

europaean baker

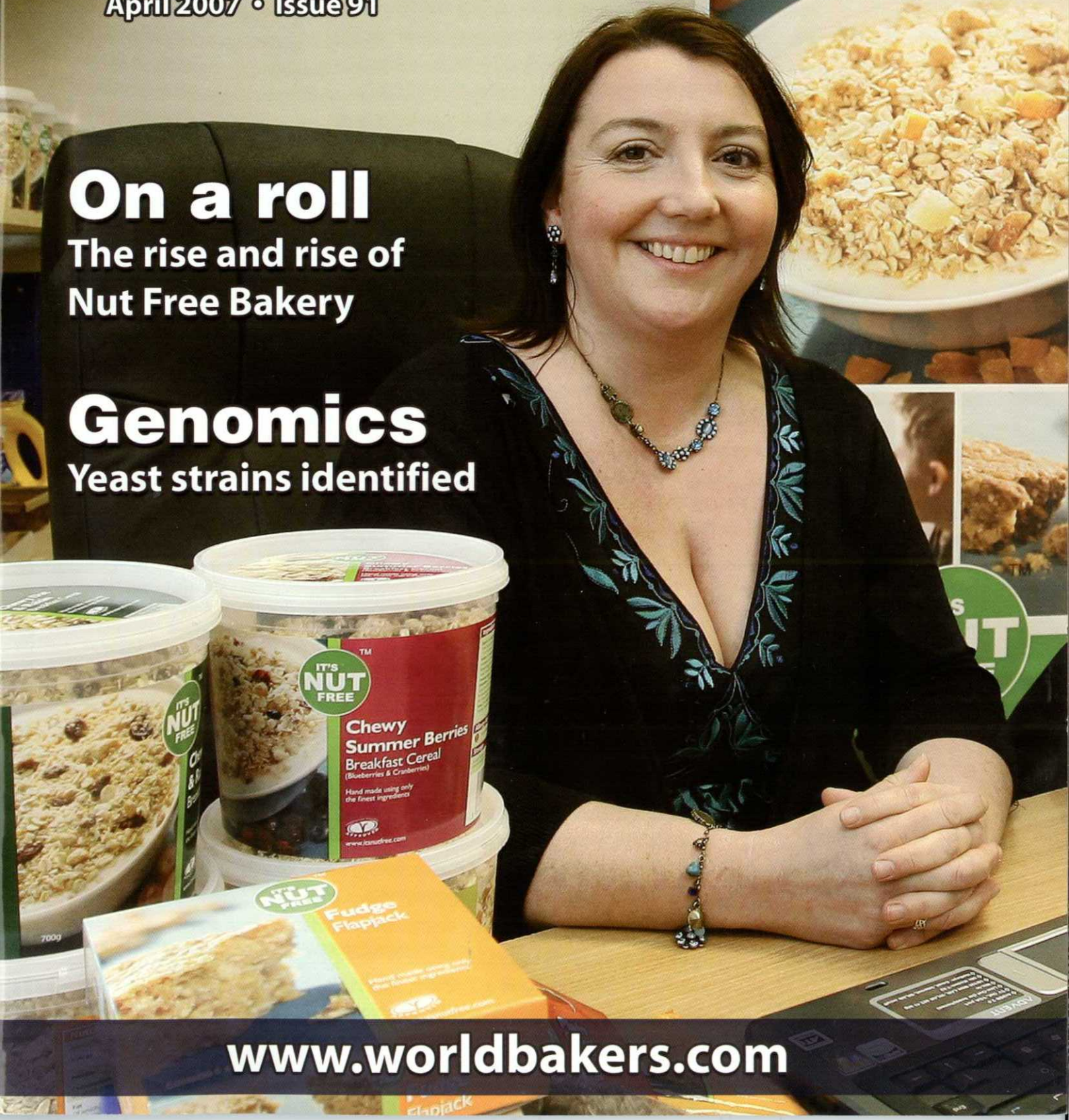
April 2007 • Issue 91

On a roll

The rise and rise of
Nut Free Bakery

Genomics

Yeast strains identified



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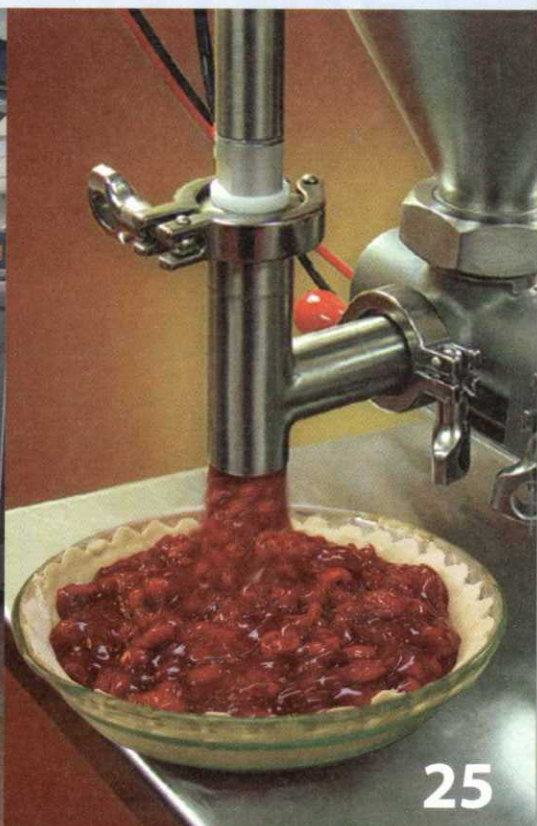
Contents



14



18



25

APRIL 2007

REGULARS

2 **Comment**

The editor's perspective on the issues affecting the European and global commercial and industrial baking market. This month, the allergen issue.

4 **News**

Sara Lee reduces its international management staff...Tate & Lyle's health and wellness centre... CSM announces strong sales growth in 2006... Royal Cosun acquires Atlanta Dethmers.

14 **National trends**

Austrian independents have a fight on their hands as supermarket in-store bakeries step up the pressure.

18 **The right mix**

Mixing technology has evolved dramatically over the last 10 years. Mixers have been developed to provide the continuous production capacity that many industrial bakers seek while maintaining quality at the lowest possible cost. Annie Launois reports.

25 **No depositor, no return**

Depositing systems are constantly under development as suppliers aim to meet the increasingly sophisticated demands of commercial bakeries. Accuracy, simplicity and ease of cleaning and maintenance are all must-haves, say the experts.

INDUSTRY FEATURES

30 **Yeast genomics**

Dr Ian Roberts, curator of the National Collection of Yeast Cultures, explains how a new genomic research project will enable the precise properties of yeasts to be identified in a more detailed way, leading to potential new product development in the future.

34 **New products**

New creme cake mix from BakeMark...Auto-Bake widens its Serpentine oven...Mono Equipment finds chocolate heaven... Thermo Fisher introduces new X-ray equipment... Bold Berliners from Cereform...Honeytop produces 24,000 naans per hour.

22 **Nuts about baking**

When Angela Russell discovered that her daughter had a serious nut allergy she turned her passion for home baking into an international bakery business. Matthew Moggridge found out that it wasn't all plain sailing.



The rising power of yeast genomics

Dr Ian Roberts, curator at the National Collection of Yeast Cultures (NCYC) explains how a new genomic research project will enable the precise properties of yeasts to be identified in a more detailed way, leading to potential new product development in the future.

Yeast and baking is an association which goes back at least 6,000 years. Over such an extraordinary expanse of time it is impossible to estimate how many different yeast strains have been used, improved, distributed and discarded to leave the pattern of variation we see in baking yeasts in use today.

However, precise details of at least one modern baking yeast strain are about to be revealed by a UK-based genome sequencing consortium.

It is now nearly a decade since the first yeast

genome sequence was completed. The yeast strain used in this pioneering project known as strain S288c was selected on scientific grounds and was derived from a laboratory strain lacking many of the genes found in industrial yeasts. The new consortium led by Richard Durbin (Sanger Institute, Cambridge) and Ed Louis (University of Nottingham) wanted to obtain a much greater representation of yeast diversity and set about sequencing a number of different isolates from around the world, including industrial strains wherever possible.



Examination of samples using the microscope is still an important part of sample analysis and is used in conjunction with molecular biology techniques.

Strains to be sequenced were selected by Gianni Liti (University of Nottingham) on the basis of geographical origin and spore viability as the ability to produce viable spores is an important technical requirement since single spore-derived genomes are simpler and easier to analyse.

Unfortunately, of the 30 or so baking strains tested only three gave an acceptable level of spore viability. Equally unfortunately, these all belonged to the osmo-sensitive grouping associated with the Western plain

dough baking method. No representatives of the osmo-resistant grouping used in sweet doughs and associated with the Eastern baking method, which implements the addition of sugar to the dough at the start of the baking process, were found to sporulate or produce viable spores.

Nevertheless, the strains selected represent an important first step in baking yeast genomics. In plain or lean dough, the ability of the yeast to rapidly ferment maltose from the breakdown of starch is of crucial industrial importance. These strains should, therefore, have been selected for enhanced maltose fermentation, either as a consequence of an increase in the number of maltose-utilisation (MAL) genes or changes in the regulation of these genes, thus providing an interesting focus for genome analysis. It is also of interest that the three strains that sporulate appear to be from geographically distinct regions. All three strains were kindly provided by Philip Bell (Macquarie University, Sydney) and are known as YS2, YS4 and YS9.

YS2 is described as "Australian bakers yeast" and is thought to represent the most common yeast strain used in low-sugar baking applications worldwide. YS2 has many industrial features that

"Specially selected industrial yeasts could potentially be exploited as a vehicle by the ingredients industry to naturally increase the content of desirable nutrients"



All cultures stored at the NCYC have their master stocks kept under liquid nitrogen as well as being freeze-dried.

distinguish it from S288c, but perhaps the most important of these features is that it probably contains at least twice as much genetic material. Such duplication of the genome is quite common in industrial yeast strains and is helpful in that it makes the yeast cells bigger and easier to harvest. It may also make them more vigorous and robust in an industrial process with improved gassing characteristics. YS2 also has very good spore viability. Subjecting YS2 to two rounds of sporulation should overcome the genome duplication effect and enable researchers to obtain a usable sequence for genome analysis and direct genomic comparison with S288c.

YS4 is listed as "Dutch bakers yeast" and shows clearly different properties to YS2. It can be used where moderate amounts of sugar are present in the dough. YS4 has been sold worldwide but it is thought that this strain was probably developed in France about 20 years ago.

The third strain, YS9, is known as "Singaporean bakers yeast", although whether it or its derivatives would still be found in use in Singapore is an open question. Nevertheless, the clear differences in the baking properties of the three strains and their geographical spread should ensure that informative comparisons can be made. Subtle differences with far-reaching effects on strain performance can be investigated with far greater precision than has hitherto been possible.

Genome sequencing of YS4 has already been completed to 1x coverage. New knowledge of genes and the way they operate in this yeast as compared to, for example, laboratory strains, brewing strains and environmental isolates is eagerly anticipated. Preliminary interpretation of strain inter-relationship, assessment of genome variation and stability, and analysis of key factors associated with baking is being performed by David Carter (Sanger Institute, Cambridge) in

collaboration with Steve James and Rob Davey (National Collection of Yeast Cultures, Norwich) together with other consortium members.

In future, YS2 and YS9 are likely to be added to the genome sequencing project and more detailed studies will become possible. For example, single nucleotide polymorphisms (SNPs), which are being used as disease markers in human genomics, will become available to help track important characteristics of baking yeasts and aid strain improvement programmes. Other outputs of the project are predicted to impact on our understanding of baking strain diversity.

In the longer term, the development of functional foods based on targeted selection of a wider range of yeasts with the potential to produce other nutritional benefits is another possibility. Specially selected industrial yeasts could potentially be exploited as a vehicle by the ingredients industry to naturally increase the content of desirable nutrients. Equally, they could be used to reduce constituents considered less desirable for particular consumer groups leading to health benefits for the population as a whole.

The actual yeast cultures used in the genome project and full information on the current status of the project can be obtained via the UK National Collection of Yeast Cultures (www.ncyc.co.uk). In addition to fully-authenticated yeast cultures, the NCYC offers a safe repository back-up for commercially valuable yeast strains and an important range of associated services for the baking industry. ■



Cultures are also plated out for full visual inspection for contaminants.

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