

Modulation of IL-10 expression by IL-10-592C / A polymorphism (rs1800872) is independent of the presence and bacterial load of classical periodontal pathogens

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Summary

Objective: We report the relationship between the single nucleotide polymorphism of IL-10-592C/A (rs1800872) and the identification/relative plentitude of the periodontal microorganisms *Porphyromonas gingivalis*, *Tannerella forsythia*, *Treponema denticola*, and *Aggregatibacter actinomycetemcomitans*. We additionally examine the impact of hereditary and microbiological determinants on IL-10 articulation levels in periodontal injuries. Approach: 117 patients with incessant periodontitis and 58 controls were enrolled. At that point microbiological tests were gotten from the clinical assessment and the presence/bacterial heap of types of periodontopathogens was evaluated by RT-PCR. The genotype for IL-10-592C/A was dictated by limitation section length polymorphism.

Results: The allelic dispersion of SNP rs1800872 in the explored populace agreed to the Tough Weinberg balance ($p = 0.64$). As has just been accounted for, polymorphic subjects indicated a lower articulation of IL-10 and an expanded danger of experiencing interminable periodontitis. The IL-10-592C/A polymorphism demonstrated no relationship with the recognition or bacterial heap of any of the explored microscopic organisms, furthermore the IL-10 articulation levels were not impacted by the microbiological profile, yet were straightforwardly associated with the genotype for the IL-10-592C/A polymorphism.

Keywords: Chronic periodontitis; Polymorphism of SN; IL-10; Interaction pathogenic host; Infecto-genomics

INTRODUCTION

Periodontitis is an infectious disease in which the dysregulated immune response of a host susceptible triggers progressive and irreversible destruction visible of dental supporting tissues. The events characteristic pathologies of periodontitis are the result of due to the complex interaction between bacteria, host immune response and mechanisms of homeostasis of supporting tissues. Moreover, the vulnerability to periodontitis is affected by hereditary and natural determinants that

produce an individual danger phenotype(1). Twin studies have determined that up to 50% of the individual difference in susceptibility to periodontitis could be under genetic influence (2). The most studied candidate genes are those related to the different stages of the response immune to infection, since destructive events of the periodontal support tissue occur mainly by exacerbation of immune control mechanisms of infection(1). IL-10 is the characteristic cytokine of the adaptive response pattern of regulatory T lymphocytes

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(Treg), characterized by having the ability to suppress adaptive inflammatory responses and differentiation of CD4 + T lymphocytes towards the Th1, Th2 and Th17 lineages. Without However, despite his ability to suppress the Th2-like clusters, IL-10 was considered a cytokine characteristic of the Th2 response before discovery and characterization of the Treg (3) lymphocyte lineage. So interestingly, it is currently recognized that there may be a interrelation between Th2 and Treg responses (involving secretion of IL-10), which would result in a protective state for the progression of tissue destruction in models experimental studies of periodontitis. In this sense, it is possible speculate that IL-10 could be a biomarker of the response effector setting of both CD4 + lymphocyte lineages (Th2 and Treg)(4). IL-10 is the main suppressor cytokine of the immune systems and has the strategic role of determine the completion of immune responses, returning tissues to a state of rest (3). From the perspective of bone metabolism, when analyzing the role of IL-10 within the context of total expressed cytokines during the progression of osteolytic lesions, it is possible establish that the expression of IL-10 correlates with the inactivation of destructive processes and that their levels present a close association with those of osteoprotegerin and the phenotypic marker of Treg(5) lymphocytes. For another hand, although IL-10 has been associated with a decrease of the efficiency of infection control mechanisms in some diseases(6), the experimental evidence in chronic periodontitis indicates that the protective role of IL-10 it does not interfere with the control of periodontal infection (7). Therefore, the relative abundance of IL-10 in tissues periodontals would be a protective factor for loss bone and disease progression. In this context, understanding of the mechanisms that regulate the levels of IL-10 in periodontal tissues becomes important, as that could constitute a possible diagnostic marker and progression. In this same sense, previous research of our group indicate that the IL-10-592C / A polymorphism has a functional effect associated with lower expression of IL-10, which results in negative modulation of the expression of osteoprotegerin and tissue inhibitor of MMP TIMP-3 in subjects carrying the polymorphic allele (TO). These decreased levels of expression of mediators osteoprotectors predispose polymorphic subjects to an increased risk of chronic periodontitis (8). Although the SNP IL-10-592C / A influences the levels IL-10 expression lesions, previous studies by our group have shown that periodontopathogens (specifically the bacteria belonging to the red *Pg* complex, *Tf* and *Td*) have a preponderant effect on regulation of pro-inflammatory cytokine levels(9,10). So interesting, despite the demonstrated association between putative periodontal pathogenic bacteria with severity, extent and response to treatment of periodontitis chronic disease, it has also been shown that bacterial infection riana by period on to pathogens not only stimulates the expression of pro-inflammatory cytokines, but exerts an effect stimulant in the expression of anti-inflammatory mediators (as IL-10) (11,12). Despite the above, so far no study has specifically investigated the role of infection by periodontopathogens in the regulation of IL-10 expression values in the presence or absence of Polymorphic genetic variations in IL-10-592C / A. Newly- Of course, studies using the strategy of association of whole genome (GWA) have established a relationship between genetic determinants and risk of specific infection by pathogenic

species (13). In this sense, various studies have established that polymorphic variations of the IL-10 gene act as modulators of host susceptibility lead to infection by various bacterial species (14,15); without However, so far no study has associated infection patterns by *Pg*, *Tf*, *Td* and *Aa* with the variations polymorphic in IL-10-592C / A. Considering all the evidence cited above, we investigated the influence of periodontal infection by red complex bacteria in association with the variations polymorphs of IL-10-592C / A (rs1800872) in the modulation of IL-10 expression levels in lesions periodontal. Additionally, we investigated the effect of IL-10-592C/Apolymorphism (rs1800872) in the frequency of detection and bacterial load of *Pg*, *Tf*, *Td* and *Aa*.

MATERIALS AND METHOD

Selection of participants

Participants were recruited from the periodical clinic. All subjects marked an educated assent. The investigation convention was endorsed by the advisory group of nearby morals for the acknowledgment of logical examination utilizing people. A detailed description of the recruitment protocols, examiners and inclusion criteria has been published previously(16). The selected subjects two for the chronic periodontitis group (n = 117) had have a minimum of 14 teeth, at least one tooth per sextant, with probing depth (PS) \geq 6 mm, clinical attachment level (CIN) \geq 4 mm, bleeding when snorting daje (SS) \geq 30% of the sites examined and require therapy periodontal surgery in at least one sextant. The subjects coughs selected for the control group (n = 58) should have a minimum of 14 teeth, no sites with PS \geq 3 mm, CIN \leq 3 mm, SS \leq 0% and require a lengthening procedure. coronary treatment for restorative reasons in at least one tooth. Subjects diagnosed with diabetes were excluded from both groups. diagnosed with diabetes mellitus, smokers, pregnant women or women who are breastfeeding, patients in treatment current or in the last 6 months with antibiotics or anti-inflammatory drugs and those who have received therapy periodontal in the last 2 years.

Quantification of interleukin 10 by RT-PCR in gingival biopsies

Gingival tissue biopsies were gotten during the careful periodontal treatment in patients in the gathering ceaseless periodontitis (n = 117) or disturbing methodology coronary glanding in the benchmark group (n = 58). RNA was extricated from the tissue utilizing TriZOL (Life Innovations, Terrific Island NY, USA) adhering to the directions producer.

Genotyping for the IL-10-592C / A polymorphism(rs1800872)

DNA was extracted from epithelial cell smears obtained nests on the inside of the cheek, with a sequence phenol / chloroform and salt precipitation / ethanol(8). For perform allelic identification of the IL-10 gene the fragments DNA samples were amplified using a primer in a PCR reaction in a final volume of 25 μ l, including also 10 \times PCR.

Identification and quantification of microorganisms by real time PCR

Before the surgical procedure, a sample was taken of the subgingival biofilm of the site to be intervened and of the deepest site of each sextant using tips of sterile paper ISO

40 (17). Bacterial DNA was extracted from biofilm samples using the DNA Purification System (Promega Corporation). The RT-PCR reactions were performed on the MiniOpticon System platform using SybrGreen MasterMix, 5 ng DNA and specific primers as previously written in detail (17)(18).

Statistical analysis

The characteristics demographic and clinical parameters were compared using Fisher's exact test and the «t» test. The equi-Hardy-Weinberg book was tested by the Chi squared. The genotypic and allelic distribution was compared using Fisher's exact test. The difference in IL-10 expression was compared using the ANOVA assay Bonferroni *post hoc*. For *Pg* detection frequency, *Tf*, *Td* and *Aa* in the different genotypes were calculated the OR and the significance of the differences with the Fisher's exact test. Differences in bacterial load were tested by the Kruskal-Wallis test. Differences between IL-10 expression levels between different genotypes in the presence or absence of infectious Specific were tested by the «t» test. The analyzes were carried out in the Stata / SE v11.1 program (College Station TX, USA) and for all essays the established a p value <0.05 as statistically significant.

RESULTS

The itemized depiction of the segment attributes and centers of the examination populace is in the table 1. Control bunch people were fundamentally more youthful than those in the incessant periodontitis gathering. As indicated by the consideration models, the PS, NIC and SS were altogether higher in the periodontitis populace ceaseless contrasted with sound controls. The populace test investigated, just as the subgroups of the gatherings control and constant periodontitis met the dispersion allelic set up by the Solid Weinberg standard ($p = 0.64$). The genotypic dispersion in the investigation populaces dyads demonstrated an essentially higher extent of hereditary homozygotes (CC) in the benchmark group, along these lines just as an altogether higher extent of heterozygous (CA) in the gathering of cases with periodontitis narrative. With respect to allelic conveyance, the people of the benchmark group exhibited a higher pervasiveness of the allele familial (C) (table 1). As recently detailed (8), people with incessant periodontitis introducing the allele polymorphic (CA and AA) demonstrated diminished degrees of IL-10 articulation (Table 2). Both the location recurrence as the quantity of DNA duplicates/test for every single one of the researched microbes was fundamentally higher in the gathering of patients with constant periodontitis corresponding to control (fig. 1 A). The identification frequencies and relative measure of *Pg*, *Tf*, *Td* and *Aa* in the gathering of subjects with ceaseless periodontitis demonstrated no contrasts between the various genotypes of the rs1800872 polymorphism (fig. 1 B-E). In Table 3 are introduced detail the fre-recognition rates for every one of the microorganisms contemplated isolated by genotype, both in the control as in the gathering of patients with incessant periodontitis. No critical contrasts were watched for the recurrence recognition proficiency when looking at tribal homozygotes (CC) with people conveying the polymorphic allele (CA + AA) in neither gathering. Then again, patients with constant periodontitis showed an expanded danger of contamination by *Pg*, *Tf*, *Td* and *Aa* comparable to the

gathering with savage (OR=10.36, $p<0.001$; OR=15.33, $p<0.001$; OR=11.33, $p<0.001$; OR=5.77, $p<0.006$, separately). The degrees of IL-10 articulation didn't show critical varieties by gathering patients as indicated by the quantity of red complex microorganisms (*Pg*, *Tf* and *Td*) recognized in the example (fig. 2A). Furthermore, by isolating these subgroups as indicated by genotype for polymorphism rs1800872 no noteworthy contrasts were seen in the degrees of IL-10 articulation (Fig. 2B). At last, the degree of articulation of IL-10 didn't show a relationship with the discovery of none of the microorganisms concentrated freely (fig. 2C-F).

DISCUSSION

IL-10 is the principle silencer cytokine of the reactions invulnerable frameworks, and in people it has been indicated that their levels are conversely related to the boundaries periodontitis centers (19). Exploratory proof backings the proof acquired in people and has set up a causal relationship in which IL-10 levels are related with cyan contrarily to bone misfortune in creature models of periodontitis (5,7). It is in this setting that one can surmise to state that any factor impacting the IL-10 levels could hypothetically influence the presence, seriousness and/or degree of periodontitis. Already we had revealed that people conveying the variation type of the IL-10-592 C/A polymorphism introduced diminished degrees of IL-10 articulation and an expanded danger influenced by incessant periodontitis (8). Strangely, disease by red complex microscopic organisms has been related with an expansion in the statement of favorable to incendiary cytokines matters, yet in addition IL-10 (11,12) and furthermore the polymorphisms of the IL-10 quality have been related with powerlessness to different contaminations (14,15), stable making a bidirectional connection between the two factors that up to this point had not been researched in patients with interminable periodontitis. In any case, the consequences of the current work demonstrate would that be able to tissue articulation levels of IL-10 are resolved indeed by genotype, and that presence/bacterial heap of periodontal microorganisms no significantly affects the declaration of this suppressive cytokine. From the point of view of our understanding current example of the pathogenesis of periodontitis appears to be sensible to believe that the period on to microorganisms of the mind bogging red, traditionally connected with the event, seriousness and degree of periodontitis, are straightforwardly connected with the creation of favorable to provocative cytokines (consistently "damaging" articulations) (9,10), and are not related unequivocally to the statement of a cytokine with a job famously suppressive and "defensive", like IL-10. Without In any case, as referenced above, considers Past investigations have demonstrated that period on to microbes can prompt IL-10 overexpression, both in vivo and in vitro (11,12). In this unique circumstance, our outcomes recommend that the guideline of the articulation levels of the IL-10 is firmly impacted by the profile hereditary qualities of the host, and that microbiological stimulation, just as compensatory administrative instruments of the host, they would just play an optional role (20). It is just as in an as of late distributed article the intricacy of IL-10 administrative components, showing that different cell types can communicate IL-10 paying little mind to outside improvements, while that in different circumstances the

force or nature of the upgrades significantly affects the statement of IL-10 (20). From an absolutely hypothetical point of view, the enlistment of IL-10 by the host looks to restrict the blow-back delivered by the nearby invulnerable reaction to battle bacterial contamination (20). Actually, as a rule the statement of supportive of fiery cytokines and IL-10 happens all the while, as a component of self-provocative regulation (20). There is proof exhibiting the relationship between the declaration of favorable to provocative cytokines rias, (for example, IL-1 β and TNF- α) with the statement of the atoms that legitimately intercede tissue obliteration in periodontitis (for instance MMP and RANKL). It is in this feeling that IL-10 can be considered «protective», restricting reaction interceded tissue demolition incendiary reaction to contamination, in spite of the fact that then again, its silencers cause a lessening in the capacity to insusceptible components of the host, making it hard to disposal of tainting microorganisms (21). So strikingly, a few microorganisms have the capacity to specifically instigate IL-10 emission as a component of its battery of reaction avoidance instruments immune (21.22). In spite of the fact that there is no particular proof with respect to with IL-10-subordinate break components between red complex microbes, an ongoing report showed that the fiery reaction to simultaneous contamination by *P. gingivalis* and *F. nucleatum* is diminished with connection to the vaccination of microscopic organisms in an unviable manner, and that this negative guideline of the host reaction is related with expanded degrees of IL-10 and restraint of phagocytosis (23). These discoveries appear to show that the varieties in IL-10 levels, for example, those identified with IL-10-592 C/A SNP polymorphism, could impact the example of subgingival microbial colonization. Nonetheless, our other proof focuses to the genotype for the polymorphism IL-10-592 C/A has no impact on the contamination profile. subgingival. Remember that the impacts IL-10 immunosuppressants have been related with lacks in contamination control in different maladies, anyway in all the past trial models-portrayed the balance of IL-10 articulation (through restraint or chemoattraction of Tregs) has not shown related with the bounty and tissue invasion of the microorganism *Aa* (21) nor with expanded metabolics of aggravation (7). This test proof is as per the outcomes introduced, where the pertors of the various alleles for the SNP IL-10-592 C/A demonstrated no relationship with changes in recurrence location or bacterial heap of periodontal microbes we examined. It is in this setting that we present the theory that varieties in IL-10 levels don't impact the example of subgingival disease by *Pg*, *Tf*, *Td* and *Aa*. In this sense, it has been recently exhibited demonstrated that hyper-fiery genotypes/phenotypes endure a more serious periodontal demolition, without this being dealt with lead to more noteworthy productivity in contamination control periodontal(23.24). From another point of view this implies subjects with a hypo-provocative genotype/phenotype endure less periodontal demolition, without influencing its ability capacity to control periodontal infection(22). In this model we could show that the subjects conveying the allele tribal for the IL-10-592 C/A polymorphism would react to the meaning of hypo-incendiary genotype/phenotype. To Regardless of the abovementioned, it is imperative to consider that solitary a predetermined number of microorganisms considered 'old style' periodontal microbes was

examined and that subgingival environment is more unpredictable, incorporating number species with conceivable balancing impact of the reaction of the host. Truth be told, a developing line of proof proposes that the presence and relative wealth of microorganisms magnanimous exercises could establish a defensive factor for run and movement of periodontitis. In this point of view the underlying improvement that would trigger the resistant reaction would be the environmental lopsidedness brought about by the expansion relative number of microorganisms to the disadvantage of commensal vegetation noble cause (25.26). Given the significant suppressive impact of IL-10 and its vital function in controlling safe reactions, It is conceivable to feel that their degrees of articulation are powerfully managed and are not dependent upon the impact of various natural improvements. The proof introduced upholds the possibility that the articulation levels of IL-10 in periodontal tissues react mostly to a hereditary program and what polymorphic varieties influence utilizing the advertiser area of the IL-10 quality could have a significant impact as danger determinants for the interminable periodontitis, being autonomous of the presence and bacterial heap of period on to microbes. The primary Shortcoming of the current examination is the restricted size of the example, making it hard to sum up your outcomes to different populaces. Replication concentrates with populace bigger numbers are expected to check the outcomes introduced here. In this article we report that the articulation IL-10 is altogether impacted by the IL-10-592 C/A polymorphism, where transporters of the allele A show diminished degrees of the cytokine. The IL-10 articulation isn't influenced by the presence or charge bacterial *Pg*, *Tf*, *Td* and *Aa*, recommending that their guideline is free of changes in the biology subgingival.

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TABLES

Table 1. Clinical and demographic characteristics of the study populations and genotypic and allelic distribution for the polymorphism IL-10-592 C → A rs1800872 of the study populations

	Healthy (n = 58)	Chronic periodontitis (n = 117)	Healthy vs chronic periodontitis
Gender distribution	34 m/24 f	59 m/58 f	p = 0,306
Age	42,83 ± 7,58	46,44 ± 7,39	p < 0,05
Probing depth (PS)	2,08 ± 0,4 (mm)	4,29 ± 0,74 (mm)	p < 0,001
Clinical insertion level (NIC)	0,91 ± 0,55 (mm)	3,95 ± 1,14 (mm)	p < 0,001
Bleeding on probing (SS)	4,77 ± 1,58 (%)	62,68 ± 11,76 (%)	p < 0,001
IL-10 -592 (C→A) rs1800872	n (%)	n (%)	
CC	27 (46,55)	34 (29,06)	p < 0,05
CA	23 (39,66)	65 (55,56)	p < 0,05
AA	8 (13,79)	18 (15,38)	p = 0,787
Alleles			
C	77 (66,37)	133 (56,83)	p < 0,05
A	39 (33,62)	101 (43,16)	

Table 2. IL-10 expression according to the genotype for the polymorphism IL-10-592 C → A rs1800872 in individuals with periodontitis chronic and healthy controls

IL-10 -592 (C→A) rs1800872	Healthy (n = 58) IL-10/βactina ^{2ΔACT} (mean ± SD)	Ancestral homozygous vs polymorphs	Chronic periodontitis (n = 117) IL-10/βactina ^{2ΔACT} (mean ± SD)	Ancestral homozygous vs polymorphs
CC	0,25 ± 0,12		1,68 ± 0,5	
CA	0,26 ± 0,18	p > ,0,05	1,3 ± 0,38	p >,0,001
AA	0,25 ± 0,15	p >,0,05	1,08 ± 0,31	p >,0,001

Table 3. Frequency detection for putative periodontal pathogens By *firomonas gingivalis*, *Tenerella forsythia*, *T replenish denticolay* *Aggregatibacter actinomycetemcomitans* in the patients conperiodontitis chroicle and control us of agreement genotype for he polymorphism IL-10-592C → A rs1800872

Microorganism	Control (n=58)				Chronic Periodontitis (n=117)				Control vsperiodontitis	
	Negativo n, (%)	Positivo n, (%)	P value *	OR*	Negativo n, (%)	Positivo n, (%)	P value	OR*	P value	OR*
<i>P. gingivalis</i>	50 (86,2)	8 (13,8)	0,06	0,37	44 (37,6)	73 (62,4)	0,55	1,03	< 0,001	10,36
CC	14 (51,8)	13 (48,2)			13 (38,2)	21 (61,8)				
CA	15 (65,2)	8 (34,8)			22 (33,8)	43 (66,2)				
AA	8 (100)	0 (0)			9 (50)	9 (50)				
CA + AA	23 (74,2)	8 (25,8)			31 (37,3)	52 (62,7)				
<i>T. forsythia</i>	53 (91,4)	5 (8,6)	0,22	3,85	47 (40,9)	68 (59,1)	0,49	1,09	< 0,001	15,33
CC	26 (96,3)	1 (3,7)			14 (42,4)	19 (57,6)				
CA	21 (91,3)	2 (8,7)			27 (42,2)	37 (57,8)				
AA	6 (75)	2 (25)			6 (33,3)	12 (66,7)				
CA + AA	27 (87)	4 (13)			33 (40,2)	49 (59,8)				
<i>T.denticola</i>	51(87,9)	7 (12,1)	0,42	0,61	45 (39,1)	70 (60,9)	0,25	1,44	< 0,001	11,33
CC	23(85,2)	4 (14,8)			15 (45,5)	18 (54,5)				
CA	20(86,9)	3 (13,1)			21 (32,8)	43 (67,2)				
AA	8(100)	0 (0)			9 (50)	9 (50)				
CA+AA	28(90,3)	3 (9,7)			30 (36,6)	52 (63,4)				
<i>A. actinoacti- nomyetem- comitans</i>	56(96,5)	2 (3,5)	0,71	0,87	97 (82,9)	20 (17,1)	0,44	1,27	0,006	5,77
CC	26 (96,3)	1 (3,7)			29 (85,3)	5 (14,7)				
CA	22 (95,6)	1 (4,4)			53 (81,5)	12 (18,5)				
AA	8 (100)	0 (0)			15 (83,3)	3 (16,7)				
CA + AA	30 (96,8)	1 (3,2)			68 (81,9)	15 (18,1)				

* OR and Fisher's exact test for the probability of detection of pathogens between ancestral homozygotes (CC) and carriers of the polymorphic allele (CA + AA).

** OR and Fisher's exact test for the probability of detection of pathogens between individuals in the control group and patients with chronic periodontitis.

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FIGURES

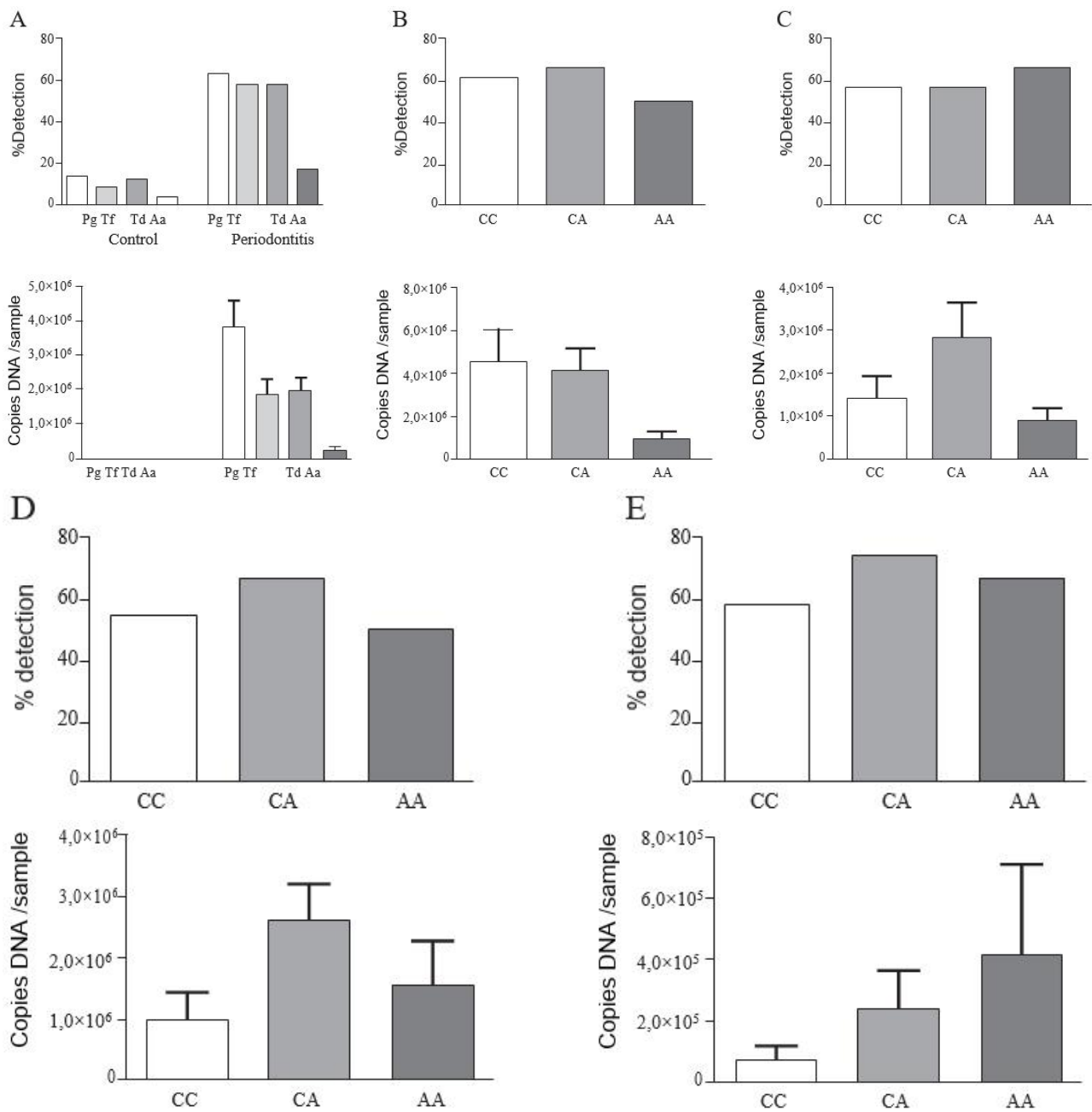


Figure 1. Recurrence of location and bacterial heap of *P. gingivalis*, *T. forsythia*, *T. denticola* and *A. actinomycetemcomitans* in people of the benchmark group and patients with constant periodontitis (A). Recurrence of recognition and bacterial burden in the various genotypes of the polymorphism IL-10-592 CA rs1800872 in patients with incessant periodontitis of *P. gingivalis* (B), *T. forsythia* (C), *T. denticola* (D) and *A. actinomycetemcomitans* (AND).

Modulation of IL-10 expression by IL-10-592C / A polymorphism (rs1800872) is independent of the presence and bacterial load of classical periodontal pathogens

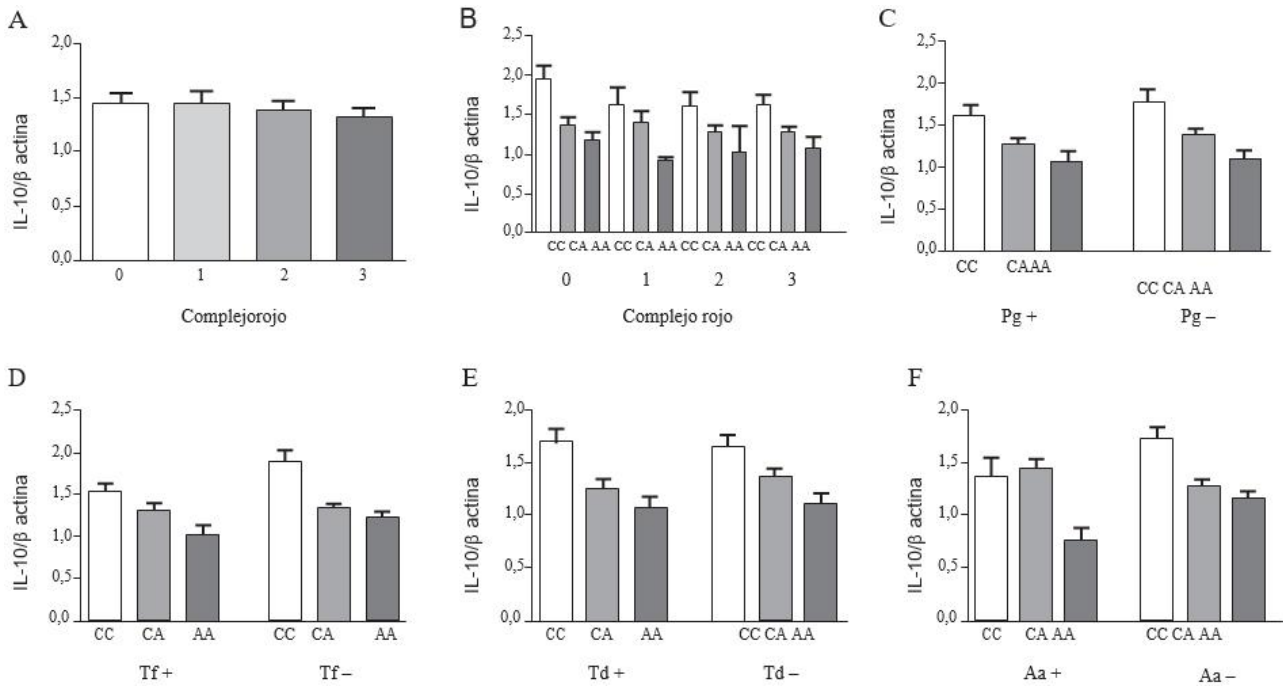


Figure 2. Relative level of IL-10 expression in patients with chronic periodontitis. A. Stratification according to the number of species of the red complex detected in the sample. B. Stratification by genotype for the polymorphism IL-10-592 C → A rs1800872 in the groups separated according to the number of species of the red complex detected in the sample. C. Stratification by genotype and detection of *P. gingivalis*. D. Stratification by genotype and detection of *T. forsythia*. E. Stratification by genotype and detection of *T. denticola*. F. Stratification by genotype and detection of *A. actinomycetemcomitans*.