiology, and may prove crucial for individual risk prediction.

Cerebral amyloid angiopathy (CAA) is characterized by \textbeta-amyloid peptide (A\textbeta) deposition and destruction of the vessel walls of capillaries, arterioles and small- and medium-sized arteries of the cerebral cortex, leptomeninges and cerebellum. In its sporadic form CAA is a common cause of intracerebral hemorrhage (ICH), [4] MRI-detected white matter hyperintensity (WMH) and cognitive dysfunction. [5,6] Vascular amyloid, like the amyloid plaques in Alzheimer disease (AD), is composed chiefly of a 39- to 43- amino acid proteolytic fragment of the \textbeta-amyloid precursor protein (\textit{APP}). A large body of data links the \textit{e2} and \textit{e4} alleles of \textit{APOE} to CAA susceptibility. [7] Epidemiological data, however, point to an even larger role for genetic variation as a risk factor for CAA, suggesting that there are other loci in the genome that modulate risk. [8]

In addition to occurring as a spontaneous condition in the elderly, CAA also manifests as a rare familial syndrome in which manifestations generally develop earlier in life. Most familial forms of CAA involve mutations within \textit{APP}, [8–14], and present with vascular deposition of A\textbeta causing a clinical phenotype akin to...
sporadic CAA, including either ICH or dementia as the primary clinical features. Besides the easily identifiable family inheritance pattern, familial CAA can be differentiated from sporadic CAA because of the average earlier age of onset (<55 years) and greater severity. All known APP mutations associated with CAA cluster within the β-coding region of the gene (exons 16 and 17). [6] In addition to point mutations within APP, duplication of the APP locus on chromosome 21 has also been identified in families with familial early-onset AD and CAA. [15] Functional studies have clarified that these mutations within APP result in altered β-amyloid biological properties and subsequent deposition, much like in sporadic CAA.

Motivated by the close phenotypic and biological overlap between sporadic and familial CAA, we investigated whether any of the established rare variants or novel variants in the same protein region of APP might contribute to susceptibility to sporadic CAA.

**Methods**

**Ethics Statement**

The Institutional Review Board of the Massachusetts General Hospital approved all aspects of this study, and written informed consent for participation in the present study was obtained from all participating subjects or their surrogates.

**Patients**

Subjects consisted of patients referred to Massachusetts General Hospital over an eleven year period who qualified for the diagnosis of probable or definite CAA according to the Boston Criteria. [4] Application of these criteria allows for reliable diagnosis of CAA in living subjects in the absence of cortical biopsy specimens, using clinical and neuroimaging data to assign patients to different groups, based on the likelihood of CAA pathology being present (Table 1).

**Sequencing of APP Exons 16 & 17**

Exons 16 and 17 of APP were amplified using a standard polymerase chain reaction (PCR) protocol. SNP detection was performed automatically with the SNP Compare analysis suite (Broad Institute of MIT and Harvard), which collates and compares SNP calls from two SNP calling algorithms, PolyDHAN and PolyPhred. [16] The quality of a given SNP is scored based on its detectability in each sequencing direction (forward and reverse) as determined by each SNP calling algorithm, as well as its estimated false positive rate. SNP Compare estimates false positive rates for detected variants using data derived from the International HapMap Consortium’s ENCODE resequencing efforts. [17]

**Copy Number Assessment**

We used multiplex ligation-dependent probe amplification (MLPA) (MRC Holland, Amsterdam, Holland) to assess for the presence of duplication of APP. Genomic DNA from ten unaffected individuals and one individual with trisomy-21 were included as negative and positive controls, respectively. Four synthetic paired probes for APP exons and four paired probes specific for genes flanking the APP locus were designed. Additional MLPA probes targeting sequences on chromosomes other than chromosome 21 were included as internal controls. All APP paired probe ligation sites were located in the coding regions of the gene. Probes for regions flanking APP were designed to detect duplications in genes previously found to show copy number variation in individuals with autosomal-dominant early-onset Alzheimer Disease with CAA. [15]

**Statistical Analyses**

Novel variants and/or duplication of the APP locus in sequenced patients were used to infer the probability of identical findings in the general population of sporadic CAA patients by computing exact confidence limits for binomial proportions based on available sample size [18]. Findings from our study were compared to the theoretical binomial distribution (any APP mutation vs. no APP mutation) in the general population the study subjects were sampled from, i.e. sporadic CAA patients diagnosed according to the Boston criteria.

**Results**

Of the 58 subjects (Table 2), 35 met criteria for probable CAA on radiographic and clinical criteria alone, while CAA was pathologically confirmed in 23 individuals (6 from autopsy reports and 17 from pathology reports from biopsy-obtained tissue). MRI data for CAA diagnosis was available for 32 (55%) subjects. Of all enrolled subjects, 13 (22%) had a single ICH before the event qualifying them for enrollment, while 2 (2%) had an history of multiple intracerebral bleeds. Five patients (9%) were being

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**Table 1. Boston criteria for CAA diagnosis.**

<table>
<thead>
<tr>
<th>Criteria</th>
<th>Clinical Data and/or Pathological Data</th>
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<tbody>
<tr>
<td>1. Definite CAA</td>
<td>Full postmortem examination demonstrating:</td>
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<td>• Lobar, cortical, or corticosubcortical hemorrhage</td>
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<td>• Severe CAA with vasculopathy*</td>
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<td>• Absence of other diagnostic lesion</td>
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<td>2. Probable CAA with supporting pathology</td>
<td>Clinical data and pathologic tissue (evacuated hematoma or cortical biopsy) demonstrating:</td>
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<tr>
<td></td>
<td>• Lobar, cortical, or corticosubcortical hemorrhage</td>
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<td></td>
<td>• Some degree of CAA in specimen</td>
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<tr>
<td></td>
<td>• Absence of other diagnostic lesion</td>
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<tr>
<td>3. Probable CAA</td>
<td>Clinical data and MRI or CT demonstrating:</td>
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<tr>
<td></td>
<td>• Multiple hemorrhages restricted to lobar, cortical, or corticosubcortical regions (cerebellar hemorrhage allowed)</td>
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<td>• Age ≥55 years</td>
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<tr>
<td></td>
<td>• Absence of other cause of hemorrhage†</td>
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<tr>
<td>4. Possible CAA</td>
<td>Clinical data and MRI or CT demonstrating:</td>
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<tr>
<td></td>
<td>• Single lobar, cortical, or corticosubcortical hemorrhage</td>
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<tr>
<td></td>
<td>• Age ≥55 years</td>
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<tr>
<td></td>
<td>• Absence of other cause of hemorrhage†</td>
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</table>

*As defined in reference 20. †Other causes of intracerebral hemorrhage include: • excessive warfarin dosing (INR >3.0) • antecedent head trauma or ischemic stroke • CNS tumor • vascular malformation • CNS vasculitis • blood dyscrasia • coagulopathy. Note: INR >3.0 or other nonspecific laboratory abnormalities permitted for diagnosis of possible CAA.

**Motivated by the close phenotypic and biological overlap between sporadic and familial CAA, we investigated whether any of the established rare variants or novel variants in the same protein region of APP might contribute to susceptibility to sporadic CAA.**
References


