

Supplementary Information

Exploratory infrared spectroscopic study of erythrocytes in cancer chemotherapy

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Fig. S2. The C-H stretching (a) and fingerprint (b) regions of averaged control and cancerous erythrocytes, as a function of number of chemotherapy cycles (CTH), and their corresponding second derivative spectra (a') and (b'). The shaded areas in (b') highlight the spectral domains where differences between the average spectra were observed: change in proportion of some secondary structures in proteic part, and changes at the CH₂ groups level, observed in the CH₂ scissoring bands, respectively.

Fig. S3. Difference spectra between the averaged data of digestive cancer cases receiving chemotherapeutics and untreated subjects, in the regions assigned to OH/NH/CH stretching (left) and fingerprint vibrations (right). The shaded areas highlight the significant differences at the CH₂/CH₃ and amide group level, respectively. The spectra noted “0 CTH” are referring to the differences between patients receiving no chemotherapy and those from the control group.

Fig. S4. (a) Normalized FTIR spectra of erythrocytes in the CH bending/scissoring vibration region for the control samples as compared to those from the cancer cases. (b) Plot of PC-1 versus PC-2 for the normal against the pathological cases: black trace – normal samples, red trace – abnormal samples. The ellipses delimitate the samples clustering. (c) Loading plots of PC-1 (A) and PC-2 (B)

Fig. S5. (a) The normalized FTIR spectra of erythrocytes in the region of phosphate group stretching vibrations for the control samples as compared to those from the cancerous cases. (b) Plot of PC-1 versus PC-2 for the normal against the pathological cases: black trace – normal samples, red trace – abnormal samples. The ellipses delimitate the samples clustering. (c) Loadings plots of the first two principal components: PC-1 (A) and PC-2 (B)

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Table S2. Independent Samples Test for digestive cancer vs. control group (healthy men group)

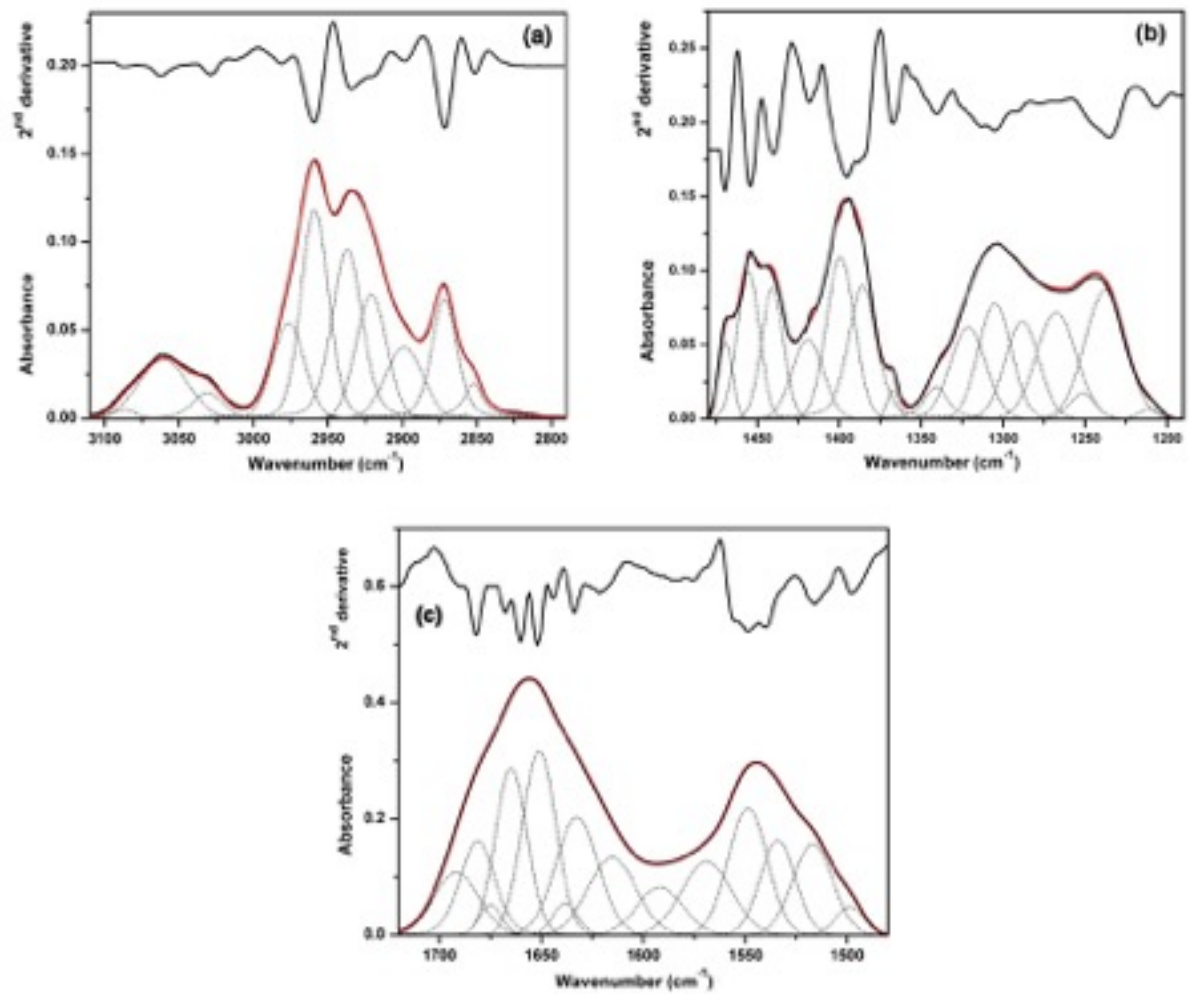


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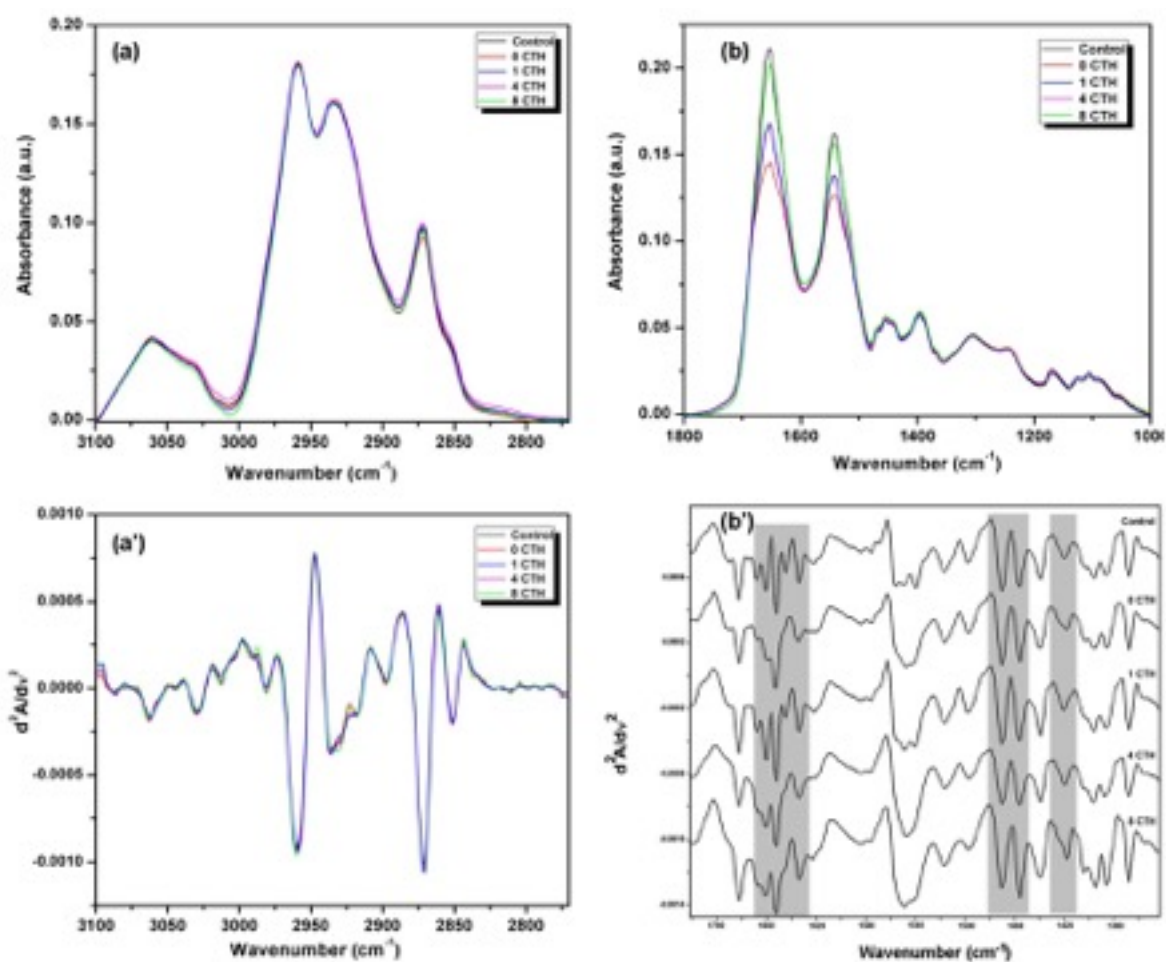


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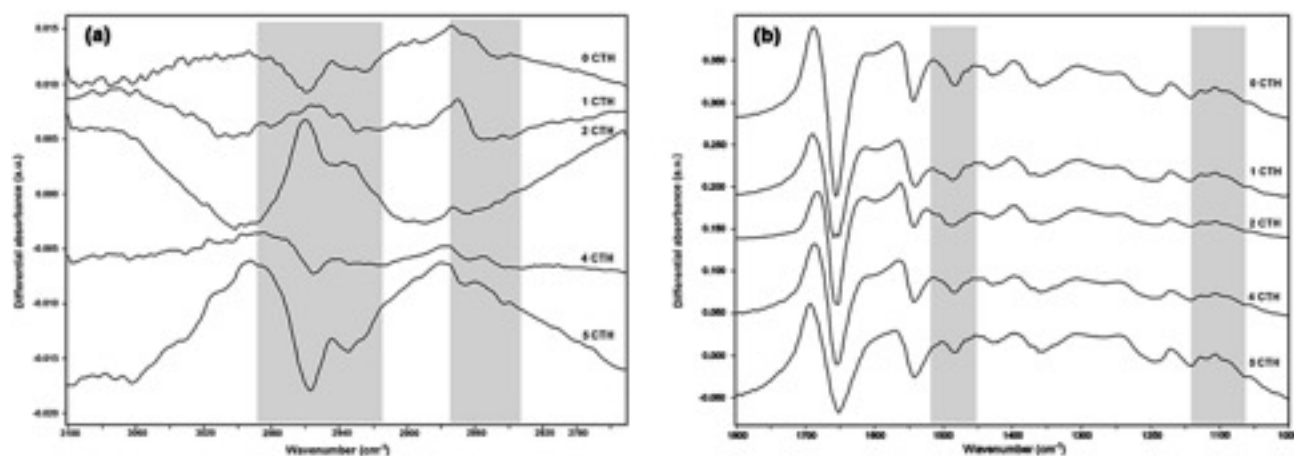


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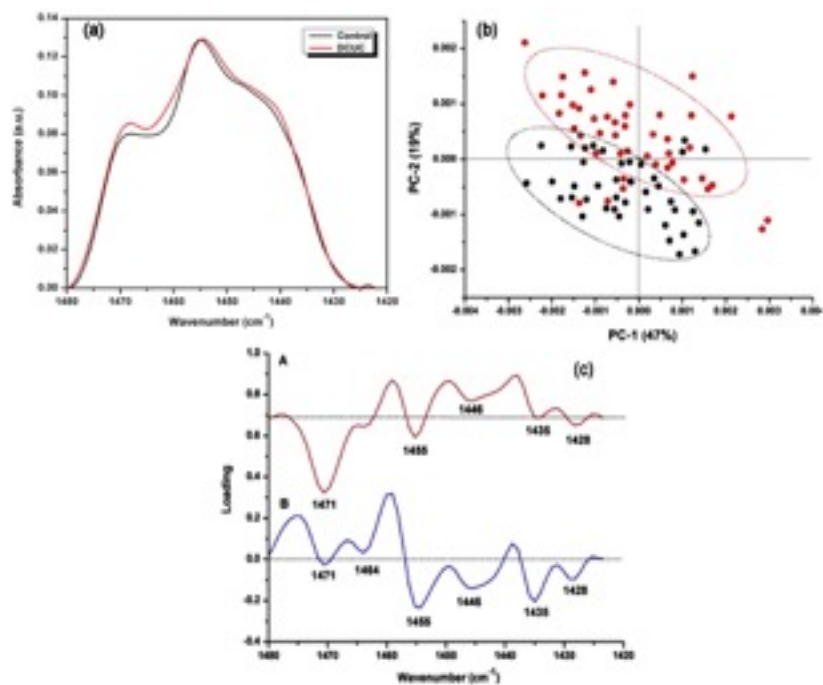


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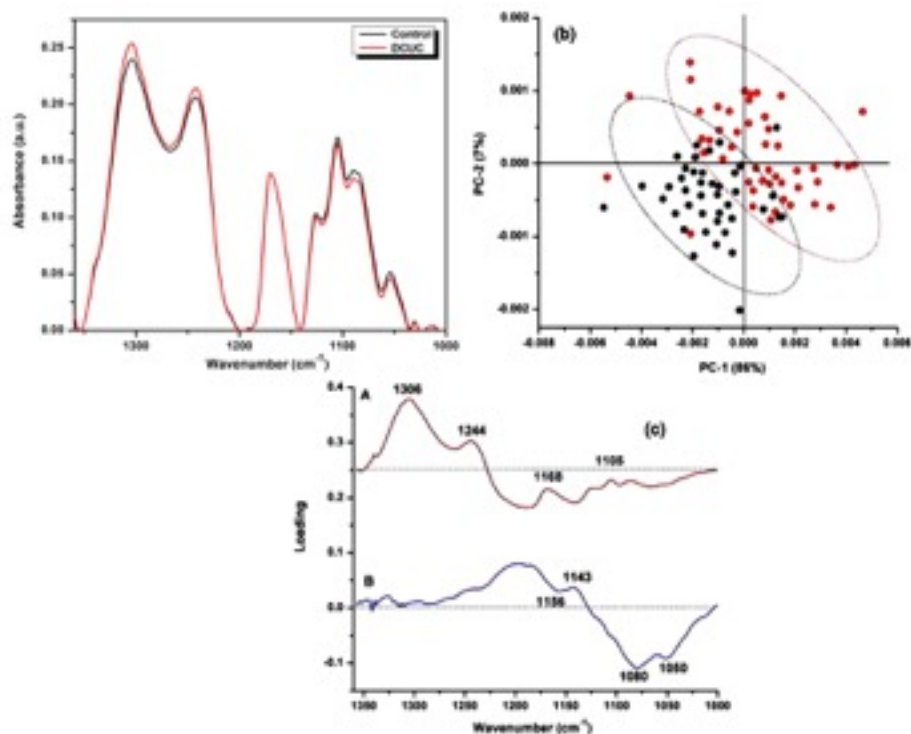


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Physiological parameters and correlation with the spectral parameters

Table S1. Hematological, biological and FTIR erythrocytes parameters correlations for digestive cancer

		$\nu(=CH)/\nu(CH_3)$	$\nu(=CH)/\nu(CH_{tot})$	$\tilde{\nu}_{\nu_{sym}(CH_2)}$	$\nu_{as}(CH_2)/\nu_{as}(CH_3)$	$\nu_{as}(CH_2)/\nu(=CH)$	$\delta_{sciss}(CH_2)/\delta_{as}(CH_3)$	Amide I/II
Age	r	-0.108	-0.134	-0.061	0.068	0.015	0.362	-0.039
	p	0.714	0.649	0.837	0.819	0.960	0.203	0.894
Cth	r	0.522	0.255	0.022	0.570*	-0.313	-0.137	-0.539*
	p	0.083	0.379	0.942	0.045*	0.275	0.642	0.047*
RBC	r	0.423	0.306	0.134	-0.270	0.364	0.559*	-0.183
	p	0.132	0.288	0.648	0.350	0.200	0.038*	0.532
HCT	r	0.253	0.109	-0.141	-0.350	0.090	0.522	-0.045
	p	0.383	0.711	0.630	0.220	0.761	0.056	0.879
Hb	r	0.257	0.120	-0.132	-0.264	0.020	0.470	-0.097
	p	0.375	0.684	0.653	0.362	0.947	0.090	0.742
PL	r	-0.259	-0.022	0.277	-0.175	0.440	-0.215	0.010
	p	0.372	0.942	0.337	0.550	0.115	0.461	0.974
Cholesterol total	r	-0.448	-0.453	-0.408	0.031	-0.035	0.026	0.312
	p	0.108	0.103	0.147	0.916	0.906	0.931	0.278
Triglycerides	r	-0.388	-0.497	-0.013	-0.318	0.439	0.128	0.070
	p	0.170	0.071	0.964	0.268	0.116	0.663	0.812
Blood glucose	r	0.189	0.149	-0.110	0.456	-0.146	0.217	-0.160
	p	0.518	0.611	0.709	0.101	0.617	0.456	0.586
Leucocytes	r	-0.395	-0.213	-0.088	-0.298	0.181	-0.067	0.001
	p	0.162	0.466	0.766	0.302	0.535	0.820	0.997
Lymphocytes	r	-0.308	-0.275	-0.103	-0.369	-0.038	-0.255	0.126
	p	0.284	0.342	0.725	0.195	0.897	0.378	0.668
VEM	r	-0.254	-0.291	-0.429	-0.149	-0.475	-0.056	0.155
	p	0.382	0.313	0.126	0.611	0.086	0.849	0.596
HEM	r	-0.126	-0.181	-0.344	-0.069	-0.455	-0.010	0.034
	p	0.669	0.536	0.228	0.814	0.102	0.974	0.908

*Statistic significant

Cth- chemotherapy cycles number, RBC- red blood cell number, HCT- hematocrit, Hb- haemoglobin level, PL- platelets

number, VEM- erythrocyte medium volume, HEM- erythrocyte medium haemoglobin

Table S2. Independent Samples Test for digestive cancer vs. control group (healthy men group)

Levene's Test for Equality of Variances				t-test for Equality of Means			
		f	Sig.	t	df	Sig. (2-tailed)	Mean Difference
RBC	Equal variances assumed	3.210	0.082	-4.910	33.000	0.000	-0.704
	Equal variances not assumed			-4.567	21.251	0.000	-0.704
HTC	Equal variances assumed	10.086	0.003	-5.923	33.000	0.000	-6.868
	Equal variances not assumed			-5.246	17.598	0.000	-6.868
Hb	Equal variances assumed	12.618	0.001	-5.960	33.000	0.000	-2.555
	Equal variances not assumed			-5.205	16.706	0.000	-2.555
PL	Equal variances assumed	3.853	0.058	2.261	33.000	0.030	57.095
	Equal variances not assumed			2.017	18.086	0.059	57.095
Total Cholesterol	Equal variances assumed	1.410	0.243	-2.795	33.000	0.009	-28.452
	Equal variances not assumed			-2.617	21.830	0.016	-28.452
Tryglicerides	Equal variances assumed	0.349	0.559	0.676	33.000	0.504	9.000
	Equal variances not assumed			0.714	32.326	0.480	9.000
Leukocytes	Equal variances assumed	0.007	0.935	-3.155	33.000	0.003	-1.613
	Equal variances not assumed			-3.226	30.067	0.003	-1.613
Limfocytes	Equal variances assumed	0.108	0.745	-3.061	33.000	0.004	-0.691
	Equal variances not assumed			-2.941	24.146	0.007	-0.691
VEM	Equal variances assumed	0.601	0.444	-0.712	33.000	0.481	-1.320
	Equal variances not assumed			-0.677	23.177	0.505	-1.320
HEM	Equal variances assumed	1.404	0.245	-1.597	33.000	0.120	-1.152
	Equal variances not assumed			-1.452	19.435	0.162	-1.152
V(=CH)/V(CH_{3as})	Equal variances assumed	7.514	0.010	-6.718	33.000	0.000	-0.001
	Equal variances not assumed			-7.794	28.392	0.000	-0.001

$V(\text{CH}_{2\text{as}})/V(\text{CH}_{3\text{as}})$	Equal variances assumed	13.483	0.001	-3.196	33.000	0.003	-0.080
	Equal variances not assumed			-3.655	30.089	0.001	-0.080
$V(=\text{CH})/V(\text{CH}_{\text{tot}})$	Equal variances assumed	8.280	0.007	-3.912	33.000	0.000	0.000
	Equal variances not assumed			-4.433	30.979	0.000	0.000
$\Delta V_{1/2}(\text{CH}_{2\text{sciss}})$	Equal variances assumed	13.642	0.001	3.163	33.000	0.003	0.907
	Equal variances not assumed			3.765	24.861	0.001	0.907
$V_{\text{as}}(\text{P-O})$	Equal variances assumed	7.540	0.010	-0.923	33.000	0.363	-0.035
	Equal variances not assumed			-1.075	27.870	0.292	-0.035
	Equal variances not assumed			-2.358	29.429	0.025	-7.364
Amide I/II	Equal variances assumed	3.160	0.085	-0.139	33.000	0.890	-0.006
	Equal variances not assumed			-0.119	15.366	0.907	-0.006