SHORT COMMUNICATION

The Long-chain Fatty Acid Compositions of Species Representing the Genera *Saccharomyces*, *Schwanniomyces* and *Lipomyces*

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The cellular long-chain fatty acid composition of 31 yeast strains representing species of *Saccharomyces*, *Schwanniomyces* and *Lipomyces* was determined by gas chromatography of fatty acid methyl esters. The fatty acid profiles of the strains representing the three genera were distinguishable from each other. The *Saccharomyces* and *Lipomyces* strains were characterized mainly by the presence of palmitic (C16:0), palmitoleic (C16:1), stearic (C18:0) and oleic (C18:1) acid as the major fatty acids. The *Schwanniomyces* strains were characterized by the presence of palmitic, palmitoleic, oleic, linoleic (C18:2) and linolenic (C18:3) acid. The 31 strains were divided into three groups on the basis of their fatty acid content. The first group was characterized by a higher concentration of linoleic and linolenic acid, the second group by the absence of linolenic acid, and the third group by the absence of both linoleic and linolenic acid.

INTRODUCTION

The conventional identification of yeasts is mainly based on sexual reproduction, microscopical appearance, and physiological and certain biochemical features (Barnett *et al.*, 1983). This procedure provides valuable information for distinction between species, but is time consuming and not always completely reliable. Several chemotaxonomic studies, which include the examination of the total cell fatty acid content, have also been done. In bacterial and yeast taxonomy, the determination of fatty acids has proved to be a most useful tool (Moss & Dees, 1976; Gunasekaran & Hughes, 1980; Cottrell *et al.*, 1985; Kock *et al.*, 1985*a, b*). Abel *et al.* (1963) demonstrated, that micro-organisms could be classified into genera and species on the basis of their chemical composition determined by gas chromatography, while Rattray *et al.* (1975) and Shaw (1974) discussed the use of cellular fatty acid composition for the identification of various yeasts. This technique was subsequently used by various workers to identify bacteria and yeasts (Kaneko, 1976; Gangopadhyay *et al.*, 1979; Moss *et al.*, 1982). Unfortunately these studies differed in the cultivation procedures used, which, according to the literature, significantly influence cellular fatty acid composition (Deinema, 1961). Therefore comparisons between previous studies are difficult. In this investigation, the cellular long-chain fatty acid contents of strains of *Saccharomyces*, *Schwanniomyces* and *Lipomyces* are described and compared.

METHODS

Cultures. The strains of *Schwanniomyces*, *Lipomyces* and *Saccharomyces* used are listed in Table 1. They were obtained from: the Centre of Biology, Gulbenkian Institute of Science, Oeiras, Portugal (IGC); the

Table 1. Percentage long-chain fatty acid composition of the 31 strains of *Saccharomyces*, *Schwanniomyces* and *Lipomyces*

Group	Name as received	Strain no.	C14:0	C14:1	C16:0	C16:1	UN1*	UN2*	C18:0	C18:1	C18:2	C18:3
1	<i>Sacch. kluyveri</i>	CBS 4569	0.3	0.1	9.6	23.4	1.9	0.1	3.8	22.8	23.5	14.2
	<i>Schw. alluvius</i> †	CBS 6472	0.1	0.1	16.0	4.7	0.1	0.2	3.5	41.6	19.5	12.4
	<i>Schw. castellii</i> ‡	CBS 2863	0.1	0.1	14.8	4.0	0.1	0.1	3.5	40.6	22.0	14.0
	<i>Schw. occidentalis</i>	CBS 819	—	0.1	14.2	4.4	0.2	0.2	3.7	41.1	21.9	14.0
		CBS 6367	—	0.1	14.5	4.5	0.2	0.2	3.6	43.6	22.9	9.5
	<i>Schw. persoonii</i> †	CBS 4869	—	0.1	13.0	6.2	0.3	0.2	0.1	41.2	24.0	13.3
2	<i>L. starkeyi</i>	CBS 2512	0.1	—	28.1	7.6	—	0.1	8.5	46.0	7.9	—
		CBS 2516	—	0.1	33.0	4.5	—	0.1	5.0	52.6	3.5	—
	<i>L. kononenkoae</i>	CBS 2514	0.1	—	31.7	8.5	—	—	8.5	41.4	7.7	0.1
	<i>L. tetrasporus</i>	CBS 5910	0.1	—	31.0	3.5	—	0.1	14.5	42.5	5.5	0.1
	<i>Sacch. dairensis</i>	CBS 421	6.1	3.3	14.2	56.8	—	—	2.4	15.6	1.6	—
	<i>Sacch. unisporus</i>	CBS 399	4.7	1.0	12.3	56.9	—	—	2.9	21.8	0.2	—
3	<i>Sacch. acetii</i> ‡	CBS 4054	0.8	0.4	9.6	45.2	0.1	0.4	5.4	37.6	—	—
	<i>Sacch. capensis</i> ‡	CBS 2247	1.5	0.3	12.8	40.6	—	0.2	2.6	41.8	—	—
	<i>Sacch. carlsbergensis</i> ‡	CSIR-Y114	0.6	0.2	6.8	42.4	—	0.1	5.4	44.3	—	—
		CSIR-Y155	1.2	1.4	5.4	48.7	—	0.2	4.4	38.3	—	—
	<i>Sacch. cerevisiae</i>	CSIR-Y2	0.5	0.4	5.6	57.1	0.1	0.4	1.9	39.2	—	—
		CSIR-Y217	0.9	0.4	6.8	45.7	—	0.1	3.0	42.7	—	—
		CSIR-Y397	1.1	0.5	9.6	49.7	0.4	0.6	4.2	32.9	—	—
		CBS 1907	0.9	0.5	6.6	44.7	—	0.2	4.0	42.6	—	—
		ATCC 4126	0.4	0.1	7.4	44.6	0.1	0.3	5.1	41.8	—	—
		ATCC 26603	0.5	0.3	4.4	49.0	0.1	0.4	1.6	43.2	—	—
		NRRL Y132	0.7	0.4	8.3	50.2	0.3	—	4.5	35.2	—	—
	<i>Sacch. chevalieri</i> ‡	CBS 400	1.0	0.6	7.4	47.1	—	0.1	4.6	39.1	—	—
	<i>Sacch. fructuum</i> ‡	CBS 1544	0.7	0.2	9.9	40.2	0.1	0.2	6.3	42.2	—	—
	<i>Sacch. globosus</i> ‡	CSIR-Y290	1.8	0.8	10.7	49.2	—	0.1	4.2	33.0	—	—
	<i>Sacch. oxidans</i> ‡	CBS 4079	0.8	0.1	16.8	33.7	—	—	3.3	45.3	—	—
	<i>Sacch. steineri</i> ‡	CSIR-Y31	0.8	0.4	8.8	47.3	0.1	0.4	5.4	36.2	—	—
	<i>Sacch. uvarum</i> ‡	ATCC 26602	0.5	0.1	9.4	42.4	0.1	2.5	4.8	42.2	—	—
	<i>Sacch. willianus</i> ‡	CSIR-Y42	0.9	0.5	8.0	44.1	0.1	—	3.6	42.6	—	—
	<i>Sacch. exiguus</i>	CBS 6750	2.5	0.4	13.6	42.7	0.4	0.2	11.5	28.2	—	—

* UN1 and UN2 were unidentified long-chain fatty acids with retention times of 13.4 and 14.2 min, respectively (retention time for C16:0 11.1 min).

† These names are regarded by Barnett *et al.* (1983) as synonyms of *Schw. occidentalis*.

‡ These names are regarded by Barnett *et al.* (1983) as synonyms of *Sacch. cerevisiae*.

Centraalbureau voor Schimmelcultures, Yeast Division, Delft, Holland (CBS); Professor J. P. van der Walt, Pretoria, South Africa (CSIR-Y); the American Type Culture Collection (ATCC); and the Northern Regional Research Laboratories, Peoria, USA (NRRL).

Procedures. Cultivation of strains, and extraction and analyses of fatty acids were done as described by Kock *et al.* (1985a).

RESULTS AND DISCUSSION

The yeast strains contained mainly saturated and unsaturated fatty acids with 14 to 18 carbon atoms (Table 1). The results were reproducible when individual strains were grown in triplicate under standard conditions. The strains all contained a relatively high proportion of palmitic (C16:0), palmitoleic (C16:1), stearic (C18:0) and oleic (C18:1) acid. They could be divided into three groups (Table 1), the first characterized by the presence of linolenic acid (C18:3), the second by the absence of linolenic acid and the third by the absence of both linoleic (C18:2) and linolenic acid.

Group 1. The strains of *Schwanniomyces* had similar fatty acid profiles, while *Saccharomyces kluyveri* contained a higher percentage of palmitoleic acid (C16:1) and a lower percentage of oleic acid (C18:1).

Group 2. The two *Saccharomyces* species in this group were characterized by a lower percentage of palmitic (C16:0) and oleic (C18:1) acid, while the palmitoleic acid (C16:1) content was much higher. *Saccharomyces dairensis* contained a lower percentage of oleic acid than *Saccharomyces unisporus*. The strains of *Lipomyces starkeyi* contained a lower mean percentage of linoleic acid (C18:2) than the *Lipomyces kononenkoae* strain. *Lipomyces tetrasporus* had the highest stearic acid (C18:0) content of all the strains examined.

Group 3. The fatty acid compositions of the *Saccharomyces* strains were similar, with the exception of *Saccharomyces oxidans*, which contained a higher percentage of palmitic acid (C16:0) and a lower percentage of palmitoleic acid (C16:1).

No distinction could be made between the different strains of *Schwanniomyces* on the basis of fatty acid content. These results, with the exception of *Schwanniomyces persoonii*, correspond with the similar proton magnetic resonance patterns of polysaccharides found for *Schwanniomyces* strains by Spencer & Gorin (1969). Price *et al.* (1978) also placed strains of *Schwanniomyces* in one species, namely *Schwanniomyces occidentalis*, on the basis of their similarity in G+C composition. The results obtained in our study provide further proof that *Schwanniomyces* strains should all be included in a single species, *Schwanniomyces occidentalis*.

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