



FACULDADE DE MEDICINA

PROGRAMA DE PÓS-GRADUAÇÃO EM MEDICINA:

CIÊNCIAS MÉDICAS

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**BIOMARCADORES LIQUÓRICOS COMO PREDITORES DE CONVERSÃO DO
COMPROMETIMENTO COGNITIVO LEVE AMNÉSICO À DEMÊNCIA DA
DOENÇA DE ALZHEIMER**

PORTO ALEGRE

2019

TESE DE DOUTORADO

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DOENÇA DE ALZHEIMER**

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Tese apresentada como requisito parcial para obtenção do título de Doutora em Medicina: Ciências Médicas, da Universidade Federal do Rio Grande do Sul, Programa de Pós-Graduação em Medicina: Ciências Médicas.

PORTO ALEGRE

2019

CIP - Catalogação na Publicação

Rizzi, Liara
BIOMARCADORES LIQUÓRICOS COMO PREDITORES DE
CONVERSÃO DO COMPROMETIMENTO COGNITIVO LEVE AMNÉSTICO
À DEMÊNCIA DA DOENÇA DE ALZHEIMER / Liara Rizzi. --
2019.
131 f.
Orientador: Matheus Roriz Silva Cruz.

Tese (Doutorado) -- Universidade Federal do Rio
Grande do Sul, Faculdade de Medicina, Programa de
Pós-Graduação em Medicina: Ciências Médicas, Porto
Alegre, BR-RS, 2019.

1. Doença de Alzheimer. 2. Comprometimento
Cognitivo Leve amnésico. 3. Biomarcadores liquóricos.
4. Proteína Beta-amilóide. 5. Proteína Tau. I. Cruz,
Matheus Roriz Silva, orient. II. Título.

AGRADECIMENTOS

Agradeço primeiramente à minha família, por ser o meu suporte e a minha força. Agradeço aos meus pais e as minhas irmãs que, mesmo estando fisicamente distantes, nunca deixaram de me apoiar, incentivar, amar e compartilhar comigo de todas as situações. Amo vocês!

Também agradeço ao meu orientador por ter confiado em mim e no nosso trabalho e por ter propiciado meios para que ele se realizasse. Aos colegas e amigos do Grupo de pesquisas em Neurogeriatria, pelo incentivo e pela torcida a cada conquista.

Gratidão à Universidade Federal do Rio Grande do Sul pelo acolhimento de tantos anos. Ao Programa de Pós-Graduação em Medicina: Ciências Médicas e ao Hospital de Clínicas de Porto Alegre pela oportunidade de desenvolver esse projeto.

À CAPES/CNPq e ao FIPE pelo incentivo financeiro.

À todos que de alguma forma auxiliaram para a realização desta tese e que contribuíram para a minha formação.

Muito Obrigada.

*“O navio está seguro quando está no porto, mas
não é para isso que se fazem navios”*

William Shedd

RESUMO

Introdução: A Doença de Alzheimer é uma desordem neurodegenerativa caracterizada pela formação de placas amilóides e emaranhados neurofibrilares. A correta identificação de indivíduos com risco de progressão para a demência da Doença de Alzheimer (DDA) é crucial em termos de diagnóstico precoce, prognóstico e tratamento. As concentrações líquóricas das proteínas $A\beta_{1-42}$ e p-Tau₁₈₁ são os biomarcadores mais promissores para o diagnóstico da patologia e podem ser identificados precocemente no *continuum* da doença. Indivíduos com Comprometimento cognitivo leve amnésico (CCL-a) possuem um alto risco de progressão para a DDA. Dessa forma, pesquisas longitudinais com indivíduos com CCL-a representam uma oportunidade para investigar os processos biológicos subjacentes (amiloidose e neurodegeneração) e prever o potencial risco de progressão para a DDA.

Objetivo: Mensurar os biomarcadores líquóricos $A\beta_{1-42}$ e p-Tau₁₈₁ em indivíduos com Comprometimento Cognitivo Leve amnésico e verificar suas capacidades preditivas para a fase demencial da Doença de Alzheimer em um estudo longitudinal.

Métodos: Quarenta e dois indivíduos diagnosticados com comprometimento cognitivo leve amnésico ou comprometimento cognitivo subjetivo foram avaliados em 2013 e reavaliados em 2018. Os níveis de $A\beta_{1-42}$ e p-Tau₁₈₁ no líquido cefalorraquidiano foram mensurados por ensaio imunoenzimático e os pontos de corte foram calculados pelo teste de Youden. Além disso, foram realizados testes neuropsicológicos, como o CERADs e o MoCA.

Resultados: 45,2% dos indivíduos com CCL-a progrediram para a DDA em cinco anos. O risco relativo de progressão para indivíduos com CCL-a e $A\beta_{1-42} < 618,5$ pg/mL foi 5,8 vezes maior do que naqueles cujos níveis foram superiores a esse ponto de corte ($P = 0,0011$). E o risco naqueles cuja razão p-Tau₁₈₁/ $A\beta_{1-42}$ foi maior de 0,135 foi 3,83 vezes maior ($P = 0,0001$). Os

níveis líquóricos de $A\beta_{1-42}$ e p-Tau₁₈₁ explicaram 47,5% da variância do Δ CERADs ($P < 0,001$), enquanto os níveis da proteína $A\beta_{1-42}$ isoladamente explicaram 38,6% ($P < 0,001$).

Conclusões: Nesse estudo, a proteína $A\beta_{1-42}$ mensurada no líquido proporcionou o melhor risco cumulativo de progressão do CCL-a para a DDA em cinco anos. A razão p-Tau₁₈₁/ $A\beta_{1-42}$ não foi melhor que a proteína $A\beta_{1-42}$ isolada na predição da progressão do CCL-a para a DDA. No entanto, os níveis de p-Tau₁₈₁ ajudaram a explicar um extra de 9% da variância do Δ CERADs em cinco anos.

Palavras-chave: Doença de Alzheimer; Comprometimento Cognitivo Leve amnésico, biomarcadores líquóricos; proteína beta-amilóide; proteína Tau.

ABSTRACT

Introduction: Alzheimer's disease (AD) is a neurodegenerative disorder characterized by the formation of amyloid plaques and neurofibrillary tangles. The correct identification of individuals at risk for developing Alzheimer's disease dementia (ADD) is of utmost importance for its early diagnosis and treatment, and for improving prognosis. Cerebrospinal fluid concentrations of $A\beta_{1-42}$ and p-Tau₁₈₁ proteins are the most promising biomarkers for the detection of AD, and may be identified early in its clinical *continuum*. Individuals with amnesic mild cognitive impairment (aMCI) are at high risk for developing ADD. Therefore, longitudinal studies with individuals diagnosed with aMCI provide an opportunity to investigate the underlying biological processes (amyloidosis and neurodegeneration) and predict the potential risk of progression to ADD.

Objective: To measure the cerebrospinal fluid biomarkers $A\beta_{1-42}$ and p-Tau₁₈₁ in individuals with aMCI and to verify whether these biomarkers are able to predict progression to the stage of dementia in Alzheimer's disease via a longitudinal study.

Methods: Forty-two patients diagnosed with aMCI or subjective cognitive decline were evaluated in 2013 and re-evaluated in 2018. $A\beta_{1-42}$ and p-Tau₁₈₁ levels in their cerebrospinal fluid were measured via an immunoenzymatic assay and cutoff points were calculated with the Youden test. Moreover, neuropsychological testing, such as the CERADs and MoCA, was performed.

Results: 45,2% of individuals diagnosed with aMCI progressed to ADD in five years. The relative risk of progression in patients diagnosed with aMCI and with $A\beta_{1-42}$ concentrations of $<618,5$ pg/mL was 5.8 times greater than that of patients with higher $A\beta_{1-42}$ concentrations ($P = 0,0011$). Those with a p-Tau₁₈₁/ $A\beta_{1-42}$ ratio above 0.135 were 3.83 times at risk of disease progression ($P = 0,0001$). Cerebrospinal fluid concentrations of $A\beta_{1-42}$ and p-Tau₁₈₁ explained

47.5% of the variance observed in the Δ CERADs ($P < 0,001$), whereas the $A\beta_{1-42}$ protein on its own was able to explain 38.6% ($P < 0,001$).

Conclusions: We hereby demonstrate that $A\beta_{1-42}$ cerebrospinal fluid protein concentration was the best measure for establishing the relative risk of evolving from aMCI to ADD in five years. The p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was not superior to isolated $A\beta_{1-42}$ protein concentration in predicting progression from aMCI to ADD. Nonetheless, p-Tau₁₈₁ protein concentrations aided in accounting for an extra 9% of the variance in Δ CERADs in five years.

Keywords: Alzheimer's disease; amnesic mild cognitive impairment; cerebrospinal fluid biomarkers; beta-amyloid protein; Tau protein.

AD: Alzheimer's disease

ADD: Alzheimer's disease dementia

aMCI: amnesic Mild Cognitive Impairment

APOE: Apolipoproteína E

APP: Amyloid Precursor Protein - Proteína Precursora Amilóide

AUC: Area Under the Curve

BACE1: enzima β -secretase

BNT: Boston Naming Test

CCL: Comprometimento Cognitivo Leve

CCL-a: Comprometimento Cognitivo Leve amnésico

CCI-na: Comprometimento Cognitivo Leve não-amnésico

CDR: Clinical Dementia Rating

CDT: Clock Drawing Test

CERADs: Consortium to Establish a Registry for Alzheimer's Disease subscore

CP: Constructional Praxis

CSF: Cerebrospinal Fluid

DA: Doença de Alzheimer

DSM-5: Manual Diagnóstico e Estatístico de Transtornos Mentais - 5ª edição

ELISA: Enzyme-Linked Immunosorbent Assay

GDS: Geriatric Depression Scale

MCI: Mild Cognitive Impairment

MMSE: Mini-Mental State Examination

MoCA: Montreal Cognitive Assessment

NIA-AA: National Institute on Aging and Alzheimer's Association

P1: Presenilina 1

P2: Presenilina 2

PET: Positron Emission Tomography

ROC: Receiver Operating Characteristic Curve

SCI: Subjective Cognitive Impairment

SPSS: Statistical Package for the Social Sciences

VFT: Verbal Fluency Test

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APRESENTAÇÃO

Esta tese está estruturada em seis capítulos

Capítulo I – Introdução

Capítulo II – Revisão Sistematizada da Literatura

Capítulo III – Justificativa, Mapa Conceitual e Objetivos

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Capítulo IV – Artigos Científicos Originais em Inglês

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CAPÍTULO I – INTRODUÇÃO

A Doença de Alzheimer (DA) é uma patologia neurodegenerativa progressiva que causa grave comprometimento cognitivo(1, 2). Dentre as doenças mais prevalentes, é uma das que

não possuem prevenção efetiva ou tratamento eficaz(3). Possui uma complexa e heterogênea fisiopatologia e é caracterizada pelo declínio insidioso e irreversível de funções cognitivas, tais como: memória, atenção, linguagem, percepção e funções executivas. O processo patológico costuma evoluir de forma lenta e a sobrevida média após o diagnóstico é curta(4).

Caracteriza-se pela presença de placas de proteína β -amilóide e emaranhados neurofibrilares de proteína *Tau* hiperfosforilada, além de processos oxidativos e inflamatórios no cérebro(5). As alterações patológicas se iniciam muitos anos antes dos primeiros sintomas clínicos(6). A ausência de terapias efetivas instiga a compreensão da fisiopatologia da doença e a busca de novos meios diagnósticos. Um dos aspectos mais importantes da pesquisa na DA é a descoberta de biomarcadores confiáveis que possam auxiliar a estabelecer o curso clínico e o prognóstico da doença(7).

Estudos têm se concentrado principalmente na correta identificação de indivíduos com comprometimento cognitivo leve (CCL), pelo fato desse estágio estar na transição entre a cognição normal e a demência(8, 9). Além disso, pesquisas demonstraram que indivíduos com CCL, especialmente do subtipo amnésico (CCL-a), têm um risco aumentado de desenvolver a DA(10-12). Esta entidade nem sempre é facilmente distinguível de casos verdadeiramente pré-demenciais. Neste sentido, o desenvolvimento de biomarcadores e métodos confiáveis capazes de identificar o declínio ou a estabilidade cognitiva em pessoas com CCL-a são importantes. Além disso, os biomarcadores podem contribuir tanto para a correta identificação de indivíduos prodrômicos à DA, quanto para a diferenciação de outras causas de CCL(13). Com base no conhecimento atual, quanto mais previamente a DA for diagnosticada, maiores são as chances de um melhor prognóstico(14, 15).

A nova estrutura de pesquisa, proposta pelo *National Institute on Aging and Alzheimer's Association* (NIA-AA), definiu que os processos patológicos subjacentes à DA podem ser

reconhecidos por exame *post-mortem* ou *in vivo* por meio dos biomarcadores(16). Há evidências de que a quantificação das proteínas envolvidas com o processo patológico, $A\beta_{1-42}$ e p-Tau₁₈₁, possa se tornar um importante instrumento de apoio ao diagnóstico da DA prodrômica(16). Essas proteínas podem atuar como verdadeiros biomarcadores, visto que podem ser detectadas no líquido cefalorraquidiano antes da emergência da sintomatologia clínica da DA(17). Então, a partir deste racional, este estudo foi proposto com o objetivo de verificar a predição dos biomarcadores liquóricos $A\beta_{1-42}$ e p-Tau₁₈₁ na progressão do CCL-a para o estágio demencial da DA.

A estrutura da apresentação desta tese seguiu as normas do Programa de Pós Graduação em Medicina: Ciências Médicas da Faculdade de Medicina da Universidade Federal do Rio Grande do Sul (UFRGS). A formatação dos artigos foi realizada de acordo com as normas dos periódicos aos quais foram ou serão submetidos.

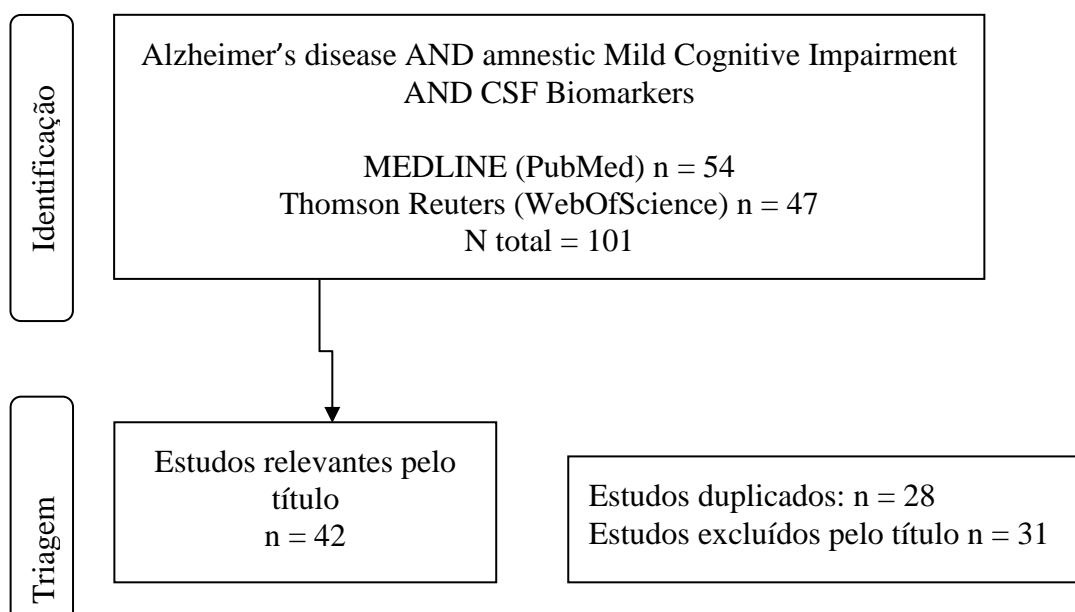
CAPÍTULO II – REVISÃO SISTEMATIZADA DA LITERATURA

1. Estratégias para localizar e selecionar informações

Para a apresentação dos aspectos epidemiológicos, conceituais, fisiológicos e sustentar as conclusões obtidas nesta tese, buscou-se suporte em artigos originais, artigos de revisão e meta-

análises. A revisão sistematizada da literatura foi realizada enfatizando-se os aspectos da DA e dos biomarcadores líquóricos $A\beta_{1-42}$ e p-Tau₁₈₁. As informações foram selecionadas nas bases de dados MEDLINE (PubMed) e Thomson Reuters (WebOfScience) através de combinações dos seguintes descritores: ‘*Alzheimer’s disease*’, ‘*amnestic Mild Cognitive Impairment*’ e ‘*CSF Biomarkers*’. Foram selecionadas publicações dos últimos cinco anos e não foi feita restrição de idioma. As referências dos artigos escolhidos e utilizados foram revisadas de modo a encontrar outras não contempladas na busca. Portanto, alguns estudos comumente referenciados e conceituadas publicações mais antigas foram posteriormente incluídas na revisão.

O critério de inclusão foram estudos que envolveram a relação dos biomarcadores líquóricos $A\beta_{1-42}$ e p-Tau₁₈₁ na predição da progressão do comprometimento cognitivo leve para a demência da Doença de Alzheimer. O diagrama de fluxo a seguir mostra os resultados obtidos na busca sistematizada. Foram encontrados inicialmente 101 estudos publicados nos últimos cinco anos. Desses, 59 foram excluídos (primeira exclusão) após rastreio por duplicações e leitura de títulos. Todos os restantes 42 artigos tiveram seus resumos cuidadosamente lidos. Dos quais, 13 foram excluídos (segunda exclusão) devido aos critérios de elegibilidade. Todos os 29 artigos restantes foram totalmente lidos e 21 foram finalmente incluídos na revisão sistematizada final e/ou nos artigos científicos.



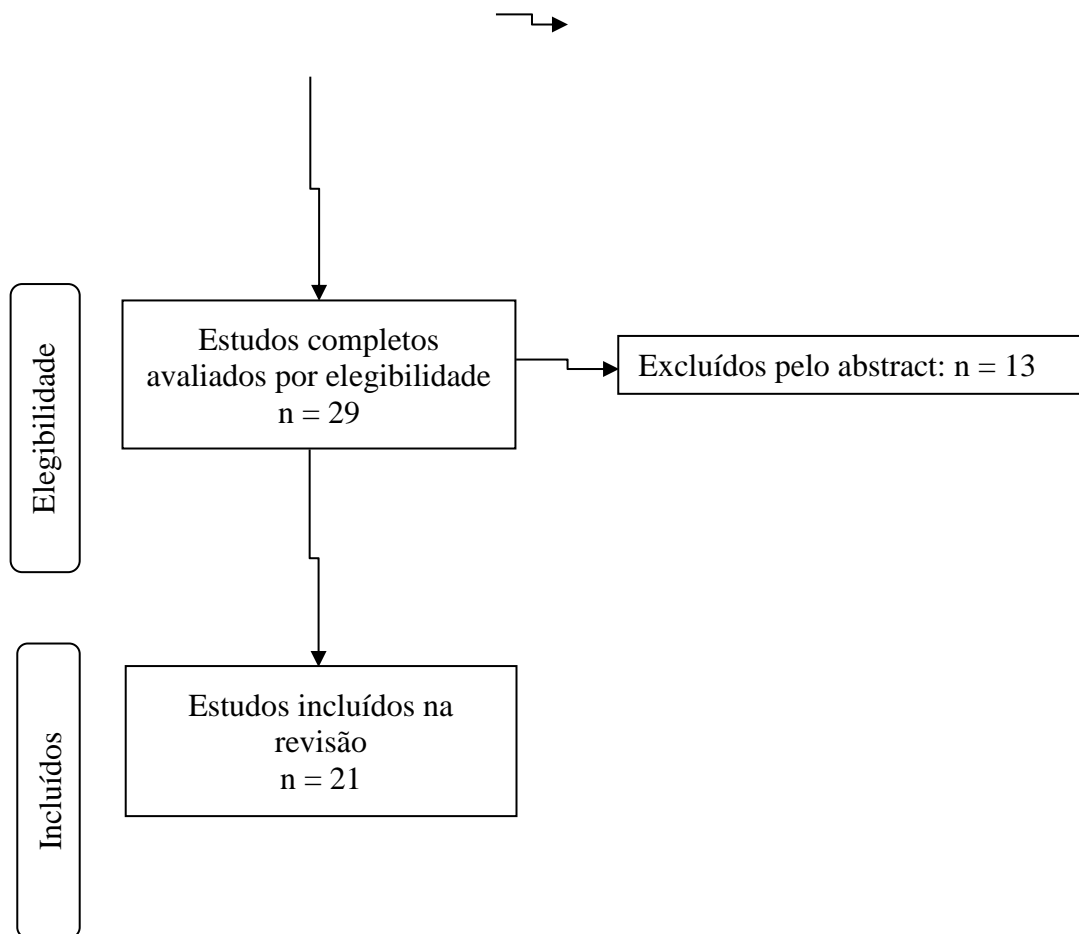


Figura 1: Diagrama de fluxo da revisão sistematizada da literatura.

2. Aspectos Conceituais e Epidemiológicos da Doença de Alzheimer

A DA foi descrita pela primeira vez em 1906 pelo médico psiquiatra Alois Alzheimer(18). Inicialmente acreditava-se tratar de uma doença rara e foram necessários mais de setenta anos desde o seu descobrimento para que ela fosse reconhecida como um tipo demência e uma das principais causas de morte(19). Hoje, a DA é considerada a causa mais prevalente de demência, responsável por cerca de 60% a 80% dos casos(3, 20, 21). A saber, o

termo “Demência” (Transtorno Neurocognitivo Maior), segundo o DSM-5, é uma síndrome clínica, que cursa com deterioração dos domínios cognitivos, alterações de comportamento e prejuízo funcional(22).

As demências em geral, e a DA em particular, são consideradas prioridades de saúde pública em nível global, devido à alta prevalência e ao impacto causado aos indivíduos e suas famílias, à sociedade e à economia(23). O número de pessoas com demência em todo o mundo estimado em 2015 era de 46,8 milhões, sendo que a previsão para 2030 é de 74,7 milhões e de 131,5 milhões para 2050. 68% desse número vivem em países de baixa e média renda(24). No Brasil, as demências afetam aproximadamente 7,5 a 8,0% da população com mais de 65 anos e estima-se a incidência de 55 mil novos casos por ano. A prevalência das demências na comunidade brasileira em geral dobra a cada cinco anos a partir dos 65 anos (2%), para atingir aproximadamente 4% aos 70 anos, 8% aos 75 anos, 15% aos 80 anos e 30% aos 85 anos. A partir dessa faixa etária essa aceleração diminui para dobrar apenas aos 100 anos (60%)(25).

A DA é neurodegenerativa, progressiva e incurável e causa a perda irreversível de funções cognitivas(1). O termo “cognição” refere-se a todo processo cerebral com tomada de consciência e que vise à tentativa de controle dos meios externo ou interno(26). Cinco são os domínios cognitivos primários, conforme descritos por Mesulam: 1) Memória; 2) Linguagem; 3) Atenção; 4) Funções Executivas e 5) Funções Visuoespaciais. Todos esses domínios possuem seus respectivos circuitos cerebrais, os quais se integram em áreas associativas(26). Portanto, o declínio das funções cognitivas pode ser caracterizado pela dificuldade progressiva em fixar fatos recentes, adquirir novos conhecimentos, fazer cálculos numéricos e julgamentos de valor, manter-se alerta, compreender e expressar-se na linguagem adequada e manter a motivação, dentre outras funções corticais superiores(27).

A DA é caracterizada pelo declínio insidioso de funções cognitivas, sendo que o comprometimento do domínio cognitivo memória é o primeiro e principal sintoma. Porém, além da disfunção cognitiva, podem ocorrer mudanças comportamentais e perda da autonomia funcional com o avançar da doença. O processo patológico, em geral, costuma evoluir de forma lenta e a sobrevida média após o diagnóstico clínico é curta(4). Modelos hipotéticos da relação temporal entre os elementos patológicos e os sintomas clínicos têm sido propostos de modo a elucidar etiologia subjacente e propiciar o diagnóstico precoce(23).

3. Fatores de risco

A idade é o principal fator de risco para o desenvolvimento da DA(28). Logo, o aumento da longevidade leva a um aumento no número de casos, os quais têm sobrecarregado os sistemas de saúde pública, principalmente de países em desenvolvimento(3). Ressalta-se, porém, que a DA não faz parte do envelhecimento biológico esperado, assim, somente idade avançada não é suficiente para causar a doença. A maioria dos casos de DA (aproximadamente 95%) se refere ao tipo de início tardio, que ocorre acima dos 65 anos de idade, resultado da interação de fatores ambientais e/ou genéticos.

O principal fator de risco genético para o desenvolvimento da DA de início tardio é ser portador do alelo $\epsilon 4$ do gene da apolipoproteína E (APOE)(29). Localizado no cromossomo 19, o gene da APOE está envolvido com o transporte de colesterol e outros lipídeos na corrente sanguínea(30). Em seres humanos há três alelos diferentes do gene: $\epsilon 2$, $\epsilon 3$ e $\epsilon 4$, os quais são herdados um de cada genitor. O tipo $\epsilon 3$ é o mais comum, seguido do $\epsilon 4$ e do $\epsilon 2$, o qual é relativamente raro. Portar APOE- $\epsilon 4$ constitui o maior fator de risco genético para a DA, sendo que a APOE- $\epsilon 3$ é neutra, não diminui nem aumenta o risco, e a APOE- $\epsilon 2$ é considerada protetora(31). Portar $\epsilon 4$ não garante que um indivíduo irá desenvolver a DA. Todavia, aqueles

que possuem uma cópia de $\epsilon 4$ apresentam três vezes maior risco de desenvolver a DA, enquanto aqueles que possuem duas cópias desse alelo têm risco de oito a doze vezes maior(32, 33). Além disso, indivíduos que possuem o alelo $\epsilon 4$ são mais prováveis de desenvolver a DA em uma idade mais jovem do que aqueles que possuem os outros alelos do gene da APOE(33). Em um estudo recente foi reportado que indivíduos com pelo menos um alelo $\epsilon 4$ têm maior probabilidade de desenvolver CCL do tipo amnésico(34).

Certas mutações genéticas, como as que ocorrem no gene da proteína precursora amilóide (APP) (cromossomo 21), ou nos genes das proteínas Presenilina 1 (P1) (cromossomo 14) ou Presenilina 2 (P2) (cromossomo 1), ambas componentes da γ -secretase, estão relacionadas ao desenvolvimento da DA com herança autossômica dominante. Uma pequena porcentagem dos casos de DA (estima-se 1% ou menos) a desenvolve como resultado de mutações em qualquer um dos três genes. Mutações na P1 e na APP estão associadas à penetrância completa, significando que todos os indivíduos que têm uma mutação na P1 ou na APP desenvolverão DA ao longo da vida. Em contraste, as mutações na P2 mostram 95% de penetrância, o que significa que nem todos indivíduos com mutação na P2 desenvolverão a doença(35, 36). Mutações na P1 são as mais comuns (30%-70%), seguido das mutações na APP (10%-15%) e na P2 (<5%)(27). Indivíduos com mutações em qualquer um desses três genes tendem a desenvolver DA precocemente, muitas vezes com a idade de 30 anos, por isso é conhecida como DA de início precoce ou pré-senil(36).

Também se identificou que indivíduos com síndrome de Down possuem maior risco de desenvolver DA, o que pode estar relacionado com a cópia adicional do cromossomo 21, cromossomo que codifica a APP. Logo, ter uma cópia extra de cromossomo 21 pode aumentar o número de fragmentos de β -amilóide no cérebro(37). Cerca de 30% das pessoas com síndrome de Down com 50 anos de idade têm DA. E com a expectativa de vida aumentando, aproximadamente 70% delas desenvolverão a DA ao longo da vida(38). Outros 4% dos casos

de DA de início precoce desenvolvem a doença devido a uma herança complexa, baseada na combinação de fatores de risco ambientais e genéticos de múltiplas causas.

Embora fatores de risco como idade e genéticos não possam ser alterados, outros podem ser modificados para reduzir a chance de desenvolver a doença: os fatores de risco ambientais(39). Um relatório que avaliou fatores de risco modificáveis concluiu que a atividade física regular e a gestão de fatores de risco cardiovasculares (especialmente diabetes, obesidade, tabagismo e hipertensão) podem reduzir o risco de declínio cognitivo e demência. Além de também contribuírem: o seguimento de uma dieta e de um estilo de vida saudável(40) e a aprendizagem ao longo da vida, o chamado treinamento cognitivo(41). É de amplo conhecimento que quanto maior o nível de escolaridade do indivíduo, maior é sua reserva cognitiva e menor o risco de desenvolver DA(42). Essa variação individual na reserva cognitiva pode, muitas vezes, obscurecer ou mascarar a relação entre a gravidade da patologia e o desempenho cognitivo apresentado pelo indivíduo(43).

Além disso, há evidências emergentes de que os mecanismos epigenéticos (modificações no genoma que são herdadas pelas próximas gerações, mas que não alteram a sequência do DNA) contribuem para a DA. Alterações epigenéticas, sejam elas protetoras ou prejudiciais, podem ajudar a explicar, por exemplo, por que um membro da família desenvolve a doença e o outro não. Cientistas estão estudando cada vez mais sobre epigenética relacionada à DA, com a esperança de desenvolver manejos individualizados(44-47).

4. Características Anatomopatológicas

A patologia da DA é caracterizada por atrofia cerebral difusa não uniforme, além de estresse oxidativo generalizado, disfunção mitocondrial e neuroinflamação(48). Os níveis dos

neurotransmissores acetilcolina, serotonina, noradrenalina e somatostatina encontram-se reduzidos, enquanto que os de glutamato geralmente estão elevados(49). Nos estágios iniciais primariamente o lobo temporal medial é afetado, seguindo progressivamente para as áreas associativas neocorticais(50).

A neuropatologia, segundo estágios de Braak, é caracterizada pela presença de emaranhados neurofibrilares que se iniciam envolvendo o córtex entorrinal (estágios I e II), progredindo para os hipocampos (III) e a ínsula (IV), para finalmente envolverem o neocórtex de forma inicial (V) ou avançada (VI)(51, 52). Essa progressão neuropatológica explica a evolução típica da forma clássica da doença, da anosmia à amnésia anterógrada - especialmente para fatos recentes – e desorientação espacial (fase III), depressão e outras alterações neuropsiquiátricas como delírios (IV), para finalmente levar a alterações nas “funções corticais superiores” (fases V e VI), incluindo afasia anômica, agnosias, apraxias, além de progressiva perda da memória autobiográfica(26). Naturalmente, a ordem da apresentação dos sintomas pode variar substancialmente de um indivíduo para outro.

Ao microscópio observa-se perda de neurônios e degeneração sináptica, os quais são resultado do processamento incorreto de proteínas do sistema nervoso central (53). Duas são as principais proteínas envolvidas com a patologia da DA: a proteína β -amilóide e a proteína *Tau*(54). Essas proteínas formam as placas amilóides e os emaranhados neurofibrilares que foram vistas por Alois Alzheimer ao estudar o cérebro de Auguste Deter, porém foram descritas cientificamente somente mais tarde, em 1984(55) e 1986(56, 57) respectivamente.

5. A Proteína β -amilóide

Desde o primeiro relato de caso da DA, as marcas neuropatológicas eram conhecidas por serem compostas de “amilóide”, isto é, depósitos proteicos que podem ser corados com corantes como o Congo Red. Somente após o desenvolvimento de um método para purificar as placas amilóides, em meados de 1984, pode-se observar a sequência completa da proteína purificada de 40 aminoácidos (4kDa) que formava placas no tecido cerebral. Com base no seu peso molecular, a proteína foi inicialmente denominada proteína A4 amilóide, a qual é hoje conhecida como β -amilóide ou $A\beta$. A identificação da sequência de aminoácidos da proteína β -amilóide facilitou posteriormente a clonagem do gene da APP(58).

β -amilóide é resultante da clivagem de uma grande proteína transmembrana, a APP, pela enzima β -secretase (BACE1), sequencialmente seguida de clivagens por γ -secretases. O peptídeo formado (sAPP β) pode, sob condições normais, ser degradado por enzimas, tais como: a neprilisina, a enzima degradadora da insulina ou ainda pela enzima conversora de endotelina; ou ser eliminado pelo líquido intersticial cerebral através da barreira hematoencefálica. Alternativamente, pode ser transportado ao líquido cefalorraquidiano para ser eliminado por essa via. No entanto, se houver alguma deficiência na degradação e/ou eliminação, ou ainda, aumento da produção de peptídeos β -amilóide, ele irá se agregar ao longo do tempo, e produzirá as conhecidas e neurotóxicas placas amilóides(59). O aumento da produção de β -amilóide por mutações ou duplicações no gene da APP e nas presenilinas está relacionado com a DA familiar, enquanto que a diminuição da degradação da β -amilóide está mais relacionada à DA esporádica(60). A função fisiológica da proteína β -amilóide ainda não está bem elucidada, mas sabe-se que em animais jovens e saudáveis a presença desses peptídeos é importante para o aprendizado e a memória(61). A APP, alternativamente, poderá seguir outra via de clivagem, na qual a enzima α -secretase atuará, seguida de clivagens por γ -secretases, o que resultará em peptídeos sAPP α , com função não-amiloidogênica e neuroprotetora(20, 62) (Figura 2).

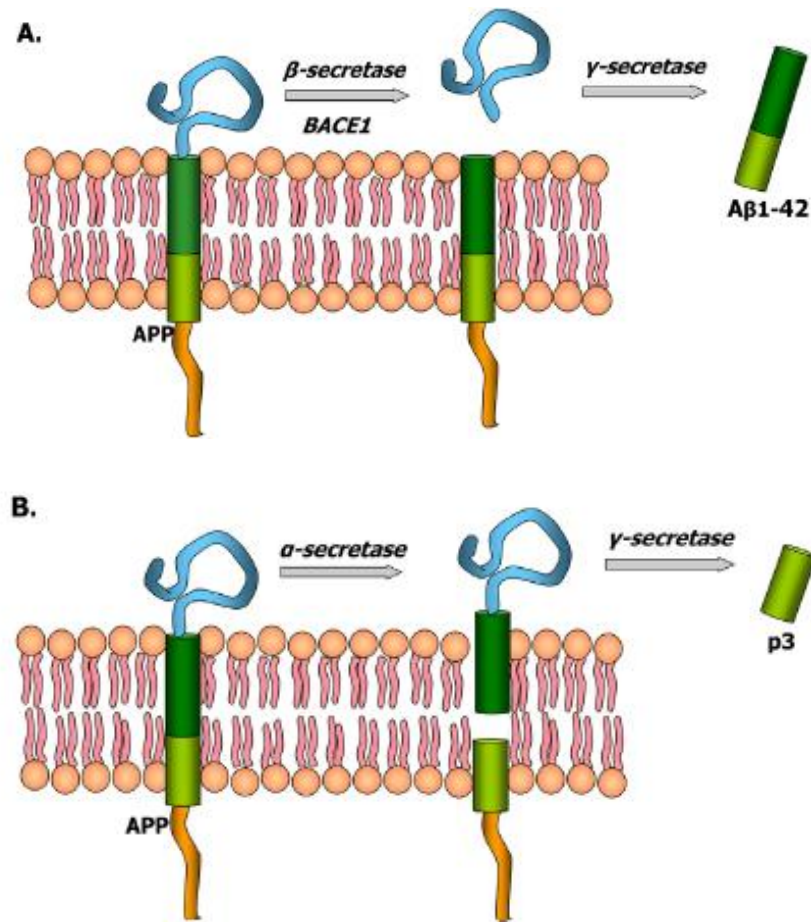


Figura 2. A) Proteólise de APP por ações enzimáticas seqüenciais de β e γ -secretases, gerando peptídeos sAPP β e liberando A β ₁₋₄₂. B) Proteólise da APP pela α -secretase, gerando peptídeos sAPP α e liberando o peptídeo p3 extracelular(63).

Os peptídeos β -amilóide são produzidos no cérebro e estão presentes também no líquido cefalorraquidiano e no plasma. Há vários tipos, o tipo A β 40 é o mais abundante, no entanto o tipo A β 42 tende a se agregar mais facilmente, por ser mais hidrofóbico e mais dinâmico(64). A β 42 é o principal peptídeo envolvido na patologia da DA e parece ser o principal tipo envolvido ‘hipótese da cascata amilóide’, a qual é a teoria mais aceita para a explicação da etiopatogenia da doença(65).

A ‘hipótese da cascata de amilóide’ na gênese da DA, foi proposta em 1991 por John Hardy e David Allsop(66) e revisada por Tanzi e Bertram em 2005(67). Tal hipótese postula que a iniciação da DA acontece pelo excesso de peptídeos β -amilóide. Mutações no gene da

APP estariam associadas às formas familiares da DA com herança autossômica dominante, enquanto interações genéticas complexas e riscos ambientais contribuiriam para a acumulação de espécies tóxicas de β -amilóide na DA de início tardio. Esse excesso e agregação de peptídeos β -amilóide no tecido cerebral desencadearia a patologia. Após esse processo ocorreria a ativação neuroglial, a formação de emaranhados neurofibrilares com a proteína *Tau*, a neuroinflamação, a disfunção sináptica e neurítica e finalmente a morte celular neuronal, resultando em declínio cognitivo e demência(68).

Essa teoria de patogênese linear da DA já foi bastante questionada pelo fato de que outros mecanismos complexos estão envolvidos na etiopatogenia da DA. Entre esses fatores destacam-se: a neuroinflamação(69), o estresse oxidativo, a redução do metabolismo energético e a redução da função sináptica, os quais interagem uns com os outros(70). No entanto, a proteína β -amilóide é considerada o principal biomarcador para a detecção precoce da DA(71). Além disso, resultados de meta-análises sugerem que a proteína β -amilóide é útil tanto para a discriminação da DA de outras demências quanto do CCL(72-74).

6. A Proteína *Tau*

Tau é uma proteína associada aos microtúbulos do citoesqueleto dos neurônios e está diretamente envolvida na estabilização celular, portanto, desempenha importante papel na manutenção da morfologia neuronal e no transporte intracelular(64). Em condições normais, o equilíbrio entre a fosforilação e a desfosforilação da *Tau* coordena a sua ligação ou não aos microtúbulos, o que mantém a estabilidade neuronal e auxilia no transporte de cargas ao longo do axônio. Assim, a perda de sua funcionalidade, geralmente por hiperfosforilação, leva a deficiências funcionais nos neurônios e, conseqüentemente, das sinapses(21).

A hiperfosforilação diminui a capacidade da *Tau* se ligar aos microtúbulos, o que resulta em um anormal aumento dos níveis de *Tau* não ligada. Logo, com as suas concentrações citosólicas aumentadas, a probabilidade de formar oligômeros e agregados é maior. Na DA ela se hiperfosforila e se torce formando filamentos helicoidais emparelhados, os chamados emaranhados neurofibrilares. Em 1986, foi demonstrado que os emaranhados neurofibrilares são compostos da forma anormal da proteína *Tau*, com cerca de três vezes mais sítios fosforilados do que *Tau* normal(56, 58). Esses emaranhados de *Tau* hiperfosforilada desestabilizam os neurônios e conseqüentemente levam à neurodegeneração(75).

A chamada *Tau* total não se mostrou específica para a DA, pois é considerada indicadora de danos que podem derivar de uma variedade de etiologias(76), como: lesão cerebrovascular, demência fronto-temporal(77), traumatismo craniano, acidente cardiovascular agudo, doença de Creutzfeldt-Jakob(78), doença de Pick(21), entre outras. A *Tau* total é considerada um “marcador de estado”, refletindo a intensidade da neurodegeneração ou a gravidade de um dano neuronal agudo. De fato, após danos cerebrais agudos, os níveis de *Tau* total aumentam em poucos dias após a lesão, permanecendo elevados por semanas até a normalização(58).

A única patologia que mostra consistentemente um aumento de *Tau* hiperfosforilada no líquido é a DA, este biomarcador encontra-se normal em outros distúrbios neurodegenerativos ou em danos cerebrais como acidente vascular cerebral isquêmico agudo(58, 79). A proteína *Tau* hiperfosforilada se mostrou eficaz no diagnóstico diferencial entre a DA, CCL e outros tipos demenciais(80, 81). Além disso, constatou-se que concentrações líquóricas de *Tau* hiperfosforilada podem estar aumentadas em aproximadamente 200% em indivíduos com DA quando comparadas a indivíduos controles(82).Em conjunto, esses dados indicam que a *Tau* total reflete a intensidade da lesão neuronal em um ponto específico, enquanto a *Tau* hiperfosforilada elevada no líquido reflete um estado patológico anormal associado à formação de filamentos helicoidais emparelhados. A proteína *Tau* hiperfosforilada é uma importante

proteína envolvida na patologia da DA, visto que emaranhados neurofibrilares estão mais intimamente associados com a gravidade da demência do que as próprias placas amilóides(83). Esse biomarcador é indicativo de um processo patológico mais tardio em relação ao causado pela proteína β -amilóide, logo, se torna dinâmico somente pouco tempo antes dos primeiros sinais clínicos da doença(6, 84).

Outra teoria proposta na etiopatogenia da DA é a ‘teoria *Tau*’, que tem como argumento que o grau de severidade das alterações cognitivas da DA correlaciona-se melhor com a severidade da patologia *Tau* do que com a da proteína β -amilóide. Além de que o depósito de placas amilóides não se correlaciona bem com a perda de neurônios. Um possível ponto de conciliação entre a ‘teoria *Tau*’ e a ‘teoria da cascata amilóide’, em termos de plausibilidade e constatação neuropatológica, seria o fato de que a proteína β -amilóide, especialmente em sua forma oligomérica, é necessária, mas não suficiente para causar apoptose e os efeitos adversos da DA(85).

Com efeito, neurônios de modelos transgênicos de camundongos hiperexpressando a proteína β -amilóide, mas geneticamente modificados para não expressar a proteína *Tau* hiperfosforilada, não desenvolveram neurodegeneração(54). Além disso, os primeiros biomarcadores que se tornam alterados em portadores de mutações determinísticas da DA são os do tipo β -amilóide(27, 86, 87). Observa-se então que a proteína β -amilóide pode ser superior à proteína *Tau* na patogênese da DA e desencadeia a conversão de *Tau* de um estado normal para um estado tóxico, isto é, promovendo tauopatia e neurodegeneração, que conduzem finalmente à deterioração cognitiva(85). Porém, deve-se considerar que a *Tau* hiperfosforilada também pode aumentar a toxicidade da proteína β -amilóide através mecanismos de feedback(54).

Alguns estudos hipotetizam que as duas proteínas envolvidas na patologia da DA podem iniciar independentemente o processo patológico, e há proposições de que uma incidente ‘betaopatia’ pode acelerar uma antecedente ‘tauopatia’(6, 88). Em suma, as proteínas que definem a DA como uma doença única entre as muitas que podem levar à demência podem não ser a via causal primária da patologia. Porém, fornecem uma explicação mecanicista para o desenvolvimento de ambas as proteinopatias diagnósticas, bem como a neurodegeneração e os sintomas clínicos da DA(16).

7. Terapêutica da DA

O diagnóstico precoce da DA é decisivo para o tratamento adequado e eficaz. A base da terapêutica tem se concentrado em retardar a evolução, tratar os sintomas e controlar as mudanças comportamentais. No entanto, não tem tido sucesso no desenvolvimento de terapias modificadoras da história natural da doença(89). Por esse motivo, dezenas de medicamentos e novas terapias estão em estudo(90, 91). As principais drogas que conseguem melhorar temporariamente os sintomas da DA agem alterando a disponibilidade de neurotransmissores, sendo que a eficácia desses fármacos varia de pessoa para pessoa. Atualmente existem apenas três modalidades terapêuticas para a DA, a saber: 1) anticolinesterásicos como o donepezil, a rivastigmina e a galantamina, 2) a memantina, única molécula antagonista NMDA aprovada para uso em humanos(49, 92) e 3) alguma evidência para o uso da vitamina E como neuroprotetora na DA(93).

A terapia colinérgica é a mais utilizada, e pode efetivamente melhorar a cognição e a funcionalidade cerebral em cerca de 20% a 30%. Na DA há uma marcada alteração do sistema colinérgico, principalmente com a diminuição (40%-90%) na atividade da colina acetiltransferase (enzima sintetizadora), sobretudo no córtex cerebral e hipocampo. Também

estão diminuídas as atividades da precursora acetilcoenzimaA, resultando em importante diminuição dos níveis de acetilcolina. Já a butilcolinesterase, que tal como a acetilcolinesterase (enzima metabolizadora) degrada a acetilcolina, está significativamente aumentada na doença. Os medicamentos inibidores de acetilcolinesterase agem diminuindo a queda dos níveis de acetilcolina, logo, aumentando a atividade colinérgica do neurotransmissor nos indivíduos com doença(94). A DA também libera moléculas de glutamato em excesso, o que permite a entrada de grande quantidade de cálcio no neurônio pós-sináptico, podendo levá-lo à morte. A Memantina (fármaco antagonista dos receptores de glutamato) coloca-se no canal de entrada para o cálcio no neurônio pós-sináptico, bloqueando sua entrada e a consequente morte neuronal(92).

Todos os fármacos aprovados para uso são indicadas para pacientes que estão nas fases iniciais e intermediárias da doença. São elegíveis os pacientes que ainda mantêm algum grau de cognição e de independência funcional, por este motivo a importância do diagnóstico precoce. Estes medicamentos são essencialmente sintomáticos e não há nenhuma evidência de que eles retardam a progressão da patologia. As perspectivas para o futuro almejam que novas drogas sejam mais seguras e capazes de interferir efetivamente no retardo da evolução natural da doença(95). As terapias mais promissoras consistem: na terapia anti-amilóide, no metabolismo da proteína *Tau* e nas neurotrofinas. Além dessas estratégias terapêuticas há estudos com relação à função mitocondrial, ao uso de antioxidantes, anti-inflamatórios e fitomedicamentos(91).

As terapias anti-amilóide consistem: na inibição tanto da β -secretase quanto γ -secretase, as quais são as duas enzimas que favorecem a via amiloidogênica; terapias antiagregação do β -amilóide em placas senis ou ainda imunoterapias, ativa ou passiva, de modo a aumentar a eliminação do β -amilóide do tecido cerebral com o uso de anticorpos para impedir a formação de placas(91, 96). Já as terapias que envolvem a proteína *Tau* se baseiam na inibição ou da

hiperfosforilação ou da agregação em emaranhados neurofibrilares. Sabe-se também que neurônios colinérgicos são sensíveis à ação do fator de crescimento neuronal. Dessa maneira, alguns estudos testam essa nova possibilidade terapêutica no tratamento da DA, reduzindo a perda de neurônios colinérgicos no córtex e hipocampo(93).

As falhas que se observam nos estudos de fármacos no sentido de alterar o curso natural da doença se devem ao fato da DA ser uma doença extremamente complexa, além da fisiopatologia não estar completamente elucidada(93, 97). Sendo assim, as pesquisas focadas em modelos lineares de mecanismos de ação, que seguem uma linha reducionista - em que o fármaco candidato agirá em um único alvo ligado à patogênese da doença - dificilmente obterão êxito na possível cura da DA. Assim, o melhor entendimento da patogenia da doença e o desenvolvimento de fármacos que possam se ligar a diferentes alvos, seguindo um modelo de rede e/ou multialvo, e com menores efeitos colaterais, poderiam prover melhores resultados na possível cura ou interrupção da progressão da patologia(91). O uso dos biomarcadores, na identificação precoce de indivíduos com alto risco de desenvolverem a DA, é um promissor caminho para que haja um completo entendimento da patologia e o desenvolvimento de drogas específicas, que consigam reverter ou interromper o processo patológico da doença.

8. A Pesquisa na Doença de Alzheimer

A partir do momento em que se evidenciou a ampla abrangência da DA na população mundial, a mesma tornou-se um foco significativo de pesquisa. Em 1984, DA foi inicialmente definida como uma entidade clínico-patológica e era diagnosticada somente *post-mortem* na autópsia ou *in vivo* como possível ou provável(98). O diagnóstico era basicamente clínico, obtido com a identificação de uma síndrome demencial, seguido da exclusão de outras etiologias por meio de uma variedade de abordagens. Algumas ferramentas utilizadas na

exclusão incluía: histórico médico e familiar (incluindo história psiquiátrica de mudanças cognitivas e comportamentais), testes cognitivos, avaliação física e exclusão de doenças cerebrovasculares ou características de outros tipos demenciais(99).

A pesquisa que se seguiu revelou que a neuropatologia da DA se inicia anos antes do aparecimento dos primeiros sintomas(100). As alterações cerebrais associadas à DA podem iniciar cerca de vinte anos ou mais antes dos sinais clínicos(6, 27) (Figura 3). Portanto, diagnosticar a DA de forma precoce se tornou decisivo para um melhor manejo da doença.

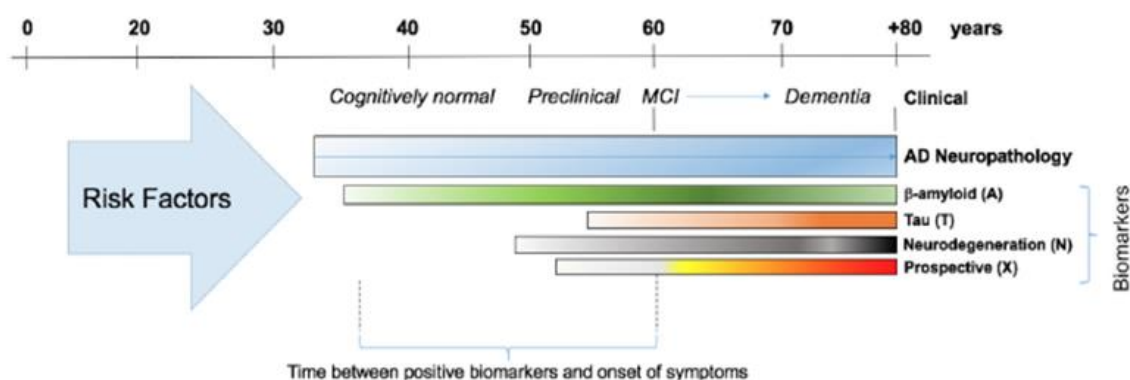


Figura 3. Neuropatologia da Doença de Alzheimer pode ser detectada cerca de 20 a 30 anos antes dos primeiros sintomas clínicos por meio de biomarcadores(101).

Em 2011, o NIA-AA atualizou as recomendações diagnósticas para a DA de 1984(98) e considerou a doença em três principais estágios: 1) pré-clínico, 2) comprometimento cognitivo leve e 3) sintomático ou demencial(102). Além do mais, com a disponibilidade de biomarcadores específicos para a patologia *in vivo* houve suporte para a mudança de definição da DA: de uma entidade clínico-patológica para uma entidade clínico-biológica.

Os estágios da DA passaram a ser caracterizados na pesquisa como segue: 1) pré-clínico: no qual os indivíduos são objetivamente caracterizados como cognitivamente normais, é pré-sintomático(20); 2) fase de CCL: fenótipo clínico específico da síndrome amnésica do tipo hipocampal(103). Em indivíduos com CCL devido à DA há um declínio cognitivo progressivo maior na memória do que o esperado para a idade e nível de escolaridade, mas sem sinais

clínicos de habilidades funcionais prejudicadas(20); e 3) demencial: onde há prejuízo funcional nas atividades da vida diária (20). A partir dessas recomendações os biomarcadores passaram a ser fortemente sugeridos nas pesquisas com a DA. Verificou-se que a aplicação conjunta de critérios clínicos com os biomarcadores resulta num maior nível de evidência no suporte à etiologia da doença. Outrossim, os biomarcadores auxiliariam na determinação da probabilidade de progressão cognitiva e funcional de um indivíduo com declínio cognitivo a um estágio demencial num determinado período de tempo(104).

O progresso científico nesse ínterim levou a uma iniciativa de atualização e unificação das diretrizes de 2011. Então, em 2018, o NIA-AA propôs uma nova estrutura de pesquisa para a DA. A partir da qual a DA fica definida pelos seus processos patológicos subjacentes, que podem ser documentados por exame *post mortem* ou *in vivo* por biomarcadores. O diagnóstico não é mais baseado nas consequências clínicas da doença - ou seja, nos sintomas - mas sim em um *continuum* da doença baseado em biomarcadores. Além disso, essa nova estrutura muda a definição da DA para pessoas vivas: de processo sindrômico para um construto biológico(16).

O novo quadro de investigação centra-se em biomarcadores agrupados nos diferentes processos patológicos da DA e que podem ser mensurados em pessoas vivas com tecnologia de imagem e/ou análise de líquido cefalorraquidiano. A proposta recomenda que o termo DA seja alocado a pessoas que tenham a comprovada presença biomarcadores positivos(23). Os biomarcadores são agrupados nos de deposição β -amilóide (A), *Tau* hiperfosforilada (T) e neurodegeneração (N) no sistema [AT(N)]. Sendo que β -amilóide e *Tau* hiperfosforilada são os depósitos proteicos anormais que definem a DA como uma doença neurodegenerativa única entre diferentes distúrbios que podem levar à demência(105). Enquanto que os biomarcadores de neurodegeneração, - a saber: dosagem de *Tau* total no líquido cefalorraquidiano, hipometabolismo cerebral com fluordesoxiglicose no PET e atrofia cerebral verificada na ressonância magnética - não são equivalentes àqueles que refletem a acumulação de β -amilóide

e *Tau* hiperfosforilada(76). Os indicadores de neurodegeneração ou lesão neuronal podem ser resultantes de várias causas, não são específicos para neurodegeneração devido à DA. No entanto, a combinação de todos esses biomarcadores pode fornecer uma predição de declínio cognitivo futuro muito mais poderosa do que o estudo das proteínas alteradas isoladamente. Logicamente, uma vez que a neurodegeneração é a alteração neuropatológica da DA que mais se correlaciona com os sintomas da patologia(106). Essa nova estrutura estabelece que quanto mais avançada a doença definida pelos biomarcadores, maior é a probabilidade e mais rápida é a predição de declínio cognitivo. Assim, há sólidas evidências de que as combinações dos biomarcadores alterados são úteis para o estagiamento do *continuum* da DA(16).

Além disso, como a DA é considerada como um *continuum*, o estagiamento cognitivo também passa a ser feito com medidas contínuas. Para esse estagiamento são disponibilizados dois esquemas: um, usando as três categorias sindrômicas tradicionais: sem comprometimento cognitivo, com CCL e demência - a qual pode ser subdividida em leve, moderada ou severa - (aplicável a todos os membros de uma coorte, ou seja, inclui todos os perfis de biomarcadores), ou outro, de estagiamento clínico numérico com seis etapas (aplicável apenas àqueles no *continuum* da DA, útil para ensaios clínicos)(101). Dessa forma, ao considerar a DA como um construto biológico, se observa uma melhor caracterização e compreensão da sequência de eventos que levam ao comprometimento cognitivo, bem como da etiologia multifatorial da demência(16).

9. O advento dos biomarcadores

Biomarcadores são cruciais para a implementação da medicina personalizada, podendo ser mensurados objetivamente em fluidos biológicos como sangue e líquido cefalorraquidiano ou em tecidos periféricos. São indicadores biológicos que aprimoram a compreensão da doença

e podem fornecer informações sobre: presença/ausência de patologia, susceptibilidade, prognóstico ou ainda resposta a um tratamento. As características de um biomarcador ideal podem resumidas em: sensibilidade e especificidade de pelo menos 80%, valor preditivo positivo próximo a 90%, fácil dosagem, confiável, não invasivo, barato, estar envolvido na patologia, permitir a detecção precoce, representar a fisiopatologia e auxiliar a diferenciar a patologia estudada de outras semelhantes(107).

Diferentes biomarcadores, em particular proteínas mensuradas no líquido cefalorraquidiano, demonstraram ser ferramentas úteis para a detecção da DA *in vivo* e estão ganhando atenção na prática clínica(16). Existem múltiplas vantagens associadas à identificação de indicadores prognósticos preditivos de progressão à DA. Por exemplo, o conhecimento da patologia subjacente permite que pacientes e familiares se preparem para o futuro, enquanto que a correta alocação de indivíduos em ensaios clínicos impede que indivíduos de improvável progressão à DA se exponham a um risco indevido.

A busca por biomarcadores que possibilitem o diagnóstico preciso da DA é uma das áreas de maior concentração de pesquisas atualmente. Principalmente busca-se biomarcadores acurados para os estágios iniciais da doença, onde medicamentos terão maior eficácia. Muitas das falhas nos ensaios clínicos se devem à imprecisão da correta identificação de indivíduos em vias de desenvolvimento da DA. É possível que mais de 30% dos indivíduos recrutados para ensaios clínicos, somente pela história natural e clínica, possuem patologias diferentes da DA(101). Além do diagnóstico precoce, o emprego dos biomarcadores pode trazer novas informações a respeito dos mecanismos fisiopatológicos envolvidos na doença, sendo vantajosos no prognóstico, no desenvolvimento de um tratamento e no monitoramento da sua eficácia(13).

Na medicina clínica os biomarcadores de fluidos corporais influenciam em até 70% das decisões médicas. Para distúrbios cerebrais, incluindo a DA, o desenvolvimento de biomarcadores iniciou-se adotando-se o líquido cefalorraquidiano como matriz, o qual, comparado ao sangue, tem a vantagem da sua proximidade com o parênquima cerebral e de receber as proteínas secretadas diretamente do espaço extracelular cerebral(58).

Há muitos anos os testes diagnósticos por meio de reações imunoenzimáticas são utilizados para a quantificação das proteínas β -amilóide e *Tau* no líquido(58). Tais estudos estabeleceram um padrão biomarcador para a DA, muitas vezes denominado “perfil para a DA”, sendo que este é caracterizado pela diminuição da concentração líquórica da proteína β -amilóide e pelo aumento da proteína *Tau*. Esses principais biomarcadores evoluíram desde os primeiros estudos baseados em ensaios simples ao seu status atual, com instrumentos totalmente automatizados e extensiva validação de desempenho(58). Os biomarcadores movem a pesquisa sobre a DA na direção de uma medicina personalizada através da codificação de alterações patológicas. As informações fornecidas pelos biomarcadores, combinada com os elementos genéticos e clínicos, promovem uma medicina personalizada(17).

Há algumas diferenças entre os biomarcadores líquóricos e os de imagem. Os biomarcadores de líquido cefalorraquidiano refletem as taxas de concentrações protéicas de produção, degradação ou remoção em um determinado ponto no tempo. As medidas de imagem, por outro lado, representam a magnitude da carga ou dano neuropatológico acumulado ao longo do tempo(108). Discordâncias entre os tipos de biomarcadores poderão ocorrer. Porém, um estado patológico ativo contínuo, denotado pelas concentrações líquóricas, e o acúmulo de carga neuropatológica, denotado pelos exames de imagem, serão concordantes a longo prazo(16). As diretrizes atuais sugerem que ambos podem ser usados na clínica, sendo que a escolha pode ser baseada na disponibilidade, nos custos, ou nas estimativas de risco (exposição

à radiação *versus* cefaleia pós-punção lombar), juntamente com as preferências do médico e do paciente(58).

Embora numerosas pesquisas tenham relatado excelente desempenho diagnóstico por meio dos biomarcadores líquóricos, ainda se observam diferenças marcantes nos níveis absolutos relatados entre os estudos, mesmo quando se utiliza a mesma variante da técnica. A ampla variação nas medidas desses biomarcadores entre estudos e laboratórios é uma das dificuldades na determinação de pontos de corte homogêneos(72). Essas diferenças podem ser causadas tanto pelos os critérios de seleção de casos e resultante diferença nas características da amostra, quanto por diferentes procedimentos pré-analíticos utilizados como, por exemplo: tipo de tubos utilizados e cronograma de congelamento e descongelamento. Além disso, a variabilidade laboratorial também pode ser devida as discrepâncias nos procedimentos analíticos entre os laboratórios ou nos procedimentos de fabricação dos imunoenaios, resultando em variações de lote para lote. Devido a essas diferenças ainda não há o estabelecimento de pontos de corte, o que dificulta a implementação generalizada de biomarcadores na rotina clínica(58). Atualmente sugere-se que grupos de pesquisa utilizem baterias de testes cognitivos e pontos de corte para os biomarcadores encontrados em suas próprias amostras de pesquisa, de modo a melhor atender os objetivos de cada estudo(16). A padronização e o controle de qualidade desses procedimentos podem reduzir a disparidade e aumentar a utilidade dos biomarcadores(109).

A pesquisa clínica sem biomarcadores continua válida e fornece informações fundamentais sobre a sobrecarga social da incapacidade cognitiva e fatores que contribuem para o comprometimento cognitivo. No entanto, as variantes sindrômicas clássicas não são sinônimos da presença de deposição de β -amilóide e da neurodegeneração. Além do mais, os critérios diagnósticos puramente clínicos para DA apresentam baixa acurácia, com valores de sensibilidade e especificidade em torno de 70-80% quando comparados à neuropatologia(58).

Portanto, estudos sem biomarcadores, que inferem associações biológicas com a DA, podem causar confusão de diagnóstico(16).

10. O Comprometimento Cognitivo Leve e os biomarcadores liquóricos

O CCL é caracterizado pela presença de déficits neuropsicológicos objetivos, em um ou mais domínios cognitivos, sem comprometimento funcional nas atividades da vida diária(9). A pesquisa na DA tem se concentrado principalmente na correta identificação de indivíduos com CCL, por ser um estágio de transição entre a cognição normal e a demência(8, 9, 103). Porém, nem todas as pessoas com CCL desenvolverão a DA(34). Estima-se que indivíduos com CCL têm um risco aumentado, com taxas de progressão anuais que variam de 5-20% e quinquenais de 40-60%(10-12). Em autópsias cerebrais de casos com CCL foi constatado que mais de 70% das amostras analisadas estavam em vias de desenvolvimento da DA(110).

Essa entidade nem sempre é facilmente distinguível de quadros verdadeiramente pré-demenciais em idosos, podendo ser confundida, por exemplo, com uma depressão com sintomas cognitivos, o que é muito mais comum de ocorrer em idosos do que em adultos de meia idade(9). Portanto, a correta identificação de indivíduos com CCL que sejam considerados prodrômicos à DA é de extrema importância(103). Com base no conhecimento atual, quanto mais previamente a DA for diagnosticada, as chances de um melhor prognóstico são maiores(14, 15). Afere-se que quando terapias modificadoras da história natural da doença estiverem disponíveis, essas pessoas com CCL serão as principais beneficiadas(13).

Na fase prodrômica, a avaliação clínico-neuropsicológica tem acurácia limitada para a predição de conversão de CCL para a demência da DA(111). Até o momento, não há métodos claramente estabelecidos para prever a progressão para DA em pessoas com CCL(72). Para

superar esse limite, os biomarcadores diagnósticos, como a análise do líquido cefalorraquidiano e a neuroimagem, foram incluídos nos critérios atuais de pesquisa(111). A utilização desses biomarcadores auxilia na resposta a questões fundamentais, no suporte à etiologia da síndrome clínica em indivíduos com CCL e na determinação da probabilidade da progressão cognitiva e funcional de um paciente com CCL a um estágio demencial, juntamente com a chance de que essa progressão irá ocorrer em um definido período de tempo(104).

Os critérios clínicos para a caracterização de sujeitos com CCL foram propostos inicialmente por Petersen em 1999(112) e atualizados em 2004(113, 114). Igualmente se enquadram nas recomendações do NIA-AA (16, 104) e nos critérios para o diagnóstico de DA no Brasil(99). Tais critérios se resumem em: a) queixa cognitiva, de preferência corroborada por informante; b) prova objetiva de perda cognitiva; c) funcionamento cognitivo geral essencialmente preservado; d) não estar demente. Os indivíduos que se enquadram nos quesitos acima ainda podem ser classificados em uma das seguintes categorias: CCL-a (CCL - amnésico) quando principalmente o desempenho nos testes neuropsicológicos de memória episódica for insatisfatório ou CCL-na (CCL - não amnésico) no caso de mau desempenho em testes neuropsicológicos relativos a outros domínios cognitivos, tais como as funções executivas, linguagem ou habilidades visuo-espaciais(9).

O padrão específico de comprometimento da memória episódica, ou seja, “amnésia do tipo hipocampal”, é o critério clínico central para o diagnóstico precoce da DA(104). Esse perfil amnésico, caracterizado por baixa capacidade de aprendizado e declínio rápido da memória em um período de tempo relativamente curto, é tipicamente associado ao envolvimento precoce do lobo temporal medial, que é o principal local anatômico para consolidação e armazenamento de memória(115). Pesquisas recentes revelam que esse padrão característico de amnésia é reconhecível em pacientes com CCL-a.

Indivíduos com CCL-a, cujo desempenho na memória episódica é pior do que em outros domínios cognitivos, têm maior probabilidade de progredir para DA(116, 117). A saber, a memória episódica pode ser subdividida de acordo com as diferentes etapas do processo de reprodução (por exemplo: recordação livre, recordação dirigida ou reconhecimento) e essa análise múltipla pode ser usada para descrever o risco real de progressão de um indivíduo com CCL à DA(116). A recordação tardia é o mais importante preditor neuropsicológico da conversão de CCL para a DA(116, 118).

Embora o CCL seja uma entidade bem conhecida, pode ser difícil para não especialistas diagnosticar adequadamente essa condição em sua prática somente pela clínica(119). Estudos longitudinais com pacientes com CCL representam uma oportunidade para investigar a intensidade dos processos biológicos subjacentes (amiloidose e neurodegeneração) e a sua relevância para a progressão para DA. Alguns estudos avaliaram o valor dos biomarcadores líquóricos na predição da progressão do CCL para a fase demencial da DA(7, 10, 73, 79, 120-122). Porém, as dificuldades em prever a progressão do CCL para a DA podem ser influenciadas pela heterogeneidade intrínseca dos indivíduos com CCL.

CCL é uma condição amplamente heterogênea, com uma gama de diferentes mecanismos neurodegenerativos subjacentes, o que dificulta a predição precoce do risco para o desenvolvimento da DA(123). Dessa forma, a generalização da pesquisa científica para a prática clínica é limitada. Os estudos envolvendo a dosagem dos biomarcadores $A\beta_{1-42}$ e p-Tau₁₈₁ disponíveis compreendem, em sua maioria, indivíduos com diagnóstico de CCL geral, não fazendo diferenciação entre os subtipos amnésico e não-amnésico, o que gera uma ampla variabilidade de resultados e nenhuma concordância no reconhecimento do risco factual para o desenvolvimento da DA(73, 74, 79, 111, 124). Nesse sentido, buscou-se nesse estudo original reportar o risco relativo da progressão de um grupo composto exclusivamente de indivíduos

com CCL amnésico para a demência da DA, baseado nos biomarcadores líquóricos $A\beta_{1-42}$ e p-Tau₁₈₁.

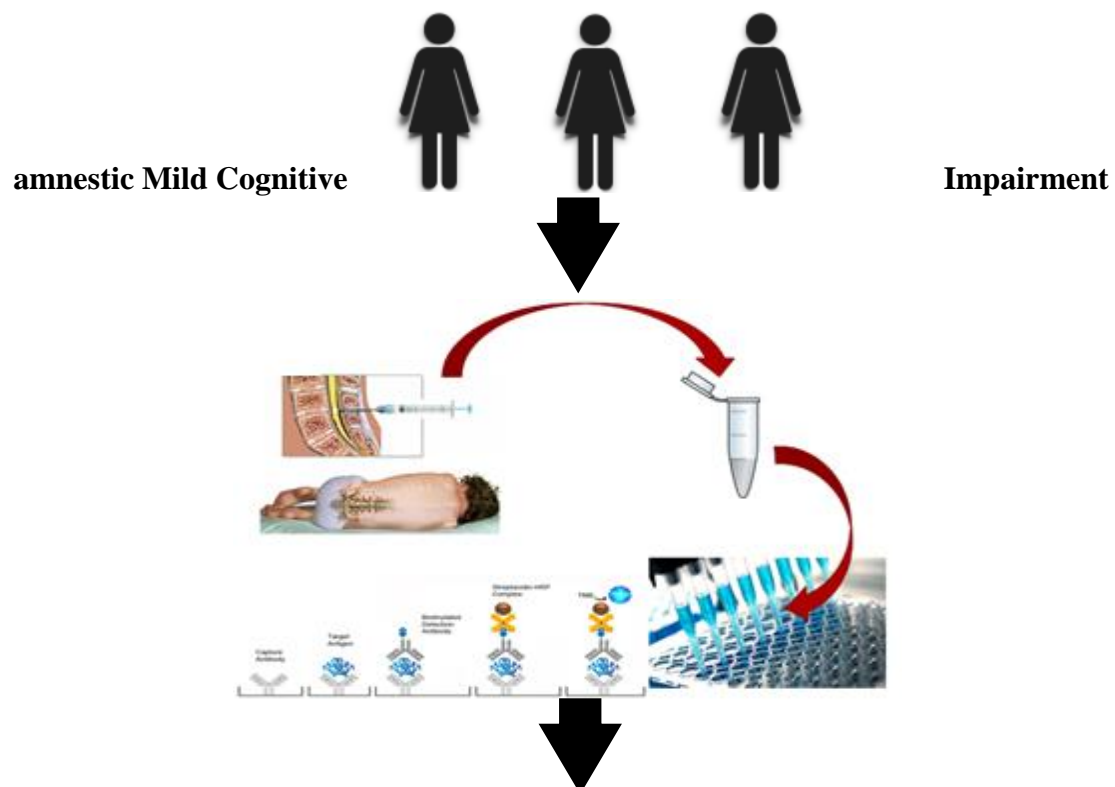
CAPÍTULO III

1. JUSTIFICATIVA

A DA é causa direta de grandes prejuízos pessoais, sociais e financeiros. Portanto, estudos que auxiliem na correta identificação de indivíduos com risco de progressão à fase demencial da doença são de máxima importância. O uso dos biomarcadores na identificação precoce de indivíduos com alto risco de desenvolverem a DA, é um promissor caminho para que haja um completo entendimento da patologia e o desenvolvimento de tratamentos específicos que consigam reverter ou interromper o processo patológico da doença. Com base no conhecimento atual, quanto mais previamente a DA for diagnosticada, maior é a chance de um melhor prognóstico. Além disso, muitas das falhas nos ensaios clínicos se devem à imprecisão na identificação de indivíduos em vias de desenvolvimento da DA.

Embora o CCL seja uma entidade bem conhecida, pode ser difícil diagnosticar adequadamente essa condição somente pelos aspectos clínicos. Estudos longitudinais com pacientes com CCL representam uma oportunidade para investigar a intensidade dos processos biológicos subjacentes e a sua relevância na progressão para DA. A capacidade dos biomarcadores em definir adequadamente o estado de risco pode, em última análise, permitir que agentes terapêuticos finalmente atinjam o status modificador da história natural da doença. Portanto, esse estudo justifica-se pela avaliação da contribuição dos biomarcadores líquóricos $A\beta_{1-42}$ e p-Tau₁₈₁ na predição do risco de progressão à fase demencial da DA em um grupo de alto risco, composto exclusivamente por indivíduos com CCL do tipo amnésico, o qual terá maior vantagem prognóstica ao ser corretamente identificado.

2. MAPA CONCEITUAL



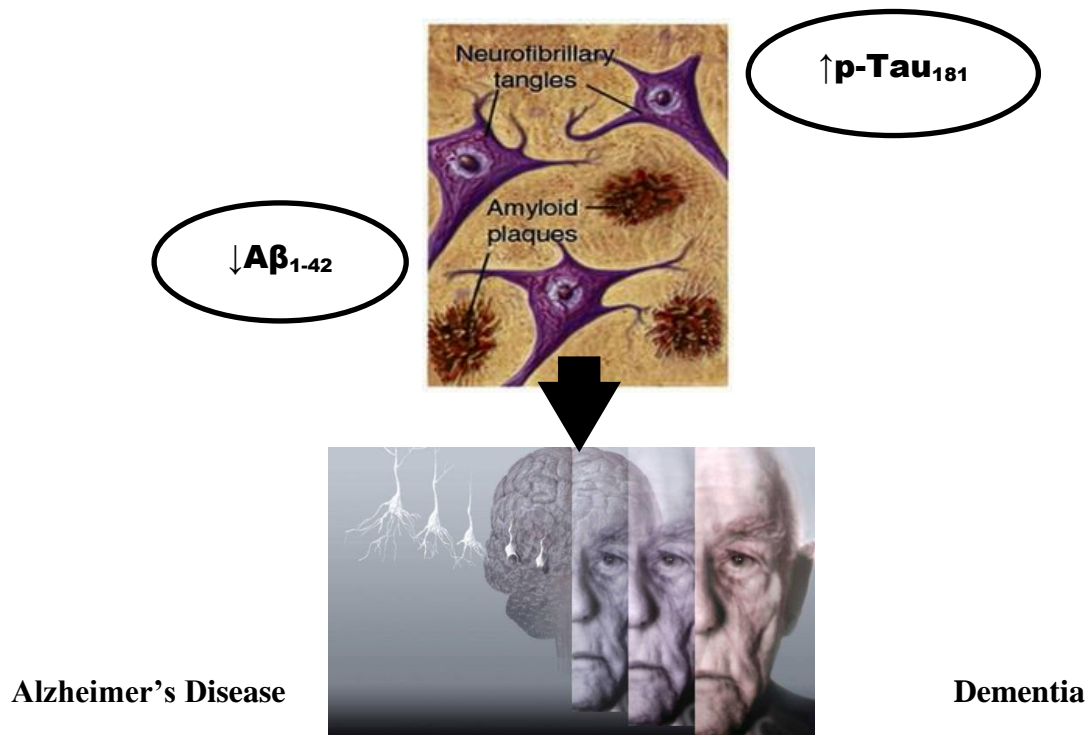


Figura 4. Mapa conceitual do estudo. Fonte: a autora utilizando figuras do Google imagens.

3. OBJETIVOS

3.1 Objetivo Geral

- Mensurar os biomarcadores líquóricos Aβ₁₋₄₂ e p-Tau₁₈₁ em indivíduos com Comprometimento Cognitivo Leve amnésico e verificar suas capacidades preditivas para a fase demencial da Doença de Alzheimer em um estudo longitudinal.

3.2 Objetivos Específicos

- Identificar e comparar os perfis dos biomarcadores líquóricos Aβ₁₋₄₂ e p-Tau₁₈₁ em indivíduos com Comprometimento Cognitivo Leve amnésico e com Comprometimento Cognitivo Subjetivo;

- Verificar a relação e a concordância desses biomarcadores com testes neuropsicológicos selecionados;

- Predizer o risco de progressão do Comprometimento Cognitivo Leve amnésico para a fase demencial da Doença de Alzheimer em cinco anos de seguimento.

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CAPÍTULO IV

1. ARTIGO CIENTÍFICO ORIGINAL I

Estudo transversal inicial disponível online na revista Brain Reasearch em 07.10.2017 (<https://doi.org/10.1016/j.brainres.2017.10.008>).

Title of the paper: CSF A β ₁₋₄₂, but not p-Tau₁₈₁, differentiates aMCI from SCI.

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Abstract and Keywords

Aim: Individuals with amnesic mild cognitive impairment (aMCI) are at a high risk to develop Alzheimer's disease (AD). We compared CSF levels of biomarkers of amyloidosis ($A\beta_{1-42}$) and neurodegeneration (p-Tau₁₈₁) in individuals with aMCI and with subjective cognitive impairment (SCI) in order to ascertain diagnostic accuracy and predict the odds ratio associated with aMCI.

Methods: We collected CSF of individuals clinically diagnosed with aMCI (33) and SCI (12) of a memory clinic of Southern Brazil. Levels of $A\beta_{1-42}$ and p-Tau₁₈₁ were measured by immunoenzymatic assay. Participants also underwent neuropsychological testing including the verbal memory test subscore of the Consortium to Establish a Registry for Alzheimer's Disease (VM-CERAD).

Results: CSF concentration of $A\beta_{1-42}$ was significantly lower (p: 0.007) and p-Tau₁₈₁/ $A\beta_{1-42}$ ratio higher (p: 0.014) in aMCI individuals than in SCI. However, isolate p-Tau₁₈₁ levels were not associated with aMCI (p: 0.166). There was a statistically significant association between $A\beta_{1-42}$ and p-Tau₁₈₁ (R^2 : 0.177; β : -4.43; p: 0.017). ROC AUC of CSF $A\beta_{1-42}$ was 0.768 and of the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio equals 0.742. Individuals with $A\beta_{1-42}$ < 823 pg/mL levels were 6.0 times more likely to be diagnosed with aMCI (p: 0.019), with a 68.9% accuracy. Those with p-Tau₁₈₁/ $A\beta_{1-42}$ ratio > 0.071 were at 4.6 increased odds to have aMCI (p: 0.043), with a 64.5% accuracy. VM-CERAD was significantly lower in aMCI than among SCI (p: 0.041).

Conclusion: CSF $A\beta_{1-42}$, but not p-Tau₁₈₁, level was significantly associated with aMCI.

Keywords: Alzheimer; Amyloid; CSF Biomarkers; MCI; Tau.

1. Introduction

Mild cognitive impairment (MCI) is a disorder situated in the continuum between normal cognition and dementia. According to National Institute on Aging and the Alzheimer's Association (NIA-AA), the clinical characterization of MCI requires the presence all items below: (1) self- or informant -reported cognitive complain, (2) objective cognitive impairment, (3) preserved independence in functional abilities, and (4) no dementia. Individuals with MCI ascertained according to these core clinical criteria could be further sub classified into two categories: amnesic MCI (aMCI) if performance on neuropsychological tests of episodic memory is poor, and non-amnesic MCI (naMCI) in the case of poor performance on tests covering cognitive domains other than memory(Petersen et al., 2014).

Only a proportion of individuals with MCI progress to AD (Alzheimer's disease). According to criteria established by NIA-AA, the use of biomarkers may aid in identifying etiological MCI subtypes by differentiating between MCI due to AD (i.e.: prodromal AD) and MCI that is unlikely to be due to AD(Albert et al., 2011; Dubois et al., 2014).

Many biomarkers have been studied to support the clinical diagnosis of AD. Nonetheless, few have successfully defined AD signature. The most consistent ones have been related to compounds of neuritic plaques such as the β -amyloid protein ($A\beta_{1-42}$) and the main constituent of the neurofibrillary tangles, i.e., the hyperphosphorylated Tau protein (p-Tau₁₈₁)(Blennow et al., 2014). They are reported to be altered at least 5-10 years before dementia diagnosis(Jack et al., 2013). However, diagnostic accuracies of CSF biomarkers in MCI are still to be defined.

Although aMCI is a well-defined entity, it may be more difficult for non-specialists to proper diagnose this condition in their practice. In this sense, an exam that helps to discriminate normal aging from aMCI would be welcomed(Brandt, 2001). Moreover, accurate identification

of prodromal AD would become crucial when a disease-modifying drug becomes a reality (Cavedo et al., 2014).

Based on core criteria above we measured and compared the concentration of ($A\beta_{1-42}$ and p-Tau₁₈₁), in individuals clinically diagnosed with aMCI and with subjective cognitive impairment (SCI) in a manner to ascertain the diagnostic accuracy and verify the odds ratio to have aMCI.

2. Results

Table 1 compares the demographics characteristics and neuropsychological scores between aMCI and SCI groups. Mean age was 67.9 ± 5.4 years and the majority was women (71.1%). There was a significant difference in median verbal memory test subscore of the Consortium to Establish a Registry for Alzheimer's Disease (VM-CERAD) (Bertolucci et al., 1998) between aMCI and SCI groups ($p: 0.041$). No differences were found when we analyzed scores of Geriatric Depression Scale (GDS) (Almeida and Almeida, 1999) ($p: 0.724$) and Clock-Drawing Test (CDT) (Shulman et al., 1993) ($p: 0.825$) between aMCI and SCI. Our sample was composed mostly of a Caucasian population, as which reflects the demographics of the Southern Brazilian population. Only one individual in each group was African-Brazilian.

Table 2 describes CSF biomarkers concentration between aMCI and SCI. CSF concentration of $A\beta_{1-42}$ protein ($p: 0.007$), but not p-Tau protein ($p: 0.166$), was significantly different between the two groups. The p-Tau₁₈₁/ $A\beta_{1-42}$ ratio displayed significant difference between groups ($p: 0.014$). A linear regression analysis demonstrated significant association between $A\beta_{1-42}$ and p-Tau₁₈₁ protein ($R^2: 0.100$; $\beta: 95.19$; $p: 0.034$), even when adjusted for age ($R^2: 0.177$; $\beta: -4.43$; $p: 0.017$). When the two outliers showed in the Figure 1 were removed, the analysis remains significant ($R^2: 0.171$; $\beta: 1.77$; $p: 0.023$, adjusted for age).

$A\beta_{1-42}$ ROC AUC was 0.768 (CI 95%: 0.618 – 0.918; p: 0.007), as shown at Table 3. Cutoff value determined by the Youden index, that stretches the maximum potential effectiveness of a biomarker, was 823 pg/mL, with sensibility of 66.7% (CI 95%: 49.6- 80.2), specificity of 75% (CI95%: 46.7 - 91.1) and predictive positive value of 88% (CI95%: 73.67 - 95.05%). The logistic linear regression analysis revealed that individuals with $A\beta_{1-42} < 823$ pg/mL were 6.0 increased odds (p: 0.019) to have aMCI. When adjusted for age, the odds ratio almost did not change (6.2; p: 0.022). At this cutoff level, 31 of 45 individuals (68.9%) were correctly classified. ROC AUC of the ratio p-Tau₁₈₁/ $A\beta_{1-42}$ was 0.742 (CI 95%: 0.589 – 0.896; p: 0.014). The optimal cutoff value was 0.071, with sensibility of 60.6% (CI 95%: 43.6 - 75.3), specificity of 75% (CI95%: 46.7 - 91.1) and predictive positive value of 87% (CI95%: 71.60 - 94.63%). Individuals with the ratio p-Tau₁₈₁/ $A\beta_{1-42} > 0.071$ were at 4.6 increased odds (p: 0.043) to have aMCI. At this cutoff 29 of 45 individuals (64.5%) were correctly classified, but all of them were also adequately classified according to $A\beta_{1-42}$ levels alone.

3. Discussion

As expected, the concentration of $A\beta_{1-42}$ protein was significantly diminished in aMCI subjects than among SCI. However, p-Tau₁₈₁ protein was not different between groups. These results are in accord with the recently proposed biomarker behavior hypothetical model of AD (Jack et al., 2010). According to this model, CSF $A\beta_{1-42}$ levels declines before the p-Tau₁₈₁ increases. It is possibly that CSF p-Tau₁₈₁ levels only start to increase expressively as neurodegeneration advances. Considering this model, we can infer that at the moment the markers were measured at our sample, CSF p-Tau₁₈₁ concentration in aMCI may not have raised expressively yet. In fact, p-Tau₁₈₁ only increase in the CSF later than $A\beta_{1-42}$ starts to decrease (Buchhave et al., 2012).

Although we found no significant difference in levels of p-Tau₁₈₁, we verified a linear association of this protein with A β ₁₋₄₂, suggesting that they could be influenced by common mechanisms and/or influence each other. p-Tau₁₈₁/A β ₁₋₄₂ ratio displayed significant difference between groups at our study. This coefficient is frequently utilized because it presumes a link between β -amyloid and p-Tau pathways(Shaw et al., 2009). Indeed, p-Tau₁₈₁/A β ₁₋₄₂ ratio was already reported (1) to predict cognitive decline in cognitively normal elderly(Fagan et al., 2007), (2) to differentiate patients with AD from individuals without objective cognitive impairment(Ferreira et al., 2014), and (3) to predict MCI progression to AD(Ferreira et al., 2014).

Patients with AD dementia tends to have lower levels of CSF A β ₁₋₄₂ and higher levels of CSF p-Tau₁₈₁ than individuals without cognitive impairment(Blennow et al., 2010). It has been reported A β ₁₋₄₂ levels are reduced in about 50% among individuals with AD relatively to age-matched people without cognitive impairment (Holtzman, 2011). Although there are no established cutoff values for these CSF biomarkers general acceptable, some studies suggests cutoffs for CSF A β ₁₋₄₂ positivity in AD, which below 650 pg/mL when utilizing immunoenzymatic assays(Blennow et al., 2015). p-Tau₁₈₁ thresholds usually vary above 60 and 80 pg/mL at the demential phase of the disease(Tang et al., 2014b).

Cutoff points for A β ₁₋₄₂ and p-Tau₁₈₁ are still scarce and even unclear for aMCI individuals. A recent meta-analysis described that the levels of A β ₁₋₄₂ in aMCI individuals ranged from 172.6 \pm 53.5 to 622.9 \pm 275.6 pg/mL, whereas among healthy cognitively people they vary between 383.5 \pm 101.8 and 1020 \pm 230 pg/mL. However, none of these studies have direct compared aMCI to SCI. This meta-analysis suggests that there is no established threshold which can distinguish AD or aMCI from healthy cognitively individuals(Mo et al., 2015). Although this study does not differentiate aMCI from SCI, some older studies compared CSF A β ₁₋₄₂ levels in general MCI individuals and healthy cognitively people(Herukka et al., 2005;

Maruyama et al., 2001). One reported that CSF A β_{1-42} levels did not differ significantly between cognitively normal subjects and MCI groups(Maruyama et al., 2001), and other showed that values of CSF A β_{1-42} were significantly lower in progressive MCI group than in progressive and stable MCI groups(Herukka et al., 2005).

The broad variation at the measurements of these biomarkers between studies and laboratories is only one of the difficulties in determining homogenous cutoff points(Tang et al., 2014a). It might results from differences in CSF sample handling techniques, analytical procedures and kits. Cases selection criteria and resultant difference in sample characteristics are other problems. Standardization and quality control of these procedures may reduce the disparity and increase the utility of these CSF biomarkers(Samtani et al., 2013). To find the best cutoff values we used the Youden index. This is a standardized and objective method to determine diagnostic cutoff points. Youden index evaluates the maximum potential effectiveness of a biomarker by choosing the best values in terms of test accuracy, taking in consideration both sensibility and specificity (Ruopp et al., 2008; YOUDEN, 1950). Such cutoff points, however, are dependent of several variables, such as study population and phase of disease. In this sense, it would be important that other cross-sectional studies on aMCI be conducted in different regions of the globe in order to find their best own distinctive cutoff point to differentiate aMCI from SCI.

At our study, individuals with A β_{1-42} <823 pg/mL were 6.0 times more likely to be diagnosed with aMCI, with reasonable accuracy. At the ratio p-Tau₁₈₁/A β_{1-42} , individuals with >0.071 were at 4.6 increased odds to have aMCI. Thus, among the CSF biomarkers studied here, CSF A β_{1-42} concentration was the best analyte for detection of aMCI subjects (ROC AUC: 0.768). Thereby, indicating that CSF A β_{1-42} might be the most single informative biomarker for prodromal AD. To our knowledge, no previous study has measured CSF biomarkers that discriminates exclusively aMCI individuals from SCI and identified cut off values and odds

ratio to have aMCI, independently from previous neuropsychological and clinical evaluation. Our finding is important in order to correctly identify people who are at an imminent risk to progress to Alzheimer's disease dementia. We also aim to help non-specialists to properly diagnose aMCI and differentiate it from normal aging in clinical practice.

As expected, performance on VM-CERAD was significantly lower at aMCI group than at SCI. This finding probably means that aMCI cases and SCI individuals were well allocated. Conversely, GDS and CDT were not different between aMCI and SCI. Depression may be a cause of cognitive deficits or simulate aMCI. Our result probably means that depressed individuals were adequately excluded from our sample. In turn, CDT evaluates more executive function and visuospatial organization than memory itself. Vascular mild cognitive impairment is characterized by more impairment in executive functions and gait apraxia than is AD (Román and Royall, 1999). Therefore, it was also expected that there will be no differences in CDT scores between our pure aMCI individuals and SCI. In fact, this finding also suggests that we have appropriately excluded MCI cases other than the purely amnesic ones.

Limitations of our study include the relatively small sample size and the fact that it is a case-control study, therefore general causality cannot be inferred. Strengths include simultaneous analysis of CSF biomarkers and neuropsychological evaluation in a group at high risk for developing AD. Moreover, biomarkers measures and cognitive and affective tests were conducted by blind persons, using validated methods.

3.1 Conclusion

To our knowledge, this is the first study that evaluated CSF $A\beta_{1-42}$ to discriminate exclusively aMCI individuals from SCI and identified cut off values and odds ratio of to have aMCI. Moreover, we found no value for CSF p-Tau₁₈₁ *vis-à-vis* CSF $A\beta_{1-42}$ alone in predicting aMCI diagnosis.

4. Methods and Materials

4.1 Study participants and clinical classification

We included thirty three subjects with aMCI, and twelve individuals with SCI, without evidence of objective impairment, in the study. All were sixty years or older. They were referred to a memory clinic of Southern Brazil called “Hospital de Clínicas de Porto Alegre”. The sample size was based in a conservative estimation of AD’s pathology among aMCI (70%) and SCI (10%). Considering a power of 90%, significance of 5% and 1/3 of losses(Markesbery, 2010).

Participants were submitted to an evaluation that was performed blindly by a behavioral neurologist and a neuropsychologist, and included a structured clinical interview, a full neurological examination, and neuropsychological assessment. NIA-AA criteria for aMCI was used(Albert et al., 2011; Petersen et al., 2014) and corroborated by Clinical Dementia Rating (CDR)(Morris, 1993). Cases fulfilled the criteria for aMCI and scored 0.5 on CDR, and SCI were individuals who had no evidence of objective cognitive decline by NIA-AA criteria and scored CDR: 0.

We excluded subjects who had evidence of dementia, stroke, cerebrovascular disease, Parkinson’s disease, depression or other neurological disease that potentially cause cognitive impairment. A questionnaire was applied in order to assess the following socio demographic data: age, sex, occupation and years of schooling.

4.2 Neuropsychological assessments

We utilized the VM-CERAD, Brazilian validated adaptation (Bertolucci et al., 1998). In order to assess verbal episodic memory function this evaluation was performed by a certified and blind neuropsychologist. The final score was composed by a possible sum of 30 points for the word list learning, 10 points for word list recall and 10 points for word list recognition (total of 50 possible points) (Chandler et al., 2005). The 0-5 points version of CDT was also utilized (Shulman et al., 1993). The GDS 15-item version, translated and validated to Brazilian Portuguese was applied (Almeida and Almeida, 1999). Presence of significant depressive symptomatology was considered for all subjects who scored ≥ 6 points in the scale.

4.3 CSF analysis

All participants underwent a fasted lumbar puncture to obtain CSF samples. Briefly, CSF (5ml) was collected in polypropylene tubes and immediately centrifuged (4,000 g X 10 minutes) at 4°C and then stored at -80°C until assay. We used commercially available ELISA kits to determine levels of A β ₁₋₄₂ (Innotest β -amyloid1-42, Fujirebio-Europe, Gent, Belgium) and p-Tau₁₈₁ (Innotest Phospho-Tau181P, Fujirebio-Europe) following the manufacturers' recommendations. CSF tests were performed blindly after clinical evaluation, in duplicate, and the laboratory technician was also blinded to any clinical and demographic information about the study participants.

4.4 Statistical analysis

Statistical analyses were performed using SPSS (the Statistical Package for Social Sciences) version 20. To compare gender distribution between the groups, a Chi-square test was performed. Subsequently, Mann–Whitney U tests were performed to compare clinical, neuropsychological and biomarker data between the groups. A linear regression analysis was used to verify the relationship between proteins. Receiver operating characteristic (ROC) curve analyses were used to obtain area under the curve (AUC), that express the probability of a

positive case test randomly chosen will exceed the outcome of a randomly chosen negative case. The optimal cutoff values were determined by calculating the maximal sum of sensitivity and specificity (i.e., maximizing the Youden index (YOU DEN, 1950)). The accuracy of the tests was determined by the proportion of true results (both true positives and true negatives) among the total number of cases examined. Logistic linear regression was performed to verify the odds ratio. All results were showed as CI95% and p value <0.05 was considered significant. Values were adjusted for age.

4.5 Ethical considerations

All participants gave their written consent, and the study was approved by the local ethics committee. This study was conducted in accord with the Declaration of Helsinki.

5. Acknowledgements

This study was supported by CAPES-CNPQ and FIPE. The funding sources had no involvement in study design, in the collection, analysis and interpretation of data, in the writing of the report, and in the decision to submit the article for publication.

6. Disclosure statement

All authors declare no actual or potential conflict of interests including any financial, personal or other relationships with other people or organizations.

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Table 1

Demographics characteristics and neuropsychological scores.

	aMCI	SCI	ρ value
n	33	12	
Age (years): median (min-max)	68 (61-78)	63.5 (60-76)	.053
Education (years): median (min-max)	11 (1-18)	11 (5-18)	.211
Gender, (male/female): n	10/23	3/9	.120
GDS: median (min-max)	2 (0-5)	1 (0-5)	.724
VM-CERAD: median (min-max)	27 (18-37)	31 (23-40)	.041
CDT: median (min-max)	4 (1-5)	4 (1-5)	.825

†aMCI: amnesic Mild Cognitive Impairment; CDT: Clock Drawing Test; GDS: Geriatric Depression Scale; SCI: Subjective Cognitive Impairment; VM-CERAD: Verbal Memory test subscore of the Consortium to Establish a Registry for Alzheimer's Disease. ‡ Mann-Whitney test was used, except for sex (Chi-Square Test).

Table 2

CSF biomarkers features.

	aMCI	SCI	ρ value
n	33	12	
A β ₁₋₄₂ (pg/mL): median (P25 – P75)	677.82 (493.72 - 913.35)	985.99 (757.67 - 1096.57)	0.007
p-Tau ₁₈₁ (pg/mL): median (P25 – P75)	64.94 (50.32 - 85.08)	55.26 (48.54 - 69.87)	0.166
p-Tau ₁₈₁ / A β ₁₋₄₂ ratio: median(P25 – P75)	0.075 (0.059 - 0.167)	0.059 (0.051 - 0.074)	0.014

†aMCI: amnesic Mild Cognitive Impairment; SCI: Subjective Cognitive Impairment. P25: percentile 25; P75: percentile 75. ‡ Mann-Whitney test was used.

Table 3

ROC Curve Parameters.

Parameters	A β ₁₋₄₂	p-Tau ₁₈₁ /A β ₁₋₄₂
ROC AUC (CI95%)	0.768 (0.618 – 0.918)	0.742 (0.589 – 0.896)
Threshold value (pg/mL)	823	0.071
Sensitivity (%) (CI95%)	66.7 (49.6 - 80.2)	60.6 (43.6 - 75.3)
Specificity (%) (CI95%)	75.0 (46.7 - 91.1)	75.0 (46.7 - 91.1)
Test accuracy (%)	68.9	64.5

†ROC: receiver operating characteristic; AUC: area under the curve ‡Youden index was used. §Both specificities were exactly the same.

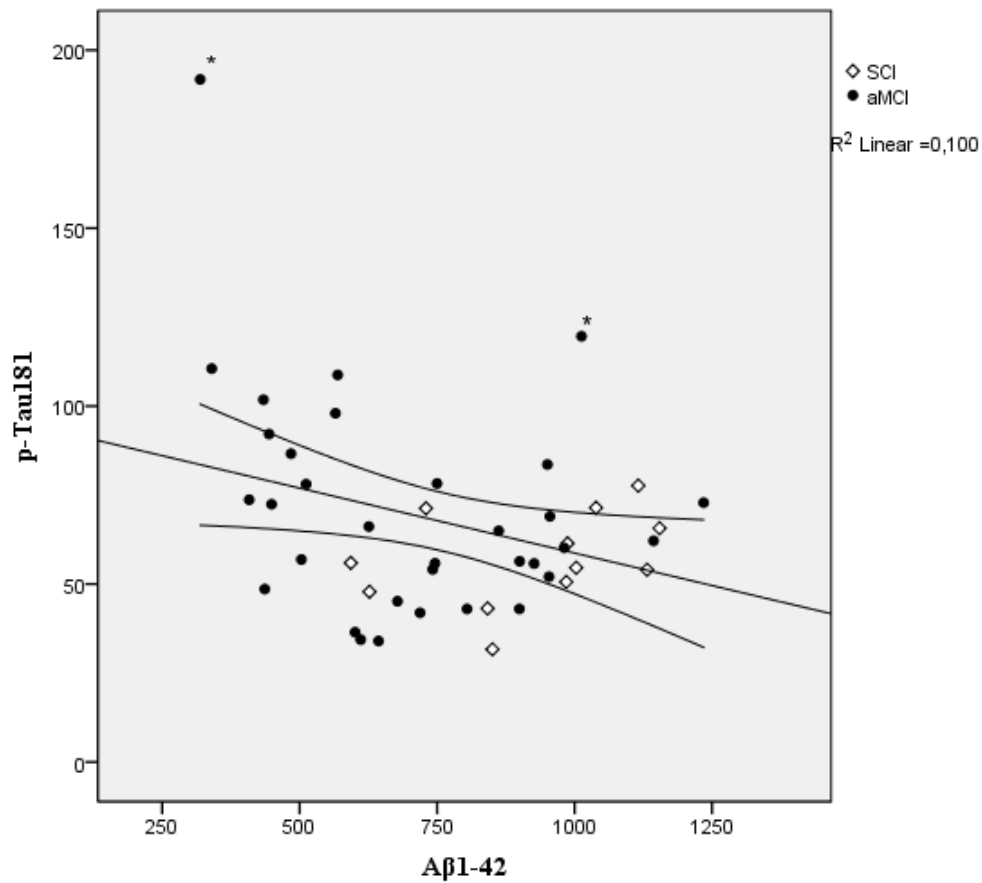


Figure 1. Linear regression analysis between $A\beta_{1-42}$ and p-Tau₁₈₁ (pg/mL) (β : 95.19; p: 0.034), showing a linear dependence. Distribution at SCI and MCI cases. When adjusted for age, R^2 : 0.177; β : -4.43; p: 0.017. Even when the two outliers (*) showed at the figure were removed, the linear regression remains significant (R^2 : 0.171; β : 1.77; p: 0.023, adjusted for age). †aMCI: amnesic Mild Cognitive Impairment; SCI: Subjective Cognitive Impairment.

2. ARTIGO CIENTÍFICO ORIGINAL II

Estudo longitudinal de três anos de seguimento da coorte com CCL-a disponível online na revista NeuroMolecular Medicine em 10.10.2018 (<https://doi.org/10.1007/s12017-018-8516-8>).

Title: CSF A β ₁₋₄₂, but not p-Tau₁₈₁, predicted progression from amnesic MCI to Alzheimer's disease dementia

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ABSTRACT

Objective: To determine whether $A\beta_{1-42}$ and p-Tau₁₈₁ cerebral spinal fluid (CSF) levels can predict progression from amnesic Mild Cognitive Impairment (aMCI) to Alzheimer's disease dementia (ADD) in a three-year follow-up study.

Methods: All participants were evaluated blindly by a behavioral neurologist and a neuropsychologist, and classified according to the Petersen criteria for aMCI and according to the Clinical Dementia Rating (CDR) scale. Individuals were also submitted to lumbar puncture at baseline. Levels of $A\beta_{1-42}$ and p-Tau₁₈₁ were measured by immunoenzymatic assay. Values were adjusted for age and sex.

Results: Thirty-one of 33 (93.9%) participants completed follow-up. Approximately 39% of aMCI individuals progressed to ADD. The relative risk of developing ADD in those with $A\beta_{1-42}$ CSF levels lower than 618.5 pg/mL was 17.4 times higher than in those whose levels were higher than 618.5 pg/mL ($P = 0.003$). p-Tau₁₈₁ alone did not predict progression to ADD ($P = 0.101$). The relative risk in those with a p-Tau₁₈₁/ $A\beta_{1-42}$ ratio higher than 0.135 was 5.7 times greater ($P < 0.001$). $A\beta_{1-42}$ and p-Tau₁₈₁ explained 40.1% of the verbal memory test subscore of the Consortium to Establish a Registry for Alzheimer's Disease (Δ CERADs) variance ($P = 0.008$).

Conclusion: $A\beta_{1-42}$ strongly predicted progression from aMCI to ADD. p-Tau₁₈₁ alone, or its relation to $A\beta_{1-42}$, was inferior than $A\beta_{1-42}$ alone as a predictor of progression to ADD.

Key words: Alzheimer's disease; amyloid protein; CSF biomarkers; MCI; Tau.

INTRODUCTION

The correct identification of people at risk to develop Alzheimer's disease dementia (ADD) is crucial in terms of early diagnosis (prodromal Alzheimer), prognosis and treatment. Research efforts to improve the positive predictive value of progression from amnesic mild cognitive impairment (aMCI) to ADD are needed, since many trials on disease modifying drugs fail because of low progression rates. In this sense, efforts to correctly identify individuals with prodromal AD are of utmost importance (McGeer and McGeer, 2013; Molinuevo et al., 2014). Even so, it is often difficult to identify who among those with aMCI will progress to ADD based solely on neuropsychological evaluations (Petersen et al., 2014).

Different biomarkers demonstrated to be useful diagnostic tools *in vivo*, and are now gaining attention in the clinical practice after being incorporated into research criteria for AD (Albert et al., 2011; Dubois et al., 2014; Morris et al., 2014). The combination of decreased concentrations of beta amyloid protein ($A\beta_{1-42}$) and increased concentrations of hyperphosphorylated Tau protein (p-Tau₁₈₁) in the CSF is related to AD pathology and may predict the progression to ADD (Jack et al., 2013; Jack et al., 2010).

Many studies have evaluated the value of CSF biomarkers in predict progression from MCI to ADD (Ferreira et al., 2014b; Prestia et al., 2015; Ritchie et al., 2014; Tondelli et al., 2015; Vos et al., 2013). However, no study has evaluated the relative risk to develop ADD in an exclusively amnesic MCI patient sample in a three-year follow-up. This study consisted of measuring the concentrations of both CSF $A\beta_{1-42}$ and p-Tau₁₈₁ proteins in a sample of exclusive amnesic MCI subjects and analyzing to which extent these biomarkers could predict progression to ADD in a three-year follow-up. The relationship and agreement of these biomarkers with neuropsychological tests was then verified.

MATERIAL AND METHODS

Participants

Thirty-three subjects diagnosed with aMCI from a memory clinic in Southern Brazil were included in the study. All individuals were evaluated by a behavioral/geriatric neurologist and the National Institute on Aging – Alzheimer’s Association (NIA-AA) criteria for MCI (Albert et al., 2011), corroborated by the Clinical Dementia Rating scale (CDR) (Morris, 1993). aMCI diagnoses were based on criteria by Petersen and colleagues (Petersen, 2004; Petersen et al., 2014). We excluded those who had diagnosis of dementia, stroke, Parkinson’s disease, depression or other neurological conditions that could possibly cause cognitive impairment. Furthermore, we also excluded individuals with normal cognition. A questionnaire was applied in order to obtain sociodemographic data.

Standard Protocol Approvals, Registrations, and Patient Consents

This study was approved by the local research ethics committee and is in accordance with the Declaration of Helsinki. All participants gave their written consent in order to participate in this study.

CSF analyses

All participants underwent a fasted lumbar puncture to measure $A\beta_{1-42}$ and p-Tau₁₈₁ proteins in the CSF. CSF (5ml) was collected in polypropylene tubes and immediately centrifuged (4,000 g x 10 minutes) at 4°C and then stored at -80°C until the assay. Commercially-available ELISA kits were used to determine the levels of $A\beta_{1-42}$ (Innotest β -amyloid1-42, Fujirebio-Europe,

Gent, Belgium) and p-Tau₁₈₁ (Innotest Phospho-Tau181P, Fujirebio-Europe). Tests were performed in duplicate and the laboratory technician was blinded to any clinical and demographic information about the participants.

Neuropsychological tests

At baseline, participants were submitted to a battery of neuropsychological evaluations performed by a certified neuropsychologist. We utilized the validated adaptation for Brazilian patients version of the verbal memory test subscore of the Consortium to Establish a Registry for Alzheimer's Disease (CERADs)(Morris et al., 1989)(Bertolucci et al., 1998). The final score was composed by a possible sum of 30 points for word list learning, 10 points for word list recall and 10 points for word list recognition (total of 50 possible points)(Chandler et al., 2005). The Geriatric Depression Scale (GDS) 15-item version(Yesavage et al., 1982), which was translated and validated to Brazilian portuguese(Almeida and Almeida, 1999), was utilized to screen for depressive symptoms.

After three years of follow-up, subjects were reassessed in order to verify whether or not they progressed to ADD. Evaluation was performed blindly by the same behavioral neurologist and neuropsychologist, and included a structured clinical interview, a full neurological examination, and neuropsychological evaluation. At this time, they were analyzed by NIA-AA criteria for ADD(McKhann et al., 2011), corroborated by the CDR, and were classified in two groups: progressors (P), and non-progressors (NP) to ADD. The neuropsychological tests, besides those performed at baseline, included the Montreal Cognitive Assessment (MoCA)(Memória et al., 2013; Nasreddine et al., 2005), Boston Naming Test (BNT)(Kaplan et al., 1983; Miotto et al., 2010), Verbal Fluency Test, animals category (VFT)(Brucki et al., 1997; Isaacs and Kennie, 1973) and Constructional Praxis (CP)(Bertolucci et al., 2001; Rosen et al., 1984), all translated

and validated to Brazilian Portuguese. Instead of MMSE, we preferred to utilize MoCA because it has been shown to be more accurate in detecting MCI than MMSE(Trzepacz et al., 2015).

Statistical analyses

Statistical analyses were performed using the Statistical Package for Social Sciences (SPSS) version 20. To compare sex distribution, a Chi-square test was performed. Mann–Whitney tests were performed to compare clinical, neuropsychological and biomarker data. Receiver operating characteristic (ROC) curve analyses were used to obtain the area under the curve (AUC) and other parameters. The optimal cutoff values were determined by calculating the maximal sensitivity and specificity (i.e., maximizing the Youden index(Youden, 1950)). The Generalized Estimating Equation Model with the Bonferroni *post-hoc* test was applied to verify the mean of CERADs score between groups, discriminated by time. Linear regressions were performed to evaluate the relationship among Δ CERADs and CSF biomarkers. Values were adjusted for age and sex. All results were showed as confidence intervals CI 95% and *P* values <0.05 were considered significant.

RESULTS

Thirty-one of 33 (93.9%) participants completed the follow-up. Of these, twelve (38.4%) progressed to ADD after three years. Mean age was 68.1 ± 5.1 years and 67.75% were female. No participants deceased during the follow-up. Table 1 lists the demographic characteristics and baseline neuropsychological scores between P and NP. There was no significant difference between groups when baseline characteristics were analyzed.

Table 2 lists the neuropsychological scores after three years of follow-up and CSF biomarker features. $A\beta_{1-42}$ concentrations in CSF were significantly different between groups ($P < 0.001$), as opposed to p-Tau₁₈₁ concentrations ($P = 0.101$). The p-Tau₁₈₁/ $A\beta_{1-42}$ ratio also displayed a significant difference between groups ($P < 0.001$). The CERADs and MoCA tests differed significantly at endpoint as well ($P = 0.006$ and $P = 0.025$, respectively).

In Table 3, cutoff values were determined by Youden's index, which stretches the maximum potential effectiveness of a biomarker. For $A\beta_{1-42}$, the threshold value was 618.5 pg/mL, with 91.7% sensitivity (CI95%: 64.6 – 98.5) and 94.7% specificity (CI95%: 75.4 – 99.0). At this cutoff level, 29 of 31 individuals (93.5%) were correctly classified in P or NP. The relative risk of developing ADD in those directly exposed ($A\beta_{1-42} < 618.5$ pg/mL) was 17.4 times higher than among those who were not exposed (CI95%: 2.5 – 118.2; $P = 0.003$). In other words, those who had values above this concentration had their risk of developing ADD reduced by 94.3%. The optimal cutoff value for the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was 0.135, with 66.7% sensitivity (CI95%: 39.0 – 86.2) and 100% specificity (CI95%: 83.2 – 100.0). At this cutoff value, 27 of 31 individuals (87%) were correctly classified as P or NP. The relative risk of developing ADD in those whose p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was higher than 0.135 was 5.7 times greater when compared to those with a lower p-Tau₁₈₁/ $A\beta_{1-42}$ ratio (CI95%: 2.3 – 14.0; $P < 0.001$).

As measure of experimental validity, Fig. 1 displays the mean and standard errors of the CERADs score for each group discriminated by the baseline and follow-up times in years (baseline in 2013; follow-up in 2016). When the time was set and the groups were compared, there was no difference in the CERADs score of the NP group ($P = 0.437$), but there was a significant difference in the P group ($P < 0.001$). When the groups were fixed and times were compared, there was no difference between groups in 2013 ($P = 0.575$), but, in 2016, a significant difference between P and NP was observed ($P = 0.004$).

Δ CERADs was defined as the difference between CERADs score from 2016 and 2013. Δ CERADs was statistically different between P and NP groups ($P = 0.002$) and correlated with $A\beta_{1-42}$ levels ($P = 0.011$), p-Tau₁₈₁ levels ($P = 0.045$) and p-Tau₁₈₁/ $A\beta_{1-42}$ ratio ($P = 0.010$). $A\beta_{1-42}$ and p-Tau₁₈₁ levels explained 40.1% of Δ CERADs variance (B:-6.2; SE: 13.7; $P = 0.008$). As demonstrated in Fig. 2, $A\beta_{1-42}$ alone explained 26.8% of Δ CERADs variance ($P = 0.036$), whereas p-Tau₁₈₁ alone accounted for 27.5% of Δ CERADs variance ($P = 0.032$).

DISCUSSION

In this study, 38.7% of aMCI individuals progressed to ADD, a rate which is consistent with previous studies (Schjønning Nielsen et al., 2016). CSF concentration of $A\beta_{1-42}$ was significantly diminished in the P group ($P < 0.001$), whereas there was no difference in p-Tau₁₈₁ levels between groups ($P = 0.101$). These results are in line with the model of dynamic pathophysiological biomarkers in AD (Jack et al., 2013), in which $A\beta_{1-42}$ levels in the CSF becomes abnormal 5–10 years or before the diagnosis of dementia. A meta-analysis of fifty studies confirmed that $A\beta_{1-42}$ is a good biomarker for discriminating ADD from MCI and other dementias (Ferreira et al., 2014a). Moreover, our group recently demonstrated that $A\beta_{1-42}$, but not p-Tau₁₈₁, is significantly associated with aMCI (Rizzi et al., 2018). Previous studies agree that p-Tau₁₈₁ levels in the CSF become progressively abnormal, and have better predictive power only 0–5 years before progression to ADD (Buchhave et al., 2012). The p-Tau₁₈₁/ $A\beta_{1-42}$ ratio also showed significant difference ($P < 0.001$) between patients that progressed to ADD versus those who did not. The literature supports the evidence that the combination of $A\beta_{1-42}$ and p-Tau₁₈₁ protein levels is a suitable measure for MCI prognosis (Ferreira et al., 2014a).

In the CSF, the $A\beta_{1-42}$ concentration displayed a cutoff value of 618.5 pg/mL for aMCI cases, with greater sensitivity and specificity when compared to similar reports in the

literature(Ferreira et al., 2014a; Ritchie et al., 2014). From this value, we can infer that the relative risk to develop ADD in those whose CSF $A\beta_{1-42}$ levels was lower than 618.5 pg/mL was about 17.4 times higher than in those whose level was above this value. Other studies described different values associated with the relative risk of developing ADD from MCI. Michaud and colleagues(Michaud et al., 2015) found a hazard ratio of developing ADD among MCI patients with high-risk biomarker levels about 4 times greater than in MCI patients with low-risk biomarker values. Tondelli and collaborators(Tondelli et al., 2015) established that $A\beta_{1-42}$ was helpful to discriminate between MCI and dementia, with a relative risk of 1.01 in MCI patients. Here we emphasizes that our cutoff value was specific for amnesic MCI patients, even though our sample size was small. The interpretation of any comparative results should be made with caution due to the heterogeneity of the population that was evaluated in this study.

For the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio in CSF, the optimal cutoff value was 0.135, with less sensitivity than $A\beta_{1-42}$ alone, but with 100% of specificity. The relative risk of developing ADD in those whose ratio was higher than 0.135 was 5.7 times greater than in those whose ration was lower than 0.135. Michaud and colleagues found that $A\beta_{1-42}$ and p-Tau₁₈₁ were the best combination among CSF biomarkers to predict the overall risk of developing ADD among MCI patients with an area under the curve of 0.77(Michaud et al., 2015). In our study, $A\beta_{1-42}$ alone (AUC: 0.961) performed better than the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio (AUC: 0.864) in predicting overall risk, but the combination of the two proteins showed a better positive predictive value (100%). Prestia and colleagues found that the best predictive accuracy was achieved by combinations of amyloidosis and neurodegeneration biomarkers(Prestia et al., 2015). Moreover, in a recent meta-review(Ferreira et al., 2014a) it was found that the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was the most accurate CSF measure in predicting ADD progression from MCI. Our finding that $A\beta_{1-42}$ levels alone is a superior, more accurate, measure when compared to the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio needs

to be confirmed in further studies with larger samples sizes and a more heterogeneous population.

Although several different possible cut-off values were proposed, there is a lack of agreement on which would be the best discriminant value. This controversy might be due to the variability in CSF measurements between laboratories that utilize different techniques (Samtani et al., 2013; Tang et al., 2014). We decided to find the best cut-off values for our sample by utilizing the Youden test (Youden, 1950), differently from other reports in which the threshold values were based on laboratory cut-off points that were based on different populations and methodologies (Ritchie et al., 2014). For instance, difficulties in predicting MCI progression to ADD could be influenced by the intrinsic heterogeneity of MCI individuals.

After three years of follow-up, only CERADs and MoCA tests reflected differences between the P and NP groups. These results agree with our baseline selection of exclusively aMCI cases, since episodic memory is the major cognitive domain impaired in this subtype of MCI patients (Gifford et al., 2015). There was no significant difference in the GDS test, although some patients who did not progress to ADD presented depressive symptoms after three years.

The CERADs test was performed at baseline and again after three years. As Fig. 1 shows, there was no difference between groups at baseline, but over time it was observed a significant decline in the episodic memory of those who progressed to ADD. This pattern was not verified in the NP group, which performed similarly at baseline and follow-up. Additionally, Δ CERADs correlated with the two proteins alone, besides correlating with their combination ratio. This finding reinforces the early and specific involvement of episodic memory in the prodromal phase of AD. Haldenwanger and colleagues already emphasized the existence of a significant correlation between $A\beta_{1-42}$ in the CSF and memory performance for aMCI patients, but not for non-amnesic MCI (Haldenwanger et al., 2010). Rami and collaborators also suggested that

memory performance is first related with $A\beta_{1-42}$ levels and then with t-Tau or p-Tau₁₈₁(Rami et al., 2011). Moreover, a recent study suggested that, in particular, $A\beta_{1-42}$ protein is associated with a delayed memory performance CERAD(Haapalinna et al., 2016), agreeing with our results. $A\beta_{1-42}$ and p-Tau₁₈₁ levels explained 40.1% of Δ CERADs variance, better than each one alone.

Often, MCI represents an intermediate stage between normal cognition and dementia(Petersen et al., 2014). In one year, about 10-15% of MCI patients develop ADD. In 5 years, this number can raise up to 40-60%(Schjønning Nielsen et al., 2016; Tondelli et al., 2015). To our knowledge, this is the first study that evaluated the relative risk of both $A\beta_{1-42}$ and p-Tau₁₈₁/ $A\beta_{1-42}$ ratio in predicting progression from aMCI to ADD in an exclusively amnesic MCI sample, in a three-year follow-up.

An important limitation of our study is the relatively small sample size. Another possible methodologic drawback is the absence of controls. Nonetheless, in this study we did not aim to evaluate differences between individuals with aMCI and controls, but, instead, to analyze the role of CSF $A\beta_{1-42}$ and p-Tau₁₈₁ in predicting progression from aMCI to ADD. In another words, we tried to answer a common question that physicians find in everyday practice: what is the predictive value of analyzing $A\beta_{1-42}$ and p-Tau₁₈₁ in the CSF of individuals with aMCI?

CONCLUSION

Taken together, our results suggest that the CSF biomarkers analyzed herein provide predictive information about progression from aMCI to ADD. $A\beta_{1-42}$ strongly predicted progression from aMCI to ADD, whereas p-Tau₁₈₁ alone or its relation to $A\beta_{1-42}$ were no better than $A\beta_{1-42}$ alone

as a progression to ADD predictor. However, the CSF p-Tau₁₈₁/A β ₁₋₄₂ ratio did improve the specificity and negative predictive value as compared to CSF A β ₁₋₄₂ levels alone.

ROLE OF THE FUNDING SOURCE

This study was supported by CAPES-CNPQ (Grant number: 476387/2013-2) and FIFE (Process: 13-0009). All authors declare that their funding source had no role in the study design, in the collection, analysis and interpretation of data, in the writing of the report, and in the decision to submit the paper for publication.

DECLARATION OF INTEREST

The authors hereby declare that there are no actual or potential conflicts of interest that may have affected the discussion presented.

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Table 1. Patients characteristics and baseline neuropsychological scores.

	Progressors	Non-Progressors	P value	
n (%)	12 (38.7%)	19 (61.3%)		
Age (years): median (min –max)	69 (63-76)	67 (61-78)	0.765	
Education (years): median (min –max)	9.5 (3-18)	11.0 (1-16)	0.191	
Gender (male/female): n	3/9	7/12	0.492	
GDS: median (min –max)	2.5 (0-5)	2.0 (0-5)	0.562	
CERADs: median (min –max)	26.5 (18-37)	27.0 (22-34)	0.535	GDS:

Geriatric Depression Scale; CERADs: Consortium to Establish a Registry for Alzheimer's Disease. All results were obtained performing the Mann-Whitney test, with the exception of gender, in which the Chi-Square Test was used.

Table 2. Relationship between baseline CSF A β ₁₋₄₂, p-Tau₁₈₁, and neuropsychological scores at follow-up.

	Progressors	Non progressors	P value
n (%)	12 (38.7%)	19 (61.3%)	
A β ₁₋₄₂ (pg/mL): median (min –max)	466.5 (319.1 – 742.0)	900.1 (503.3 – 1234.6)	<0.001
p-Tau ₁₈₁ (pg/mL): median (min –max)	82.3 (34.3 – 191.7)	56.4 (33.9 – 119.6)	0.101
p-Tau ₁₈₁ / A β ₁₋₄₂ ratio: median (min –max)	0.17 (0.05 – 0.60)	0.06 (0.04 – 0.11)	<0.001
GDS: median (min –max)	2 (1 – 5)	2 (0 – 11)	0.857
CERADs: median (min –max)	19 (5 – 36)	27 (18 – 35)	0.006
MoCA: median (min –max)	18.5 (9 – 27)	23.0 (14 – 28)	0.025
BNT: median (min –max)	13 (9 – 15)	14 (8 – 15)	0.509
VFT: median (min –max)	15 (5 – 27)	15 (8 – 20)	0.646
CP: median (min –max)	6 (2 – 10)	7 (2 – 11)	0.326

GDS: Geriatric Depression Scale; CERADs: Consortium to Establish a Registry for Alzheimer's Disease; MoCA: Montreal Cognitive Assessment; BNT: Boston Naming Test; VFT: Verbal Fluency Test, animals category; CP: Constructional Praxis. All results were obtained via the Mann-Whitney test.

Table 3. ROC curve parameters of CSF biomarkers in predicting progression from aMCI to ADD.

Threshold values	Progressors	Non-Progressors	ROC AUC (CI95%)	Sensitivity (%) (CI95%)	Specificity (%) (CI95%)	Test accuracy (%)	Positive Predictive Value (%)	Negative Predictive Value (%)
$A\beta_{1-42} < 618.5 \text{ pg/mL}$	11	1	0.961 (0.898 - 1.00)	91.7 (64.6 - 98.5)	94.7 (75.4 - 99.0)	93.5	91.7	94.7
$A\beta_{1-42} > 618.5 \text{ pg/mL}$	1	18						
$p\text{-Tau}_{181} / A\beta_{1-42} > 0.135$	8	0	0.864 (0.721 - 1.00)	66.7 (39.0 - 86.2)	100 (83.2 - 100.0)	87.0	100.0	82.6
$p\text{-Tau}_{181} / A\beta_{1-42} < 0.135$	4	19						

aMCI: amnesic mild cognitive impairment; ADD: Alzheimer's disease dementia; ROC: receiver operating characteristic; AUC: area under the curve. Youden index was used.

Figures

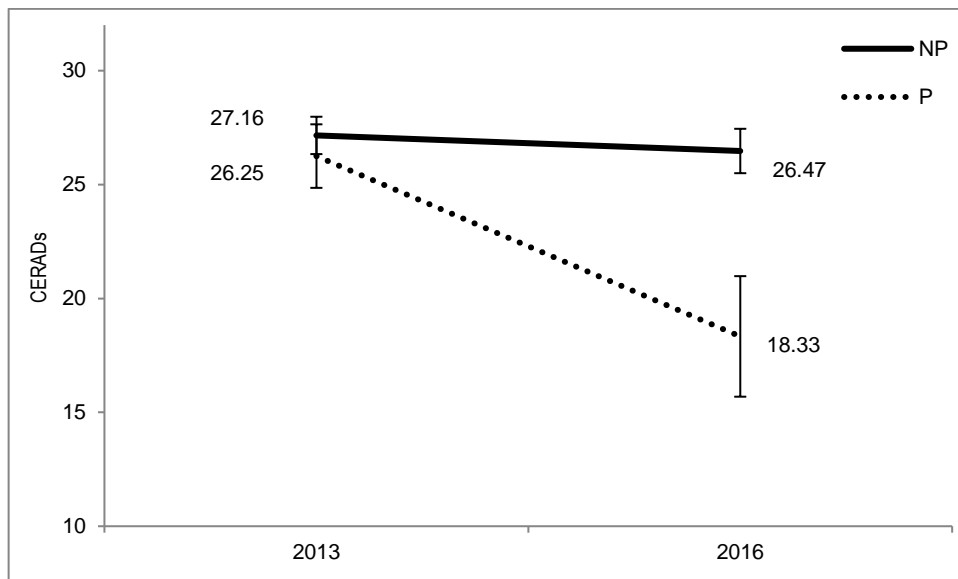


Fig. 1 Line chart of the means and standard errors of the CERADs score of each group. There was an association between variables ($P < 0.001$). When the time was set and the groups were compared, there was no difference in the NP group ($P = 0.437$) but there was a significant difference in the P group ($P < 0.001$). When the groups were fixed and times were compared in 2013 (baseline), there was no difference between groups ($P = 0.575$). When times were compared in 2016 (follow-up), there was a statistical difference between groups ($P = 0.004$). P: Progressors; NP: Non-progressors; CERADs: Consortium to Establish a Registry for Alzheimer's Disease. Generalized Estimating Equation Model with the Bonferroni *post-hoc* test was used

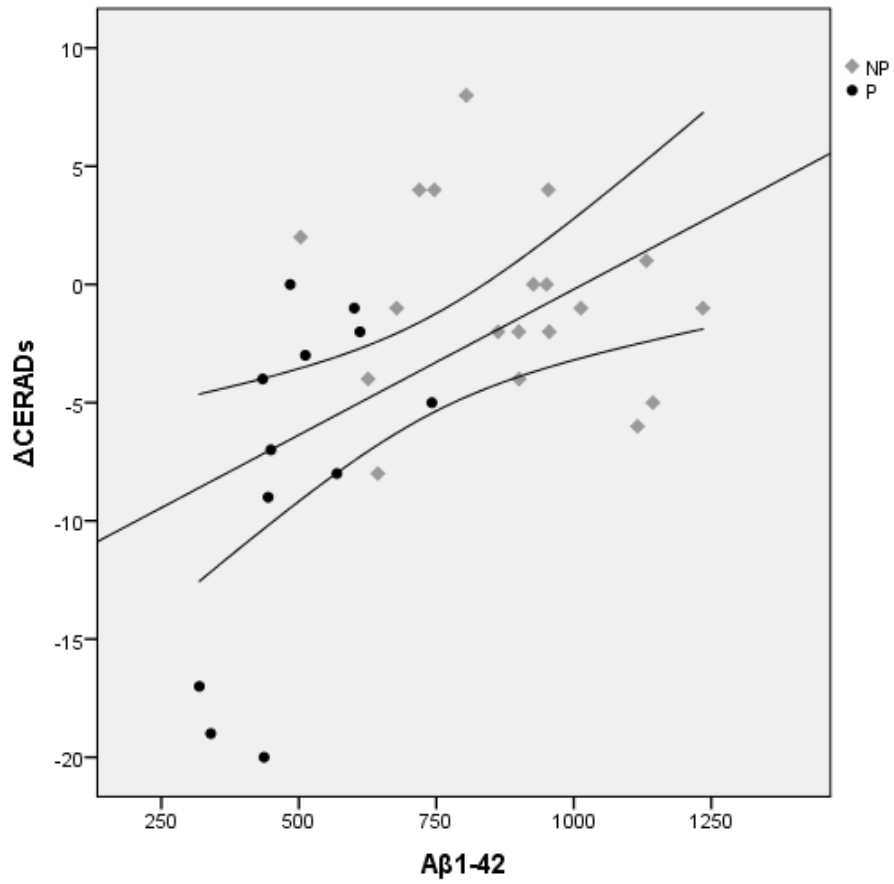


Fig. 2 Linear relationship between $A\beta_{1-42}$ (pg/mL) and Δ CERADs (R^2 : 0.268; P = 0.036). Values were adjusted for age and sex. Distribution at P and NP. P: Progressors; NP: Non progressors; CERADs: Consortium to Establish a Registry for Alzheimer's Disease

3. ARTIGO CIENTÍFICO ORIGINAL III

Estudo longitudinal final de cinco anos de seguimento da coorte inicial a ser submetido.

Title: Value of CSF biomarkers in predicting risk of progression from aMCI to ADD: a 5-year follow-up study

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ABSTRACT

Objective: To approach cerebrospinal fluid (CSF) $A\beta_{1-42}$ and p-Tau₁₈₁ as risks factors in predicting progression from amnesic mild cognitive impairment (aMCI) to Alzheimer's disease dementia (ADD) in a 5-year follow-up.

Methods: Forty-two individuals diagnosed as aMCI or SCI were evaluated in 2013 and reevaluated in 2018. CSF $A\beta_{1-42}$ and p-Tau₁₈₁ were measured by immunoenzymatic assay, and cutoffs were calculated with the Youden test. Differences in performance between endpoint and baseline were verified by neuropsychological tests, such as the Consortium to Establish a Registry for Alzheimer's Disease (CERADs) and Montreal Cognitive Assessment (MoCA). Values were adjusted for age.

Results: 45.2% of the aMCI individuals progressed to ADD. The cumulative risk to develop ADD in individuals with aMCI and $A\beta_{1-42} < 618.5$ pg/mL was 5.8 times higher than in those whose levels were above this cutoff ($P = 0.0011$). Moreover, the relative risk among those in which the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was higher than 0.135 was 3.83 times greater ($P = 0.0001$). Both $A\beta_{1-42}$ and p-Tau₁₈₁ levels explained 47.5% of Δ CERADs variance ($P < 0.001$), whereas $A\beta_{1-42}$ alone explained 38.6% ($P < 0.001$).

Conclusion: The p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was no better than $A\beta_{1-42}$ alone in predicting progression from aMCI to ADD. However, p-Tau₁₈₁ levels helped to explain an extra 9% of Δ CERADs variance in 5 years.

Key words: Alzheimer's disease; amyloid protein; CSF biomarkers; MCI; Tau.

INTRODUCTION

The new research framework, proposed by the National Institute on Aging and Alzheimer's Association (NIA-AA), defined that Alzheimer's disease (AD) underlying pathologic processes can be acknowledged by *postmortem* examination or *in vivo* by biomarkers[20]. Especially, cerebrospinal fluid (CSF) concentrations of $A\beta_{1-42}$ and p-Tau₁₈₁ proteins seem to be the most promising biomarkers related to AD and can be early identified in the disease continuum[37]. Therefore, it is extreme important to estimate the added value of these biomarkers to identify the real risk of progression to the dementia phase of this disease.

Longitudinal research on mild cognitive impairment (MCI) individuals represent an opportunity to investigate the underlying biological processes (amyloidosis and neurodegeneration) and their relevance in the progression to AD. However, MCI remains a largely heterogeneous condition with a range of different underlying neurodegenerative mechanisms, which blurs both the ability to predict an individual's risk and the early detection of AD in its course. For this reason, individuals with amnesic mild cognitive impairment (aMCI) are the focus of ongoing research, since they are more likely to develop Alzheimer's disease dementia (ADD)[47].

Reports from studies regarding dominantly inherited AD genetic mutations support the concept of a protracted preclinical period during which biomarkers become abnormal[25]. It has been observed that the first changes in CSF $A\beta_{1-42}$ begin at least 20 years prior to the first symptoms, and CSF p-Tau₁₈₁ almost 15 years before[21]. However, few studies have evaluated the specific role of these biomarkers in patients diagnosed with aMCI regarding prediction of progression to ADD[13, 14, 24, 35, 36, 40, 50]. We have previously demonstrated the relative risk of developing ADD in 3 years, by following-up an exclusively aMCI cohort[43]. Here, we report the 5-year follow-up of this sample. The overarching aim of the present study was to

analyze whether or not these biomarkers, $A\beta_{1-42}$ and p-Tau₁₈₁, might predict the cumulative risk of progressing from aMCI to ADD in a 5-year follow-up.

MATERIALS AND METHODS

Subjects

In 2013, we began a longitudinal assessment of 33 patients diagnosed with aMCI and 12 patients diagnosed with subjective cognitive impairment (SCI) at a memory clinic in Southern Brazil. This cohort underwent lumbar puncture followed by CSF biomarkers evaluation and was enrolled in the study until 2018. The baseline cross-sectional and the 3-year follow-up studies have already been previously published [42, 43]. In brief, patients were enrolled in a systematic way with clinical evaluations by a behavioral/geriatric neurologist and a neuropsychological specialist in order to detect progression to ADD in the aMCI group. Those who followed-up until they developed dementia or until they had been deemed cognitively stable comprised the longitudinal study-group. This study was approved by the local research ethics committee (number 13-0009) and is in accordance with the Declaration of Helsinki. All participants gave their written consent in order to participate in this study.

Clinical and Neuropsychological Procedures

At baseline, aMCI diagnoses were based on criteria established by Petersen [38, 39] and on NIA-AA criteria for MCI[1]. SCI individuals included were those without objective evidence of cognitive impairment. All diagnoses were corroborated by the Clinical Dementia Rating scale (CDR)[31], in which aMCI scored 0.5 on CDR, and SCI scored 0 on CDR. As an exclusion criteria for enrolment we considered the diagnosis of dementia, stroke, Parkinson's

disease, depression or other neurological conditions that could possibly cause cognitive impairment.

Diagnostic investigation included a standard clinical evaluation and a battery of neuropsychological tests performed by a certified neuropsychologist. At baseline, the comprehensive diagnostic battery-protocol included: the verbal memory test subscore of the Consortium to Establish a Registry for Alzheimer's Disease (CERADs)[6, 32] to test memory performance, the 0-5 points version of the CDT (Clock Drawing Test)[3, 48] to measure executive functions, and the 15-item version of the Geriatric Depression Scale (GDS)[2, 53] to measure depressive symptomatology, all translated and validated to Brazilian Portuguese. The final CERADs score was composed by a possible sum of 30 points for word list learning, 10 points for word list recall and 10 points for word list recognition (total of 50 possible points)[10]. The presence of significant depressive symptomatology on GDS was considered for all subjects who scored ≥ 5 points in the scale. All the available information was used to reach a consensus diagnosis.

A similar approach was used in the follow-up evaluations, which were performed blindly by the same behavioral neurologist and neuropsychologist, and included a structured clinical interview, a full neurological examination, and other neuropsychological tests. Besides those performed at baseline, other the tests included were: the Montreal Cognitive Assessment (MoCA)[27, 34], Boston Naming Test (BNT)[22, 28], Verbal Fluency Test, animals category (VFT)[8, 19] and Constructional Praxis (CP)[5, 44], all translated and validated to Brazilian Portuguese. At the endpoint, individuals were reassessed in order to verify whether or not they had progressed to ADD. At this time, aMCI individuals were evaluated to verify whether they fulfilled the NIA-AA criteria for ADD[26], corroborated by changes in global CDR rating from 0.5 to 1 or more, in order to confirm the cognitive profile of dementia. Afterwards, the aMCI

group was subdivided accordingly into two groups: those who progressed to ADD (Progressors) or those who did not (Non-Progressors).

Laboratory Determinations

CSF samples were collected from all participants. They underwent a fasted lumbar puncture from the L3/L4 or L4/L5 intervertebral region. No adverse events were reported. CSF (5ml) was collected in sterile polypropylene tubes and immediately centrifuged (4,000 g x 10 minutes) at 4°C, aliquoted in polypropylene Eppendorfs, and then stored at -80°C until analysis. CSF A β ₁₋₄₂ and p-Tau₁₈₁ were measured separately by commercially-available sandwich enzyme-linked immunosorbent assay (ELISA) kits (Innotest, Fujirebio-Europe, Ghent, Belgium). Tests were performed in duplicate and the laboratory technician was blinded to any clinical and demographic information about the participants.

Statistical analyses

Statistical analyses were performed using the Statistical Package for Social Sciences (SPSS, version 20.0) (IBM SPSS, Chicago, IL). Normality of continuous variables was assessed by the Kolmogorov-Smirnov test. Non-parametric tests were used. The Kruskal-Wallis followed by the Dunn *post-hoc* tests were utilized to compare clinical, neuropsychological and biomarker data among the groups. ANCOVA test followed by the Bonferroni *post-hoc* test was performed to assess the statistical significance adjusted for age. Groups' differences between categorical variables were examined using the Chi-square (χ^2) test. Receiver operating characteristic (ROC) curve analyses were performed to obtain the area under the curve (AUC) and related parameters. The optimal cutoff values were determined by the Youden test[54]. The

Generalized Estimating Equation Model with the Bonferroni *post-hoc* test was applied to verify the mean of CERADs between those who were above and under the cutoff established for A β and in the SCI group, discriminated by time. Linear regressions were performed to evaluate the relationship between Δ CERADs and CSF biomarkers. Values were adjusted for age. All results are showed as confidence intervals CI 95% and *P* values <0.05 were considered significant.

RESULTS

At baseline, 33 aMCI and 12 SCI individuals were included in the study. Initially, these two groups differed only in the CERADs ($P = 0.041$; $P_{\text{adj.}} = 0.009$). Thirty-one aMCI and 11 SCI individuals completed the follow-up. After five years, 45.16% of the aMCI individuals progressed to ADD, corresponding to an annual conversion rate of 9.03%. The group of aMCI individuals was then dichotomized between those who were cognitively stable in the last observation, called Non-Progressors (17), and those who evolved to ADD, called Progressors (14). Additionally, we also verified that two (18.18%) SCI individuals progressed to aMCI in five years. None developed another kind of dementia. Moreover, our sample was composed mostly of a Caucasian population, which reflects the demographics of the Southern Brazilian population[33]. Only one individual in each group was African-Brazilian. No participants deceased during the follow-up, and those missed were due to no-shows.

Baseline demographic, neuropsychological and CSF biomarker data of the study population that completed the follow-up are presented in Table 1. The groups did not show significant differences in gender, educational level, and age. However, we corrected all data for age to discard any possible bias. CSF A β_{1-42} and p-Tau $_{181}$ /A β_{1-42} ratio were significantly different between groups. Table 2 describes the demographic and neuropsychological endpoint

data of the study population. Δ CERADs, defined as the difference between CERADs scores in 2018 compared to 2013, and the MoCA test were significantly different between aMCI Progressors and the SCI group ($P = 0.001$ and $P < 0.001$, respectively).

Table 3 describes ROC curve parameters of CSF biomarkers for predicting progression from aMCI to ADD. The best cutoff values were determined as described previously[43]. For $A\beta_{1-42}$, the threshold value was 618.5 pg/mL, with 78.5% sensitivity (CI95%: 52.2 – 92.4) and 94.1% specificity (CI95%: 73.0 – 98.9). The relative risk of developing ADD after five years among those with aMCI and $A\beta_{1-42} < 618.5$ pg/mL was 5.8 times higher than among those who were above this cutoff value (IC95%: 2.02 - 16.62; $P = 0.0011$). The optimal cutoff value for the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was 0.135, with 57.1% sensitivity (CI95%: 32.6 – 78.6) and 100% specificity (CI95%: 81.6 – 100.0). The relative risk of developing ADD after five years of follow-up in those whose p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was higher than 0.135 was 3.83 times higher when compared to those with a lower p-Tau₁₈₁/ $A\beta_{1-42}$ ratio (IC95%: 1.92 - 7.62; $P = 0.0001$).

Table 4 summarizes the demographic and neuropsychological endpoint data between those who were above and below the cutoff for $A\beta$. At this time, Δ CERADs was significantly different in those were below the cutoff for $A\beta$ as compared to those who were above the cutoff, or in the SCI group ($P < 0.001$). MoCA and BNT tests differed from those who were under the cutoff for $A\beta$ and in the SCI group ($P < 0.001$ and $P = 0.035$, respectively). Although the Δ GDS, defined as the difference between GDS scores in 2018 compared to 2013, presented some variation throughout this time, it did not affect the group with $A\beta < 618.5$ pg/mL.

The CERADs was applied three times during the follow-up. Figure 1 displays the line chart of CERADs in those who were above and below the cutoff for $A\beta$, and in the SCI group. The figure shows significant differences only in those who presented $A\beta$ levels < 618.5 pg/mL over time ($P < 0.001$). Moreover, in 2013 (baseline), when the groups were fixed and times

were compared, there was no difference between groups ($P = 0.078$), but there was a statistical significant difference at the 3-year (2016) and 5-year (2018) follow-up ($P = 0.004$ and $P = 0.002$, respectively). Furthermore, both $A\beta_{1-42}$ and p-Tau₁₈₁ levels explained 47.5% of Δ CERADs variance (B:-13.13; SE: 10.52; $P < 0.001$), whereas $A\beta_{1-42}$ alone explained 38.6% ($P < 0.001$), and p-Tau₁₈₁ accounted for 23.1% ($P = 0.006$). p-Tau₁₈₁ levels helped explain an extra 9% ($P = 0.015$) of Δ CERADs variance in 5 years.

DISCUSSION

We verified that the 5-year cumulative risk of developing ADD in individuals with aMCI and $A\beta_{1-42} < 618.5$ pg/mL was 5.8 times higher than among those whose levels were above this cutoff. Similarly, in those whose p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was greater than 0.135, the relative risk was 3.83 times higher of developing ADD. Interestingly, these relative risk values are lower than the ones we have reported in our 3-year follow-up study[43]. Moreover, we verified that 45.16% of aMCI individuals who completed the follow-up progressed to ADD after five years, corresponding to an annual conversion rate of approximately 9%, and which is in agreement with previous studies[29, 46, 49, 50]. Prediction of ADD in a short period of time appears much more relevant in a clinical perspective than prediction of dementia in a more distant future. The proportion of aMCI patients progressing to ADD is not constant over time, is highest during the first years of follow-up, and decreases at longer follow-up intervals[14, 24]. Additionally, most people with MCI will not progress to dementia even after 10 years of follow-up[29].

$A\beta_{1-42}$ was the best biomarker to predict ADD, which is also supported by others in clinical and neuropathological studies[18, 20, 45]. Furthermore, human and animal model data suggest a causal upstream role for $A\beta_{1-42}$ in the pathogenesis of AD[21]. This resembles studies

of AD-related neurodegeneration, in which amyloid deposition acts as the trigger for further disease progression[11]. Although $A\beta_{1-42}$ alone is insufficient to cause cognitive deterioration directly, it may be sufficient to cause tauopathy and neurodegeneration, which ultimately leads to cognitive deterioration[4, 7]. Biomarkers of neuronal injury appeared to best predict conversion from shorter time intervals before developing ADD[9].

It is important to note that, in the present study, the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio showed good predictive value in the progression from aMCI to ADD. Moreover, it combines measures of two different pathological processes into a single diagnostic biomarker. This result is also consistent with previous studies, in which the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio was found to be an accurate measure for progression to ADD[12, 23, 40]. It was also demonstrated that, in subjects with MCI and evidence of amyloid pathology, the injury markers, such as CSF p-Tau₁₈₁, can predict further cognitive decline[52]. In our study, we verified that p-Tau₁₈₁ levels helped to explain an extra 9% of Δ CERADs variance in 5 years.

In line with the approach of a proxy routine clinical practice, we exclusively included patients with aMCI at baseline, since the focus in implementing biomarkers, and in developing new treatments, when available, is specially in this clinical setting[20]. Despite few studies that have been conducted in this field, [13, 14, 24, 35, 36, 40, 50], this is, to our knowledge, the first study to verify the relative risk of CSF $A\beta_{1-42}$ and of the p-Tau₁₈₁/ $A\beta_{1-42}$ ratio in predicting ADD in an exclusively aMCI sample in a 5-year follow-up.

Decline in episodic memory is one of the hallmark features of AD and is also a defining feature of aMCI[15]. To assess episodic memory, we applied the verbal memory test of the CERAD. Figure 1 clearly demonstrates that, in those with $A\beta_{1-42} < 618.5$ pg/mL, CERADs declined dramatically along time, which did not occur in the other groups. Moreover, this decline happened mainly in the first three years, demonstrating that those who have low levels of $A\beta_{1-42}$ have an earlier impairment in episodic memory than those whose levels are above

618.5 pg/mL [16, 41]. Both $A\beta_{1-42}$ and p-Tau₁₈₁ levels explained 47.5% of CERADs variance, whereas $A\beta_{1-42}$ alone explained 38.6%, adjusted for age. This data is in agreement with our rigorous inclusion criteria of aMCI individuals and with the statement that a decline in episodic memory correlates with $A\beta_{1-42}$ in other aMCI studies[17].

At baseline, there was no difference in the GDS. It was important to include this scale, since depressive symptoms are very prevalent in subjects with MCI. Since depression displays a similar pattern of symptoms as AD, it could be a possible bias[30]. Although some individuals developed depression during the follow-up, there were no significant differences between groups at the endpoint. Moreover, the Δ GDS showed that the variation in the score along time did not affect the aMCI Progressors group, and, therefore, did not influence our results. Additionally, we observed that there were no significant differences in other cognitive domains, such as executive functions measured by CDT, which are more associated with other forms of MCI[38, 39].

The MoCA test is a cognitive screening scale that assesses several cognitive domains[27, 34]. Instead of the Mini-Mental State Examination (MMSE), we preferred to utilize MoCA because it has been shown to be more accurate in detecting MCI than MMSE [51]. In our study, we observed that, at the endpoint, this test showed a significant difference between those who had $A\beta_{1-42}$ levels below the cutoff point as compared with the SCI group. This endorses that the prodromal aMCI individuals had higher global cognition deterioration than those who had normal CSF $A\beta_{1-42}$ levels. The BNT scale was different between those who had CSF $A\beta_{1-42} < 618.5$ pg/mL and the SCI group. Nonetheless, because of the non-homoscedasticity of the data, we cannot make conclusions regarding this finding.

Strengths of this study are the rigorous methodology adopted in the inclusion criteria of exclusively aMCI or SCI individuals, and in their progression, avoiding misclassifications. Moreover, the use of neuropsychological instruments that were validated and administered by

the same experienced neuropsychologist may improve reliability and diagnostic consistency. Differently from studies that used threshold values based on laboratory standards, and that evaluated different populations with diverse methodologies, we preferred to utilize our own cut-offs to improve the reliability of our results. The main limitations of this study are, in the first place, the small sample size. Secondly, since only the amnesic subtype of MCI was considered, the generalization of the results to more heterogeneous population should be made with caution. And, lastly, we have measured the aforementioned CSF biomarkers only in the baseline.

CONCLUSIONS

In this study, $A\beta_{1-42}$ provided the best cumulative risk to the progression from aMCI to ADD in a 5-year follow-up cohort. $p\text{-Tau}_{181}/A\beta_{1-42}$ ratio was no better than $A\beta_{1-42}$ alone in predicting progression from aMCI to ADD. However, $p\text{-Tau}_{181}$ levels helped to explain an extra 9% of ΔCERADs variance in 5 years. The value of CSF biomarkers in predicting progression to ADD in aMCI individuals is more relevant during the first three years of follow-up than at longer intervals.

ACKNOWLEDGEMENTS

This study was supported by CAPES-CNPQ (Grant number: 476387/2013-2) and FIPE (Process: 13-0009). All authors declare that their funding source had no role in the study design, in the collection, analysis and interpretation of data, in the writing of the report, and in the decision to submit the paper for publication.

DECLARATION OF INTEREST

The authors hereby declare that there are no actual or potential conflicts of interest that may have affected the discussion presented.

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Table 1. Baseline demographic, neuropsychological and CSF biomarker data of the study population that completed the follow-up.

	SCI	aMCI Non-Progressors	aMCI Progressors	P value	Adjusted P value
n	11	17	14		
Age (years): median (min – max)	62 (60 – 76)	66 (60 – 78)	69 (63 – 76)	0.069	
Education (years): median (min – max)	11 (5 – 18)	11 (1 – 20)	11 (3 – 18)	0.354	
Gender (female/male): n	8/3	12/5	9/5	0.237	
Aβ 1-42 (pg/mL): median (P25 – P75)	850.58 (593.06 – 1002.89) ^b	900.17 (732.17 – 1064.29) ^b	497.91 (436.03 – 627.89) ^a	<0.001	<0.001
p-Tau₁₈₁ (pg/mL): median (P25 – P75)	55.94 (47.84 – 71.45)	56.40 (47.54 – 67.58)	80.80 (47.72 – 103.54)	0.202	0.279*
p-Tau₁₈₁/Aβ 1-42 ratio: median(P25 – P75)	0.062 (0.051 – 0.094) ^b	0.060 (0.053 – 0.075) ^b	0.156 (0.071 – 0.214) ^a	0.003	0.001*
CERADs: median (min – max)	29 (23 – 40)	27 (22 – 34)	26.5 (18 – 37)	0.137	0.128
GDS: median (min – max)	1 (0 – 5)	2 (0 – 5)	2.5 (0 – 5)	0.728	0.820
CDT: median (min – max)	4 (1 – 5)	4 (1 – 5)	5 (1 – 5)	0.061	0.293

† aMCI: amnesic Mild Cognitive Impairment; CDT: Clock Drawing Test; CERADs: Consortium to Establish a Registry for Alzheimer's Disease subscore; GDS: Geriatric Depression Scale; SCI: Subjective Cognitive Impairment; P25: percentile 25; P75: percentile 75. ‡ Results were obtained performing the Kruskal-Wallis test followed by the Dunn *post-hoc* test. ^{a, b} Equal letters do not differ according to the Dunn *post-hoc* test at 5% significance. Regarding gender, the Chi-Square Test was used. P values adjusted for age were obtained performing the ANCOVA test, *with logarithmic transformation.

Table 2. Demographic and neuropsychological endpoint data of the study population.

	SCI	aMCI Non-Progressors	aMCI Progressors	P value	Adjusted P value
n	11	17	14		
Age (years): median (min – max)*	66 (63 – 80)	70 (64 – 82)	73.5 (67 – 80)	0.057	
ΔCERADs: median (min – max)	-2 (-11 – 7) ^{ab}	3 (-9 – 9) ^b	-6.5 (-22 – 4) ^a	0.002	0.001
ΔGDS: median (min – max)	1 (3 – 11)	1 (-2 – 11)	0 (-5 – 3)	0.120	0.127
MoCA: median (min – max)	27 (18 – 29) ^b	23 (17 – 27) ^{ab}	16.5 (5 – 28) ^a	0.001	<0.001
BNT: median (min – max)	15 (13 – 15)	15 (11-15)	13 (5-15)	0.057	0.040 [‡]
VFT: median (min – max)	16 (11 – 19)	12 (8 – 21)	13 (0 – 20)	0.306	0.185
CP: median (min – max)	7 (3 – 11)	7 (0 – 11)	4.5 (2 – 8)	0.058	0.102
CDT: median (min – max)	5 (1 – 5)	4 (1 – 5)	4 (0 – 5)	0.150	0.311

†aMCI: amnesic Mild Cognitive Impairment; BNT: Boston Naming Test; CDT: Clock Drawing Test; CERADs: Consortium to Establish a Registry for Alzheimer's Disease subscore; CP: Constructional Praxis; GDS: Geriatric Depression Scale; MoCA: Montreal Cognitive Assessment; SCI: Subjective Cognitive Impairment; VFT: Verbal Fluency Test; Δ: values from 2018 minus 2013; P25: percentile 25; P75: percentile 75. ‡ Results were obtained performing the Kruskal-Wallis test followed by the Dunn *post-hoc* test. ^{a, b} Equal letters do not differ according to the Dunn *post-hoc* test at 5% significance. P values adjusted for age were obtained performing the ANCOVA test. [‡] Levene's Test for Equality of Variances: P = 0.004. *Differences in median age from the baseline to endpoint were due to small differences between time of reevaluation and birthdate.

Table 3. ROC curve parameters of CSF biomarkers in predicting progression from aMCI to ADD.

Threshold values [‡]	aMCI Progressors	aMCI Non-Progressors	ROC AUC (CI95%)	Sensitivity (%) (CI95%)	Specificity (%) (CI95%)	Test accuracy (%)	Positive Predictive Value (%)	Negative Predictive Value (%)
$A\beta_{1-42} < 618.5$ pg/mL	11	1	0.912 (0.676 – 0.964)	78.5 (52.4 – 92.4)	94.1 (73.0 – 98.9)	87.1	91.7	84.2
$A\beta_{1-42} > 618.5$ pg/mL	3	16						
$p\text{-Tau}_{181} / A\beta_{1-42} > 0.135$	8	0	0.849 (0.71–0.984)	57.1 (32.6 – 78.6)	100.0 (81.6 – 100.0)	80.6	100.0	73.9
$p\text{-Tau}_{181} / A\beta_{1-42} < 0.135$	6	17						

[†] ADD: Alzheimer's disease dementia; aMCI: amnesic mild cognitive impairment; AUC: area under the curve; ROC: receiver operating characteristic. [‡] Youden index was used.

Table 4. Demographic and neuropsychological endpoint data between those above and under the cutoff for A β .

	SCI	A β > 618.5 pg/mL	A β < 618.5 pg/mL	P value	Adjusted P value
n	11	19	12		
Age (years): median (min – max)	66 (63 – 80)	70 (64 – 82)	72.5 (67 – 80)	0.067	
Education (years): median (min – max)	11 (5 – 18)	11 (1 – 20)	9.5 (3 – 18)	0.243	
Gender (female/male): n	8/3	12/7	9/3	0.749	
ΔCERADs: median (min – max)	-2 (-11 – 7) ^b	2 (-9 – 9) ^b	-7 (-22 – 3) ^a	0.001	<0.001
ΔGDS: median (min – max)	1 (-2 – 7) ^{ab}	1 (-1 – 11) ^b	0 (-5 – 3) ^a	0.046	0.066
MoCA: median (min – max)	27 (18–29) ^b	23 (16 – 28) ^{ab}	16.5 (5 – 27) ^a	0.001	<0.001
BNT: median (min – max)	15 (13–15) ^b	15 (11 – 15) ^{ab}	12.5 (5 – 15) ^a	0.035	0.016 [#]
VFT: median (min – max)	16 (11–19)	13 (8 – 21)	13 (0 – 18)	0.194	0.062
CP: median (min – max)	7 (3–11)	7 (0 – 11)	4.5 (2 – 8)	0.118	0.166
CDT: median (min – max)	5 (1–5)	4 (1–5)	4 (0 – 5)	0.145	0.312

†aMCI: amnesic Mild Cognitive Impairment; BNT: Boston Naming Test; CDT: Clock Drawing Test; CERADs: Consortium to Establish a Registry for Alzheimer's Disease subscore; CP: Constructional Praxis; GDS: Geriatric Depression Scale; MoCA: Montreal Cognitive Assessment; SCI: Subjective Cognitive Impairment; VFT: Verbal Fluency Test; Δ : values from 2018 minus 2013; P25: percentile 25; P75: percentile 75. ‡ Results were obtained performing the Kruskal-Wallis followed by the Dunn *post-hoc* test. ^{a, b} Equal letters do not differ according to the Dunn *post-hoc* test at 5% significance. P values adjusted for age were obtained performing the ANCOVA test. [#] Levene's Test of Equality of Variances: P = 0.005.

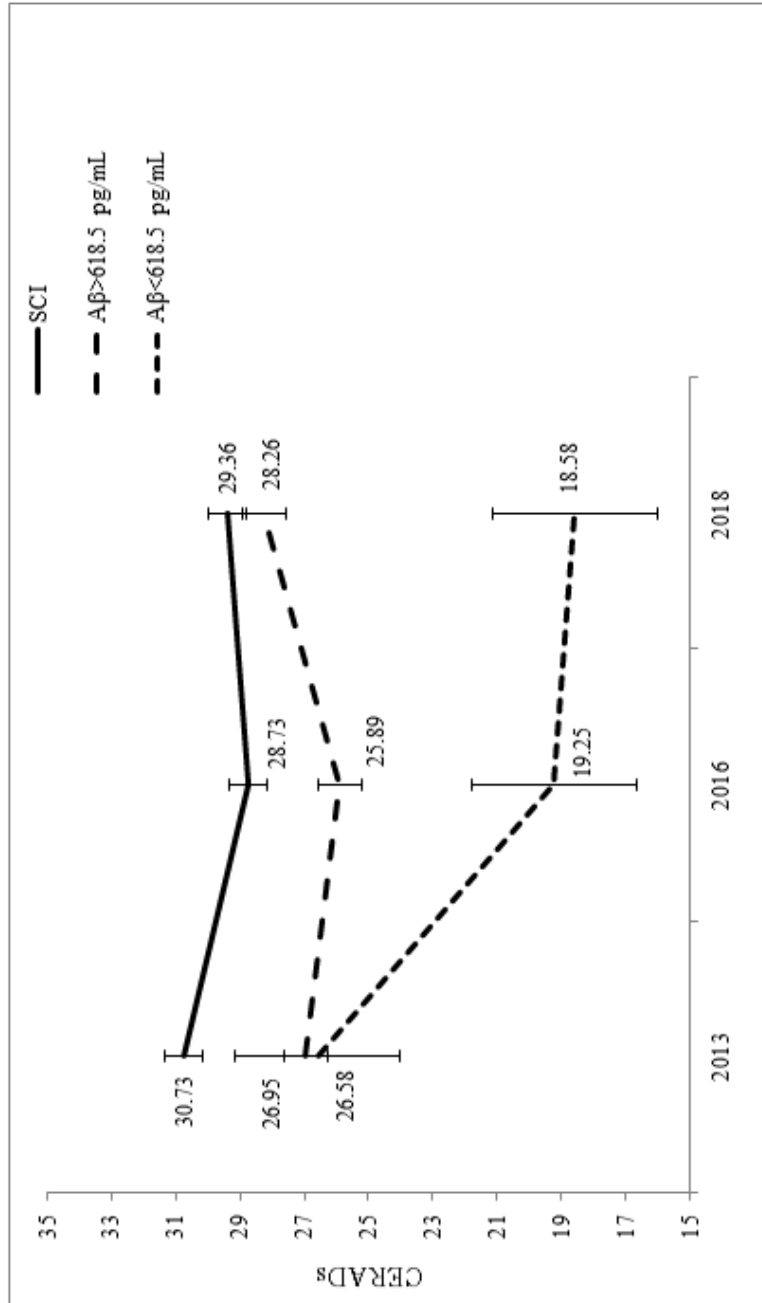


Fig. 1 Line chart of the means and standard errors of CERADs among those above and under the cutoff for A β , and the SCI group. There was an interaction between variables ($P = 0.002$). When the time was set and the groups were compared, there was no difference in the SCI ($P = 0.316$) and A $\beta > 618.5$ pg/mL ($P = 0.063$) groups, but there was a significant difference in the A $\beta < 618.5$ pg/mL group ($P < 0.001$; 2013 versus 2016 and $P = 0.001$; 2013 versus 2018 $P < 0.001$). When the groups were fixed and times were compared, there was no difference between groups in 2013 ($P = 0.078$), but there was a significant difference at the follow-up in 2016 ($P = 0.004$; A $\beta < 618.5$ pg/mL versus SCI $P = 0.005$), and in 2018 ($P = 0.002$; A $\beta < 618.5$ pg/mL versus SCI $P = 0.001$; A $\beta < 618.5$ pg/mL versus A $\beta > 618.5$ pg/mL $P = 0.002$). †CERADs: Consortium to Establish a Registry for Alzheimer's Disease subscore; SCI: Subjective Cognitive Impairment. ‡Generalized Estimating Equation Model followed by the Bonferroni *post-hoc* test.

CAPÍTULO V

1. CONSIDERAÇÕES FINAIS

A presente tese agregou conhecimento na avaliação dos biomarcadores líquóricos $A\beta_{1-42}$ e p-Tau₁₈₁ na predição do risco de progressão à demência da DA em um grupo de indivíduos com CCL-a. Em nosso estudo, 45,2% dos indivíduos com CCL-a progrediram para a DDA em cinco anos. A proteína $A\beta_{1-42}$ mensurada no líquido proporcionou o melhor risco cumulativo de progressão do CCL-a para a fase demencial da DA. Enquanto que a razão p-Tau₁₈₁/ $A\beta_{1-42}$ não foi melhor que a proteína $A\beta_{1-42}$ isolada na predição da progressão do CCL-a para a DDA. No entanto, os níveis de p-Tau₁₈₁ ajudaram a explicar um extra de 9% da variância Δ CERADs em cinco anos. Além disso, verificou-se que, numa perspectiva clínica, o valor dos biomarcadores líquóricos na predição da progressão de indivíduos com CCL-a para demência da DA é mais relevante durante os primeiros anos de acompanhamento do que em intervalos mais longos.

Um progresso substancial foi feito ao longo das últimas décadas na compreensão DA e no uso dos biomarcadores. No entanto, ainda não há padronização na utilização dos mesmos de modo que possam ser implementados efetivamente na prática clínica, o que atrasa o diagnóstico e, conseqüentemente, as intervenções farmacológicas e terapêuticas que poderiam retardar ou impedir a progressão da patologia da DA. Este estudo parte de uma linha de pesquisa cuja abordagem visa integrar a pesquisa à assistência e colabora para que o conhecimento gerado seja transferido ao paciente e à sociedade, auxiliando no diagnóstico clínico. Desta forma, buscou-se contribuir com o desenvolvimento científico e tecnológico e, com isto, auxiliar no fortalecimento da pesquisa brasileira no cenário nacional e internacional.

2. PERSPECTIVAS FUTURAS

Embora numerosas pesquisas tenham relatado bom desempenho diagnóstico por meio dos biomarcadores, ainda observam-se diferenças marcantes entre os estudos. Dessa forma, mais pesquisas nessa área se tornam necessárias, com amostras populacionais maiores e com rigor na seleção de indivíduos, de modo a melhor esclarecer a performance dos biomarcadores e promover a sua implementação generalizada na prática clínica.

Este estudo encoraja novas pesquisas com os biomarcadores na DA, envolvendo amostras maiores, bem como estudos de coorte com dosagens iniciais e seriadas das proteínas β -amilóide e Tau, juntamente com avaliações clínicas e neuropsicológicas intermitentes de modo a melhor elucidar os mecanismos etiopatogênicos e fisiopatológicos da doença. As perspectivas futuras consistem no seguimento desses indivíduos visando reavaliação quanto à progressão à DA em um período maior de tempo, além de novas dosagens e possíveis correlações com outros biomarcadores.

CAPÍTULO VI


1. ANEXOS

1.1 Artigos científicos publicados durante o período de doutoramento

doi: 10.1111/ggi.12704 Medline Indexed

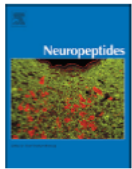
Current Contents In 2016
Neuropeptides 71 (2018) 54–60

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News and reviews

Sirtuin 1 and Alzheimer's disease: An up-to-date review

Liara Rizzi^{a,b,*}, Matheus Roriz-Cruz^{a,b}

<https://doi.org/10.1016/j.npep.2018.07.001>

Alzheimer's, Dementia & Cognitive Neurology

Research Article

Haemodialysis improves uraemic patients' cognition: a pilot study

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doi: 10.15761/ADCN.1000101 *Alzheimers Dement Cogn Neurol*, 2016 **1.2**Guideline STARD

STARD checklist for the reporting of studies of diagnostic accuracy.

Section and Topic	Item #		On page #

TITLE/ABSTRACT/ KEYWORDS	1	Identify the article as a study of diagnostic accuracy (recommend MeSH heading 'sensitivity and specificity').	99, 100
INTRODUCTION	2	State the research questions or study aims, such as estimating diagnostic accuracy or comparing accuracy between tests or across participant groups.	102
METHODS			
<i>Participants</i>	3	Describe the study population: The inclusion and exclusion criteria, setting and locations where the data were collected.	102
	4	Describe participant recruitment: Was recruitment based on presenting symptoms, results from previous tests, or the fact that the participants had received the index tests or the reference standard?	102, 103
	5	Describe participant sampling: Was the study population a consecutive series of participants defined by the selection criteria in items 3 and 4? If not, specify how participants were further selected.	102, 103
	6	Describe data collection: Was data collection planned before the index test and reference standard were performed (prospective study) or after (retrospective study)?	102, 103, 104
<i>Test methods</i>	7	Describe the reference standard and its rationale.	104
	8	Describe technical specifications of material and methods involved including how and when measurements were taken, and/or cite references for index tests and reference standard.	104
	9	Describe definition of and rationale for the units, cutoffs and/or categories of the results of the index tests and the reference standard.	104, 106
	10	Describe the number, training and expertise of the persons executing and reading the index tests and the reference standard.	104
	11	Describe whether or not the readers of the index tests and reference standard were	

		blind (masked) to the results of the other test and describe any other clinical information available to the readers.	104
<i>Statistical methods</i>	12	Describe methods for calculating or comparing measures of diagnostic accuracy, and the statistical methods used to quantify uncertainty (e.g. 95% confidence intervals).	104, 105
	13	Describe methods for calculating test reproducibility, if done.	NA
RESULTS			
<i>Participants</i>	14	Report when study was done, including beginning and ending dates of recruitment.	102, 105
	15	Report clinical and demographic characteristics of the study population (e.g. age, sex, spectrum of presenting symptoms, comorbidity, current treatments, recruitment centers).	105
	16	Report the number of participants satisfying the criteria for inclusion that did or did not undergo the index tests and/or the reference standard; describe why participants failed to receive either test (a flow diagram is strongly recommended).	105
<i>Test results</i>	17	Report time interval from the index tests to the reference standard, and any treatment administered between.	NA
	18	Report distribution of severity of disease (define criteria) in those with the target condition; other diagnoses in participants without the target condition.	106
	19	Report a cross tabulation of the results of the index tests (including indeterminate and missing results) by the results of the reference standard; for continuous results, the distribution of the test results by the results of the reference standard.	123
	20	Report any adverse events from performing the index tests or the reference standard.	NA
<i>Estimates</i>	21	Report estimates of diagnostic accuracy and measures of statistical uncertainty (e.g. 95% confidence intervals).	106, 123
	22	Report how indeterminate results, missing responses and outliers of the index tests were	NA

		handled.	
	23	Report estimates of variability of diagnostic accuracy between subgroups of participants, readers or centers, if done.	NA
	24	Report estimates of test reproducibility, if done.	NA
DISCUSSION	25	Discuss the clinical applicability of the study findings.	108

*NA: Not applicable.