

SCIENTIFIC CORRESPONDENCE

Yeast budding forages through redundancy!

Among yeasts, *S. cerevisiae* grows by budding and soon after the division the mother and the daughter cells separate. Simplicity of the organism and its amenability to genetic methods have made yeasts the most popular and convenient eukaryotic model system to study biology. In the process, they turn out to be among the best explored organisms. However, surprises continue to come. The discovery of filamentary mode of growth in budding yeast by Gimeno *et al*¹ is one of such surprises and, perhaps, a promise that many more may be in stock. The discovery also provides a new look at the function of several genes from evolutionary and developmental viewpoint.

Budding in yeast is controlled by complex sets of genes². The pattern of budding, i.e. decision of sites of budding with respect to the preceding bud site is made with the help of BUD1, BUD2, BUD3, BUD4 and BUD5 genes. Next in the hierarchy are bud site assembly genes: CDC4, CDC42, CDC43, BEM1, BEM2, MSB1, MSB2, etc. These genes control functions, leading to cytoskeleton assembly, viz. organization of: a) neck filament involving CDC3, CDC10, CDC11 and CDC12 genes, b) actin filament using, among others, ABP gene, and c) microtubules using SPA2, etc. Of these, 'a' and 'b' facilitate bud growth by channelizing secretory pathway and organelle transport while 'c' positions nucleus spindle orientation.

Genes RSR1/BUD1, BUD2 and BUD5 convert the default 'random' pattern to a 'bipolar' pattern and the subsequent action of BUD3 and BUD4 converts the 'bipolar' pattern to an 'axial' pattern (Figure 1). The exact mechanism of bud site selection is not understood. However, the homology of

BUD1/RSR1 and CDC43 to the p^{21ras}, a family of GTP-binding proteins and that of BUD5 to CDC25 class of proteins that catalyse GDP-GTP exchange, suggests the involvement of RAS signal transduction pathway (Figure 2). Also, the interaction of BUD1 with CDC42 whose function is needed for isoprenylation of RAS strengthens this view. More convincing evidence came from studies wherein a RAS2 dominant gain-of-function mutation increased filamentous growth while a RSR1/BUD1 loss-of-function allele showed no filamentous growth. In short, BUD1/RSR1 may act as a switch which is activated by BUD5 when appropriate positioning of macromolecular assemblies is achieved, allowing the bud to emerge from selected site (Figure 2). For a better understanding in molecular terms the gaps in this pathway need to be filled.

The loss of a gene responsible for bud site selection, however, does not affect the propagation of the cells. Why, then, has this elaborate genetic mechanism evolved and continued to be maintained? Are these genes redundant? Now it is possible to answer this question. Upon starvation, yeast cells switch over from

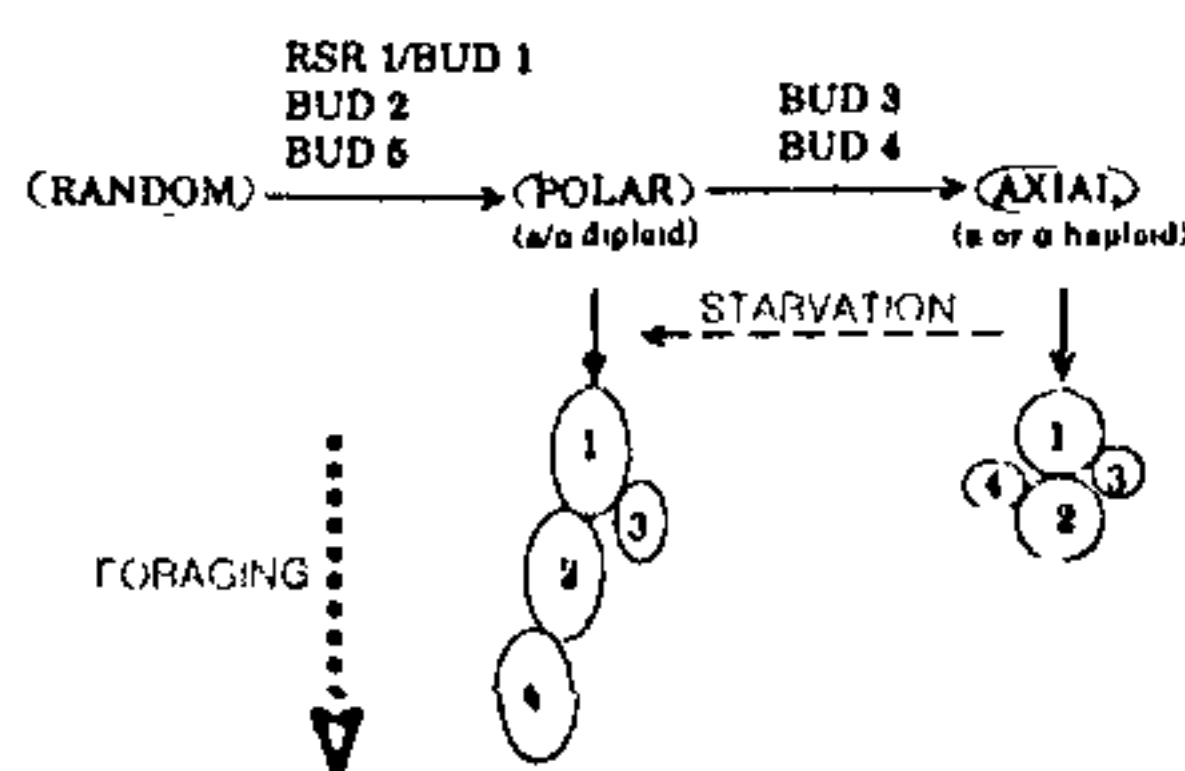


Figure 1. Bud site selection and resultant pattern. Starvation signal, leading to diploidy through sexual cycle enables a colony of cells to forage for a better niche

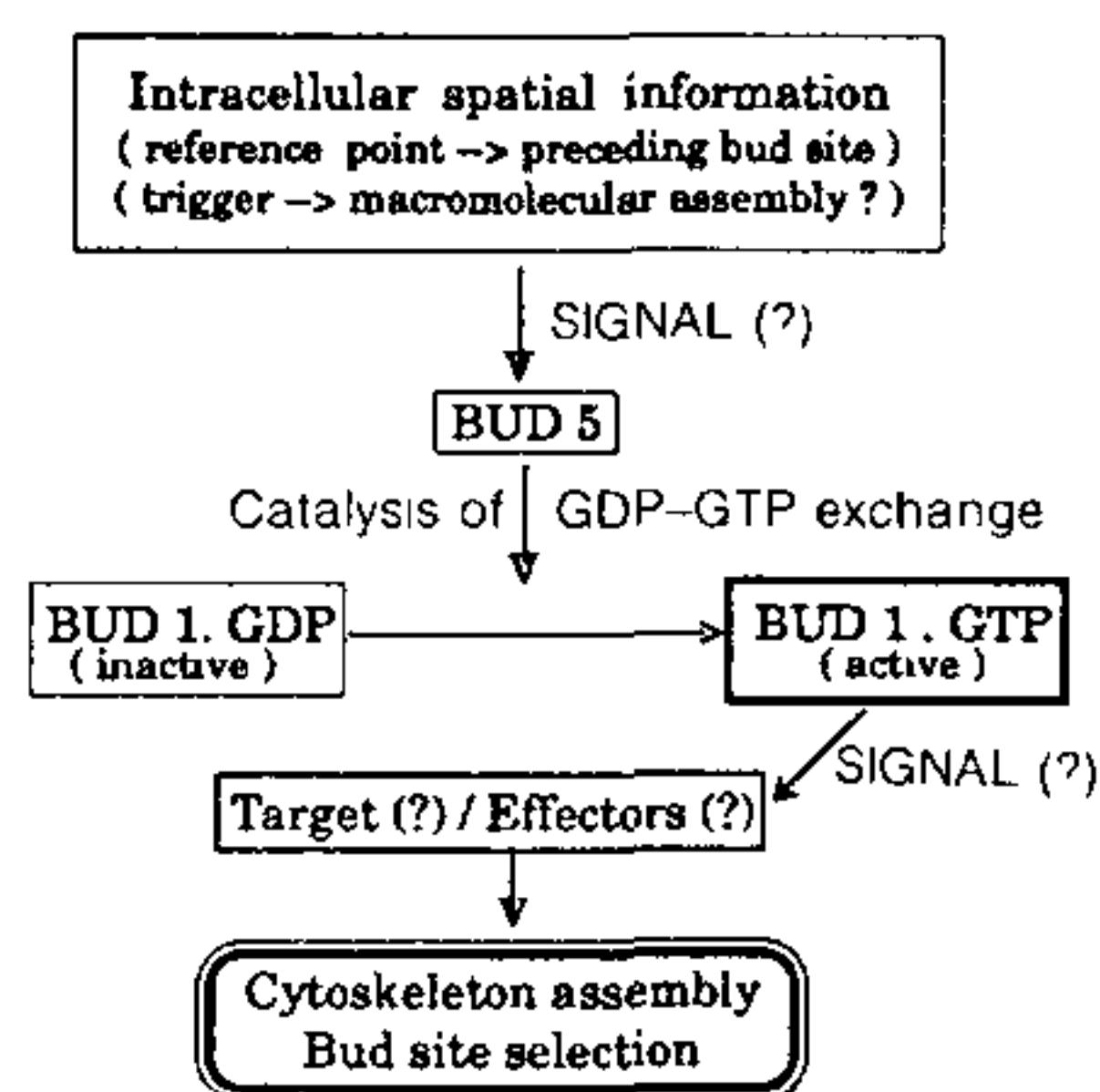


Figure 2. Signal transduction pathway of yeast bud site selection.

the vegetative to the sexual mode of reproduction. This is marked by mating of *a* and *α* haploid cells to give rise to *a/α* diploid cells. Such diploid cells have two fates. One is to form ascospore and wait for the suitable growth condition and the alternative one is to divide as diploid cells. This later division is characteristically different from the haploid cell division (Figure 1). Gimeno *et al.* show that diploid cells have unipolar budding pattern with strikingly elongated cell shape leading to the filamentous structure. Using such a budding strategy, the colony is able to forage for a better niche.

This observation converts an apparently redundant phenomenon into the one extremely important for the survival and better propagation under adverse conditions. This also warns us of the limitations of our criteria of 'survival' and 'essentiality' under laboratory conditions. After going through the process of natural selection, are there truly redundant genes or pathways maintained?

The real significance and evolutionary history of increasing number of functionally redundant genetic pathways are still matters of debate. This may remain so as evolution cannot be tested experimentally and the survival or essentiality in evolutionary terms cannot be determined. Such a redundancy or overlapping function may, however, be a necessary requirement for development and evolution of complex forms of life³.

A lot of repetitive DNA, likewise discarded as junk at one time, now appears to be of significance in the structure and function of chromatin. Repetitive DNA sequences are uniquely

distributed along the chromosomes and with the help of specific proteins that recognize such repetitive DNA stretches in association with non-histone chromosomal proteins provide means for global structuring of chromatin and gene regulation. Role of repetitive DNA has also been noticed in general fitness⁴. In order to explain trans-sensing effects⁵ the interaction of homologous regions of the genome at higher order chromatin organization is crucial and the need of non-coding repetitive sequences that help in such organization and spatial disposition of 'functional DNA' should, therefore, justify their evolution

and maintenance.

1. Gimeno, C. J., Ljungdahl, Styles, C. A and Fink, G. R., *Cell*, 1992, 68, 1077-1090.
2. Drabin, D. G., *Cell*, 1991, 65, 1093-1096.
3. Tautz, D., *BioEssays*, 1992, 14, 263-266.
4. Wu, C-L., True, J. R. and Johnson, N., *Nature*, 1989, 341, 248-251.
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NEWS

Brain storming sessions in the area of plant sciences

The Department of Science and Technology through its Science and Engineering Research Council (SERC) has been instrumental in promoting front-line areas of research in the country. The period 1975-80 was one of exploring mechanisms for supporting R&D projects to individual scientists to carry out specific time-bound research projects in the areas of their interests. During 1980-85, the need to initiate an innovative approach for promoting R&D activities through identification of 'thrust areas' was felt and Programme Advisory Committees (PACs) consisting of experts, in the different identified areas, were constituted.

In the late eighties, an in-depth exercise to review and update thrust areas was taken up through a series of national seminars. In the area of life sciences, such a seminar was organized at Lucknow during 6-8 December, 1988 and 'new challenging areas' that needed support were identified. The details of these were published in *Current Science* (1989, 58, 1275-1315), and in the DST document 'Challenging Areas in Life Sciences' (1990).

Each of the PACs in life sciences has been evolving action plans for considering new strategies and mechanisms for supporting the identified areas in the future. It was decided that the programme advisory committee on plant

sciences would organize brain storming sessions in order to review state-of-the-art in the identified area, to identify special areas of relevance to the country and to suggest appropriate mechanisms for developing and supporting the areas identified.

Experts in the identified areas were invited to review the state-of-the-art. Special areas of relevance to the country were identified based on the presentations by experts and through discussions with participants. Middle career and young scientists were invited to present pre-proposals which were discussed by the experts who helped in focusing and evolving meaningful projects.

The need for setting up of units/core groups around outstanding scientists, generate co-ordinated/network programmes, national facilities, organizing training programmes or summer/winter schools for human resource development was also discussed. The brain storming sessions were planned in great detail and well in advance so that a well-focused agenda was available and the sessions were more effective.

The list of brain storming sessions organized so far is given in Table 1.

The brain storming sessions were held in different parts of the country in order to enable interaction with a wider cross section of the scientific community.

One of the salient features of the brain storming sessions has been the publication of a series of technical reports highlighting the importance of the emerging areas and recommendations, indicating steps that need to be initiated in order to grow these identified areas. Three such technical reports have already been brought out in consultation with experts. These have been circulated to the scientific community as well as to various government agencies. A summary of the recommendations of the first three brain storming sessions is summarized below for general information. Summaries of the other brain storming sessions will follow after detailed reports are brought out.

Plants in relation to their environment

Plant ecology in its broadest sense has acquired global importance in view of the large-scale damage to natural ecosystems. Deforestation is one of the major causes of climatic and edaphic changes. Recurrent climatic aberrations like droughts, floods, etc. affect plant ecosystems, which subsequently influence animals and finally humans. Many of the issues have assumed global dimensions. There is significant reduction in the protective ozone layer and