

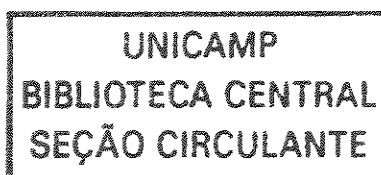
PAULA CRISTINA TREVILATTO

***SUSCETIBILIDADE GENÉTICA
À SEVERIDADE DA DOENÇA PERIODONTAL***

Tese apresentada à Faculdade de Odontologia de
Piracicaba da Universidade Estadual de
Campinas, para a obtenção do título de Doutor em
Biologia e Patologia Buco-Dental.

Piracicaba


2002



PAULA CRISTINA TREVILATTO

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Assinatura do Orientador

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Piracicaba

2002

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A Comissão Julgadora dos trabalhos de Defesa de Tese de DOUTORADO, em sessão pública realizada em 10 de Outubro de 2002, considerou a candidata PAULA CRISTINA TREVILATTO aprovada.

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5. Prof. Dr. ANTONIO WILSON SALLUM

DEDICATÓRIA

*A DEUS, que nos proporciona
tantas oportunidades...*

*Aos meus pais, NARCISO e DORA, pelos
ensinamentos constantes ao longo de nossa
caminhada evolutiva e por ampararem
toda a minha existência*

*Aos meus irmãos CLAUDIA e NARCISO Jr.,
pela convivência e por iluminarem meu caminho*

Ao ANDRÉ, pelo amor e pelo companheirismo incansável

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*“A felicidade tem base
no dever cumprido”*

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RESUMO

Citocinas constituem importantes mediadores inflamatórios que influenciam o início e a progressão de diversas doenças inflamatórias crônicas, incluindo a doença periodontal. Polimorfismos gênicos têm sido relacionados ao aumento da expressão das citocinas correspondentes. O objetivo do presente estudo foi investigar a correlação entre os polimorfismos nos genes da *IL-1 α* , *IL-1 β* , *IL-1ra*, *IL-6* e *TNF- α* e a severidade da periodontite crônica. Cento e treze indivíduos não-aparentados, não-fumantes, acima dos 25 anos (média: 41,6 anos), foram divididos de acordo com o nível de severidade da doença periodontal crônica: 44 indivíduos saudáveis, 31 com periodontite moderada e 38 com periodontite severa. O DNA genômico foi obtido de células epiteliais da mucosa bucal através de um bochecho com 5 mL de solução de glicose a 3 % e leve raspagem da mucosa jugal. Foram analisados os seguintes polimorfismos: *IL-1A* (-889), *IL-1B* (-511), *IL-1B* (+3953), *IL-1RA* (intron 2), *IL-6* (-174) e *TNFA* (-308), pela técnica PCR-RFLP. A significância das diferenças nas frequências dos polimorfismos no grupo controle e em grupos com periodontite foi acessada pelo teste qui-quadrado ($p < 0,05$). Diferenças significantes nas frequências alélicas e genotípicas foram encontradas nos polimorfismos *IL-1B* (-511), *IL-1RA* (intron 2) e *IL-6* (-174). Concluiu-se que os polimorfismos *IL-1A* (-889), *IL-1B* (+3953) e *TNFA* (-308) não se correlacionaram à severidade da periodontite, enquanto que os polimorfismos *IL-1B* (-511), *IL-1RA* (intron 2) e

IL-6 (-174) se relacionaram à susceptibilidade à periodontite crônica na população estudada. Os mesmos polimorfismos foram investigados em uma família com periodontite agressiva, juntamente com parâmetros microbiológicos. Os resultados microbiológicos e genéticos não foram suficientes para prever a susceptibilidade à periodontite agressiva na família estudada.

ABSTRACT

Inflammatory cytokines represent important pathological mediators in chronic inflammatory diseases, including periodontitis. Polymorphisms in cytokine genes have been associated with enhanced expression of cytokines, which mediate the development of inflammatory diseases. The aim of this study was to investigate the association between polymorphisms in the *IL-1 α* , *IL-1 β* , *IL-1ra*, *IL-6* and *TNF- α* genes and severity of chronic periodontitis in Brazilians. One hundred and thirteen unrelated non-smoking subjects, over 25 years (mean age 41.6), were divided according to the severity level of periodontal disease: 44 healthy individuals, 31 subjects with moderate and 38 with severe periodontitis. DNA was obtained from epithelial cells through a mouthwash with 5 mL 3% glucose and scraping of oral mucosa. The samples were analyzed for *IL-1A* (-889), *IL-1B* (-511), *IL-1B* (+3953), *IL-1RA* (intron 2), *IL-6* (-174) and *TNFA* (-308) polymorphisms using PCR-RFLP. The significance of the differences in the frequencies of the polymorphisms in the control and groups with periodontitis was assessed by Chi-square test ($p < 0.05$). Significant differences in the allele and genotype frequencies were found among the groups regarding *IL-1B* (-511), *IL-1RA* (intron 2) and *IL-6* (-174) polymorphisms. It was concluded that *IL-1A* (-889), *IL-1B* (+3953) and *TNFA* (-308) polymorphisms were not associated with the severity of chronic periodontal disease in the study population whereas polymorphisms *IL-1B* (-511), *IL-1RA* (intron 2) and *IL-6* (-174) correlated to disease

susceptibility. These polymorphisms were also investigated in a family with aggressive periodontitis, together with clinical and microbiological parameters. The results showed that the microbiological and genetic parameters did not predict the susceptibility to periodontitis in the study family.

1. INTRODUÇÃO

A doença periodontal (DP) é constituída por um grupo de afecções inflamatórias crônicas causadas por bactérias específicas, como *Porphyromonas gingivalis*, *Actinobacillus actinomycetemcomitans* e *Bacteroides forsythus* (NONNENMACHER *et al.*, 2001; SLOTS & KAMMA, 2001). As bactérias ativam mecanismos inflamatórios que acabam por destruir colágeno e osso dos tecidos de suporte periodontal (POTEMPA *et al.*, 2000). Embora as bactérias sejam essenciais para a iniciação da periodontite, a quantidade e os tipos de bactérias não são variáveis suficientes para explicar diferenças na severidade da DP (KORNMAN *et al.*, 1997). Nas doenças inflamatórias crônicas, há fatores modificadores que não causam a doença, mas amplificam alguns mecanismos que tornam a doença mais severa. O cigarro (HABER, 1994; SCHENKEIN *et al.*, 1995; JOHNSON & SLACH, 2001), o estresse psicossocial (LINDEN *et al.*, 1996), certas doenças sistêmicas (MEALEY, 2000; WACTAWSKI-WENDE, 2001) e determinados polimorfismos genéticos (KORNMAN *et al.*, 1997; TREVILATTO *et al.*, *in press*) são exemplos de fatores que tornam os indivíduos suscetíveis à progressão/gravidade da DP.

Polimorfismos são variações genéticas encontradas na população, nas quais a frequência do alelo mais raro de um determinado loco é maior que 1% (THOMPSON *et al.*, 1991). Existem polimorfismos que influenciam a atividade de fatores reguladores da resposta inflamatória, estando assim associados ao

aumento significativo do risco à severidade da doença (POCIOT *et al.*, 1992; DANIS *et al.*, 1995; WILSON *et al.*, 1997; SHIRODARIA *et al.*, 2000).

1.1 Mediadores inflamatórios da DP

Bactérias específicas, predominantemente anaeróbias gram-negativas, ativam mecanismos teciduais que produzem uma série de alterações inflamatórias e imunológicas que levam à destruição do tecido conjuntivo e osso alveolar. Em humanos, a resposta imune às bactérias é promovida e regulada em parte por um número de citocinas (GEMMELL & SEYMOUR, 1994). Como ocorre em outras infecções, a inflamação nos tecidos gengivais protege o organismo contra o ataque microbiano local e impede os microrganismos de se disseminarem. No entanto, a resposta inflamatória causa danos às células e estruturas periodontais, incluindo o osso alveolar.

1.1.1 Interleucina-1 (IL-1)

As interleucinas são mediadoras-chave do processo inflamatório, pois modulam componentes da matriz extracelular e osso que compõem os tecidos periodontais (GENCO, 1992). Níveis mais altos de IL-1 foram encontrados na gengiva (HONIG *et al.*, 1989) e em sítios ativos (STASHENKO *et al.*, 1991a,b) de pacientes com periodontite crônica, e diminuídos no fluido gengival após tratamento da DP (MASADA *et al.*, 1990). A IL-1 α e a IL1 β são produzidas e liberadas localmente na DP, apresentando atividades biológicas similares pró-

inflamatórias e catabólicas, como induzir a desmineralização óssea, aumentar a adesão de leucócitos às células endoteliais, proporcionar a desgranulação de neutrófilos, e estimular a síntese de prostaglandina e a atividade colagenolítica pelas células do tecido conjuntivo. Além disso, promovem a proliferação epitelial e são quimiotáticas para neutrófilos e macrófagos, tornando-os ativos (MASADA *et al.*, 1990).

1.1.2 Antagonista do receptor da IL-1 (IL-1 ra)

O antagonista do receptor da interleucina-1 compete com a IL-1 pela ocupação de receptores de superfície celular, desempenhando papel inibitório no desenvolvimento de doenças mediadas por esta citocina. Constitui importante regulador endógeno do processo inflamatório (TARLOW *et al.*, 1993), estando associado à susceptibilidade a diversas doenças inflamatórias (MANSFIELD *et al.*, 1994; BOIARDI *et al.*, 2000; BUCHS *et al.*, 2000; SHU *et al.*, 2000).

1.1.3 Interleucina-6 (IL-6)

A interleucina-6, assim como a IL-1, está envolvida em mecanismos de reabsorção óssea (GEMMELL & SEYMOUR, 1994) e se encontra presente em concentrações mais elevadas no fluido gengival de pacientes com DP refratária (REINHARDT *et al.*, 1993).

1.1.4 Fator de necrose tumoral- α (TNF- α)

O fator de necrose tumoral- α (TNF- α) é uma citocina pró-inflamatória produzida por macrófagos, que desempenha papel similar às IL-1 e IL-6 (ALEXANDER & DAMOULIS, 1994). Ele induz a secreção de collagenase, prostaglandina E₂ (PGE₂) e IL-6 por fibroblastos e osso em cultura (MEIKLE *et al.*, 1989), além de estimular a reabsorção óssea (BERTOLINI *et al.*, 1986). O fator de necrose tumoral- α está presente no fluido gengival de pacientes com gengivite e periodontite (ROSSOMANDO *et al.*, 1990). No entanto, o TNF- α é cerca de 500 vezes menos potente que a IL-1 na indução de reabsorção óssea (STASHENKO *et al.*, 1991a; ALEXANDER & DAMOULIS, 1994).

Como se vê por estes exemplos, o número de mediadores da resposta do hospedeiro, que atuam na destruição dos tecidos periodontais, é vasto e com ação interdependente. Estudos em periodontite crônica indicam que grande parte da perda de inserção e da reabsorção do osso alveolar pode ser prevenida pela ação de drogas antiinflamatórias não-esteróides (HOWELL & WILLIAMS, 1993; JEFFCOAT *et al.*, 1993). Portanto, alterações gênicas que resultem em modificação da resposta inflamatória merecem ser estudadas.

Mais que ser o interesse principal focalizar níveis de higiene oral, identificando-se e quantificando-se a microbiota potencialmente patogênica, o principal desafio para o futuro parece ser encontrar meios de identificar grupos de risco para a severidade da doença periodontal. Clinicamente, estes fatores podem

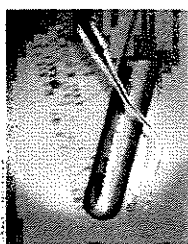
ser usados para a identificação de indivíduos com uma resposta desfavorável ao ataque microbiano, isto é, pessoas que sejam suscetíveis à doença periodontal, para que sejam priorizados programas de prevenção, antes que ocorra a destruição irreversível dos tecidos periodontais, e para que se conheça melhor o curso da doença. Como a placa bacteriana parece explicar, apenas em parte, o desenvolvimento da DP (GENCO, 1992), fatores sistêmicos diretos e indiretos que influenciam a resposta do hospedeiro parecem ser de grande relevância e merecem atenção nesta fase do desenvolvimento científico. A DP compreende um grupo de doenças crônicas multifatoriais complexas cuja etiopatogênese é pobremente compreendida, desta forma, dificultando testes diagnósticos do risco à sua severidade e progressão (KORNMAN & DI GIOVINE, 1998). Mediadores pró-inflamatórios parecem ser o foco de atenção neste momento em que a resposta do hospedeiro se mostra determinante na intensidade da destruição periodontal. Assim, a busca de marcadores genéticos que permitam a detecção de indivíduos com maior probabilidade de desenvolver a doença é fundamental para a prevenção da instalação do processo destrutivo, ou na instauração de terapêutica individualizada e preservação adequada de pacientes, nos quais sinais clínicos da doença já se manifestaram.

2. PROPOSIÇÃO

O presente trabalho, composto por sete artigos, teve como objetivo geral avaliar a associação entre polimorfismos genéticos e susceptibilidade à doença periodontal em uma família com periodontite agressiva e em pacientes com diferentes graus de periodontite crônica. Os polimorfismos *IL-1A* (-889), *IL-1B* (-511), *IL-1B* (+3953), *IL-1RA* (intron 2), *IL-6* (-174) e *TNFA* (-308) foram estudados pela técnica PCR-RFLP.



3. ARTIGOS



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DIAGNÓSTICO MOLECULAR DA DOENÇA PERIODONTAL

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DIAGNÓSTICO MOLECULAR DA DOENÇA PERIODONTAL

SINOPSE

O cigarro, o estresse psicossocial e certos polimorfismos gênicos são exemplos de fatores que aumentam o risco à periodontite, tornando os indivíduos mais suscetíveis à progressão ou ao agravamento da doença. Polimorfismos em genes de mediadores pró-inflamatórios, que caracterizam a resposta do hospedeiro, têm sido alvo de estudos recentes, que objetivam diagnosticar precocemente mecanismos destrutivos da doença. A realização de um simples bochecho com solução açucarada pelo paciente pode permitir a análise de seu perfil de susceptibilidade genética à doença periodontal, o que pode ser de grande valia na prevenção da instalação e progressão da doença periodontal em pacientes de risco.

UNITERMOS: *Periodontite. Polimorfismo genético. Suscetibilidade.*

MOLECULAR DIAGNOSIS OF PERIODONTAL DISEASE

ABSTRACT

Smoking, stress and genetic polymorphisms are examples of factors that increase the risk of periodontitis, making the individuals more susceptible to the progression or aggravation of periodontal disease. Polymorphisms in genes of pro-inflammatory mediators, which characterize the host response, have been investigated with the aim of accomplishing the early diagnosis of the destructive mechanisms of the disease. A simple mouthwash performed by the patient can determine the individual pattern of genetic susceptibility to periodontal disease, which can help to prevent the beginning and progression of the disease in high-risk patients.

DESCRIPTORS: *Periodontitis. Genetic risk. Polymorphisms.*

A periodontite (DP) constitui doença inflamatória crônica em resposta à presença de bactérias específicas, como *Porphyromonas gingivalis*, *Actinobacillus actinomycetemcomitans* e *Bacteroides forsythus*. As bactérias ativam mecanismos inflamatórios que acabam por destruir colágeno e osso dos tecidos de suporte periodontal. Embora as bactérias sejam essenciais para a iniciação da periodontite, a quantidade e os tipos de bactérias não são suficientes para explicar diferenças na progressão e severidade da DP. O cigarro e o estresse psicossocial são exemplos de fatores que aumentam o risco à doença, tornando os indivíduos mais suscetíveis à progressão ou ao agravamento da doença periodontal. No entanto, há indivíduos que, mesmo sofrendo exposição a esses fatores ambientais e apresentando pobre higiene oral, e, portanto, possuindo altos índices de placa, não mostram níveis significativos de doença. O contrário também é verdadeiro: pacientes com baixos índices de placa podem desenvolver altos níveis de doença e responder mal ao tratamento periodontal, o que caracteriza a periodontite refratária. Nas doenças inflamatórias crônicas, há fatores modificadores que não causam a doença, mas amplificam alguns mecanismos que tornam a doença mais severa. Esses fatores são geneticamente determinados e constituem a resposta do hospedeiro.

FATORES RELACIONADOS À DOENÇA PERIODONTAL

1. Placa Dental

Diferenças na prevalência e gravidade da DP foram associadas à raça, à área geográfica, ao sexo, à condição sócio-econômica e ao nível educacional. A partir da década de 60, com o emprego do Índice de Higiene Oral (OHI), foi observado que diferenças raciais, geográficas e demográficas aparentes na gravidade da DP desaparecem quando os níveis de doença são relacionados diretamente com índices de higiene oral. A associação entre a DP e a higiene oral foi demonstrada epidemiologicamente (LINDHE⁸, 1992). A quantidade de placa e cálculo, juntamente com a idade, poderia explicar até 90 % da experiência da doença.

2. Resposta do Hospedeiro

A reação imunoinflamatória representa a resposta do hospedeiro à microbiota da placa dental e seus produtos. A própria qualidade da placa (quais as bactérias e em que quantidade relativa estão presentes) é determinada pela resposta individual do hospedeiro, que apresenta componentes imunológicos próprios que permitirão ou não o desenvolvimento da microflora em questão. O tipo e a severidade da DP são reflexo da

competência da resposta do hospedeiro mais do que da virulência da microflora patogênica, o que torna difícil determinar se um certo tipo de microflora bacteriana associado a doenças periodontais específicas seria a causa ou condição da doença. Muito embora placa e cálculo estejam indubitavelmente relacionados com a gengivite e a destruição dos tecidos periodontais, há pacientes que, tendo placa e cálculo em abundância e restaurações mal-adaptadas pela vida inteira, não mostram evidências de alterações destrutivas no sistema de inserção. Inversamente, pacientes jovens com higiene oral satisfatória podem revelar destruição avançada de tecidos periodontais (LINDHE⁸, 1992). Assim, em cada paciente isoladamente, o grau de DP não é determinado apenas pela presença da placa microbiana. Qualquer alteração patológica em nível periodontal é consequência direta da resposta individual do hospedeiro em função da presença da placa. A idade poderia, talvez, refletir a manifestação da queda imunológica e o desequilíbrio de fatores que regulam a atividade colagenolítica. Dessa forma, o argumento de que 90 % dos casos de DP podem ser explicados com base na idade e higiene oral, no mínimo, não é ideal. Embora estudos epidemiológicos revelem que a frequência e a severidade da DP aumentam com a idade e com a higiene oral inadequada, não basta somente avaliar os tipos de microrganismos presentes

na placa e sua quantidade relativa, juntamente com fatores retentivos. A associação etiológica direta entre a colonização bacteriana sobre a superfície dentária e a destruição da inserção periodontal pela inflamação é clara, mas a taxa de destruição em resposta a esta colonização varia consideravelmente de uma pessoa para outra, dependendo de diferenças na resposta tecidual à irritação bacteriana. Isto explica por que a gengivite, que reflete a presença da colonização bacteriana, não resulta em destruição periodontal em todos os casos. Apesar de as bactérias serem essenciais para a iniciação da periodontite, não há mecanismos seguros que determinem a trajetória clínica da doença em nível individual, diferenciando pacientes que apresentarão uma forma de leve à moderada da doença e responderão bem ao simples cuidado profissional, daqueles que são suscetíveis a desenvolver formas mais severas, que demandem terapia intensiva e resultem na morbidade dental.

MEDIADORES PRÓ-INFLAMATÓRIOS DA DP

A preocupação com aspectos causais é enorme, mas pouco se conhece ainda acerca de sinalizadores/mediadores fundamentais na patogênese e evolução da doença. Diferenças individuais na expressão de determinadas citocinas têm efeito dramático na progressão da doença (KORNMAN et al.⁷,

1997). O número de fatores que atuam na destruição dos tecidos periodontais, mediadores da resposta imunoinflamatória do hospedeiro, é enorme e com ação interdependente. Estudos sobre periodontite do adulto indicam que 2/3 da perda de inserção e reabsorção de osso alveolar são passíveis de prevenção pela ação de drogas antiinflamatórias não-esteróides. Aspectos da resposta imunoinflamatória do hospedeiro à infecção bacteriana, que são o elemento-chave do início e da progressão da periodontite, podem ser geneticamente determinados (HART⁴, 1994). Portanto, alterações em nível gênico, que resultam em modificação da resposta via mediadores, merecem ser estudadas. Dessa forma, nos últimos anos, atenção tem sido amplamente dirigida para fatores do hospedeiro, que aumentam significativamente o risco à doença, especialmente polimorfismos em genes de mediadores pró-inflamatórios, moduladores ou intensificadores dos mecanismos destrutivos da doença. Polimorfismos são variações genéticas encontradas na população, consideradas dentro da normalidade. Há polimorfismos que influenciam a atividade de fatores que regulam a intensidade da resposta inflamatória, estando assim associados ao aumento significativo do risco à severidade da doença. Desde que o grau de destruição nos tecidos periodontais, que caracteriza a DP severa, seja essencialmente resultado da resposta

inflamatória, faz-se necessário o estudo de polimorfismos genéticos que alteram a produção de fatores relacionados com a intensidade da resposta inflamatória e a severidade da DP em adultos e em indivíduos com doença periodontal de início precoce (EOP).

MARCADORES GENÉTICOS DE SUSCETIBILIDADE À DP

São recentes as primeiras descrições de polimorfismos gênicos associados à DP. Polimorfismos nos genes da interleucina-1 α e β (IL-1 α e β) e fator de necrose tumoral- α (TNF- α) foram os primeiros marcadores genéticos da DP a serem descritos, identificando indivíduos suscetíveis à severidade da doença periodontal (KORNMAN et al.⁷, 1997, GORE et al.³, 1998, DIEHL et al.¹, 1999 e MCGUIRE; NUNN¹⁰, 1999). As interleucinas (IL) são mediadoras-chave do processo inflamatório, pois modulam a síntese e degradação de componentes da matriz extracelular e osso que constituem os tecidos periodontais (GENCO², 1992). Níveis mais altos de IL-1 foram encontrados na gengiva (HONIG et al.⁵, 1989) e em sítios ativos (STASHENKO et al.^{13,14}, 1991a e b) de pacientes com periodontite do adulto, e diminuídos no fluido gengival após tratamento da DP (MASADA et al.⁹, 1990). Diferenças individuais nos níveis de interleucina relacionados aos diferentes graus de

suscetibilidade à DP são atribuídas a alelos de genes polimórficos da interleucina-1. O alelo 2 do polimorfismo IL-1 β ⁺³⁹⁵³ está associado ao aumento da produção de IL-1 β *in vitro* (POCIOT et al.¹¹, 1992) e por polimorfonucleares do sangue periférico (GORE et al.³, 1998). Em adultos, o polimorfismo no gene da IL-1 β ⁺³⁹⁵³ (alelo 2) sugere fortemente um papel desta citocina na patogênese da DP (KORNMAN et al.⁷, 1997; GORE et al.³, 1998). A frequência do alelo 2 do polimorfismo IL-1 β ⁺³⁹⁵³ esteve significativamente aumentada em pacientes com DP avançada quando comparados com aqueles com DP leve à moderada, o que fornece subsídios para a implicação desse polimorfismo na suscetibilidade à severidade da DP em adultos (GORE et al.³, 1998). Indivíduos heterozigotos para o alelo 2 (polimorfismo IL-1 β ⁺³⁹⁵³) produzem 2 vezes mais IL-1 β , enquanto a homozigose para esse alelo proporciona o aumento de 4 vezes na produção desta interleucina-1 β (POCIOT et al.¹¹, 1992). KORNMAN et al.⁷ (1997) associaram um genótipo composto por alelos resultantes de polimorfismos no gene da IL-1 β ⁺³⁹⁵³ (alelo 2) e da IL-1 α ⁻⁸⁸⁹ (alelo 2) à severidade do desenvolvimento da DP em adultos e estimaram a frequência desse genótipo composto na população em cerca de 30 %. Foi demonstrado estatisticamente, num estudo longitudinal de 14 anos, que a presença de genótipos variantes (chamados de genótipos positivos para a

IL-1), resultantes de polimorfismos, aumenta as chances de morbidade dental em 2,7 vezes e, num efeito combinado com o fumo, pode resultar num risco 7,7 vezes maior de perda dental (MCGUIRE; NUNN¹⁰, 1999). Estes autores observaram um alto grau de colinearidade entre a combinação fumo-genótipo positivo para IL-1 e parâmetros clínicos relacionados à perda dental, tais como profundidade de sondagem, envolvimento de furca e mobilidade. Para os autores, é possível prever quais pacientes são passíveis de perder mais dentes, especialmente quando fumantes, o que denota a relevância clínica da informação genética. O valor dos parâmetros clínicos tradicionalmente usados na determinação do prognóstico da DP parece estar pelo menos em parte na dependência de genótipos específicos. A associação entre uma dada doença e um marcador genético conhecido, além de permitir a identificação de indivíduos de maior risco ao desenvolvimento da doença em questão, contribui para decifrar a heterogeneidade etiológica da mesma na elucidação de sua patogênese (SOFAER¹², 1990).

DIAGNÓSTICO MOLECULAR DA DOENÇA PERIODONTAL

Mais do que focalizar níveis de higiene oral, identificando-se e quantificando-se a microbiota potencialmente patogênica, o principal desafio

para o futuro parece ser encontrar meios de identificar grupos de risco para a severidade da doença periodontal. Clinicamente, esses fatores podem ser usados para a identificação de indivíduos com uma resposta desfavorável ao ataque microbiano, isto é, pessoas que sejam suscetíveis à doença periodontal, para que sejam priorizados programas de prevenção, antes que ocorra a destruição irreversível dos tecidos periodontais, e para que se conheça melhor o curso da doença. A DP compreende um grupo de doenças crônicas multifatoriais complexas cuja etiopatogênese é pobremente compreendida, dessa forma dificultando testes diagnósticos do risco de sua severidade e progressão (KORNMAN; DI GIOVINE⁶, 1998). Mediadores pró-inflamatórios parecem ser o foco de atenção neste momento em que a resposta do hospedeiro mostra-se determinante na intensidade da destruição periodontal. Assim, a busca de marcadores genéticos que permitam a detecção de indivíduos com maior probabilidade de desenvolver a doença é fundamental para a prevenção da instalação do processo destrutivo, ou para a instauração de terapêutica individualizada e preservação adequada de pacientes, nos quais sinais clínicos da doença já se manifestaram. Sendo a DP uma doença multifatorial complexa, quanto mais genes forem considerados, mais efetivo será o diagnóstico.

A mensuração da perda óssea através de sondagem na dentição mista e em dentes apenas parcialmente erupcionados é considerada difícil. Devido à severidade das periodontites de início precoce (EOP) e à sua tendência a progredir para a morbidade dental em curto espaço de tempo e em indivíduos jovens, a detecção precoce da EOP em crianças e adultos jovens é de suma importância para o diagnóstico de indivíduos suscetíveis a desenvolverem a doença a partir da infecção. Pelo fato de a EOP apresentar tendência à agregação familiar, a investigação genética em indivíduos jovens, principalmente naqueles descendentes de pais que perderam dentes pela DP, poderia garantir acompanhamento mais cuidadoso do profissional quanto ao controle de placa, juntamente com aconselhamento contra hábitos de risco, como o fumo. A descoberta de marcadores genéticos relacionados à EOP pode ser de inestimável valia para a compreensão de sua etiologia e patogênese e, no futuro, para a instalação de análise epidemiológica preventiva.

A análise de DNA humano é amplamente empregada em estudos genéticos de famílias e populações. Na maioria dos casos, é realizada em amostras obtidas de sangue periférico. No entanto, constitui um procedimento invasivo, além de esbarrar em problemas éticos, tais como em casos que envolvem pessoas extremamente doentes, idosos e crianças; também requer

supervisão médica e equipamento específico, o que aumenta os custos. A obtenção de células epiteliais da mucosa bucal como fonte de DNA permite uma análise genética fácil, rápida e sem entraves do ponto de vista ético. Ela consiste na realização de um bochecho com solução de glicose a 3 % pelo paciente por 1 minuto (SCAREL et al.¹⁵, 2000; TREVILATTO; LINE¹⁶). Essa solução transporte contém as células epiteliais nucleadas, a partir das quais se extrai o DNA, o que permite as análises de suscetibilidade genética à DP. O perfil de suscetibilidade representa a somatória das análises individuais de genes que expressam mediadores/fatores celulares envolvidos na patogênese da doença.

CONCLUSÃO

Num futuro muito próximo, a prática da coleta de um simples bochecho do paciente poderá permitir ao cirurgião-dentista o conhecimento do perfil individual de risco à progressão e severidade da doença periodontal. Essa técnica de coleta é simples, rápida e não-invasiva, de apropriada execução durante uma consulta clínica e indicada, por exemplo, para pacientes cujos progenitores perderam elementos dentários em consequência da DP. Dessa forma, sugere um acompanhamento mais próximo do paciente pelo CD e

desaconselha hábitos de risco, como o fumo. Ainda, do ponto de vista do cirurgião-dentista, este terá como se proteger judicialmente se de posse de termo de compromisso devidamente assinado pelo paciente, em ciência de sua condição genética.

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CLINICAL, GENETIC AND MICROBIOLOGICAL FINDINGS IN A
BRAZILIAN FAMILY WITH AGGRESSIVE PERIODONTITIS

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Clinical, Genetic and Microbiological Findings in a Brazilian Family with Aggressive Periodontitis

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Short title: *Clinical, Genetic, Microbiologic aspects.*

Abstract. In this study, the clinical, genetic and microbiological profile of a 14-individual family with Aggressive Periodontitis was reported. Microbiological samples were obtained from subgingival plaque of affected sites and PCR was utilized to detect pathogenic bacteria. RFLP-PCR was used to determine cytokine genetic polymorphisms. Localized Aggressive Periodontitis was diagnosed for a 18-yr-old systemically healthy non-smoking female (proband), associated with *Actinobacillus actinomycetemcomitans* infection and detectable levels of *Porphyromonas gingivalis*, *Bacteroides forsythus* and *Treponema denticola*. The siblings displayed clinically detectable Aggressive Periodontitis. *Bacteroides forsythus* and *T. denticola* were the most frequent pathogens found. *P. gingivalis* was detected in 50 % of the individuals. Allele 2 of the IL-1 α (-889) polymorphism was found in all the individuals as well as allele 1 of the IL-1 β (+3953). Alleles 1 and 2 (50 % each) of the IL-1 β (-511), allele 1 of the TNF- α (-308) and allele 2 (in homo or heterozygosity) of the gene IL-RN (intron 2) were present. The low prevalence of *A. actinomycetemcomitans* in this family may question the validity of the microbiological analysis to diagnose Localized Aggressive Periodontitis. The results clearly show that microbiological and genetic parameters were irrelevant for the prediction of periodontitis susceptibility in this family.

Key words: Aggressive Periodontitis; cytokine; risk factors; gene polymorphism; periopathogens

Aggressive Periodontitis comprises a group of rare (roughly 1 % of the population), rapidly progressive forms of periodontitis, characterized by severe destruction of periodontal attachment apparatus at an early age. Aggressive Periodontitis seems to be inherited in a Mendelian Fashion, and both X-linked and autosomal modes of transmission have been proposed (Hart et al. 1992, Hodge et al. 2000). Diagnosis of Aggressive Periodontitis requires exclusion of the presence of systemic diseases that may severely impair host defenses and lead to premature tooth loss (Tonetti & Mombelli 1999). The short time of manifestation of clinically detectable levels of disease is generally interpreted as being the expression of either aggressive etiological agents, that implies infection with a highly virulent microbiota, or a high level of subject susceptibility to Periodontal Disease (PD), or a combination of the two (Tonetti & Mombelli 1997). *Actinobacillus actinomycetemcomitans* (*A.a.*) has received particular attention in recent years for being considered a key microorganism in Localized Aggressive Periodontitis. Bacterial lipopolysaccharide (LPS) activates host cells to secrete inflammatory mediators such as prostaglandins, interleukin-1 beta (IL-1 β) and tumor necrosis factor alpha (TNF- α). Subject differences in the interleukin levels are related to the different degrees of susceptibility to periodontal disease and are due to polymorphic alleles of some genes.

Polymorphisms in the IL-1 α , IL-1 β and TNF- α can identify individuals susceptible to periodontitis (Gore et al. 1998, Diehl et al 1999, McGuire & Nunn 1999). These cytokines are key regulators of the host immuno-inflammatory responses to microbial infection (Kornman et al. 1997). They modulate the synthesis and resorption of extracellular matrix components and bone of the periodontal tissues (Genco 1992). Interleukin-1 (IL-1) has been implicated in disease pathogenesis because it is considered to be a multifunctional pro-

inflammatory cytokine (Birkedal-Hansen 1993). Besides participating in several aspects of the immune response (Tatakis 1993), it enables ingress of inflammatory cells into sites of infection, stimulates release of metalloproteinases that degrade proteins of the extracellular matrix and promotes bone resorption (Birkedal-Hansen 1993, Diehl et al 1999). The allele 2 of IL-1 β (+3953) gene was associated with increased production of IL-1 β *in vitro* (Pociot et al. 1992) and by peripheral blood leukocytes (Gore et al. 1998). Heterozygous individuals for the IL-1 β (+3953) allele 2 can produce twice as IL-1 β , while homozygosity promotes a 4-fold increase in the production of IL-1 β (Gore et al. 1998). A longitudinal study with a follow up of 14 years (McGuire & Nunn 1999) showed a close relationship between a positive IL-1 genotype (allele 2 of the IL-1 β ⁺³⁹⁵³) status and tooth loss. However, alleles 1 of IL-1 α (-889) and IL-1 β (+3953) polymorphisms were shown to be associated with Aggressive Periodontitis and the variation at the IL-1 α (-889) marker does not seem to be closely linked with this disease (Diehl et al. 1999). It was also observed that homozygous individuals for allele 2 of IL-1 α (-889) marker were quite rare (only 3 % of the patients with Aggressive Periodontitis).

In spite of its rare occurrence, Aggressive Periodontitis has been the focus of many investigations aimed at understanding its etiology and pathogenesis. In this study we report the clinical and microbiological profile, as well as the analysis of specific inflammatory mediator genotypes of a 14-individual Brazilian family with Aggressive Periodontitis.

Materials and Methods

Clinical procedure

Within a protocol approved by an institutional review board, subjects signed a consent form after being advised of the nature of the study. The two-generation family was formed by 14 individuals: 8 women and 6 men. The average age was 21 years, with a range between 10 and 48 years. Evaluations in each family member consisted of medical and dental history, full-mouth periapical radiographic survey and dental examination. Patients did not smoke and did not have any systemic disease. Clinical examination consisted of visual inspection and photography of the teeth and oral tissues. Measurements of probing depth and of attachment level were made at four sites for each tooth using standard periodontal probe (Hu-Friedy, Chicago, IL). Inflammation was measured using the Gingival Index (GI) and microbial deposits were assessed using the Plaque Index (PI) (Löe 1967). Alveolar bone loss was verified by the use of periapical radiographs (Rx). Any tooth with a clinical attachment loss (CAL) ≥ 5 mm was considered to be affected (Flemming 1999, Hedge et al. 2000). Siblings 3 and 4 refused from clinical and radiographic examination. It should be noted that the detection of clinically evident disease is very unlikely in patients less than 13 years of age, unless they are suffering from any variety of systemic conditions that interferes with resistance to bacterial infection in addition to or as part of their Aggressive Periodontitis (Armitage 1999).

Microbiological analysis

Sampling

Microbiological samples were obtained from subgingival plaque of affected sites. Sample sites were isolated and air-dried. Supragingival plaque was removed and paper points were

inserted to the depth of the pockets, held in place for 15 s and placed into a vial containing 0.5 mL sterile water. The samples were boiled for 10 min, centrifuged, and the supernatant was subsequently used for PCR analysis.

Bacterial samples

The following bacterial strains were obtained from American Type Culture Collection and used as positive and/or negative controls: *Porphyromonas gingivalis* (*P.g.*) (ATCC 33277), *Porphyromonas endodontalis* (*P.e.*) (ATCC 35406), *Bacteroides forsythus* (*B.f.*) (ATCC 43037), *Actinobacillus actinomycetemcomitans* (*A.a.*) (ATCC 29522), *Prevotella intermedia* (*P.i.*) (ATCC 25611), *Prevotella nigrescens* (*P.n.*) (NCTC 9336) and *Treponema denticola* (*T.d.*) (clinical isolate).

Primers

The primers used have been described previously: *P. gingivalis* (Benkirane et al. 1995); *B. forsythus*, *T. denticola* and *A. actinomycetemcomitans* (Slots et al. 1995); *P. endodontalis*; *P. intermedia* and *P. nigrescens* (Guillot et al. 1997). Most of these bacteria are considered to be predictors for the progression of periodontitis (Flemming 1999).

PCR

Amplifications were performed in a reaction mixture containing 5 µL of sample, 1X PCR buffer (10 mM Tris-HCl, pH 9.0; 50 mM KCl; 1.5 mM MgCl₂), 200 µM of each of the 4 dNTPs, 1.25 U Taq DNA polymerase, 1.0 µM of each primer in a final volume of 50 µL. The PCR temperature profile included an initial denaturation step at 95°C for 2 min, followed by 36 cycles of denaturation at 95°C for 30 s, primer annealing at 65°C for 1 min and extension at 72°C for 1 min, with a final extension step of 72°C for 2 min. PCR

amplification products were analyzed in 1.5 % agarose gel electrophoresis. The gel was stained with ethidium bromide and photographed on a ultraviolet light transilluminator.

Genes of the host inflammatory response

Sampling

Fourteen individuals undertook a mouthwash after 2 min, containing 5 mL 3 % glucose. Following mouthwash, a sterile wood spatula was used to scrape oral mucosa. The tip of the spatula was then shaken into the retained mouthwash solution. Buccal epithelial cells were pelleted by centrifugation at 2000 rpm for 10 min. The supernatant was discarded and the cell pellet resuspended in 500 µL of extraction buffer [10 mM Tris-HCl (pH 7.8), 5 mM EDTA, 0.5 % SDS]. The samples were then frozen at -20 °C until used for DNA extraction.

DNA extraction

After defrosted, samples were incubated overnight with 100 ng/mL proteinase K (Sigma Chemical Co., St. Louis, MO, USA) at 37°C with agitation. DNA was then purified by sequential phenol/chloroform extraction and salt/ethanol precipitation (Sambrook et al. 1989). DNA was dissolved in 70 µL TE buffer [10 mM Tris (pH 7.8), 1 mM EDTA]. The concentration was estimated by measurements of OD 260.

Analysis of genetic polymorphisms

Amplification reactions (PCR) were performed with 300 to 700 ng DNA in a volume of 50 µL in reaction mixture containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, deoxyribonucleotides (200 µM each), 2 U *Taq* DNA polymerase (Amersham Pharmacia Biotech, Uppsala, Sweden). Five genetic markers, considered to be predictors of Adult Periodontitis severity by Kornman et al. (1997), were investigated: IL-1 α (-889),

IL-1 β (-511), IL-1 β (+3953), TNF- α (-308) and IL-RN (intron 2) genes. The primers, MgCl₂ concentration, cycle parameters and restriction assays (RFLP) were used as described (Kornman et al. 1997). Amplification was carried out in a *Perkin-Elmer GeneAmp 2400* thermal cycler. Restriction products were visualized by electrophoresis on vertical 5 % polyacrylamide gels in 1X TBE (89 mM Tris-Borate, 89 mM boric acid, 2 mM EDTA), followed by silver staining (Bio-Rad Silver Stain Kit).

Results

Case report

Proband features

The proband (subject 10: Fig.1, Table 1) was examined and complained about tooth mobility. The patient was systemically healthy and did not present susceptibility to infections. She suffered from red, swollen and easy-bleeding gingiva, progressive mobility on all first molars and gingival recessions. At the moment of clinical examination, the right maxillary and mandibular first molars and the left maxillary first molar were extremely mobile. The teeth were free from caries and calculus was not found. Radiographs revealed extensive alveolar bone loss on the first molars. Deep pockets were clinically detected by probing. Localized Aggressive Periodontitis was diagnosed for the proband according to the criteria of the *1999 World Workshop for a Classification of Periodontal Diseases and Conditions* (Armitage 1999).

Siblings

Subjects 11, 13, 14, 15 (Fig.1, Table 1) did not show any clinical attachment loss. At their age (10 to 16 years) the disease phenotype may not have developed sufficiently so that could

be reliably differentiated from diseased subjects. The youngest siblings of the family (13, 14 and 15) were in the period of mixed dentition. Six siblings (5, 6, 7, 8, 9 and 12: Fig.1, Table 1) presented signs of Aggressive Periodontitis. Siblings 5, 6, 7 and 8 presented several missing teeth and clinical attachment loss were in the range of 5 to 7 mm; radiographs revealed angular defects affecting the related teeth, especially in sibling 7. Siblings 5 and 6 showed a moderate amount of calculus and plaque. Sibling 7 did show neither calculus nor amounts of plaque. Localized Aggressive Periodontitis was diagnosed for subjects 5 and 8. Incipient LAP was diagnosed for subject 9, which presented only two affected sites, and sibling 12, with affected sites on the first molars (she was in the period of mixed dentition). The large number of missing teeth and loss of attachment $\geq 5\text{mm}$ in other teeth than molars and incisors in patients 6 and 7 suggest a generalization of the process of disease. The clinical condition of the mother (subject 2: Fig. 1) suggests that she used to portrait periodontal disease (Table 1).

Microbiological findings

The specificity of PCR primers was confirmed against the tested species. No cross reaction was observed for all tested species. The most frequent pathogens found in the subgingival microbiota of the analyzed patients were *B. forsythus* and *T. denticola* (detected in 45 % plaque samples). *Porphyromonas gingivalis* was found in about 50 % of the aggressive periodontitis individual plaque samples. The proband (subject 10) was colonized by *A. actinomycetemcomitans*, *B. forsythus*, *T. denticola* and *P. gingivalis* (Table 2).

Genetic analysis

The following alleles of the polymorphisms studied were observed in the family: allele 2 of IL-1 α gene (-889), allele 1 for the IL-1 β gene (+3953), alleles 1 and 2 (50 % each) for IL-1 β

gene (-511), allele 1 for TNF- α gene (-308) and allele 2 (in homo or heterozygosity) for IL-RN gene (intron 2) (Table 3).

Discussion

Gram-negative organisms are believed to constitute approximately two thirds of the inhabitants of aggressive periodontitis pathogenic microbiota. *Actinobacillus actinomycetemcomitans*, a facultative anaerobic, is considered to be closely associated with LAP (Tonetti & Mombelli 1999). In fact, this microorganism was detected in the proband sites of infection. Together with the clinical attachment loss and alveolar bone loss localized in the mesial aspect of the first molars, the presence of this pathogen is considered to be an important factor in the diagnosis of LAP (Lench et al. 1988). Generalized aggressive periodontitis has been frequently associated with *P. gingivalis*, *B. forsythus* and *A. actinomycetemcomitans* (Tonetti & Mombelli 1999). One of the siblings with generalized aggressive periodontitis had *P. gingivalis* and the two presented *B. forsythus*. Sibling 15 was infected with *A.a.*, *P.g.*, *P.e.* and *T.d.*. This patient had a significant microbiota and should be monitored. He did not present signs of disease, which could be due to low age (10 years).

Since bacteria alone will not explain periodontal disease progression, genetic risk factors implicated in the host immune and inflammatory response to bacterial etiologic agents might significantly contribute to the comprehension of the pathogenesis of this group of diseases.

Allele 1 (genotype 1/1) of the IL-1 β (+3953) polymorphism was present in all the family members analyzed. If the presence of allele 1 for the IL-1 β (+3953) polymorphism determines low levels of IL-1 β (and we found it in homozygosity for all the family members), other mediators should be playing a role and having an effect on severity of

periodontal disease. Perhaps, the lower expression of the IL-1 β may be compensated by the homozygosity of the IL-1 α gene (allele 2). All the individuals studied did present allele 2 (genotype 2/2) of the IL-1 α (-889) marker. Although IL-1 α is about 15-fold less potent than IL-1 β (Stashenko et al. 1991 b), polymorphism in this gene has been associated with juvenile arthritis, a chronic inflammatory disease (McDowell et al. 1995). Otherwise, allele 1 of the IL-1 β (+3953) polymorphism associated or not with IL-1 α (-889) allele 2 can possibly cause individuals to be more susceptible to aggressive periodontitis. It is possible that the non-affected siblings of this study do not show signs of disease because of low age (principally individuals 14 and 15 who carry pathogenic bacteria). The distinct roles of IL-1 α and β in periodontal diseases indicate a possible association between periodontitis severity and IL-1 genotypes, but conclusive data about which allele of both polymorphisms really and undoubtedly contributes to the increase of susceptibility to periodontal disease remain to be deciphered.

Regarding the IL-1 β (-511) polymorphism, we have found alleles 1 and 2 in homo or heterozygosity, with a similar frequency. The frequency of alleles 1 and 2 has been estimated as about 60 % and 40 % respectively (Di Giovine et al. 1992).

The tumor necrosis factor alpha (TNF- α) is a pro-inflammatory cytokine, produced by macrophages, with a similar role as IL-1 (Alexander & Damoulis 1994). It induces the secretion of collagenase, prostaglandin E₂ (PGE₂) and interleukin-6 (IL-6) by fibroblasts and bone in culture (Meikle et al. 1989), stimulates bone resorption, and has important immunological activities (Bertolini et al. 1986). It is present in the crevicular fluid of patients with gingivitis and periodontitis (Rossomando et al. 1990). However, TNF- α is about 500-fold less potent than IL-1 in inducing bone resorption (Stashenko et al. 1991 a,

Alexander & Damoulis 1994). Polymorphism within TNF- α locus (allele 2) has been associated with autoimmune diseases (Wilson et al. 1993). In our study, we observed only allele 1 (in homozygosity) in all individuals analyzed. In fact, the frequency of this allele was around 84 % when a sample of forty unrelated individuals was screened (Wilson et al. 1992).

The IL-1 receptor antagonist (IL-1ra), expressed by IL-RN gene, is an IL-1 antagonist by blocking IL-1 receptors, inhibiting the development of diseases mediated by IL-1. Out of the four alleles described allele 2 is more frequent in patients with some forms of immunoinflammatory diseases (Tarlow et al. 1993, Blakemore et al 1994, Clay et al. 1994, Mansfield et al. 1994). Allele 2 was present in all genotypes studied at least in heterozygosity.

We have investigated some already reported markers, but also have to consider the effect of other host modifying factors, acting in antagonistic or synergistic ways with the genes of principal effect, that can modulate the severity of the inflammatory response. Besides, it is not certain yet whether IL-1 is indeed the major factor determining the genetic susceptibility to periodontitis. It is possible that the findings and definitions of factors composing the host response, together with the local microbiota associated, could help clarify the etiology and pathogenesis of this heterogeneous disease, this way providing the best way to prevent and monitor the treatment of this pathology. Analysis of families which portrait forms of aggressive periodontitis may help to add information to clarify the factors that really contribute to progress disease.

It is also worth mentioning that the use of buccal epithelial cells as source of DNA for PCR amplifications has several advantages over blood sampling (Trevilatto & Line 1999, Scarel et al. 2000). The collection of material is fast and inexpensive, buccal samples can be

easily obtained from patients who are reluctant to donate blood and there is no need of medical supervision during sampling (Lench et al. 1988, Meulenbelt et al 1995). Besides, children's consent becomes easier, which is suitable for epidemiological analysis and diagnostic assays involving a large number of individuals.

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Table 1. Clinical features of the individuals within the family with aggressive periodontitis.

Patient	Age	Sex	Missing Teeth	Teeth = CAL (mm) [tooth face*]	Alveolar Bone Loss (Rx)
2	48	Female	All the maxillary 37/38/46/47/48	absent	31/32/41/42/ 43/44 /45
5	25	Female	16/12/11/21/22/24/26 36/37/32/46	27=7[m]	27/33/ 31/41/42
6	24	Male	17/14/12/11/21/22/26/36/ 34/32/33/31/41/42/46	16=5[m]; 24=5[m]; 37=5[v] 43=7[m]	16/24/25/26/ 36/43/47
7	23	Female	12/11/21 31/32/41/42	16=5[m]; 24=7[m]; 46=7[m]; 44=7[v]; 36=5[b]	16/22/24/26/34/ 35/36/ 44/45/46
8	20	Female	36/45/46	16=7[m/d]; 21=5[d]; 22=5[m]; 24=9[m]; 26=7[m]	absent
9	19	Female	absent	16=7[m]; 26=5[m/d]	16/26
10 Proband	18	Female	absent	16=7[m]; 26=5[m]; 36=7[m]; 46=8[d]	16/36/46
11	16	Female	absent	absent	absent
12	14	Female	absent	16=5[d]; 26=5[d]; 36=5[d]; 46=5[d]	absent
13	13	Male	absent	absent	absent
14	11	Male	absent	absent	absent
15	10	Male	absent	absent	absent

* *m*=mesial; *d*=distal; *v*=vestibular; *b*=buccal

Table 2. Presence of specific bacteria in crevicular sites of the aggressive periodontitis patients.

<i>Patients</i>	<i>A.a.</i>	<i>B.f.</i>	<i>P.e.</i>	<i>P.g.</i>	<i>P.i.</i>	<i>P.n.</i>	<i>T.d.</i>
2	-	-	-	-	-	-	-
3	-	+	-	-	-	-	+
4	-	-	-	-	-	-	-
5 [§]							
6	-	+	-	+	-	+	+
7	-	+	+	-	-	-	-
8	-	+	-	+	+	-	+
9	-	+	+	-	-	-	+
10	+	+	-	+	-	-	+
11	-	-	-	-	-	-	-
12	-	-	-	-	-	-	-
13	-	-	-	-	-	-	-
14	-	+	-	+	-	-	+
15	+	-	+	+	-	-	+

+ positive PCR reaction; - negative PCR reaction.

[§] This patient was not analyzed because she had already started taking antibiotics.

Table 3. Gene markers analyzed with the respective genotypes of each individual of the Brazilian family with aggressive periodontitis.

<i>Patient</i>	IL-1α⁻⁸⁸⁹ (alleles 1/2)	IL-1β⁺³⁹⁵³ (alleles 1/2)	IL-1β⁻⁵¹¹ (alleles 1/2)	TNF-α⁻³⁰⁸ (alleles 1/2)	IL-RN (alleles 1/2/3/4/5)
2	(2/2)	(1/1)	(1/2)	(1/1)	(2/2)
3	(2/2)	(1/1)	(2/2)	(1/1)	(2/4)
4	(2/2)	(1/1)	(1/1)	(1/1)	(2/2)
5	(2/2)	(1/1)	(1/2)	(1/1)	(2/2)
6	(2/2)	(1/1)	(1/2)	(1/1)	(2/2)
7	(2/2)	(1/1)	(1/2)	(1/1)	(2/4)
8	(2/2)	(1/1)	(1/2)	(1/1)	(2/2)
9	(2/2)	(1/1)	(1/1)	(1/1)	(2/2)
10	(2/2)	(1/1)	(1/2)	(1/1)	(2/2)
11	(2/2)	(1/1)	(1/2)	(1/1)	(2/2)
12	(2/2)	(1/1)	(1/1)	(1/1)	(2/2)
13	(2/2)	(1/1)	(2/2)	(1/1)	(2/2)
14	(2/2)	(1/1)	(2/2)	(1/1)	(2/4)
15	(2/2)	(1/1)	(1/1)	(1/1)	(2/2)

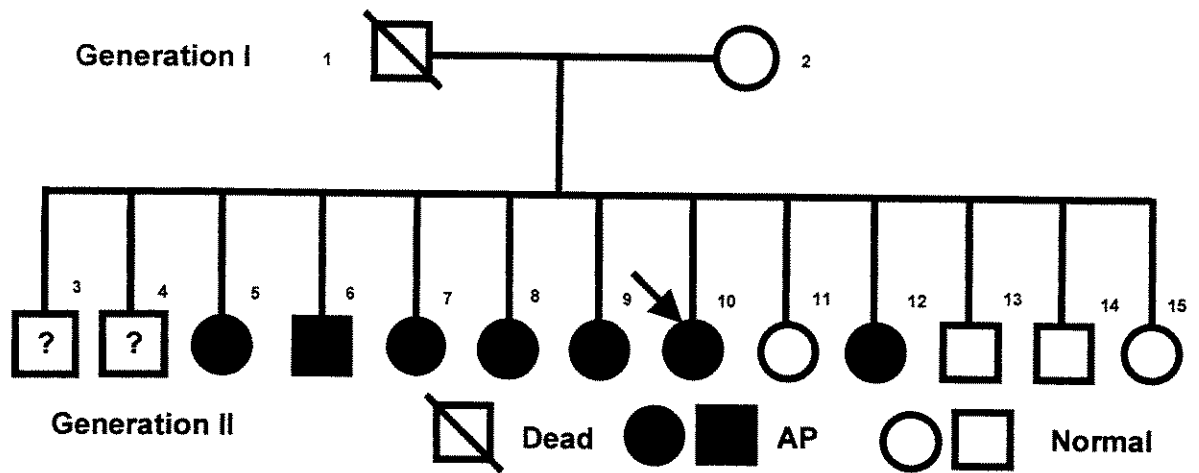
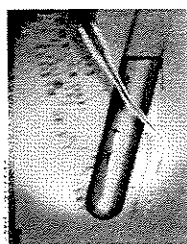


Fig.1. Pedigree of the family. Circles designate female and squares males. The proband is indicated with an arrow.



POLYMORPHISMS IN THE IL-1 α AND IL-1 β GENES ARE NOT ASSOCIATED
WITH SUSCEPTIBILITY TO CHRONIC PERIODONTITIS IN A BRAZILIAN
POPULATION

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Title: Polymorphisms in the IL-1 α and IL-1 β Genes Are Not Associated with Susceptibility to Chronic Periodontitis in a Brazilian Population

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Abstract

The aim of this study was to investigate the association between polymorphisms in the $IL-1\alpha$ and $IL-1\beta$ genes and severity of chronic periodontitis in Brazilians. 113 non-smoking subjects over 25 years (mean age 41.6) were divided according to the severity level of periodontal disease: 44 healthy individuals (control group), 31 subjects with moderate and 38 with severe periodontitis. DNA was obtained from epithelial cells through a mouthwash with 3 % glucose and scraping of oral mucosa. The samples were analyzed for $IL-1A$ (-889) and $IL-1B$ (+3953) polymorphisms using PCR-RFLP. The significance of the differences in the frequencies of the polymorphisms in the control and groups with periodontitis was assessed by Chi-square test ($p<0.05$). No significant differences in the allele and genotype frequencies were found among the groups. It was concluded that neither $IL-1A$ (-889) nor $IL-1B$ (+3953) polymorphism was associated with the severity of chronic periodontal disease in the study population.

Periodontal diseases (PD) comprise a group of infectious immuno-inflammatory diseases, characterized by irreversible loss of tissue support around the teeth, which often leads to tooth loss. Bacterial lipopolysaccharides (LPS) of the dental plaque activate cells to produce cytokines such as interleukin-1 (IL-1), which plays a central role in the pathogenesis of many autoimmune and infectious diseases, including periodontitis [1]. Interleukin-1 is a pro-inflammatory cytokine that has been observed in up to 100 % of the gingival crevicular fluid (GCF) from periodontally diseased sites [2]. It has been postulated that this cytokine could be considered a clinical indicator of the active phase of periodontal disease [3].

Together with age, race and smoking, polymorphisms in immuno-regulatory genes seem to be risk factors for the onset and progression of PD. Within the *IL-1 β* gene, a polymorphism in exon 5 (at position +3953) has been reported to influence the production of *IL-1 β* protein. Genotype 2/2 of *IL-1B* (+3953) polymorphism has been associated with a 4-fold increase in *IL-1 β* production [4]. A composite genotype formed by allele 2 of a bi-allelic polymorphism at position -889 of *IL-1A* plus allele 2 of *IL-1B* (+3953) occurred in 80 % of the individuals severely affected and did correlate to the clinical status of chronic periodontitis [1].

In this study we investigated the association between polymorphisms *IL-1A* (-889) and *IL-1B* (+3953) and the severity of chronic periodontitis in a Brazilian population.

Methods

Subject Selection. A convenience sample of 113 unrelated, non-smoking subjects over 25 years of age (mean age 41.6 years) from the Southeastern region of Brazil were recruited for study from the patient pool at the Dental Clinics of the Faculty of Dentistry of Piracicaba - UNICAMP. The baseline clinical parameters for the subject population are presented in table 1. The criteria of exclusion and diagnosis were described elsewhere [5]. Subjects were divided into the following categories according to PD severity: 44 healthy individuals (control group), with no signs of disease, 31 subjects with moderate periodontitis and 38 patients with severe periodontitis.

Sampling. DNA was obtained from epithelial buccal cells and extraction was performed as described by Trevilatto & Line (2000) [6].

Polymorphism in the IL-1 α gene at position -889. The oligonucleotides 5'-AAGCTTGTTCTACCACCTGAACTAGGC-3' and 5'-TTACATATGAGCCTTCCATG-3' were used as primers. Polymerase chain reaction (PCR) was carried out with 500 ng genomic DNA in a total volume of 50 μ L, containing 10 mM Tris-HCl

(pH 8.3), 50 mM KCl, 1 μ M of each primer, 200 μ M each dATP, dCTP, dGTP and dTTP, 2.5 mM MgCl₂ and 2.5 units *Taq* DNA polymerase (Amersham Pharmacia Biotech, Uppsala, Sweden). The reaction was incubated for 3 min at 95°C, followed by 35 cycles of 1 min at 95°C, 1 min at 55°C and 1 min at 72°C and a final extension at 72°C for 5 min. Amplifications were carried out in a Perkin-Elmer GeneAmp 2400 thermal cycler. Restriction fragment length polymorphism (RFLP) was performed with 3 U per 25 μ L reaction of *Nco*I at 37°C overnight (ON) to detect allele 1 [T] (16 bp + 83 bp) and allele 2 [C] (99 bp).

Polymorphism in the IL-1 β gene at position +3953 (5th exon). The region that contains the *Taq*I polymorphic site within exon 5 of IL-1 β gene was amplified by polymerase chain reaction (PCR). The oligonucleotides 5'-CTCAGGTGTCCTCGAAGAAATCAAA-3' and 5'-GCTTTTTTGCTGTGAGTCCCG-3' flanking this region were used as primers. Amplification reactions were carried out with 500 ng genomic DNA in a total volume of 50 μ L, containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1 μ M of each primer, 200 μ M each dATP, dCTP, dGTP and dTTP, 2.5 mM MgCl₂, and 2.5 units *Taq* DNA polymerase (Amersham Pharmacia Biotech, Uppsala, Sweden). The solution was incubated for 2 min at 95°C, 1 min at 67.5°C and 1 min at 74°C by 2 cycles followed by 35 cycles of 1 min at 95°C, 1 min at 67.5°C and 1 min at 74°C and 3 cycles of

1 min at 95°C, 1 min at 67.5°C and 5 min at 74°C. The products were digested with 3 U per 25 µL reaction of *TaqI* at 65°C ON to yield allele 1 [C] (85 bp + 97 bp) and allele 2 [T] (182 bp). In both cases a constant 12 bp band was also produced

Statistical Analysis. The allele ratio and genotype distribution of periodontitis patients and healthy control subjects were analyzed with Chi-square test. A *p*-value <0.05 was considered significant.

Results

There was no significant difference in the genotype distribution between healthy controls and periodontitis patients in the polymorphisms *IL-A*⁻⁸⁸⁹ (*p*=0.903) and *IL-IB*⁺³⁹⁵³ (*p*=0.663), neither was observed statistical variation in the frequency of the alleles in either polymorphisms studied: *IL-A*⁻⁸⁸⁹ (*p*=0.647) and *IL-IB*⁺³⁹⁵³ (*p*=0.351). The distribution of the genotype frequencies and the frequencies of the alleles for both polymorphisms studied are shown in table 2. Allele 2 of the *IL-A* (-889) polymorphism was carried by 51.3% (58/113) of the subjects; of these, only 5.3% (6/113) were homozygous. Allele 2 of the *IL-IB* (+3953) polymorphism was rarer with 31% (35/113) of the study population carrying this allele; of these, 3.5% (4/113) were homozygous. There was no difference in the frequency of the composite genotype, consisting of

IL-A (-889) allele 2 and *IL-1B* (+3953) allele 2, between the healthy group and the groups with periodontitis ($p=0.386$). Only 33 of the 113 subjects (29.2%) carried the composite genotype.

Discussion

Although the indications that more than half of the increased susceptibility to periodontal disease may depend on genetic factors [7], the genetic factors contributing to periodontitis susceptibility remain poorly understood. Among potential new candidate susceptibility genes, there is a strong evidence to support investigation of the IL-1 gene family on chromosome 2q13, encoding three proteins, IL-1 α , IL-1 β and the IL-1 receptor antagonist (IL-1ra), which competes with IL-1 α and IL-1 β for binding to the IL-1 receptors and is a potent inhibitor of IL-1 activity. In this study polymorphisms in the pro-inflammatory *IL-1A* and *IL-1B* were investigated. It was not realized significant association between *IL-1A* and *IL-1B* polymorphisms and severity of periodontal disease. Neither was observed a correlation between the composite genotype (formed by at least one copy of the allele 2 of both polymorphisms) and periodontitis in the study population.

When Caucasians were taken alone, differences in the allele and genotype frequencies among the groups were not observed as well (data not shown).

As can be noted in table 1, the majority (77 %) of the individuals belonging to the population studied is of Caucasian heritage. The high number of white individuals in the sample can be explained by the predominance of European ancestry in South and Southeast of Brazil and is consistent with the data from the Official Brazilian Census. Allele 2 carriage rate for both *IL-1A* (-889) and *IL-1B* (+3953) polymorphisms in the Caucasians was respectively 54% (47/87) of the population, with 5.8% (5/87) of homozygous, and 35.6% (31/87) of the subjects, being 3.5% (3/87) homozygous. Studies on the relationship between IL-1 polymorphisms and periodontitis in Caucasians found the following allele 2 carriage rates: 48% [8], 50.3% [1], 40.6% [9], 52% [10] and 56.4% [11] at the *IL-1A* (-889), and 44.2% [1], 40.6% [9], 32.3% [12] and 49% [11] at the *IL-1B* (+3953) locus. The composite genotype was carried by 33.3% (29/87) of the study Caucasians, similar to that (36.3%) reported by Kornman et al. (1997) [1]. Lower prevalence of 28% was obtained by McDewitt et al (2000) [13] and 29.1% by Duff and di Giovine in Northern Europeans subjects of unknown periodontal status [1], similar to what was obtained in this study for the whole Brazilian population (29.2%).

Recently, a number of single nucleotide polymorphisms (SNPs), which quantitatively affect mRNA synthesis, have been identified in the IL-1 gene cluster, and their frequency is associated with the incidence and severity of

several infectious and inflammatory diseases, such as rheumatoid arthritis [14], meningococcal disease [15] and chronic periodontitis [1, 9, 11, 12].

Our results failed to detect an association between specific alleles of *IL-1A* (-889) and *IL-1B* (+3953) polymorphisms and chronic periodontal disease in a Southeastern Brazilian population. Even though the IL-1 genes do affect the production of the cytokines, we speculate the total influence might be weak and these alleles may not represent a risk factor for Brazilian periodontitis patients. Although the role IL-1 plays in leading to tissue destruction, it is worth mentioning the need for evaluation of other potential candidate genes as contributors to periodontitis, since the existence of a unique gene of principal effect has not yet been confirmed, and chronic periodontitis may possibly represent a polygenic disease. Besides, an individual may also increase susceptibility to severe disease due to non-genetic factors, such as economic status, poor education or lack of professional dental care and bacterial challenge. Probably, in each population an individual risk factor may explain a different proportion of severe periodontitis cases than in other population groups. Polymorphisms in these and/or other genes of the host response, yet to be identified, may bring more information as to which factors could indeed be implicated in the process of disease.

It was concluded that neither *IL-1A* (-889) nor *IL-1B* (+3953) polymorphism was associated with the severity of chronic periodontal disease in the population studied. Although the prevalence of the polymorphisms studied for the Brazilian population was similar to that reported for Europeans, findings from this study bring into question the usefulness of the cited polymorphisms as a method for determining the susceptibility of Brazilian patients to chronic periodontitis.

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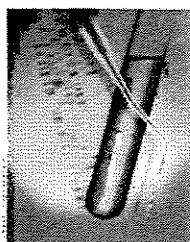
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Table 1. Baseline clinical parameters of the subject population (n=113)

	Healthy (n=44)	Moderate (n=31)	Severe (n=38)
<i>Age (years)</i>			
Mean (\pm SD)	43.2 (\pm 14.0)	36.9 (\pm 11.2)	43.6 (\pm 14.4)
<i>Gender %</i>			
Female	68.2	80.6	84.2
Male	31.8	19.4	15.8
<i>Ethnic Group %</i>			
Caucasoid	84.1	77.4	68.4
Afro-American	6.8	16.1	13.2
Mulatto	6.8	6.5	18.4
Japanese	2.3	0.0	0.0

Table 2. Distribution of the *IL-1A* (-889) and *IL-1B* (+3953) alleles (n=226) and genotypes (n=113) in the healthy group and in groups with moderate and severe periodontitis of the whole Brazilian population

	IL-1A (-889)				IL-1B (+3953)			
	Genotype- n (%)			<i>p</i> value	Genotype- n (%)			<i>p</i> value
	1/1	1/2	2/2		1/1	1/2	2/2	
<i>Healthy</i>	20 (45.5)	21 (47.7)	3 (6.8)	0.903	27 (61.5)	15 (34.0)	2 (4.5)	0.663
<i>Moderate</i>	15 (48.5)	14 (45.0)	2 (6.5)		24 (77.5)	6 (19.3)	1 (3.2)	
<i>Severe</i>	20 (52.7)	17 (44.7)	1 (2.6)		27 (71.0)	10 (26.3)	1 (2.7)	
	Allele - n (%)				Allele - n (%)			
	1	2			1	2		
<i>Healthy</i>	61 (69.3)	27 (30.7)	0.715		69 (78.4)	19 (21.6)	0.351	
<i>Moderate</i>	44 (71.0)	18 (29.0)			54 (87.0)	8 (13.0)		
<i>Severe</i>	57 (75.0)	19 (25.0)			64 (84.2)	12 (15.8)		



ASSOCIATION BETWEEN IL-1 β -511 (C \rightarrow T) POLYMORPHISM AND
CHRONIC PERIODONTITIS IN A BRAZILIAN POPULATION
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Association between IL-1 β -511 (C→T) Polymorphism and Chronic Periodontitis in a Brazilian Population

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SHORT TITLE: IL-1 β (-511) polymorphism, periodontitis

ABSTRACT

Polymorphisms in the interleukin-1 (IL-1) gene cluster have been associated with many types of inflammatory diseases including chronic periodontitis. The aim of this study was to investigate the association between IL-1 β (-511) polymorphism and severity of chronic periodontitis in Brazilians. 113 non-smoking subjects over 25 years (mean age 41.6) belonging to different ethnic groups were divided according to the severity level of periodontal disease: 44 healthy individuals, 31 subjects with moderate and 38 with severe periodontitis. DNA was obtained from epithelial cells through a mouthwash with 3% glucose and scraping of oral mucosa. The samples were analyzed for IL-1 β (-511) polymorphism using PCR-RFLP. The significance of the differences in the frequencies of the polymorphism in the control and groups with periodontitis was assessed by Chi-square test ($p < 0.05$). Significant differences in the allele ($p = 0.018$) and genotype ($p = 0.051$) frequency were found between control and groups with periodontitis only in the subgroup of Brazilian blacks and mulattos. We concluded that allele 2 of IL-1 β (-511) polymorphism was associated with susceptibility to chronic periodontitis in the subpopulation composed of blacks and mulattos, which may suggest a racial component in the determination of the degree of periodontitis severity.

INTRODUCTION

Periodontitis comprises a group of chronic immuno-inflammatory diseases that affect the tissues surrounding teeth and can lead to tooth loss. The etiology of periodontal disease (PD) has been primarily attributed to the interaction of bacterial antigens and inflammatory cells resulting in the production of cytokines [1]. Monocytes are activated by lipopolysaccharides (LPS) to produce cytokines such as interleukin-1 (IL-1), which may contribute to the destruction of periodontal tissues [2].

Interleukin-1 β (IL-1 β) is a member of the interleukin-1 family that has a broad spectrum of biological actions. The degradation of type I collagen by fibroblasts when stimulated with IL-1 β suggests that connective tissue destruction could be initiated by this cytokine [3]. This molecule also promotes bone resorption by stimulating proliferation, differentiation and activation of osteoclasts [4]. Interleukin-1 β has been observed in up to 100% of the gingival crevicular fluid (GCF) from periodontally diseased sites [1, 4-6]. It was postulated that this cytokine could be considered a clinical indicator of the active phase of periodontal disease [1].

Together with age, sex, race, stress and smoking [7-10], genetic polymorphisms seem to be risk factors for the onset and pathogenesis of PD.

Polymorphisms in the IL-1 β gene (chromosomal localization: 2q13) have been reported. A single base polymorphism at position -511 (C→T) was described [11]. Allele 2 (T) of the IL-1 β -511 gene polymorphism has been associated with certain infectious and immuno-inflammatory diseases, such as asthma [12], meningococcal disease [13], cirrhosis [14], hippocampal sclerosis [15], inflammatory bowel disease [16, 17] and gastric carcinoma [18].

Epidemiological studies indicate that periodontitis is widespread among the Brazilian population [19-23]. Since IL-1 β seems to have key roles in the development of chronic periodontitis, in this study we investigated the association between the IL-1 β (-511) polymorphism and the severity of chronic periodontitis in a Brazilian population.

MATERIAL AND METHODS

Subject Selection. A convenience sample of 113 unrelated, non-smoking subjects >25 years of age (mean age 41.6 years old), were recruited for study from the patient pool at the Dental Clinics of the Faculty of Dentistry of Piracicaba - UNICAMP (approved by the Ethical Committee in Research at FOP/UNICAMP, protocol 63/99). The patients are from the Southeastern

region of Brazil. The principal ethnic groups that constitute the Southeast Brazilian population [24, 25] were included in this study: 87 Caucasian (white), 13 Afro-American (black), 12 mulatto and 1 Japanese individuals. The baseline clinical parameters for the subject population are presented in table 1. All subjects were in good general health and had at least 20 teeth in the mouth. Subjects did not have any of the following exclusion criteria: diseases of the oral hard or soft tissues except caries and periodontal disease; use of orthodontic appliances; need for pre-medication for dental treatment; chronic usage of anti-inflammatory drugs; a history of diabetes, hepatitis or HIV infection; immunosuppressive chemotherapy; history of any disease known to severely compromise immune function; present acute necrotizing ulcerative gingivitis or current pregnancy or lactation. Subjects completed personal medical and dental history questionnaires, and within a protocol approved by an Institutional Review Board, signed a consent form after being advised of the nature of the study. Diagnosis and classification of disease severity were made on the basis of clinical parameters and consisted of physical examination, medical and dental history, probing depth, assessment of clinical attachment loss (CAL), tooth mobility, gingival recession and observation of bleeding on probing. Measurements of probing depth and

attachment level were recorded at 4 points around each tooth. Subjects were included in clinical categories according to PD severity:

- 1) *Healthy group*: Subjects found to exhibit no signs of periodontal disease as determined by the absence of clinical attachment loss and no sites with probing depth >3 mm ($n = 44$),
- 2) *Moderate Periodontitis*: Patients with tooth sites exhibiting ≥ 3 mm and <7 mm CAL ($n = 31$),
- 3) *Severe Periodontitis*: Patients with teeth exhibiting ≥ 7 mm CAL ($n = 38$).

Sampling. The sampling of epithelial buccal cells was performed as described by Trevilatto & Line [26]. Briefly, 113 individuals undertook a mouthwash after 1 min, containing 5 mL 3 % glucose. Following mouthwash, a sterile wood spatula was used to scrape oral mucosa. The tip of the spatula was then shaken into the retained mouthwash solution. Buccal epithelial cells were pelleted by centrifugation at 2000 rpm for 10 min. The supernatant was discarded and the cell pellet resuspended in 500 μ L of extraction buffer [10 mM Tris-HCl (pH 7.8), 5 mM EDTA, 0.5 % SDS]. The samples were then frozen at -20°C until used for DNA extraction.

DNA Extraction. After defrosted, samples were incubated overnight (ON) with 100 ng/mL proteinase K (Sigma Chemical Co., St. Louis, MO, USA) at 37°C with agitation. DNA was then purified by sequential phenol/chloroform

extraction and salt/ethanol precipitation. DNA was dissolved in 70 μ L TE buffer [10 mM Tris (pH 7.8), 1 mM EDTA]. The concentration was estimated by measurements of OD 260.

Polymorphism in the IL-1 β gene at position -511 (C \rightarrow T). The oligonucleotides 5'-TGGCATTGATCTGGTTCATC-3' and 5'-GTTTAGGAATCTTCCCCACTT - 3' were used as primers. Amplification reactions were performed with 500 ng genomic DNA in a total volume of 50 μ L, containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1 μ M of each primer, 200 μ M each dATP, dCTP, dGTP and dTTP, 4 mM MgCl₂, and 2.5 units *Taq* DNA polymerase (Amersham Pharmacia Biotech, Uppsala, Sweden). Cycling was 2 cycles of 2 min at 95°C, 1 min at 53°C and 1 min at 74°C, followed by 38 cycles of 1 min at 95°C, 1 min at 53°C and 1 min at 74°C. The products were digested with 3 U per 25 μ L reaction of *Ava*I at 37°C ON to detect allele 1 (C) (114 bp + 190 bp) and allele 2 (T) (304 bp).

Gel electrophoresis. Restriction products were visualized by electrophoresis on vertical 10% non-denaturing polyacrylamide gels in 1X TBE (89 mM Tris-Borate, 89 mM boric acid, 2 mM EDTA), followed by silver staining (Bio-Rad Silver Stain Kit).

Statistical Analysis. The differences in allele and genotype frequency of periodontitis patients and healthy control subjects were analyzed with Chi-

square test. *P*-values less than 0.05 were considered to be statistically significant. The analyses were performed by the program BioEstat [27].

RESULTS

There was no significant difference in the genotype distribution between healthy controls and periodontitis patients on the IL-1 β (-511) polymorphism ($p=0.433$), neither was observed statistical variation in the frequency of the alleles for the polymorphism studied ($p=0.522$). The distribution of the genotype frequencies for the polymorphism studied in the whole sample is shown in table 2 and the frequencies of the alleles are shown in table 3. Allele 2 was carried by 65.5% (74/113) of the study population, being 14% (16/113) homozygous.

When Caucasians alone were investigated, there were no differences among the groups in the genotype ($p=0.716$, Table 4) and allele ($p=0.955$, Table 5) frequencies for the IL-1 β (-511) polymorphism. However, there was a significant difference in the genotype ($p=0.051$, Table 6) and allele ($p=0.018$, Table 7) frequencies between the healthy group and groups with periodontitis in the subgroup comprising the Afro-Americans (blacks) and mulattos for the IL-1 β (-511) locus. For genotypes 1/1 vs 1/2 together with 2/2 [odds ratio:

control vs moderate/severe disease = 18 (1.37-235.69), $p=0.049$]. For allele 1 vs allele 2 [odds ratio: control vs moderate/severe disease = 6.5 (1.48-28.4), $p=0.020$]. Allele 2 was carried by 84% (21/25) of the whole Afro-American and mulatto individuals, being 32% (8/25) homozygous. The allele 2 carriage rate for the patients with moderate and severe periodontitis was 94.7% (18/19), of whom 42% (8/19) were homozygous.

DISCUSSION

Polymorphisms in certain host-response genes have been related to hypersecretion of several cytokines upon microbiological challenge [28-30]. Recently, a number of polymorphisms, which quantitatively affect mRNA synthesis, have been identified in the IL-1 gene cluster [11, 28, 31, 32] and their frequency has been associated with several chronic inflammatory diseases [15-17, 32-41]. The allele 2 carriage rate for a polymorphism in the 5th exon of IL-1 β gene [28] appears to be related to the incidence and severity of periodontal disease [42-45].

In order to elucidate the genetic background to chronic periodontitis it is useful to investigate associations with genetic polymorphisms of immune response genes, whose products play a role in the inflammatory process. The

aim of this study was to examine IL-1 (-511) polymorphism in unrelated Brazilian patients with several degrees of periodontal disease.

As can be noted in table 1, the majority (77 %) of the individuals belonging to the population studied is of Caucasian heritage. The sample is consistent with the data from the Official Brazilian Census [24, 25], which shows that the population of São Paulo State (Southeast of Brazil) is composed by 71.8% of white subjects. The high number of white individuals can be explained by the predominance of European ancestry in South and Southeast of Brazil [24, 25].

Allele 2 carriage rate for the IL-1 β (-511) polymorphism in the white Caucasians was 58% (52/87), being 9% (8/87) of the individuals homozygous. A similar 60% allele 2 carriage rate at IL-1 β (-511) locus was found by Kornman *et al.* [42] in Caucasians of north European origin. Studies on other cytokine genes have shown similar allele frequencies in European and Southeastern Brazilian populations, reinforcing a common ancestry [46].

No association was found between chronic periodontitis and IL-1 β (-511) polymorphism in the Caucasian subgroup. Kornman *et al.* [42] also failed to detect an association between this polymorphism and chronic periodontitis in Caucasians.

As can be observed in table 1, the percentage of black and mulatto individuals increases in the groups with periodontitis. Besides, the prevalence of black and mulatto subjects is higher in the periodontitis groups than the prevalence of whites (75% vs 60%). In the severe disease group the difference is still more evident (50% vs 30%). Destructive periodontal diseases and differences in subgingival microbiota and host immune response have been reported disproportionately more prevalent and severe in African-Americans, indicating that risk factors for disease progression may differ for these populations [10]. However, it is not yet clear whether these differences are really genetic or due to confounding variables such as social economic status, poor education or lack of professional dental care [9]. Sometimes genetic and environmental factors can interact to influence aspects of disease. In black subjects, but not in the whites, smoking in patients with chronic periodontitis was associated with IgG1 lower concentration [47].

Allele 2 carriage rate is high in the black and mulatto subgroup (84%) and is still greater if only the diseased patients are taken into account (94.7%). Allele 2 carriage rate was higher in the subgroup of blacks and mulattos than in whites for all status of disease (84% vs 60%) and this difference was more expressive in patients with periodontitis (94.7% vs 42%). In addition to the higher frequency of allele 2 in the black and mulatto population, this allele

was associated with chronic periodontitis only in this racial group ($p=0.018$). The present results indicate that blacks and mulattos are at higher risk of chronic periodontitis than their white neighbors when they present allele 2 of IL-1 (-511) polymorphism in their genotypes [OR: 18 (1.37-235.69), $p=0.049$]. The fact that allele 2 only correlates to disease in the group composed of black and mulatto individuals may suggest a race-related genetic susceptibility to this disease. It could also indicate that additional efforts are needed to identify complex relationships between allele 2 of IL-1 (-511) gene and other inflammatory modifying genes. Our results point at genetic racial components as contributing risk factors for chronic periodontal disease progression. The substantial ethnic variability in the frequency of allele 2 of the IL-1 β (-511) gene reinforces the concept of the complexity of the causative mechanisms of chronic periodontitis and the variety of genetic interactions that are likely to determine the diseased phenotype.

It was concluded that allele 2 of the IL-1 β (-511) polymorphism was associated with susceptibility to chronic periodontal disease in the Brazilian sub-population of blacks and mulattos studied. This is the first study relating the IL-1 β (-511) polymorphism to susceptibility of chronic periodontitis. Although the sample size of blacks and mulattos is small (25 subjects), this

finding may indicate that ethnic and racial differences could interfere with disease-associated polymorphisms.

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Table 1. Baseline clinical parameters of the subject population (n=113)

	Healthy (n=44)	Moderate (n=31)	Severe (n=38)	Total (n=113)
<i>Age (years)</i>				
Mean (\pm SD)	43.2 (\pm 14.0)	36.9 (\pm 11.2)	43.6 (\pm 14.4)	41.6 (\pm 12.4)
<i>Gender %</i>				
Female	68.2	80.6	84.2	78
Male	31.8	19.4	15.8	22
<i>Ethnic Group %</i>				
Caucasoid	84.1	77.4	68.4	77.2
Afro-American	6.8	16.1	13.2	11.5
Mulatto	6.8	6.5	18.4	10.5
Japanese	2.3	0.0	0.0	0.8

Table 2. Distribution of the IL-1 β (-511) genotypes in the healthy group and in groups with moderate and severe chronic periodontitis in the whole Brazilian population

Genotype	Healthy		Moderate		Severe		<i>p</i> value
	n	(%)	n	(%)	n	(%)	
1/1	17	(38.7)	11	(35.5)	11	(29.0)	0.433
1/2	23	(52.3)	13	(42.0)	22	(58.0)	
2/2	4	(9.0)	7	(22.5)	5	(13.0)	

Table 3. Distribution of the IL-1 β (-511) alleles in healthy, moderate and severe groups with chronic periodontitis in the whole Brazilian population

Allele	Healthy		Moderate		Severe		<i>p</i> value
	n	(%)	n	(%)	n	(%)	
1	57	(64.8)	35	(56.5)	44	(57.9)	0.522
2	31	(35.2)	27	(43.5)	32	(42.1)	

Table 4. Distribution of the IL-1 β (-511) genotypes in the healthy group and in groups with moderate and severe chronic periodontitis in the Caucasian Brazilian population

Genotype	Healthy		Moderate		Severe		<i>p</i> value
	n	(%)	n	(%)	n	(%)	
1/1	14	(37.8)	11	(46.0)	10	(38.5)	0.7157
1/2	20	(54.0)	10	(41.5)	15	(57.5)	
2/2	3	(8.2)	3	(12.5)	1	(4.0)	

Table 5. Distribution of the IL-1 β (-511) alleles in healthy, moderate and severe groups with chronic periodontitis in the Caucasian Brazilian population

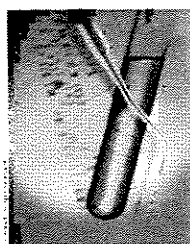
Allele	Healthy		Moderate		Severe		<i>p</i> value
	n	(%)	n	(%)	n	(%)	
1	48	(64.8)	32	(66.5)	35	(67.5)	0.9555
2	26	(35.2)	16	(33.5)	17	(32.5)	

Table 6. Distribution of the IL-1 β (-511) genotypes in the healthy group and in groups with moderate and severe chronic periodontitis in the subgroup composed of Brazilian black and mulatto individuals

Genotype	Healthy n (%)	Moderate n (%)	Severe n (%)	<i>p</i> value
1/1	3 (50.0)	0 (0.0)	1 (8.3)	0.0515
1/2	3 (50.0)	3 (43.0)	7 (58.3)	
2/2	0 (0.0)	4 (57.0)	4 (33.4)	

Table 7. Distribution of the IL-1 β (-511) alleles in healthy, moderate and severe groups with chronic periodontitis in the Brazilian blacks and mulattos

Allele	Healthy n (%)	Moderate n (%)	Severe n (%)	<i>p</i> value
1	9 (75.0)	3 (21.5)	9 (37.5)	0.0184
2	3 (25.0)	11 (78.5)	15 (62.5)	



INTERLEUKIN-1 RECEPTOR ANTAGONIST (IL-1RA) GENE POLYMORPHISM
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Cytokine, submitted

Interleukin-1 receptor antagonist (IL-1ra) gene polymorphism is associated with the severity of chronic periodontitis in a Brazilian population

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Short title: *IL-1ra and chronic periodontitis*

ABSTRACT

Inflammatory cytokines represent important pathological mediators in chronic inflammatory diseases. Interleukin-1 receptor antagonist (IL-1ra) regulates interleukin-1 (IL-1) activity in inflammatory disorders, including chronic periodontitis. Polymorphism in the IL-1ra gene was associated with enhanced production of IL-1ra protein. This study aimed to investigate the association between IL-1ra polymorphism and severity of chronic periodontitis in Brazilians. 113 non-smoking subjects over 25 years (mean age 41.6) were divided according to the severity level of periodontal disease: 44 healthy individuals, 31 subjects with moderate and 38 with severe periodontitis. Genomic DNA was obtained through a mouthwash with 3 % glucose and scraping of oral mucosa. Polymerase chain reaction (PCR) amplification was used to identify the IL-1 receptor antagonist intron 2 variable number of tandem repeat (VNTR) polymorphism. The significance of the differences in the genotype and allele frequencies of the polymorphism in the healthy, moderate and severe groups with periodontitis was assessed by Chi-square test ($p < 0.05$). Significant differences in the genotype frequencies of the polymorphism were found between control/moderate and severe periodontitis groups ($p = 0.029$). It was concluded that IL-1ra intron 2 polymorphism was associated with the severity of chronic periodontal disease in the Brazilian population.

Periodontitis is a complex multifactorial condition involving multiple genes and environmental factors. Approximately half of the variance in periodontal disease seems to be attributed to genetic factors.¹ Inflammatory mediators, such as interleukin-1 (IL-1) and IL-1 receptor antagonist (IL-1ra), play a key role in the pathogenesis of several inflammatory disorders, including chronic periodontitis.^{2,3} Interleukin-1 receptor antagonist regulates IL-1 β activity by inhibiting its competitive binding to the IL-1 β receptor, thus suppressing the IL-1 β induction of cytokines.⁴ Some cytokine gene polymorphisms may contribute to inter-individual variation in cytokine production upon microbial challenge⁵⁻⁷. The polymorphism in human IL-1ra gene intron 2 is caused by variable number of an 86-bp tandem repeat.⁸ The number of repeats at the polymorphism site may be of functional significance because the repeated sequence contains possible binding sites for transcription factors.⁸ Allele 2 was reported to be associated with enhanced production of IL-1ra protein.⁹ Recently, the IL-1ra gene allele 2 was reported to be associated with inflammatory bowel disease,¹⁰ rheumatoid arthritis,¹¹ nephropathy,¹² polymyalgia rheumatica,¹³ alopecia areata,¹⁴ lichen sclerosus,¹⁵ multiple sclerosis,¹⁶ systemic lupus erythematosus,¹⁷ Sjögren's syndrome¹⁸ and myasthenia gravis.¹⁹

Since periodontitis is a chronic inflammatory disease, this study aimed to investigate the association between the IL-1ra (intron 2) polymorphism and chronic periodontitis in Southeast Brazilians.

RESULTS

Fifty-four percent of the individuals studied (61/113) had the A1A1 genotype and 33.6% (38/113) had A1A2 type; only 3.5% (4/113) A2A2 type individuals were included; 0.9% (1/113) was of A1A3 type; 0.9% (1/113) of A2A3 genotype; 5.3% (6/113) were of A1A4, and 1.8% (2/113) were of the A2A4 type. There was no significant difference in the genotype distribution between healthy controls and periodontitis patients at the study polymorphism ($p=0.1536$) (Table 2). But, when the groups comprising control healthy individuals and subjects with moderate periodontitis were analyzed together against the severe periodontitis group, we found a statistically significant association of the genotype A2A2 (genotype frequency 10.5% vs 0%, Table 2) of the IL-1ra polymorphism with severe disease ($p=0.029$). There was no statistical variation in the frequencies of the alleles between controls and groups with periodontal disease ($p=0.799$) (Table 3). The allele frequencies in the study population were: allele 1, 73.9%; allele 2, 21.7%; allele 3, 0.9%; allele 4, 3.5% and allele 5, 0% (Table 4). The corresponding carriage rates were: 94%, 37%, 1.7%, 7% and 0%, respectively. Allele 2 carriage rate at

IL-1ra polymorphism was not different (37%) when only the diseased patients were taken in account, and when severely impaired patients alone were analyzed (37%).

DISCUSSION

Interleukin-1 β and its endogenous antagonist, interleukin-1 receptor antagonist, play important roles in immune responses. interleukin-1 receptor antagonist inhibits IL-1 β activity competitive binding to the IL-1 β receptor, thus suppressing the IL-1 β induction of cytokine.⁴ It may therefore play a crucial role in many IL-1 mediated diseases, acting as an important endogenous regulator of inflammation. Polymorphism in the IL-1ra gene may account for variation in the production of IL-1ra and IL-1 β proteins.^{9,20} Interleukin-1 β and IL-1ra may function as immunomodulators of chronic periodontitis,²¹ so that allelic variation in those genes might be expected to have an impact on periodontal disease. Allele 2 of IL-1ra polymorphism has been associated with many chronic inflammatory diseases, but studies on its implication in periodontal disease are rare, if they so far exist. The allele frequencies in the study population were very similar to that obtained by Tarlow *et al.* (1993)⁸ (Table 4). The allele 2 frequency obtained in the present study was 21.7%. The following similar frequencies for allele 2 were reported: 21.4%⁸ and 27%¹⁸. Allele 2 was carried by 37% of the study population and by 36% of

Caucasian controls of northern European ancestry.¹⁸ A study on the relationship between the IL-1ra polymorphism and periodontitis in Caucasians found an allele 2 carriage rate of 47%,²² but it can be much rarer in other population groups.^{4,12} Studies have demonstrated a significant increase in both the frequency and carriage rate of allele 2 in several diseases.^{17,18}

In the study population, the allele 2 (homozygous genotype) was related to risk of severity for chronic periodontitis. It was concluded that IL-1ra intron 2 polymorphism is associated with the severity of, but not with susceptibility to, chronic periodontal disease in the Brazilian population studied. Although IL-1ra represents an anti-inflammatory cytokine, with allele 2 increasing the production of the corresponding protein, these results implicate the potential involvement of both pro- and anti-inflammatory cytokines in the regulation of chronic periodontitis. The paradox of the association of allele 2 with inflammatory diseases, and with increased production of IL-1ra, perhaps resides in the fact that beyond being anti-inflammatory, it stimulates IL-1 β production, which, at a time, is a potent pro-inflammatory mediator. Another point of consideration is that A2 effect on local and systemic IL-1ra production may be distinct. That can be illustrated by the fact that lower salivary levels of IL-1ra could be detected in patients with severe Sjögren's Syndrome, in contrast with the increase of this protein in the patients serum, suggesting specific regulation in different compartments.^{18,23}

MATERIAL AND METHODS

Subject selection

A convenience sample of 113 unrelated, non-smoking subjects >25 years of age, were recruited for study from the patient pool at the Dental Clinics of the Faculty of Dentistry of Piracicaba – UNICAMP (approved by the Ethical Committee in Research at FOP/UNICAMP, protocol 63/99). The patients are from the Southeastern region of Brazil. The baseline clinical parameters for the subject population are presented in table 1. All subjects were in good general health and had at least 20 teeth in the mouth. Subjects did not have any of the following exclusion criteria: diseases of the oral hard or soft tissues except caries and periodontal disease; use of orthodontic appliances; need for pre-medication for dental treatment; chronic usage of anti-inflammatory drugs; a history of diabetes, hepatitis or HIV infection; immunosuppressive chemotherapy; history of any disease known to severely compromise immune function; present acute necrotizing ulcerative gingivitis or current pregnancy or lactation. Subjects completed personal medical and dental history questionnaires, and within a protocol approved by an Institutional Review Board, signed a consent form after being advised of the nature of the study.

Diagnosis and classification of disease severity were made on the basis of clinical parameters and consisted of physical examination, medical and dental

history, probing depth, assessment of clinical attachment loss (CAL), tooth mobility, gingival recession and observation of bleeding on probing. Measurements of probing depth and attachment level were recorded at 6 points around each tooth. Subjects were included in clinical categories according to periodontal disease severity:

- 1) *Healthy group*: Subjects found to exhibit no signs of periodontal disease as determined by the absence of clinical attachment loss and no sites with probing depth >3 mm ($n = 44$),
- 2) *Moderate Periodontitis*: Patients with tooth sites exhibiting ≥ 3 mm and <7 mm CAL ($n = 31$),
- 3) *Severe Periodontitis*: Patients with teeth exhibiting ≥ 7 mm CAL ($n = 38$).

Sampling

The sampling of epithelial buccal cells was performed as described by Trevilatto & Line (2000).²⁴ Briefly, 113 individuals undertook a mouthwash after 1 min, containing 5 ml 3% glucose. Following mouthwash, a sterile wood spatula was used to scrape oral mucosa. The tip of the spatula was then shaken into the retained mouthwash solution. Buccal epithelial cells were pelleted by centrifugation at 2000 rpm for 10 min. The supernatant was discarded and the cell pellet resuspended in

500 µl of extraction buffer [10 mM Tris-HCl (pH 7.8), 5 mM EDTA, 0.5% SDS]. The samples were then frozen at -20°C until used for DNA extraction.

DNA extraction

After defrosted, samples were incubated overnight (ON) with 100 ng/mL proteinase K (Sigma Chemical Co., St. Louis, MO, USA) at 37°C with agitation. DNA was then purified by sequential phenol/chloroform extraction and salt/ethanol precipitation. DNA was dissolved in 70 µL TE buffer [10 mM Tris (pH 7.8), 1 mM EDTA]. The concentration was estimated by measurements of OD 260.

Polymerase chain reaction (PCR) and variable number of tandem repeat (VNTR)

Polymorphism in the IL-1ra (intron 2) gene

The oligonucleotides 5'-CTCAGCAACACTCCTAT-3' and 5'-TCCTGGTCTGCAGGTAA-3' were used as primers. Amplification reactions were performed with 500 ng genomic DNA in a total volume of 50 µL, containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1 µM of each primer, 200 µM each dATP, dCTP, dGTP and dTTP, 1.5 mM MgCl₂, and 2.5 units *Taq* DNA polymerase (Amersham Pharmacia Biotech, Uppsala, Sweden). The reaction was incubated for 1 min at 96°C, followed by 35 cycles of 1 min at 94°C, 1 min at 60°C and 2 min at 70°C, and additional 5 min at 70°C and 55°C for 5 min. Amplifications were

carried out in a *Perkin-Elmer GeneAmp 2400* thermal cycler. In the second intron of IL-1ra gene, five alleles are defined by different numbers of a 86-bp segment repeat. Genotypes were determined by comparing the size of the bands with a molecular weight ladder, with separation into allele 1 (4 repeats - 412 bp), allele 2 (2 repeats - 240 bp), allele 3 (3 repeats - 326 bp), allele 4 (5 repeats - 498 bp) and allele 5 (6 repeats - 584 bp).²²

Gel electrophoresis

Restriction products were visualized by electrophoresis on vertical 10% non-denaturing polyacrylamide gels in 1X TBE (89 mM Tris-Borate, 89 mM boric acid, 2 mM EDTA), followed by silver staining (Bio-Rad Silver Stain Kit).

Statistical Analysis

The allele ratio and genotype distribution of periodontitis patients and healthy control subjects were analyzed with Chi-square test. A p -value <0.05 was considered significant.

Acknowledgements

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<i>Gender %</i>			
Female	68.2	80.6	84.2
Male	31.8	19.4	15.8
<i>Ethnic Group %</i>			
Caucasoid	84.1	77.4	68.4
Afro-American	6.8	16.1	13.2
Mulatto	6.8	6.5	18.4
Japanese	2.3	0.0	0.0

TABLE 2. Distribution of the IL-1ra genotypes in the healthy group and in groups with moderate and severe chronic periodontitis

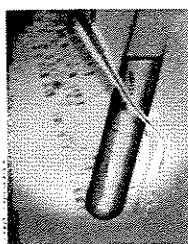
Genotype	Healthy		Moderate		Severe		<i>p</i> value
	n	(%)	n	(%)	n	(%)	
<i>1/1</i>	25	(56.8)	15	(48.4)	21	(55.2)	0.1536
<i>1/2</i>	16	(36.4)	14	(45.2)	8	(21)	
<i>2/2</i>	0	(0)	0	(0)	4	(10.5)	
<i>1/3</i>	1	(2.3)	0	(0)	0	(0)	
<i>2/3</i>	0	(0)	0	(0)	1	(2.7)	
<i>1/4</i>	2	(4.5)	1	(3.2)	3	(7.9)	
<i>2/4</i>	0	(0)	1	(3.2)	1	(2.7)	

TABLE 3. Distribution of the IL-1ra alleles in healthy, moderate and severe groups with chronic periodontitis

Allele	Healthy		Moderate		Severe		<i>p</i> value
	n	(%)	n	(%)	n	(%)	
<i>1</i>	69	(78.4)	45	(72.6)	53	(69.7)	0.799
<i>2</i>	16	(18.2)	15	(24.2)	18	(23.7)	
<i>3</i>	1	(1.1)	0	(0)	1	(1.3)	
<i>4</i>	2	(2.3)	2	(3.2)	4	(5.3)	
<i>5</i>	0	(0)	0	(0)	0	(0)	

TABLE 4. Frequencies (%) of the IL-1ra alleles in the Brazilian population* and in the population studied by Tarlow et al. (1993)^{8}**

Allele	*	**	<i>p</i> value
1	73.9	73.6	0.1213
2	21.7	21.4	
3	0.9	0.7	
4	3.5	3.6	
5	0	0.7	



POLYMORPHISM AT POSITION -174 OF IL-6 GENE IS ASSOCIATED WITH
SUSCEPTIBILITY TO CHRONIC PERIODONTITIS IN A CAUCASIAN
BRAZILIAN POPULATION

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Polymorphism at position -174 of IL-6 gene is associated with susceptibility to chronic periodontitis in a Caucasian Brazilian population

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Short title: *IL-6 polymorphism and chronic periodontitis*

Abstract

Background: Interleukin-6 (IL-6) is a multifunctional cytokine that mediates inflammatory tissue destruction. A G to C substitution at position -174 in the promoter of IL-6 influences in vitro transcription of IL-6. This polymorphism has been associated with inflammatory diseases like chronic arthritis.

Objective: The aim of this study was to investigate the association between the IL-6⁻¹⁷⁴ polymorphism and susceptibility to chronic periodontitis in Brazilians.

Material and Methods: 84 non-smoking subjects over 25 years (mean age 42.4) were divided according to the severity level of periodontal disease: 37 healthy individuals (control group), 24 subjects with moderate and 24 with severe periodontitis. Genomic DNA was obtained from epithelial cells through a mouthwash with 3 % glucose and scraping of oral mucosa. The samples were analyzed for IL-6⁻¹⁷⁴ polymorphism using PCR-RFLP. The significance of the differences in the frequencies of the polymorphism in the control and groups with periodontitis was assessed by Chi-square test ($p < 0.05$).

Results: Differences were found between control and groups with periodontitis in the genotype ($p = 0.0036$, OR=3.0) and in the allele ($p = 0.0838$, OR=1.9) frequencies.

Conclusion: We concluded that the IL-6⁻¹⁷⁴ polymorphism is associated with susceptibility to chronic periodontitis in the population studied.

Key words: chronic periodontitis; interleukin-6, polymorphism

Interleukin-6 (IL-6) plays a role in B-cell differentiation and T cell proliferation (Lotz et al 1988). It also stimulates hematopoiesis (Revel 1989) and accelerates bone resorption (Ishimi et al 1990). High levels of IL-6 in biological fluids and blood have been determined in infections, trauma, chronic inflammatory diseases and neoplasia (Hirano et al. 1990). It is involved in the pathogenesis of several inflammatory diseases such as rheumatoid arthritis (Hirano et al 1988, Houssiau et al. 1988) and psoriasis (Grossman et al 1989), therefore constituting a major mediator of the host response to injury and infection.

Higher levels of IL-6 were found in sites with gingivitis when compared to healthy sites (Kono et al. 1991, Matsuki et al. 1992, Takahashi et al 1994, Atilla & Kütükçüler 1998). Significantly higher expression of IL-6 mRNA was reported in diseased tissues when compared to healthy ones in periodontitis patients (Prabhu et al. 1996). Interleukin-6 levels were higher in culture supernatants of gingival tissues from gingivitis and periodontitis patients than in healthy control patients (Kamagata et al. 1989). It has been therefore suggested that this cytokine may be considered a useful indicator or a diagnostic marker for periodontal disease (Geivelis et al. 1993, Reinhardt et al. 1993).

Some polymorphisms in cytokine genes promoter sequences are associated with transcriptional activity (Pociot et al. 1992, Wilson et al. 1997, Olomolaiye et al. 1998, Shirodaria et al. 2000). A G to C substitution at position -174 in the promoter of IL-6 is located immediately upstream of the multiresponsive element (MRE), located at positions -173 to -151 relative to the transcription start site (Morse et al. 1999). The C allele was shown to alter the IL-6 gene transcription response to stimuli such as LPS and IL-1 (Fishman et al. 1998). The C allele creates an *Nla*III restriction site and has been assigned Genbank accession number AF005845 (Yasukawa et al. 1987, Ray et al. 1988, Olomolaiye et al. 1998, Morse et al. 1999).

Since cytokines like IL-6 seem to have key roles in the development of several chronic inflammatory diseases including periodontitis, in this study we investigated the possible association between IL-6⁻¹⁷⁴ polymorphism and susceptibility to chronic periodontitis in Caucasian Brazilians.

Material And Methods

Subject Selection

A convenience sample of 84 unrelated, non-smoking Caucasian subjects >25 years of age (mean age 42.4), were recruited for study from the patient pool at the Dental Clinics of the Faculty of Dentistry of Piracicaba – UNICAMP

(approved by the Ethical Committee in Research at FOP/UNICAMP, protocol 63/99). The patients are from the Southeastern region of Brazil. The baseline clinical parameters for the subject population are presented in table 1. All subjects were in good general health and had at least 20 teeth in the mouth. Subjects did not have any of the following exclusion criteria: diseases of the oral hard or soft tissues except caries and periodontal disease; use of orthodontic appliances; need for pre-medication for dental treatment; chronic usage of anti-inflammatory drugs; a history of diabetes, hepatitis or HIV infection; immunosuppressive chemotherapy; history of any disease known to severely compromise immune function; present acute necrotizing ulcerative gingivitis or current pregnancy or lactation. Subjects completed personal medical and dental history questionnaires, and within a protocol approved by an Institutional Review Board, signed a consent form after being advised of the nature of the study. Diagnosis and classification of disease severity were made on the basis of clinical parameters and consisted of physical examination, medical and dental history, probing depth, assessment of clinical attachment loss (CAL), tooth mobility, gingival recession and observation of bleeding on probing. Measurements of probing depth and attachment level were recorded at 4 points around each tooth. Subjects were included in clinical categories according to periodontal disease severity:

- 1) *Healthy group*: Subjects found to exhibit no signs of periodontal disease as determined by the absence of clinical attachment loss and no sites with probing depth > 3 mm (n = 37),
- 2) *Moderate Periodontitis*: Patients with tooth sites exhibiting ≥ 3 mm and <7 mm CAL (n = 24),
- 3) *Severe Periodontitis*: Patients with teeth exhibiting ≥ 7 mm CAL (n = 24).

Sampling

The sampling of epithelial buccal cells was performed as described by Trevilatto & Line (2000). Briefly, 85 individuals undertook a mouthwash after 1 min, containing 5 ml 3 % glucose. Following mouthwash, a sterile wood spatula was used to scrape oral mucosa. The tip of the spatula was then shaken into the retained mouthwash solution. Buccal epithelial cells were pelleted by centrifugation at 2000 rpm for 10 min. The supernatant was discarded and the cell pellet resuspended in 500 μ l of extraction buffer [10 mM Tris-HCl (pH 7.8), 5 mM EDTA, 0.5 % SDS]. The samples were then frozen at -20°C until used for DNA extraction.

DNA Extraction

After defrosted, samples were incubated overnight (ON) with 100 ng/mL proteinase K (Sigma Chemical Co., St. Louis, MO, USA) at 37°C with agitation. DNA was then purified by sequential phenol/chloroform extraction and salt/ethanol precipitation. DNA was dissolved in 70 µL TE buffer [10 mM Tris (pH 7.8), 1 mM EDTA]. The concentration was estimated by measurements of OD 260.

Polymerase Chain Reaction (PCR) and Restriction Fragment Polymorphism (RFLP)

Polymorphism in the IL-6 gene at position -174

The following primer pair was used for PCR amplification of genomic DNA samples: 5'-TTGTCAAGACATGCCAAGTGCT-3' (Forward) and 5'-GCCTCAGAGACATCTCCAGTCC-3' (Reverse). Amplification reactions were carried out with 500 ng genomic DNA in a total volume of 50 µL, containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1 µM of each primer, 200 µM each dATP, dCTP, dGTP and dTTP, 1.5 mM MgCl₂, and 2.5 units *Taq* DNA polymerase (Amersham Pharmacia Biotech, Uppsala, Sweden). The reaction was incubated for 5 min at 95°C, followed by 35 cycles of 1 min at 95°C, 1 min at 60°C and 1 min at 72°C and a final extension at 72°C for 5 min.

Amplifications were carried out in a *Perkin-Elmer GeneAmp 2400* thermal cycler. The products were digested with 1 U per 25 μ L reaction of *Nla*III (CATG↓) at 37°C overnight (ON) to detect allele G (13 bp + 227 bp + 59 bp) and allele C (13 bp + 118 bp + 109 bp + 59 bp).

Gel electrophoresis

Restriction products were visualized by electrophoresis on vertical 10 % non-denaturing polyacrylamide gels in 1X TBE (89 mM Tris-Borate, 89 mM boric acid, 2 mM EDTA), followed by silver staining (Bio-Rad Silver Stain Kit).

Statistical Analysis

The allele ratio and genotype distribution of periodontitis patients and healthy control subjects were analyzed with Chi-square test. A p -value <0.05 was considered significant.

Results

There was a significant difference in the genotype ($p=0.0036$) distribution and a less significant but still suggestive one in the allele frequency ($p=0.0838$) between healthy controls and periodontitis patients for the polymorphism

IL-6⁻¹⁷⁴. The distribution of the genotype and allele frequencies for the polymorphism studied is shown in tables 2 and 3, respectively. For genotypes G/G vs G/C together with C/C [odds ratio: control vs moderate/severe disease = 3.05 (1.27-7.52), $p=0.0253$]. For G allele vs C allele [odds ratio: control vs moderate/severe disease = 1.9 (0.97-3.71), $p=0.0838$]. Allele G of the IL-6⁻¹⁷⁴ polymorphism was carried by 91.6% (77/84) of the study Caucasians; of these 48.8% (41/84) were homozygous [29.3% (12/41) belonged to the healthy group and 70.7% (29/41) to the diseased group]. The frequency of allele G in the Caucasians studied was 70.2% and of allele C was 29.8%, respectively.

Discussion

Cytokines are regulatory proteins believed to be involved in the initiation and progression of chronic inflammatory diseases, such as arthritis and periodontitis (Masada et al. 1990, Wilton et al. 1992, McDowell et al. 1995, Yavuzyilmaz 1995, Kornmann et al. 1997, Dongari-Bagtzoglou et al. 1998, Fishman et al. 1998, Bozkurt et al. 2000, McDewitt et al. 2000, Boch et al. 2001, Buchs et al. 2001, Papapanou et al. 2001). Many recent studies have been reporting positive, equivocal or negative associations between cytokine gene polymorphisms and periodontal disease (Roberts et al. 1997, Gore et al.

1998, Gaibraith et al. 1999, Armitage et al. 2000, Cullinan et al. 2000, Scarel-Caminaga et al. *in press*).

Interleukin-6 is a multifunctional cytokine that regulates immune responses and its effects overlap those of interleukin-1 (IL-1) and tumor necrosis factor (TNF). It is widely distributed among cells of the periodontium and is thought to play a role in the elevated B-cell response observed in the gingival tissues of patients with chronic periodontitis (Fujihashi et al. 1993).

In the study Caucasian Brazilians genotype G/G was statistically associated with susceptibility to chronic periodontitis ($p=0.0036$, OR=3.0). Fishman et al. (1998) have found G/G showing circulating IL-6 concentrations approximately twice as high as those homozygous for allele C. In fact, it was found a reduction in the frequency of the C/C genotype in patients with systemic-onset juvenile arthritis, suggesting that this genotype confers a protective influence against the development of the disease. The presence of the C allele therefore would result in a lower IL-6 expression after a given inflammatory stimulus compared with the G/G genotype (Fishman et al. 1998). On the contrary to what happens to the G/G genotype frequency, that augments as increases the degree of severity of periodontitis (33.3% in healthy, 50% in the moderate and 70.8% in the severe periodontitis), the frequency of heterozygous individuals (G/C) decreases as increases the degree

of severity of disease (58.3% with this genotype were healthy, 50% had moderate and only 12.5% had severe periodontitis) (Table 2). Maybe this represents a protective function of allele C, whose presence may reduce IL-6 production. The low frequency of the C/C genotype in all groups possibly is related to the low frequency of allele C in the population studied (29.8%). This low frequency is smaller than that of 41% found by Olomolaiye et al (1998) and 40.3% encountered by Fishman et al. (1998) in healthy Caucasian populations.

The G→C substitution in the promoter (position -174) of IL-6 gene has been considered to increase the in vitro transcription of IL-6 gene by two-fold (Morse et al. 1999). We found an association between allele G of the IL-6⁻¹⁷⁴ polymorphism and susceptibility to chronic periodontal disease. If the C allele really increases the transcriptional rate of the IL-6 gene, the paradox of the association of IL-6 allele G with chronic periodontal disease, perhaps resides in the fact that beyond being pro-inflammatory, IL-6 stimulates interleukin-4 (IL-4) production, which is a potent anti-inflammatory mediator (Alexander & Damoulis 1994). Interleukin-4 has been reported to be a negative regulator of bone resorption by inhibiting the secretion of pro-inflammatory cytokines, such as IL-1, TNF and IL-6 (Shapira et al. 1992). Most cytokines are multifunctional, some of them having antagonistic effects by interaction with

other inflammatory mediators, and this can be the case of IL-6 in the microenvironment of the periodontium. The decrease of heterozygous individuals (G/C) as increases the degree of severity of disease maybe would be representing a protective function of allele C, whose presence may decrease IL-4 production, which, at a time, inhibits IL-6 and other potent pro-inflammatory mediators production. However it is more probable that allele C decreases the IL-6 production because the polymorphism at position -174 is located in a negative regulatory domain (NRD), between -225 and -164 (Morse et al. 1999), having been previously reported to demonstrate a negative regulatory effect on gene expression (Ray et al. 1990).

The overall genotype distribution of the whole patient group was significantly different than the controls. When the genotype frequencies of the PD patients and the controls were compared, there was a statistically significant augment in G/G genotype frequency in the periodontitis patients. It was concluded that genotype G/G of the IL-6⁻¹⁷⁴ polymorphism was significantly associated with susceptibility to chronic periodontal disease, suggesting that allele G may play a role in the pathogenesis and development of periodontal disease. To our knowledge this is the first report associating a polymorphism in the IL-6 gene with periodontal disease. The outcome and progression of periodontal disease constitute, however, an imbricate process

depending on the interaction of various cytokines pro- and anti-inflammatory of synergistic and antagonistic effects. Like IL-6, other pro-inflammatory mediators may play significant roles in the pathogenesis of chronic periodontitis. The study of cytokine gene polymorphisms may contribute to an understanding on the host mediator interactions that determine the disease phenotype.

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Table 1. Baseline clinical parameters of the subject population (n=84)

	Healthy (n=37)	Moderate (n=24)	Severe (n=24)	Total (n=84)
Age (years)	43.7 (14.7)	37.9 (11.5)	44.9 (11.6)	42.4 (13.2)
Mean (\pm SD)				
Gender (%)				
Female	25 (70.3)	18 (75.0)	20 (83.3)	63 (75.3)
Male	11 (29.7)	6 (25.0)	4 (16.7)	21 (24.7)

Table 2. Distribution of the IL-6 genotypes in the healthy group and in groups with moderate and severe chronic periodontitis in the Caucasian Brazilians

Genotype	Healthy n (%)	Moderate n (%)	Severe n (%)	p value
G/G	12 (33.3)	12 (50.0)	17 (70.8)	0.0036
G/C	21 (58.3)	12 (50.0)	3 (12.5)	
C/C	3 (8.4)	0 (0)	4 (16.7)	

Table 3 Distribution of the IL-6 alleles in the healthy and moderate/severe groups with chronic periodontitis in the Brazilian Caucasian individuals

Allele	Healthy n (%)	Moderate/Severe n (%)	p value
G	45 (62.5)	73 (76.0)	0.0838
C	27 (37.5)	23 (24.0)	



POLYMORPHISM IN THE TUMOR NECROSIS FACTOR- α (G-308A) GENE
IS NOT ASSOCIATED WITH THE SUSCEPTIBILITY TO CHRONIC
PERIODONTITIS IN A BRAZILIAN POPULATION
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**Polymorphism in the tumor necrosis factor-alpha (G-308A) gene
is not associated with susceptibility to chronic periodontitis in a
Brazilian population**

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genetic risk factor

Abstract

Tumor necrosis factor- α (TNF- α) is a major mediator of the immunoinflammatory response and may play an important role in the pathogenesis and progression of chronic periodontal disease (PD). Polymorphisms in the promoter of the TNF- α gene have been associated with some types of inflammatory diseases, such as asthma and rheumatoid arthritis. The aim of the present study was to investigate the association between a single-nucleotide polymorphism (SNP) of the TNF- α (G-308A) gene and severity of chronic periodontitis in Brazilians. One hundred and thirteen (113) non-smoking subjects over 25 years (mean age 41.6) were divided according to the severity level of periodontal disease: 44 healthy individuals (control group), 31 subjects with moderate and 38 patients with severe periodontitis. Genomic DNA was obtained from epithelial cells through a mouthwash with 3 % glucose and scraping of oral mucosa. The samples were analyzed for TNF- α (-308) polymorphism using polymerase chain reaction-restriction fragment length polymorphism techniques. The significance of the differences in the allele and genotype frequencies of the polymorphism between the control and groups with periodontitis was assessed by Chi-square test ($p < 0.05$). No significant differences in the genotype distribution and allele frequency were found between control and groups with periodontitis. It was concluded that TNF- α (-308) polymorphism was not associated either with susceptibility to or with the severity of chronic periodontal disease. Other polymorphisms in this or/and other genes of the host inflammatory response might be involved in determining susceptibility to periodontitis in the study population.

Bacterial lipopolysaccharides (LPS) activate monocytes of inflamed periodontal tissues to produce cytokines. Tumor necrosis factor- α (TNF- α) is an important immune mediator and a pluripotent proinflammatory cytokine, that is able to induce bone resorption (1). TNF- α gene is encoded on chromosome 6 inside the HLA region (2) and its biological activities have raised the possibility that polymorphisms within this gene might contribute to genetic association to diverse immuno-inflammatory diseases. In fact, this cytokine has been implicated in the pathogenesis of a large number of human diseases (3-7).

Within the promoter region of TNF- α gene, a biallelic polymorphic site at position -308 has been reported to influence the production of TNF- α protein (8). Allele A of TNF- α (-308) polymorphism has been positively associated with asthma (7) and ulcerative colitis (6).

Epidemiological studies indicate that periodontitis is widespread among the Brazilian population (9-13). TNF- α mRNA was significantly more frequent in diseased than in healthy gingival biopsies (14), suggesting a role of this cytokine in the development of periodontal disease. Increased production of TNF- α associated with the G/A genotype was detected in patients with advanced adult periodontitis (15). Because of the increasing evidence that genetic variations within the TNF- α locus are important in determining

susceptibility to periodontitis, this study aimed to investigate the possible link between the polymorphism at position -308 (G→A) of TNF- α gene promoter and chronic periodontitis in a Brazilian population.

Material and methods

Subject selection

A convenience sample of 113 unrelated, non-smoking subjects >25 years of age, were recruited for study from the patient pool at the Dental Clinics of the Faculty of Dentistry of Piracicaba - UNICAMP (approved by the Ethical Committee in Research at FOP/UNICAMP, protocol 63/99). The patients are from the Southeastern region of Brazil. The baseline clinical parameters for the subject population are presented in table 1. All subjects were in good general health and had at least 20 teeth in the mouth. Subjects did not have any of the following exclusion criteria: diseases of the oral hard or soft tissues except caries and periodontal disease; use of orthodontic appliances; need for pre-medication for dental treatment; chronic usage of anti-inflammatory drugs; a history of diabetes, hepatitis or HIV infection; immunosuppressive chemotherapy; history of any disease known to severely compromise immune function; present acute necrotizing ulcerative gingivitis or current pregnancy

or lactation. Subjects completed personal medical and dental history questionnaires, and within a protocol approved by an Institutional Review Board, signed a consent form after being advised of the nature of the study. Diagnosis and classification of disease severity were made on the basis of clinical parameters and consisted of physical examination, medical and dental history, probing depth, assessment of clinical attachment loss (CAL), tooth mobility, gingival recession and observation of bleeding on probing. Measurements of probing depth and attachment level were recorded at 4 points around each tooth. Subjects were included in clinical categories according to PD severity:

- 1) *Healthy group*: Subjects found to exhibit no signs of periodontal disease as determined by the absence of clinical attachment loss and no sites with probing depth >3 mm ($n = 44$),
- 2) *Moderate Periodontitis*: Patients with tooth sites exhibiting ≥ 3 mm and <7 mm CAL ($n = 31$),
- 3) *Severe Periodontitis*: Patients with teeth exhibiting ≥ 7 mm CAL ($n = 38$).

Sampling

The sampling of epithelial buccal cells was performed as described by Trevilatto & Line (16). Briefly, 113 individuals undertook a mouthwash after

1 min, containing 5 ml 3 % glucose. Following mouthwash, a sterile wood spatula was used to scrape oral mucosa. The tip of the spatula was then shaken into the retained mouthwash solution. Buccal epithelial cells were pelleted by centrifugation at 2000 rpm for 10 min. The supernatant was discarded and the cell pellet resuspended in 500 μ l of extraction buffer [10 mM Tris-HCl (pH 7.8), 5 mM EDTA, 0.5 % SDS]. The samples were then frozen at -20°C until used for DNA extraction.

DNA extraction

After defrosted, samples were incubated overnight (ON) with 100 ng/mL proteinase K (Sigma Chemical Co., St. Louis, MO, USA) at 37°C with agitation. DNA was then purified by sequential phenol/chloroform extraction and salt/ethanol precipitation. DNA was dissolved in 70 μ L TE buffer [10 mM Tris (pH 7.8), 1 mM EDTA]. The concentration was estimated by measurements of OD 260.

Polymorphism in the TNF- α gene at position -308

The oligonucleotides 5'- AGGCAATAGGTTTTGAGGGCCAT - 3' and 5'- TCCTCCCTGCTCCGATTCCG - 3' were used as primers. Amplification reactions were performed with 500 ng genomic DNA in a total volume of

50 μ L, containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 2 μ M of each primer, 200 μ M each dATP, dCTP, dGTP and dTTP, and 2.5 units *Taq* DNA polymerase (Amersham Pharmacia Biotech, Uppsala, Sweden). Cycling was 2 cycles of 3 min at 94°C, 1 min at 60°C and 1 min at 72°C, followed by 35 cycles of 1 min at 94°C, 1 min at 60°C and 1 min at 72°C, with a final extension of 7 min at 72°C. The products were digested with 3 U per 25 μ L reaction of *Nco*I at 37°C ON to detect allele 1 [G] (20 bp + 87 bp) and allele 2 [A] (107 bp).

Gel electrophoresis

Restriction products were visualized by electrophoresis on vertical 10 % non-denaturing polyacrylamide gels in 1X TBE (89 mM Tris-Borate, 89 mM boric acid, 2 mM EDTA), followed by silver staining (Bio-Rad Silver Stain Kit).

Statistical analysis

The allele ratio and genotype distribution of periodontitis patients and healthy control subjects were analyzed with Chi-square test. A *p*-value <0.05 was considered significant.

Results

There was no significant difference in the genotype distribution between healthy controls and periodontitis patients in the polymorphism $\text{TNF-}\alpha^{-308}$ ($p=0.289$), neither was observed statistical variation in the frequency of the alleles $\text{TNF-}\alpha^{-308}$ ($p=0.845$). The distribution of the genotype and the frequencies of the alleles for the polymorphism studied are shown in tables 2 and 3, respectively. Allele 2 was carried by 19.5% (22/113) of the subjects, with 1.8% (2/113) of homozygous. When Caucasians were taken alone, the following allele 2 carriage rate for the $\text{TNF-}\alpha$ (-308) polymorphism was found: 20.7% (18/87), with 1% (1/87) of homozygous.

The alleles distribution in the study population was consistent with Hardy-Weinberg equilibrium.

Discussion

Because of their frequent presence in diseased sites, it has been postulated that cytokines such as interleukin-1 (IL-1) and $\text{TNF-}\alpha$ may be indicators of the active phase of periodontal disease (17). Recently, a number of single nucleotide polymorphisms (SNPs) have been identified in the $\text{TNF-}\alpha$ promoter, and the less common A allele of $\text{TNF-}\alpha$ (-308) has been associated

with certain chronic inflammatory diseases, including asthma (7), cerebral malaria (3), multiple sclerosis (4), Alzheimer disease (5), ulcerative colitis (6) and chronic bronchitis (18).

As can be noted in table 1, the majority (77%) of the individuals belonging to the population studied is of Caucasian heritage. We found an allele 2 carriage rate of 20.7% (18/87) for our Caucasians. In their study, Kornman *et al.* (19) found an allele 2 carriage rate of 28.5% at TNF- α (-308) locus. In neither studies was observed any link between this polymorphism and periodontal disease. However, a study has been reported in which the frequency of TNF- α (-308) allele G was significantly greater in patients with advanced periodontitis (20). This finding is intriguing once allele A has been found to give a two-fold greater level of transcription than the -308G form (21) and the nature of periodontitis is inflammatory. There is an evidence that allele A is over-represented in diseases where TNF- α levels are associated with poor prognosis (22). In cerebral malaria TNF- α is of major importance for the pathology. Individuals homozygous for the TNF- α (-308) A allele carry a 7-fold higher risk of death or severe neurological sequelae due to cerebral malaria.

Polymorphisms in certain host-response genes have been related to hypersecretion of several cytokines upon microbiological challenge (8, 23,

24). Allele A of TNF- α (-308) polymorphism has been found to increase in two-fold the production of TNF- α cytokine. Although the role TNF- α play in leading to tissue destruction, it is worth mentioning the need for evaluation of other potential candidate genes as contributors to periodontitis, since chronic periodontitis may possibly represent a polygenic disease. Analysis in other cytokine promoter genes in the same Brazilian patients have revealed positive associations with chronic periodontal disease (25-27). More studies on polymorphisms in genes of the host response can increase information with regard to which factors could indeed be implicated in the process of disease.

It was concluded that TNF- α (-308) polymorphism was not associated with the severity of chronic periodontal disease in the population studied. Although the prevalence of the polymorphism studied for the Brazilian population was similar to that reported for Europeans, we observed no significant differences in genotype and allele distributions of the TNF- α (-308) gene polymorphism between control and periodontitis groups. Tumor Necrosis Factor- α (-308) G-to-A polymorphism is not a useful marker for predicting susceptibility to chronic periodontal disease in the study population.

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Polymorphism at position -174 of IL-6 gene is associated with
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J Clin Periodontol (In press)

Table 1. Baseline clinical parameters of the subject population
(n=113)

	Healthy (n=44)	Moderate (n=31)	Severe (n=38)
<i>Age (years)</i>			
Mean (\pm SD)	43.2 (\pm 14.0)	36.9 (\pm 11.2)	43.6 (\pm 14.4)
<i>Gender %</i>			
Female	68.2	80.6	84.2
Male	31.8	19.4	15.8
<i>Ethnic Group %</i>			
Caucasoid	84.1	77.4	68.4
Afro-American	6.8	16.1	13.2
Mulatto	6.8	6.5	18.4
Japanese	2.3	0.0	0.0

Table 2. Distribution of the TNF- α genotypes in the healthy group and in groups with moderate and severe chronic periodontitis.

Genotype	Healthy		Moderate		Severe		<i>p</i> value
	n	(%)	n	(%)	n	(%)	
G/G	37	(84.0)	24	(77.4)	31	(81.6)	0.289
G/A	7	(16.0)	7	(22.5)	5	(13.1)	
A/A	0	(0.0)	0	(0.0)	2	(5.3)	

Table 3. Distribution of the TNF- α alleles in healthy, moderate and severe groups with chronic periodontitis.

Allele	Healthy		Moderate		Severe		<i>p</i> value
	n	(%)	n	(%)	n	(%)	
G	81	(92.0)	55	(88.7)	67	(88.0)	0.674
A	7	(8.0)	7	(11.3)	9	(12.0)	

4. CONCLUSÃO

Artigo 1. A obtenção de DNA a partir de um bochecho com solução de glicose a 3 % e leve raspagem da mucosa jugal permite a execução de análises de suscetibilidade genética à doença periodontal.

Artigo 2. Os resultados microbiológicos e genéticos não foram suficientes para prever a suscetibilidade à periodontite agressiva na família estudada.

Artigo 3. Os polimorfismos *IL-1A* (-889) e *IL-1B* (+3953), respectivamente nos genes da *IL-1 α* e *IL-1 β* , não se relacionaram à doença periodontal crônica na população estudada.

Artigo 4. A presença do alelo 2 do polimorfismo *IL-1B* (-511) no genótipo dos indivíduos negros e mulatos associou-se fortemente [OR: 18; $p=0,049$] à doença periodontal crônica, sugerindo a existência de um componente racial na determinação da suscetibilidade à periodontite.

Artigo 5. O alelo 2 do polimorfismo *IL-1RA* (intron 2) esteve associado à severidade da doença periodontal crônica na população estudada ($p=0,029$).

Artigo 6. Indivíduos apresentando o genótipo G/G do polimorfismo *IL-6*⁻¹⁷⁴ (G→C) mostraram aumento da suscetibilidade à doença periodontal crônica (OR=3,0; $p=0,0036$).

Artigo 7. O polimorfismo *TNFA* (-308) não apresentou correlação com a suscetibilidade à doença periodontal crônica na população estudada.

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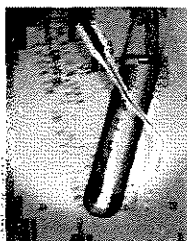
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USE OF BUCCAL EPITHELIAL CELLS FOR PCR AMPLIFICATIONS
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USE OF BUCCAL EPITHELIAL CELLS FOR PCR AMPLIFICATION OF LARGE DNA FRAGMENTS

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ABSTRACT

The analysis of human DNA is widely employed in the genetic studies of families and populations, and in most cases is performed with samples obtained from peripheral blood. The use of buccal epithelial cells as a source of DNA for PCR amplifications has several advantages over blood sampling but has only been used to amplify small fragments of DNA. Its use in forensic analysis has been limited to cases where the sampling of peripheral blood is not feasible. In the present study we show that buccal epithelial cells are a reliable source of DNA for the PCR amplification of high molecular mass fragments, which could be used in large-scale population sampling. Since most PCR gender-typing systems rely on the amplification and electrophoretic separation of the amelogenin gene, our results show that buccal epithelial cells may be the preferred source of DNA for gender -typing analysis. (*J Forensic Odontostomatol* 2000; 18:6-9)

Keywords: PCR, buccal epithelium, amelogenin.

INTRODUCTION

The analysis of human DNA is widely employed in genetic studies of families and populations and in most cases is performed with samples obtained from peripheral blood. Blood sampling is however an invasive procedure and sample collection may involve ethical problems in cases such as extreme illness, elderly persons and babies. Additionally, it requires medical supervision and specific equipment, which contribute to the increased overall costs of the procedure.

The polymerase chain reaction (PCR) provides a rapid and sensitive approach for the analysis of polymorphisms and mutations of the human genome. The use of buccal epithelial cells as a source of DNA for PCR reactions has been limited to studies of infectious agents present in oral mucosa;^{1,2} and in forensic analysis, where the sampling of peripheral blood is not feasible.^{3,4} Invariably, these studies report the amplification of small fragments of DNA (< 300 base pairs), which are suitable for the identification of viral and bacterial sequences, as well as

the analysis of highly polymorphic loci in the human genome. However, amplification of larger DNA fragments may be desirable in some instances such as PCR-RLFP,⁵ mismatch cleavage mutation analysis,^{6,7} cloning, and sequencing of amplified sequences.⁸ In the present study, we show that buccal epithelial cells are a reliable source of DNA for the PCR amplification of high molecular mass fragments, which could be used in large-scale population sampling and epidemiological studies, as well as in forensic analysis. As will be seen our results show that buccal epithelial cells may be the preferred source of DNA for gender -typing analysis.

MATERIALS AND METHODS

Sampling

A group of 83 consenting female subjects undertook a mouthwash containing 5 mL of 3 % sucrose rather than water in order to prevent osmotic imbalance that would cause rupture of cells and loss of genomic DNA, for 2 min. A sterile wood spatula was then

used to scrape the buccal oral mucosa and the tip of the spatula shaken into the retained mouthwash solution. Buccal epithelial cells were pelleted by centrifugation at 2000 rpm for 10 min, the supernatant was discarded and the cell pellet resuspended in 500 μ L of extraction buffer [10 mM Tris-HCl (pH 7.8), 5 mM EDTA, 0.5 % SDS] with antibiotics. The samples were then frozen at -20°C until used for DNA extraction.

DNA extraction

After defrosting, the samples were incubated at 37°C with 100 ng/mL proteinase K^{*}, and agitated overnight. DNA was then purified by sequential phenol/chloroform extraction and salt/ethanol precipitation and dissolved in 70 μ L TE buffer [10 mM Tris (pH 7.8), 1 mM EDTA]. The concentration was estimated by measurements of OD 260.

Polymerase chain reaction

Amplification reactions were performed with 300 to 700 ng DNA in a volume of 50 μ L in reaction mixture containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 4 mM MgCl_2 , deoxyribonucleotides (200 μ M each), 1 μ M primers, 2U *Taq* DNA polymerase^{**} and five pairs of primers were used. The primer sequences are as follows:

AMX1- 5' GGATTGGTTGTTACAGATGCC 3'
 AMX2- 5' TTACTCAGGCATGGCAAAAGCTGC 3'
 AMX3- 5' CATTTCAAGACCATCAAGAAATGGG 3'
 AMX4- 5' CTTTACAGAGCCCCAGGGCATTG 3'
 AMX5- 5' CCTCCCTGTAAAAGCTACCACC 3'
 AMX6- 5' AATGTCTACATACCGGTGGCC 3'
 AMX7- 5' GTAGAACTCACATTCTCAGGC 3'
 AMX8- 5' GGCTTCAAAATATACTCACCACCTCC 3'
 AMX9- 5' CCAGCCCCAGCCTGTTTCAGCCAC 3'
 AMX10- 5' TGTCTGCTAATGGTACTTTTITAG 3'

Samples were heated initially to 95°C for 5 min, each cycle comprising denaturation at 95°C for 50 sec, primer annealing at 67°C for 1 min and polymerization at 72°C for 2 min. Samples were subjected to 35 cycles of amplification followed by a final extension of 72°C for 7 min. Amplification was carried out in a *Perkin-Elmer GeneAmp 2400 thermal cycler*[#]. Amplification products were visualized by electrophoresis on vertical 5% polyacrylamide gels in 1 X TBE (89 mM Tris-Borate, 89 mM boric acid, 2 mM EDTA), followed by silver staining[¶].

RESULTS AND DISCUSSION

The use of buccal epithelial cells as a source of DNA for PCR amplifications has several advantages over blood sampling. The collection of material is fast and inexpensive, buccal samples can easily be obtained from people who are reluctant to donate blood, consent becomes simplified, there is no need of medical supervision during sampling, and the risk of contamination is reduced.^{9,10}

The amplifications produced specific reaction products of 1690 base pairs [bp] (AMX1-AMX2), 1986 bp (AMX3-AMX4), 1550 bp (AMX5-AMX6), 879 bp (AMX7-AMX8), and 2039 bp (AMX9-AMX10), spanning the whole amelogenin X gene.

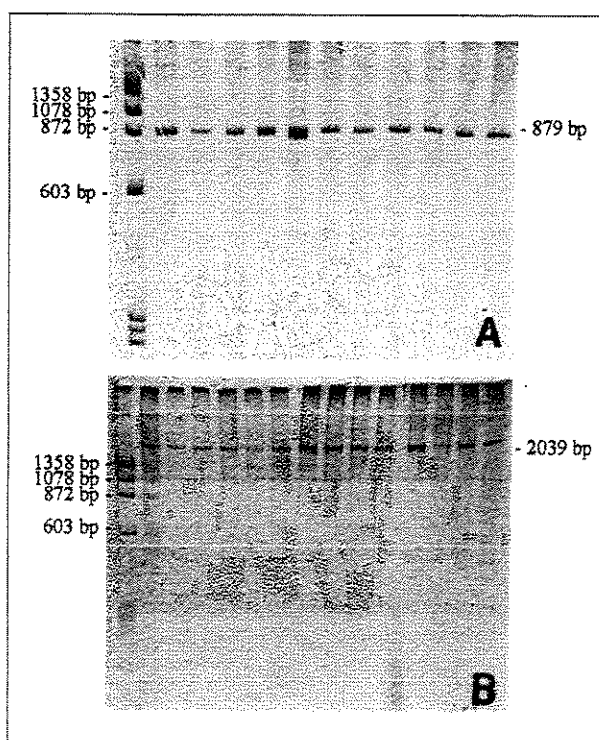


Figure 1. Polyacrylamide gel electrophoresis showing PCR products from total genomic DNA derived from buccal epithelium. A: 879 bp product of amplification with primers AMX7 and AMX8. B: 2039 bp product of amplification with primers AMX9 and AMX10. Lane 1- ϕ X-174-RF DNA *Hae* III digest molecular weight marker (Pharmacia).

* Sigma Chemical Co., St. Louis, MO, USA

** Amersham Pharmacia Biotech, Uppsala, Sweden

Perkin-Elmer, Perkin-Elmer Co., Norwalk CT 06859, USA

¶ Bio-Rad Silver Stain Kit, Bio-Rad Laboratories, 200 Alfred

Fig. 1 illustrates typical PCR products from total genomic DNA derived from buccal epithelial cells showing that buccal epithelial cells can be used for the PCR amplification of large DNA fragments. The amount of DNA extracted ranged from 2.1 µg to 360 µg, which is sufficient to enable PCR amplification, with a success rate of identification of the gender gene, in this case the female, of around 90% of large fragments ranging from 879 to 2039 base pairs (Table 1). Failure to amplify DNA may result from degradation or from the presence of inhibitors which interfere with PCR reaction and can in most cases be overcome by adding bovine serum albumin to the PCR reaction,¹¹⁻¹³ or by repurification of DNA with Chelex extraction.¹⁴ The use of small volumes of DNA extract is also recommended in order to reduce the amount of inhibitors.^{3,14}

Primers	Fragment size (bp)	% positive
AMX1-AMX2	1690	91.5
AMX3-AMX4	1986	92.5
AMX5-AMX6	1550	88
AMX7-AMX8	879	88
AMX9-AMX10	2039	88

Table 1: Positive amplification percentages of amelogenin X gene of 83 individuals.

Gender determination can be a valuable piece of information in forensic investigations. Most PCR gender-typing systems rely on the amplification and electrophoretic separation of the amelogenin gene which produce small PCR products with 106-112 bp^{15,16} or 330-218 bp¹⁴ from the X and Y chromosomes respectively. However, the main difference between X and Y loci is a 177 bp insertion in the X gene¹⁷ and the X and Y sequences can be amplified using a single set of primers which produce a 977 bp and 780 bp fragments,¹⁸ which can be clearly distinguished in agarose or polyacrylamide gels. The results presented here show that buccal epithelial cells

may be the preferred source of DNA for gender-typing analysis. Finally, it is worth mentioning that DNA extracted from this source has been routinely used in our laboratory for RFLP and direct sequencing of PCR products.

ACKNOWLEDGEMENTS

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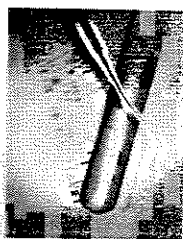
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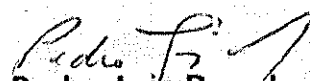
CERTIFICADO

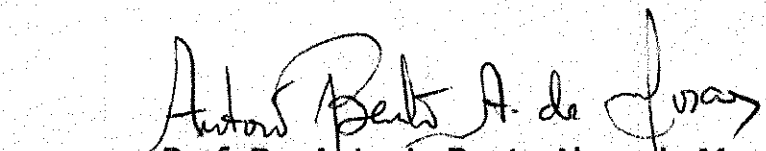
Certificamos que o Projeto de pesquisa intitulado "Suscetibilidade genética à severidade da doença periodontal em adultos e em famílias com periodontite de início precoce", sob o protocolo nº **63/99**, do Pesquisador(a) **Paula Cristina Trevilatto**, sob a responsabilidade do Prof(a). Dr(a). **Sérgio Roberto Peres Line**, está de acordo com a Resolução 196/96 do Conselho Nacional de Saúde/MS, de 10/10/96, tendo sido aprovado pelo Comitê de Ética em Pesquisa - FOP.

Piracicaba, 10 de setembro de 1999

We certify that the research project with title "Genetic susceptibility to severity of periodontal disease in adults and in families with early-onset periodontitis", protocol nº **63/99**, by Researcher **Paula Cristina Trevilatto**, responsibility by Prof. Dr. **Sérgio Roberto Peres Line**, is in agreement with the Resolution 196/96 from National Committee of Health/Health Department (BR) and was approved by the Ethical Committee in Research at the Piracicaba Dentistry School/UNICAMP (State University of Campinas).

Piracicaba, SP, Brazil, 10 september 99


Prof. Dr. Pedro Luiz Rosalen
Secretário - CEP/FOP/UNICAMP


Prof. Dr. Antonio Bento Alves de Moraes
Coordenador - CEP/FOP/UNICAMP