

PREVALENCE OF ANTIBIOTIC RESISTANCE GENES (*TEM*, *TetM*, *TetQ*, *cfxA*, *MefA*, *Erm*, *Nim* genes) IN PERIODONTIC INFECTIONS OF A PORTUGUESE POPULATION

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Introduction and Purpose

Periodontitis is one of the most common diseases in dentistry and results from the accumulation of bacterial biofilm on the tooth surface. Black-pigmented, Gram negative oral anaerobes such as *Porphyromonas gingivalis* and *Prevotella intermedia* are thought to be pathogens in adult periodontitis [1, 2]. Odontogenic local infections require surgical treatment and, if required, a probabilistic antibiotherapy is needed that is effective on most recognized oral pathogens [3]. In most cases, antibiotic prescription is empirical and based on the clinical condition of the patient.

Reports from different countries show an increasing prevalence of patients with oral antibiotic resistant bacteria. However, in Portugal there is no data concerning antibiotic resistance of oral flora.

The **main goal of this study** was to identify *Porphyromonas gingivalis* and *Prevotella intermedia* strains from periodontal pockets of Portuguese adults suffering of periodontitis infections. Moreover, the isolated strains were also tested for the presence of antibiotic resistance genes.

Methodology

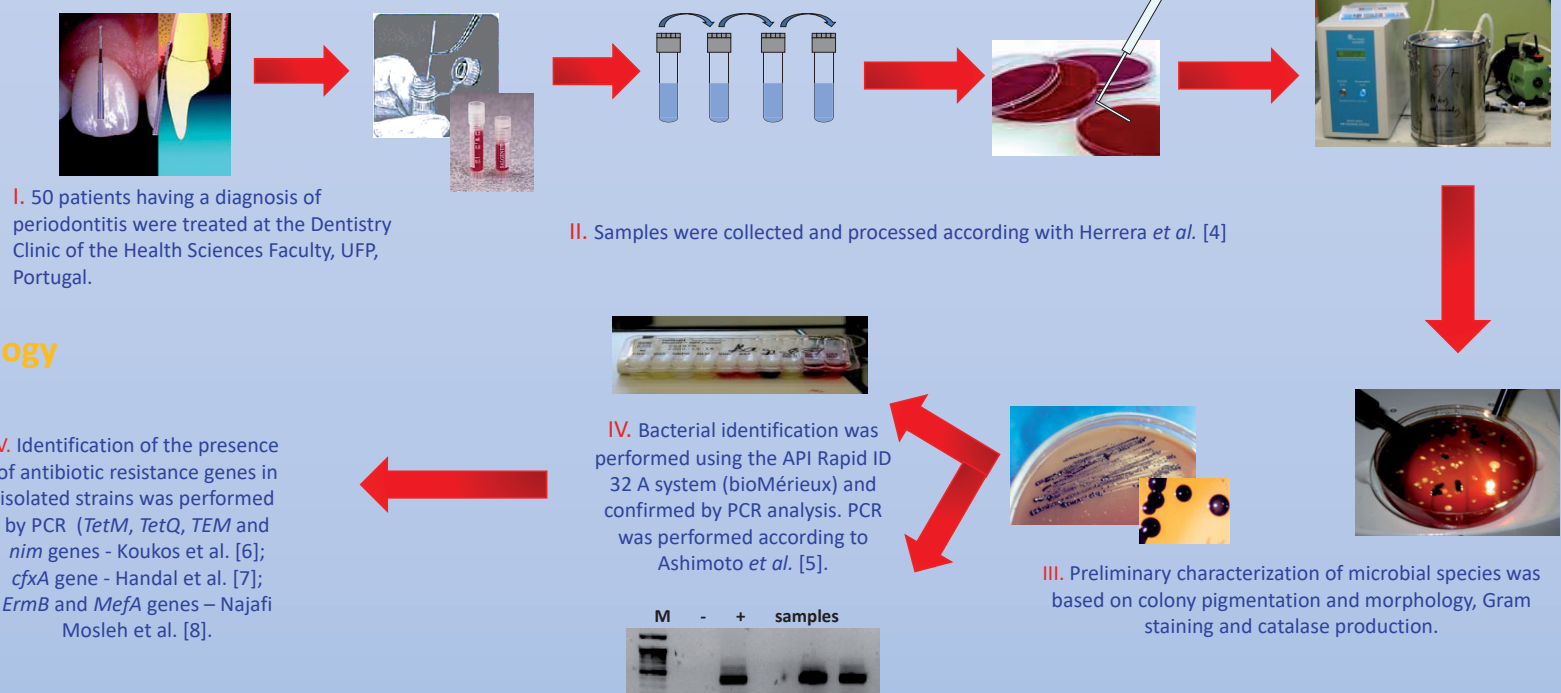


Table 1 – Identification of *P. gingivalis* and *P. intermedia* using classical methods and PCR and identification of antibiotic resistance genes.

Strain	% identified by API* and PCR	Antibiotic Resistance Genes							
		Tetracycline		β-Lactamases		Erythromycin		Metronidazol	
		<i>Tet Q</i>	<i>Tet M</i>	<i>CfxA</i>	<i>TEM</i>	<i>Erm B</i>	<i>Mef A</i>	<i>Nim</i>	
<i>P. gingivalis</i>	20%	0%	0%	0%	2%	0%	0%	0%	
<i>P. intermedia</i>	44%	4%	2%	2%	20%	2%	0%	0%	
Other black-pigmented	36%	0%	2%	0%	8%	0%	0%	0%	
Total isolates	100%	4%	4%	2%	30%	2%	0%	0%	

*API Rapid ID 32 A system (bioMérieux)

In this study *Prevotella intermedia* represented 44% and *Porphyromonas gingivalis* 20% of total isolates, with a good correlation between employed methods. The remaining 36% strains belonged to other black-pigmented species (Table 1). These results were in accordance with several authors, which report that *P. intermedia* and *P. gingivalis* are commonly isolated from periodontitis infections being considered the most abundant putative black pigmented species [1, 3, 9].

Concerning the presence of antibiotic resistance genes, it was observed that 8% of isolated strains had one of the tetracycline resistance genes (*TetQ* or *TetM*). The *cfxA* gene was detected in 2% of isolated strains and the *TEM* gene was present in 30% of strains. It was also observed that 2% of isolates had the *ermB* gene. None of the isolates showed the presence of the *mefA* or *nim* genes. Our results are in accordance with most studies where a high prevalence of β-lactam resistance genes is observed. In fact, these results would be expected since β-lactam antibiotics are the major prescribed choice. However, due to the sampling size, results should be confirmed with a bigger collection of sample isolates from periodontal infections.

This study contributes to the knowledge on subgingival microbiota and its resistance genes present in periodontal infections. Knowing the prevalence of resistance genes could impact on their clinical prescription and could raise awareness to the appropriate use of antibiotics.

1. The most frequently isolated anaerobic species from periodontal pockets was *P. intermedia*.
2. Most strains (64%) with the *TEM* gene were identified as *P. intermedia*.
3. Only 7% of identified *P. gingivalis* had one of the analyzed resistance genes.
4. No tetracycline resistance gene was observed in *P. gingivalis*.
5. The *ermB* gene was detected in strains that also had *TEM* and *TetM* genes.

Conclusions

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References

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