



MOLECULAR IDENTIFICATION OF YEAST SPECIES ASSOCIATED WITH THE PRODUCCION OF TEQUILA

Elda Rodríguez, José Lucas, Claudia Maldonado, Conrado Soto, Olivia Rodríguez, <u>Armando Arias</u> Lab. de Biotecnología, Depto. de Botánica y Zoología, Universidad de Guadalajara, Km. 15.5 Guadalajara a Nogales, Zapopan, Jalisco, 45100, MÉXICO, jaariasgarcia@gmail.com

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Introduction. The process of production of tequila involves 4 major steps: cooking, grinding, fermentation with yeast and distilled agave juice. Fermentation is performed with yeast of *Saccharomyces cerevisiae* or sometimes it performs a natural fermentation or spontaneous without an inoculum. Despite being a very important economical activity, there is little information on the different yeast species associated with this fermentation.

The objective of this work is the molecular identification of strains isolated from tequila environments.

Methods. Yeast strains were isolated from fields or agave juice of *Agave tequilana* Weber var. azul of Jalisco state. The molecular identification of the strains was carried out by means of the RFLPs of the ITS-5.8S genetic region (1). In some cases, to confirm the correct identification the sequence was compared with those deposited in the type strains.

Results. The species with the sizes of the PCR products and their patterns of restriction with enzymes *Hha* I, *Hae* III and *Hinf* I of the isolated yeast are shown in the Table 1. The patterns of restriction were compared (http://www.yeast-id.com/), and found that correspond to *Candida ethanolica, Clavispora lusitaniae, Issatchenkia orientalis, Kluyveromyces* spp., *Pichia gulliermondii,* and *Saccharomyces cerevisiae.*

The yeast species *Clavispora lusitaniae*, *Kluyveromyces* spp., *Candida ethanolica* and *Saccharomyces cerevisiae* have been isolated from tequila environments, fresh cooked or fermented plants of *Agave tequilana* for the production of tequila (2, 3) or *Agave salmiana* for the production of mezcal (3, 4, 5). On the other hand, *I. orientalis* and *P. gulliermondii* have been isolated from Togwa, a fermented food of Tanzania, sourdough bread, fermented fruit, but not reported in a tequila environment.

The frequency of the restriction patterns of the yeast species is shown in Fig. 1.

Species	Ар	Hha I	Hae III	Hinf I
	(pb)			
C. lusitaniae	380	220+80	380	190+180
Kluyveromyces	700	280+190+	620+70	270+190+
spp.		180+80		130+50
S. cerevisiae	850	375+340+	320+230+	380+370+
		130	175+125	120
I. orientalis	500	200+180+	360+75	230+160+
		50		140
P. gulliermondii	600	290+250	390+120+	300+275
			60	
C. ethanolica	450	150+90+8	320+90	240+190
		0+50		

Table 1. Nucleotide fragment length of 5.8S-ITS profiles

Fig.1 Frequency (%) of the yeast species isolated from a tequila environment.

Conclusions. The predominant species of yeast in a tequila environment was *Clavispora lusitaniae*.

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