



Proceeding Paper

Amide I Band Analysis Applied to Vibrational Micro-Spectroscopies of Gingival Crevicular Fluid Samples for Orthodontic Treatment Monitoring [†]

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Abstract: Vibrational micro-spectroscopies were applied to investigate the gingival crevicular fluid (GCF) for monitoring orthodontic treatment with fixed appliances. The GCF samples were investigated using Fourier transform infrared, Raman, and surface-enhanced Raman micro-spectroscopies. The GCF spectra collected at different times of orthodontic tooth movement were used to characterize the biochemical changes occurring during the treatment. We examined the amide I band region by means of deconvolution analysis using Gaussian–Lorentzian curves for infrared spectra and Lorentzian curves for Raman spectra. This analysis allowed us to evidence the contribution of the different subcomponents of the amide I band and the changes occurring during orthodontic treatment. These changes can be ascribed to modifications in the secondary structure of protein content and could contribute to make vibrational spectroscopies a useful tool for monitoring the individual patient's response to orthodontic force application.

Keywords: amide I; band deconvolution; Raman spectroscopies; infrared spectroscopies; orthodontic tooth movement; gingival crevicular fluid



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1. Introduction

The analysis of the vibration modes of the amide I band allows essential information to be obtained on the structure of the biological tissues and fluids. For this reason, this band has been widely considered to monitor protein molecular changes due to pathology or stress mechanisms [1,2]. Typically, the spectroscopy investigation is performed on a dried sample of the fluid to limit the signal from the water. This is a demanding condition for Fourier transform infrared (FT-IR) spectroscopy, while a direct spectroscopic assessment is allowed on hydrated samples in the cases of conventional and surface-enhanced Raman (SERS) spectroscopies. The amide I band is mainly related to the vibrational modes of C=O bonds. Due to the different mechanisms involved, the intensity and positions of the observed modes differ for FT-IR and Raman spectroscopy. This aspect has to be considered when data from these spectroscopies are compared. Our previous work has evidenced that the use of these optical techniques for the investigation of gingival crevicular fluid (GCF) can be a useful tool for investigating the changes occurring during orthodontic treatment [3–6]. In the present work, we focused our attention on the amide I region of

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FT-IR, Raman, and SERS spectra to monitor changes induced by the orthodontic treatments. Data were compared and the changes occurring in the amide I band were discussed in relation to the orthodontic treatment time. The relevance of the analysis of GCF for diagnostic purposes was initially recognized by Orban and Stallard who investigated the volume of the GCF as being sufficiently indicative of the inflammatory state [7]. Later in the 1980s, the attention moved to the analysis of the protein content of the GCF, and any quantitative and qualitative changes induced by external factors or pathologies [8,9]. For this reason, the spectroscopy methods provide a reliable and sensitive tool to assess the biochemical composition [2–6,10,11].

2. Materials and Methods

The GCF samples were collected from two different group of subjects with dental malocclusion needing orthodontic treatment with fixed appliances: the first was constituted by young subjects ranging between 11 and 18 years, whereas the second group was composed by adults over 18 years of age. Bracket bonding was applied to the patients and GCF was collected during the process of orthodontic tooth movements (OTM) before the treatment (T0 samples) and after 2 (T1), 7 (T2), and 14 (T3) days of OTM treatment, respectively [3–5]. Paper points were inserted into the gingival crevice for about 30 s and stored in an 80 °C refrigerator before analysis. After adding 10 μ L of distilled water, the samples were vortexed and centrifuged to extract the GCF [3,4].

A Perkin Elmer Spectrum One FT-IR spectrometer was used to record FT-IR spectra. Spectral acquisitions were performed in specular reflection mode with a few microliter drops of sample placed on a metallic IR-reflective surface and left to dry. All spectra were collected using 64 scans in the range from 1500 to 1800 cm⁻¹ with a 4 cm⁻¹ spectral resolution [4].

Raman spectroscopy was performed using a He-Ne laser as excitation source at a nominal power of 17 mW. The Jobin-Yvon 180 monochromator, equipped with a liquid N2-cooled CCD and a grating of 1800 grooves/mm, allowed a spectral resolution of 4 cm $^{-1}$. A $100\times$ optical objective (N.A. 0.90) and an excitation spot area of about 5 μm of size were used, with accumulation times ranging from 60 to 300 s. SERS spectra were collected using the same apparatus with a $50\times$ (N.A. 0.75) objective and by adopting an accumulation time of 300 s. A small amount (5 μL) of the GCF sample was dropped on the microscope glass decorated with dried gold nanoparticles and SERS measurements were performed immediately after [3].

The Raman spectroscopy and SERS data were numerically treated to remove background signal by using a wavelet-based algorithm described in Ref. [12]. The spectra were then analyzed in terms of convoluted peak functions to determine the basic vibrational modes that contribute to the signal using a best-fit peak fitting routine of the GRAMS program, based on the Levenberg–Marquardt nonlinear least-square method. Peaks constituting the spectrum were manually selected in order to define the starting conditions for the best-fit procedure. The best-fit was then performed to determine the optimized intensity, position, and width of the peaks using the χ^2 parameter to evaluate the performance of the procedure. Lorentzian functions were used to fit Raman and SESR data, while Gaussian–Lorentzian mixed functions were used for FT-IR data.

3. Results and Discussion

The amide I band of the FT-IR spectra of the GCF samples collected at OTM increasing times from one of the subjects considered in the study are reported in Figure 1a. The reported signals have been normalized assuming unitary the band area and the spectra have been deconvoluted in terms of Gaussian–Lorentzian mixed functions to outline the component modes. The red curve modes were assigned to α -helix secondary structure vibration, while the component at about 1620 cm⁻¹ was assigned to 3_{10} -helix and/or β -sheet [6], and the modes in the 1660–1690 cm⁻¹ range were ascribed to β -turn and β -sheet contributions as indicated in Figure 1b(i) [3,13]. The broad mode at about 1600 cm⁻¹

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was assigned to C=C stretching of amino acids [6]. We have already observed that the relative intensity of the amide I band with respect to amide II band intensity decreases with the OTM times, indicating a protein rearrangement [4]. The center of the amide I band moved to a higher wavenumber for the increasing OTM times, especially for the T2 and T3 spectra. The FT-IR spectrum of the T0 sample was compared with the spectrum resulting from Raman spectroscopy in Figure 1b(ii). The Raman spectrum was deconvoluted in terms of Lorentzian functions and the main secondary structure modes were individuated and assigned to β -sheet (at about 1627 cm⁻¹), α -helix (at about 1652 cm⁻¹), β -sheet (at about 1677 cm⁻¹), and β -turn (at about 1699 cm⁻¹). The dependence of the wavenumber positions of the protein secondary structure on the OTM time are reported in Table 1 for data concerning the FT-IR measurements and in Table 2 for Raman spectroscopy data. The maximum intensity of the amide I band of the FT-IR signal occurred at a wavenumber value lower than the one of the Raman spectrum, in agreement with data reported in Ref. [14].

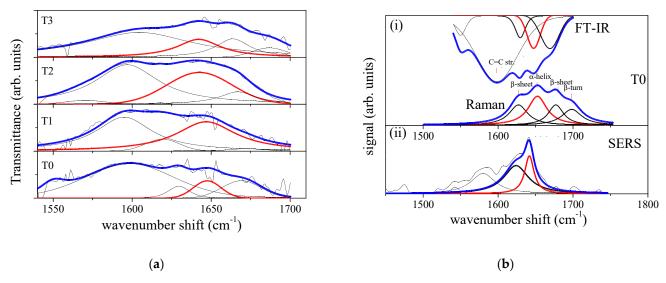


Figure 1. (a) Amide I region of the FT-IR spectra of GCF sample before orthodontic treatment (T0, reference sample) and after 2 (T1), 7 (T2) and 14 days (T3) of OTM. The deconvolution of the spectra in terms of Gaussian–Lorentzian mixed functions is reported. The red curves refer to α -helix of the amide I band. (b) (i) Comparison of amide I region of the FT-IR and Raman spectra of GCF sample before orthodontic treatment (T0). (b) (ii) SERS spectrum of GCF (T0 sample).

Table 1. Assignment of the protein secondary structure modes (in cm⁻¹) for amide I band of FT-IR spectra.

	T0 (Reference)	T1 (2 Days)	T2 (7 Days)	T3 (14 Days)
β-sheet; 3 ₁₀ -helix	1630	1619	1617	-
α-helix	1647	1647	1643	1642
β-sheet; β-turn	1669	1672	1687	1667/1690

Table 2. Assignment of protein secondary structure modes (in cm⁻¹) for amide I band of Raman spectra.

	T0 (Reference)	T1 (2 Days)	T2 (7 Days)	T3 (14 Days)
β-sheet	1622	1619	1618	1621
α-helix	1652	1643	1641	1642
β-sheet	1677	1662	1661	1666
β-turn	1699	1687	1690	1695

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The SERS signal is reported in Figure 1b(ii). In this case, the α -helix mode was the prevalent component in the amide I band region. This indicates that the peptide bonds are on the proximity of the gold nanoparticle surface. Otherwise, the presence of bulky side chain groups orients the peptide bonds too far from the evanescent field of the surface plasmon resulting in a suppression of the amide I band in the spectra [15]. A comparison of the effect of OTM time on the FT-IR and SERS response in the amide I spectral region is shown in Figure 2. Differently from FT-IR behavior, the amide I band center of the SERS spectra shifted to lower wavenumbers when the OTM time increased, from 1641 cm⁻¹ to 1611 cm⁻¹. This feature can be correlated to a change of both the relative amount and quality of helix secondary structure components. The helix protein secondary structure is typically of type α -helix (3.6 residues/turn), but the 3₁₀-helix form (3 residues/turn) can also occur. The 3_{10} -helices are typically shorter than α -helices [16] and are presumed to serve as intermediary steps in the formation and folding of α -helices, due to a low reciprocal barrier energy [17]. The energy of the 3₁₀-helix mode in the SERS spectrum is lower than the one of α -helix [18,19], thus we argued that the 1611 cm⁻¹ observed SERS peak could be assigned to this mode.

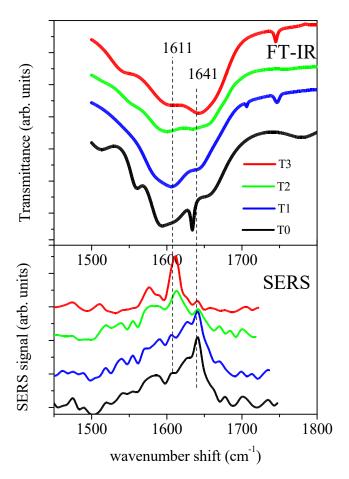


Figure 2. FT-IR and SERS spectra of GCF (T0) and at increasing OTM times, namely 2 days (T1), 7 days (T2), and 14 days (T3), respectively.

4. Conclusions

Changes occurring in the protein secondary structure of GCF during orthodontic processes were assessed in young adults by a comparing the analysis of the amide I region of FT-IR, Raman scattering and SERS spectra. This complementary approach allowed a deep insight into the molecular response of GCF component proteins to the OTM stresses, exploiting the complementary information that the considered spectroscopy methods offer. The center of the amide I band of the FT-IR spectra moves to a higher wavenumber for

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increasing OTM times, indicating a decrease of the α -helix secondary structure component content compared to an increase of unordered and β -sheet components due to protein unfolding processes. Differently from the FT-IR behavior, the amide I band center of the SERS spectra shifts to lower wavenumbers when the OTM time increases, from 1641 cm $^{-1}$ to 1611 cm $^{-1}$. The SERS response is directly correlated to the protein helix configurations and the observed features can be accounted for by the formation of 3_{10} -helix structures when the OTM time increases, indicating the occurrence of the molecular restoring mechanisms of GCF and the alveolar environment after an initial molecular unfolding and disorder increase due to OTM stress.

In the case of FT-IR analysis, a partial overlap of the 3_{10} -helix and β -sheet spectral ranges do not permit the unequivocal sensing of the presence of the 3_{10} -helix, differently from SERS.

These studies demonstrated that the vibrational spectroscopies could be a potentially useful tool for immediate monitoring of the individual patient's response to the orthodontic tooth movement, aiming for a more personalized treatment reducing any side effects.

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Informed Consent Statement: Informed consent was obtained from all subjects involved in the study.

Data Availability Statement: Data are available on request.

Conflicts of Interest: The authors declare no conflict of interest.

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