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Selection of lactic yeast producing glucosylceramide from cheese whey

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1 Abstract

2 From 2,150 isolates from raw milk and milk products, yeast strains were surveyed to produce 3 glucosylceramide from cheese whey. Most of the 54 strains that had accumulated a detectable amount of glucosylceramide were identified as Kluyveromyces lactis var. lactis. The cells of K. 4 5 lactis var. lactis strain M-11 derived from domestic raw milk accumulated glucosylceramide 6 2.5-fold higher than K. lactis var. lactis NBRC 1267, the reference strain selected from the 7 culture collections. Strain M-16 of K. lactis var. lactis derived from the same origin was found to 8 synthesize a considerable amount of steryl glucoside in addition to glucosylceramide. Sequence 9 analysis of ribosomal DNA intergenic spacer 2 regions revealed that strains M-11 and M-16 10 were diverged from a type strain of K. lactis var. lactis in the same species. 11 Key words: Glucosylceramide; steryl glucoside; cheese whey; Kluyveromyces lactis var. lactis 12 13 14

1 1. Introduction

2 Dairy farms are located on large grasslands in the cool climate of Eastern and Northern 3 Hokkaido, the northernmost island of Japan. The annual production of raw milk in Hokkaido 4 amounts to 3.9 million tons, corresponding to 47% of the overall domestic production. A gradual 5 increase in the recent market for natural cheese requires 350,000 tons of raw milk in Japan, 6 predominantly from Hokkaido. During the production of natural cheese, the whey containing 7 5% lactose, 1.9% protein and fats, 0.9% salt and a small amount of vitamins emerges from 8 clotted milk as a by-product (Ghaly and Kamal, 2004). In Europe and North America, about half 9 of the whey is used as animal feed, as a food ingredient or for microbial fermentation and as the 10 material for ethanol fermentation (González-Siso, 1996). The remainder places high levels of 11 biological and chemical oxygen demands on sewage treatment plants even after the protein 12 concentrate has been separated by ultrafiltration (Ghaly and Kamal, 2004). These problems are 13 common to the cheese industry in Japan and demand further methods for the economic 14 utilization of whey.

15 Ceramides are the predominant lipid of lamellae in the stratum corneum responsible for the epidermal permeability barrier (Hamanaka et al., 2002) and paid attention in Japan as a material 16 17 for food supplements since oral intake has shown to improve skin symptoms and reduced 18 allergic responses (Miyanishi et al., 2005). Commercially available ceramide is extracted from 19 plant tissues including rice bran, wheat germ, konjac tuber and mushrooms, and is usually 20 glucosylated, being referred to as glucosylceramide or cerebroside. In 2005, domestic market for 21 ceramide preparation was 5.8 tons as a crude extract of <5% purities, which corresponded to 22 11.4 million U.S. dollars, and is increasing by 20% annually as application to usual food 23 materials has expanded. These situations have encouraged us to propose various alternative 24 sources of glucosylceramide from agricultural by-products to respond to growing demands with 25 low costs.

1 Among 31 samples of crop tissues and by-products from their processing, apple pulp was 2 shown to include the highest amount of glucosylceramide (Takakuwa et al., 2005b). Yeasts 3 synthesizing glucosylceramide are Saccharomyces kluyveri, Zygosaccharomyces cidri, Z. 4 fermentati, K. lactis, K. thermotolerans, K. waltii (Takakuwa et al., 2002), Debaryomyces 5 hansenii (Takakuwa et al., 2005a) and Candida lipolytica (Rupčić and Marić, 2004). Some 6 strains of S. kluyveri and K. thermotolerans can be used for the production of glucosylceramide 7 from beet molasses (Tamura et al., 2006; Tamura et al., 2005). However, these strains cannot 8 grow in cheese whey due to a defect in the function of lactose fermentation. In the present study, 9 yeast strains accumulating high amounts of glucosylceramide were surveyed in the isolates from 10 raw milk and milk products.

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12 **2. Methods**

13 2.1. Yeast strains and culture

Each portion of 21 samples from raw milk, yogurt and cheese was inoculated to 10% (w/v) skim 14 15 milk and incubated for two days. The culture broth was diluted and spread on potato dextrose 16 agar. After incubation for several days, 2,150 yeast-like colonies were isolated for subsequent 17 examinations. Other strains classified as Kluveromyces lactis var. lactis were obtained from 18 NBRC (NITE Biological Research Center, Chiba, Japan). Strain NBRC 1267 was shown to 19 accumulate higher amounts of glucosylceramide than the other strains, NBRC 0433, NBRC 0648, NBRC 1090^T and NBRC 1903 and was, thus, used as a reference. Yeast cells were 20 21 routinely grown in the medium composed of 2.0% lactose as whey powder, 1.0% corn steep liquor, 0.5% ammonium sulfate, 0.075% $\rm KH_2PO_4$ and 0.075% $\rm MgSO_4$ (pH 5.5). 22

23 2.2. Extraction, purification and analysis

24 Purified preparations (98%<) of glucosylceramide and steryl glucoside derived from soybean

25 were purchased from Matreya LLC (Pleasant Gap, PA). Glucosylceramide and steryl glucoside

1 were extracted and quantified according to a method described elsewhere (Takakuwa et al., 2 2005b). Briefly, alkali-stable lipids were extracted from 0.2 g of the lyophilized cells by the 3 extraction with chloroform-methanol and successive hydrolysis in KOH-methanol and dissolved 4 in 0.2 ml of chloroform:methanol (2:1, v/v). For the analysis of alkaline-stable lipids, 5 μ l of the 5 extract was subjected to thin layer chromatography (TLC) development by chloroform: methanl: 6 acetic acid: water (20:3.5:2.3:0.7, v/v). The orcinol-sulfuric acid reagent visualized the spots, 7 which were determined by comparing their densities to those of authentic standards with a Lane 8 & Spot Analyzer (Atto Co., Tokyo).

9 2.3. Analysis of the DNA sequence

The internal transcribed spacer (ITS) and intergenic spacer 2 (IGS2) of the rRNA genes were amplified by PCR as described elsewhere (Naumova et al., 2004; Oda et al., 1997). The DNA fragments were sequenced on both strands with an automated DNA sequencer (Applied Biosystems Model 310). A phylogenetic tree was constructed using the CLUSTAL W and TreeView programs (http://taxonomy.zoology.gla.ac.uk/rod/treeview.html). The nucleotide sequences for IGS2 have been assigned EMBL/GenBank/DDBJ accession numbers AB266620 to AB266630.

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18 **3. Results and discussion**

Among the 2,150 isolates tested, 480 strains grew on an agar medium composed of cheese whey as the sole carbon source. The original raw milk and milk products seemed to contain an appreciable number of yeasts depending on the monosaccharides produced from lactose by the action of other microorganisms. When each colony on the agar medium was subjected to TLC analysis, 54 strains showed clear spots derived from glucosylceramide. From the sequence analysis of ITS, these strains were classified into three groups. The species and number of strains were: *Kluyveromyces lactis* var. *lactis*, 41; *Debaryomyces hansenii*, 9 and *Candida*

1 intermedia, 4. D. hansenii is a salt-tolerant yeast and was shown to form glucosylceramide 2 (Takakuwa et al., 2005a). All of the 54 strains were individually cultured on 40 ml of a liquid 3 medium for comparison with the reference strain (Fig. 1). Four strains identified as K. lactis var. 4 lactis M-6, M-8, M-11 and M-16, isolated from domestic raw milk, accumulated relatively high amounts of glucosylceramide (>0.40 mg g^{-1}) and that of M-11 (0.71 mg g^{-1}) attained 2.5-fold 5 that of strain NBRC 1267 (0.28 mg g^{-1}). The biomass of this strain was not so high, but the yield 6 of glucosylceramide per culture medium by strain M-11 (0.10 mg ml⁻¹) was greater than that of 7 strain NBRC 1267 (0.06 mg ml⁻¹). 8

9 The results of the TLC analysis were interesting. Surprisingly, strain M-16 produced a 10 compound corresponding to steryl glucoside that is usually below the detection limit among 11 cells grown under normal conditions (Fig. 2). In the methanol-utilizing yeast Pichia pastoris, 12 stress, such as heat shock or a high concentration of ethanol, increased the content of steryl glucoside (Sakaki et al., 2001). A steryl glucosyltransferase gene from this yeast was also shown 13 14 to be involved in the vacuole-dependent selective degradation of peroxisomes (Oku et al., 2003). 15 These findings indicate that the synthesis of steryl glucoside is strictly regulated in response to 16 changes in the environment. The accumulation of steryl glucoside in the cells of strain M-16 17 may be explained by its derepressed synthesis, but the mechanism is still unknown.

For further taxonomical analysis of strains M-6, M-8, M-11 and M-16, the IGS2 sequences, which appear to be a powerful technique to differentiate between phylogenetically intimately related species (Sugita et al., 2002), were determined. Some divergences were observed in the four strains of *K. lactis* var. *lactis*, but included in differences of individual strains as judged from the position of *K. lactis* var. *drosophilarum* as the outgroup (Fig. 3).

Cheese whey and beet molasses usually emerge in agricultural region under the cool
climate in the world. Recent reports on utilization of cheese whey are concerned with lactose
removal (Aktas et al., 2006), single cell protein production (Schultz et al., 2006) and ethanol

1	fermentation (Kourkoutas et al., 2002) by K. marxianus but not with valuable products from the		
2	yeast cells. The present study indicates that glucosylceramide can be produced from cheese		
3	whey in addition to our previous finding for beet molasses (Tamura et al., 2006; Tamura et al.,		
4	2005). The two production methods will compensate each other and contribute stable supply of		
5	glucosylceramide for growing markets.		
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1 Figure legends

3	Fig. 1. Distribution of glucosylceramide contents in yeast strains isolated from raw milk and	
4	milk products. Fifty-four strains were identified as Kluyveromyces lactis var. lactis (shaded ba	
5	Debaryomyces hansenii (closed bar) and Candida intermedia (open bar) by the sequence	
6	analysis of ITS. An arrow indicates the level in the reference strain NBRC 1267.	
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9	Fig. 2. TLC analysis of alkali-stable lipids of the four strains isolated from domestic raw milk	
10	and the five NBRC strains of K. lactis var. lactis. Strain NBRC 1673, which cannot grow in a	
11	medium composed of cheese whey, was not included in this experiment. The lane at both ends	
12	represents the authentic standards of glucosylceramide and steryl glucoside at 5 μ g.	
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15	Fig. 3. Phylogenetic tree constructed by the neighbor-joining method from IGS2 sequences of <i>K</i> .	
16	lactis var. lactis strains. K. lactis var. drosophilarum NBRC 1012 was used as the outgroup. The	
17	bar indicates one estimated substation per 100 nucleotide positions. Bootstrap values were	
18	calculated from 1,000 trees.	



Fig. 1. Sugai et al.



Fig. 2. Sugai et al.

NE	BRC 1267·M-11	
-N	BRC 1903·M-6· M-8·M-16	
594		
NE	BRC 1090	
l		K. lactis var. drosophilarum NBRC 1012

0.01

Fig. 3. Sugai et al.