

Prediction of the Genetic Variety of Extra Virgin Olive Oils Produced at *La Comunitat Valenciana*, Spain, by Fourier Transform Infrared Spectroscopy

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Fourier transform infrared spectroscopy (FTIR), followed by multivariate treatment of the spectral data, was used to classify extra virgin olive oils (EVOOs) according to their genetic variety. EVOO samples corresponding to seven different genetic varieties (Arbequina, Borriolenca, Canetera, Farga, Hojiblanca, Picual, and Serrana) were analyzed. The wavelength scale of the FTIR spectra of the oils was divided into 20 regions. The normalized absorbance peak areas within these regions were used as predictor variables. Classification of the EVOO samples according to their genetic variety was achieved by linear discriminant analysis (LDA). A good resolution among all categories was achieved using a LDA model constructed with only nine predictor variables. With this LDA model, 88% of the EVOOs were correctly classified, with assignment probabilities higher than 95%. This method is helpful for olive oil producers because it provides useful information related to the genetic variety of EVOOs, which is required by European Community regulations.

KEYWORDS: Extra virgin olive oil; genetic variety; Fourier transform infrared spectroscopy; linear discriminant analysis

INTRODUCTION

Extra virgin olive oil (EVOO) is a traditional Mediterranean food product, whose market has recently been expanded because of its highly appreciated organoleptic attributes and its health and nutritional properties (1). Along the last few years, the consumption of EVOOs has increased considerably in relation to the consumption of virgin and refined olive oils. Owing to its distinctive and peculiar intense taste, EVOOs obtained from some pure genetic varieties are highly appreciated.

To establish the authenticity of edible oils, a number of chromatographic (2–4), thermal (5), and spectroscopic methods, including fluorescence (6), near-infrared spectroscopy (7, 8), Fourier transform infrared spectroscopy (FTIR) (8–14), FT-Raman (8), nuclear magnetic resonance (15), and mass spectrometry (MS) (16–18), followed by multivariate statistical analysis of data, have been described. For this purpose, the contents of fatty acids (2, 14), tocopherols (6), volatile compounds (4), amino acids (17), and sterols (3, 18), among others, have been used.

The development of methods to distinguish the genetic variety and also the geographical origin of EVOOs is important because, according to the European Community (EC) regulation 182/2009 (19), olive oil producers have to include in their manufactured products the genetic variety and also the geographical origin of the olives. In fact, authentication methods for genetic varieties of

EVOO have been mainly addressed by gas chromatography (20–28) and high-performance liquid chromatography (20–24). Other techniques, such as MS (29), have also been used for these purposes.

FTIR is a rapid and nondestructive powerful analytical tool for the study of edible oils and fats, requiring minimum sample preparation. FTIR is also an excellent tool for quantitative analysis, because the intensities of the spectral bands are proportional to the concentration. For this reason, FTIR has mainly been used to distinguish oils from different botanical origins using non-supervised classificatory techniques (10, 11), to distinguish EVOOs from different geographical origins (30, 31), and to detect olive oil adulteration with other low-cost edible oils (9, 12, 13). FTIR has also been used to distinguish mixtures of three Turkish monovarietal olive oils using principal component analysis (32).

In this work, FTIR, jointly with the application of linear discriminant analysis (LDA), is used to classify EVOOs from seven different genetic varieties, commonly produced at *La Comunitat Valenciana*, Spain. For this purpose, FTIR spectra were divided into 20 wavelength regions, using the normalized absorbance peak areas as predictor variables.

EXPERIMENTAL PROCEDURES

Oil Samples. The EVOO samples employed in this study were mainly produced at *La Comunitat Valenciana*, Spain. Other samples, such as Hojiblanca and Picual, which were not commonly cultivated at *La Comunitat Valenciana*, were also included in this study because, jointly with the Arbequina variety, they are the main varieties in the

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Table 1. Genetic Variety, Number of Samples, Geographical Origin, and Supplier of the EVOOs

genetic variety	number of samples	geographical origin	supplier	crop season
Arbequina	2	Altura (Castellón)	Intercoop	06/07, 07/08
	2	Maestrat comarca (Castellón)	Intercoop	06/07, 07/08
	2	Alicante	Intercoop	05/06, 07/08
	2	Palancia comarca (Castellón)	Intercoop	06/07, 07/08
Borriolenca	3	Alcalatén comarca (Castellón)	Intercoop	05/06, 06/07, 07/08
	4	La Plana comarca (Castellón)	Intercoop	05/06, 06/07, 07/08
Canetera	3	Maestrat comarca (Castellón)	Intercoop	05/06, 07/08
	2	Adzaneta (Castellón)	Intercoop	06/07, 07/08
	3	La Plana comarca (Castellón)	Intercoop	05/06, 06/07, 07/08
Farga	4	Maestrat comarca (Castellón)	Intercoop	05/06, 06/07, 07/08
	3	Alcalatén comarca (Castellón)	Intercoop	06/07, 07/08
	3	La Plana comarca (Castellón)	Intercoop	05/06, 06/07, 07/08
Hojiblanca	2	Estepa (Sevilla)	Carbonell	06/07, 07/08
	2	Luque (Córdoba)	Coosur	06/07, 07/08
	3	Puente Genil (Córdoba)	Borges	06/07, 07/08
	5	Fuente de Piedra (Málaga)	Grupo Hojiblanca	05/06, 06/07, 07/08
	1	Santaella (Córdoba)	Columela	05/06
Picual	2	Martos (Jaén)	Carbonell	06/07, 07/08
	2	Villanueva del Arzobispo (Jaén) and Porcuna (Jaén)	Coosur	06/07
	3	Quesada (Jaén)	Borges	05/06, 06/07, 07/08
	1	Montoso (Córdoba)	Grupo Hojiblanca	06/07
	1	Tabernas (Almería)	Castillo de Tabernas	06/07
	1	Canena (Jaén)	Castillo de Canena	07/08
Serrana	9	Altura (Castellón)	Cooperativa Altura and Intercoop	05/06, 06/07, 07/08
	3	Artana (Castellón)	Intercoop	06/07, 07/08
	3	Jérica (Castellón)	Intercoop	06/07, 07/08
	5	Viver (Castellón)	Intercoop	05/06, 06/07, 07/08

Spanish market. The genetic variety, number of samples, geographical origin, sample suppliers, and crop season are shown in **Table 1**. All Valencian samples were kindly donated by *Intercoop Olival* (Almassora, Castellón, Spain) and the *Cooperativa de Altura* (Castellón, Spain). Other samples were purchased at the local market, with their genetic variety and geographical origin being certified by the suppliers. All of the samples were stored in amber glass bottles at $-20\text{ }^{\circ}\text{C}$ prior to their analysis.

FTIR Spectra. FTIR spectra were obtained using a Jasco 4100 type A spectrophotometer (Jasco, Easton, MD) fitted with a single reflection attenuated total reflectance (ATR) accessory. The ATR accessory (ATR-PRO410-S, Jasco) was equipped with a ZnSe reflection crystal. All analyses were carried out at room temperature. Measurements were obtained using 15 scans at 2 cm^{-1} resolution. Spectra were recorded in the absorbance mode from 4000 to 600 cm^{-1} , with only the regions being from 2500 to 750 cm^{-1} considered in this study. Data handling was performed with the Spectra Manager version 2.07.00 software (Jasco).

For each sample (ca. $20\text{ }\mu\text{L}$ were put on the crystal surface), the absorbance spectrum was collected against a background obtained with a dry and empty ATR cell. Two spectra were recorded for each sample. Before each spectrum was acquired, the ATR crystal was cleaned with a cellulose tissue soaked in *n*-hexane, rinsed with acetone, and dried.

Data Treatment and Construction of Data Matrices. FTIR spectra were divided into the 20 wavelength regions described in **Table 2**. Each selected region corresponds to a peak or a shoulder, which represent structural or functional group information, either about the lipids or minor components of the oil samples (see **Table 2**). For each region, the peak/shoulder area was measured. To reduce the variability associated with the total amount of oil sample used and to minimize other sources of variance also affecting the intensity of all of the peaks, such as the radiation source intensity, normalized rather than absolute areas were used. To normalize the variables, the area of each region was divided by each one of the areas of the other 19 regions; in this way and because any pair of areas

should be considered only once, $(20 \times 19)/2 = 190$ normalized variables were obtained.

A matrix containing 76 objects, which corresponded to the average of 2 replicates (**Table 1**), and 190 predictors, was constructed. A response column, containing the categories corresponding to the 7 genetic varieties of the oils, was added to this matrix. Only the means of the replicates of the samples were included in this matrix; in this way, the internal dispersion of the categories was reduced, which was important to reduce the number of variables selected during model construction. The matrix was randomly divided into two groups, training and evaluation sets. The training set was composed of 6 samples for each genetic variety ($6 \times 7 = 42$ objects), while the evaluation set was performed with the remaining samples (34 objects). Statistical data treatment of the normalized variables was performed using the SPSS package (version 12.0.1, Statistical Package for the Social Sciences, Chicago, IL).

RESULTS AND DISCUSSION

FTIR spectra of the 76 EVOO samples shown in **Table 1** were collected. **Figure 1** shows the spectra of seven oils, corresponding to the seven genetic varieties. As it can be observed, FTIR spectra were closely similar. To enhance small differences that were not appreciated straight away in the spectra of oils obtained from different genetic varieties, the peak areas of the 20 selected regions were conveniently handled by multivariate statistical techniques.

Classification of EVOOs According to Their Genetic Variety Using LDA. LDA, a supervised classificatory technique, is widely recognized as an excellent tool to obtain vectors showing the maximal resolution between a set of previously defined categories. In LDA, vectors minimizing Wilks' lambda, λ_w , are obtained (35). This parameter is calculated as the sum of squares of the distances between points belonging to the same category

Table 2. FTIR Spectral Regions Selected as Predictor Variables for Statistical Data Treatment

identification number	range (cm ⁻¹)	functional group	nominal frequency	mode of vibration
1	2393–2347	alcane ^a		
2	2347–2279	alcane ^a		
3	1870–1712	–C=O (ester)	1746 ^b	stretching
4	1712–1693	–C=O (acid)	1711 ^b	stretching
5	1693–1671	–C=O	^a	stretching
6	1671–1590	–C=C– (cis)	1654 ^b	stretching
7	1467–1426	–C–H (CH ₂)	1465 ^a	bending (scissoring)
		–C–H (CH ₃)	1450 ^a	bending (asym)
8	1426–1407	=C–H (cis)	1417 ^b	bending (rocking)
9	1407–1380	=C–H	1400 ^a	bending
10	1380–1336	–C–H (CH ₃)	1377 ^b	bending (sym)
		O–H	1359 ^a	bending (in plane)
11	1336–1309	non-assigned	1319 ^b	bending
12	1309–1292	=C–H (cis)	1294 ^c	bending
13	1292–1257	=C–H	– ^c	bending
		–C–O		stretching
14	1257–1216	–CH ₂ –	1238 ^b	bending
		–C–O	1163 ^b	stretching
15	1216–1127	–CH ₂ –	1163 ^b	bending
		–C–O	1138 ^a	stretching
		–C–O	1118 ^b	stretching
16	1127–1109	–C–O	1097 ^b	stretching
17	1109–1045	–C–O	1097 ^b	stretching
18	1045–998	–C–O	1033 ^b	stretching
		–HC=CH– (trans)	968 ^b	bending (out of plane)
19	998–883	–HC=CH– (cis)?	914 ^b	bending (out of plane)
		=CH ₂	850 ^a	wagging

^a According to ref 34. ^b According to ref 33. ^c According to ref 8.

divided by the total sum of squares. Values of λ_w approaching 0 are obtained with well-resolved categories, whereas overlapped categories made λ_w approach 1. Up to $N - 1$ discriminant vectors are constructed by LDA, with N being the lowest value for either the number of predictors or the number of categories.

Using the normalized variables, a LDA model capable of classifying the EVOO samples according to their genetic varieties was constructed. To select the variables to be included in the model, the SPSS stepwise algorithm was used. According to this algorithm, a predictor is selected when the reduction of λ_w produced after its inclusion in the model exceeds F_{in} , the entrance threshold of a test of comparison of variances or F test. However, the entrance of a new predictor modifies the significance of those predictors that are already present in the model. For this reason, after the inclusion of a new predictor, a rejection threshold, F_{out} , is used to decide if one of the other predictors should be removed from the model. The process terminates when there are no predictors entering or being eliminated from the model. The default probability values of F_{in} and F_{out} , 0.05 and 0.10, respectively, were adopted.

A good resolution between the seven categories was achieved when the LDA model was constructed ($\lambda_w = 0.576$). This λ_w value was higher than those previously reported in our previous work (29); however, in this previous study, just three categories were simultaneously distinguished. The variables selected by the SPSS stepwise algorithm and the corresponding standardized coefficients of the model, showing the predictors with large discriminant capabilities, are given in **Table 3**. According to this table, the main IR regions selected by the algorithm to construct the LDA model corresponded to –C=O (acid, stretching), –C–H (CH₂, bending scissoring), –C–H (CH₃, bending sym), =C–H (bending), –C–O (stretching), and –CH₂– (bending).

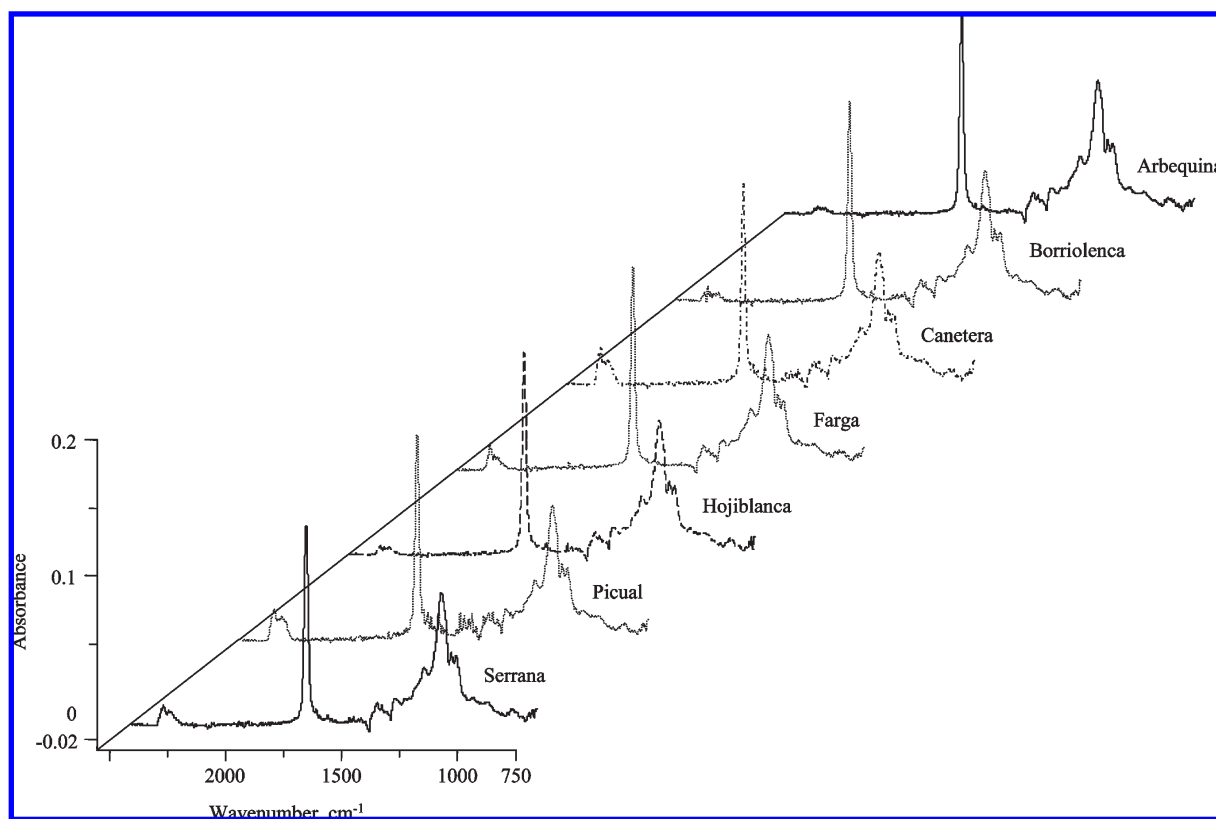


Figure 1. FTIR spectra of EVOO samples of (A) Arbequina from Alicante (crop season 05/06), (B) Borriolenca from Alcalatén comarca (crop season 07/08), (C) Canetera from La Plana comarca (crop season 06/07), (D) Farga from Maestrat comarca (crop season 06/07), (E) Hojiblanca from Luque, Córdoba (crop season 07/08), (F) Picual from Martos, Jaén (crop season 06/07), and (G) Serrana from Altura, Castellón (crop season 05/06).

Table 3. Predictors Selected and Corresponding Standardized Coefficients of the LDA Model Constructed To Predict the Genetic Variety of EVOOs

predictors ^a	f_1	f_2	f_3	f_4	f_5	f_6
1/5	0.13	-0.91	-0.96	-0.06	-0.60	-2.04
1/7	5.85	4.36	-1.51	4.00	4.07	-2.22
1/9	-6.01	-3.57	3.91	-3.71	-3.11	4.03
3/6	-0.13	0.30	0.47	0.58	0.95	0.76
4/12	9.48	15.43	12.74	16.47	-7.05	-6.22
4/14	-9.00	-14.54	-12.66	-16.58	7.15	6.35
12/15	0.85	1.32	1.25	1.30	-0.89	0.35
13/16	-0.28	-0.55	0.69	-0.11	1.03	-0.48
14/17	1.06	-0.10	-0.37	-0.32	-0.41	0.43

^aPairs of wavelength regions were identified according to Table 2.

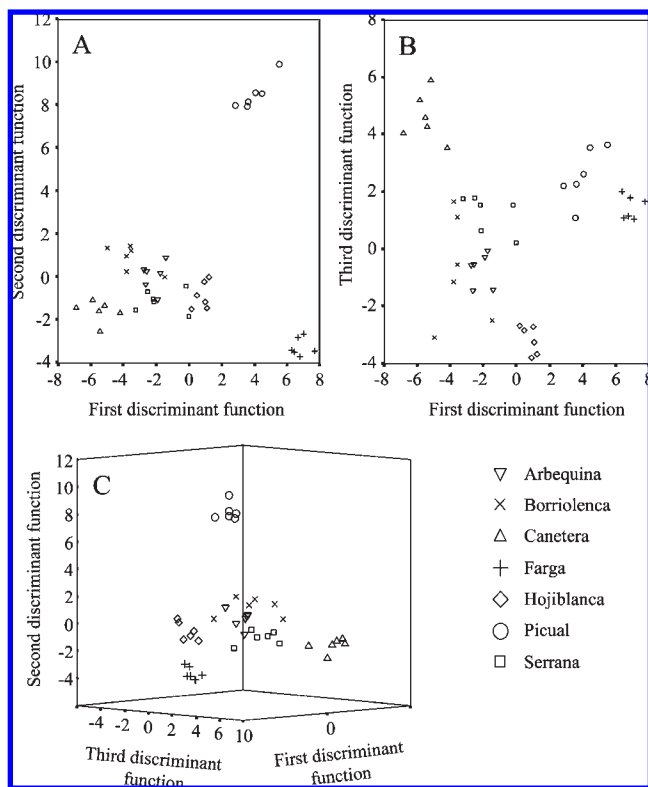


Figure 2. Score plots on the planes of the (A) first and second and (B) first and third discriminant functions and (C) an oblique perspective of the 3D space defined by the three discriminant functions of the LDA model constructed to classify EVOOs according to their genetic variety.

The projections of the samples on the six discriminant functions allowed for the distinction of at least a different category. As shown in **Figure 2A**, a large resolution between Farga, Picual, and the other categories was achieved along f_1 . On the other hand, the variance gathered by f_2 was mainly associated with the resolution between Picual and the rest of categories as a whole. According to **Figure 2B**, Canetera, Picual, and Hojiblanca were resolved from the rest of categories along f_3 . Finally, **Figure 2C** shows a score plot from an oblique perspective of the 3D space defined by the three first discriminant functions. When this 3D figure was rotated, the separation between all of the different categories was evident. Because of the fact that a large number of categories (seven) were included in this work in relation to the three categories described in our previous work (29), it is logical that it was more difficult to appreciate separation between categories when represented in a plane. When the leave-one-out validation method was applied to the training set, all of the points

were correctly classified. Concerning the evaluation set, all of the objects were correctly assigned to an assignment probability higher than 95%, except four objects, which corresponded to two Borriolenca, one Hojiblanca, and one Arbequina samples.

Thus, the possibility of classifying EVOO samples according to their genetic variety using FTIR data has been demonstrated. Using only nine predictors, all of the EVOO samples belonging to seven different genetic varieties mainly produced at *La Comunitat Valenciana* were correctly classified with a good resolution among the categories. According to the EC regulation (19), this reliable procedure provides useful information regarding the genetic varieties, which is important for olive oil producers.

On the other hand, this method is faster than other methods described in the literature (20–23, 26), which are based on chromatographic separations, using fatty acids (20–22, 26), sterols (21), *n*-alkanes (23), and triglycerides (22) as variables. For classification purposes, these methods have used both non-supervised and supervised statistical tools. The first one just led to a preliminary distribution according to the genetic varieties (20). The second approach produced satisfactory resolution among the categories (21–23, 26); however, in these studies, no more than five categories were simultaneously resolved.

ABBREVIATIONS USED

EVOO, extra virgin olive oil; LDA, linear discriminant analysis; MS, mass spectrometry.

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