

## Biodiversity

## Gut feeling for yeasts

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The startling news that has emerged from studies of the intestines of beetles is a reminder of how little is known about the diversity of even such comparatively well-characterized groups as the yeasts.

There is no doubt that many species of fungi have yet to be described, yeast species included. Many of them must lurk in habitats and hosts that have still to be investigated. But who would have thought to look in the guts of beetles? Suh and colleagues did so, as they report in *Mycological Research*<sup>1</sup>, and have found a hotspot of yeast diversity. About 1,000 yeast species are known worldwide, to which Suh *et al.* add at least 200 more, identified from a variety of beetles sampled in the southeastern United States and Panama. Many of the yeasts belong to such familiar genera as *Candida* and *Pichia*, some species of which are respectively human pathogens and agents used for the production of drugs.

Yeasts are among the best-studied groups of microbes, but this research provides a dramatic indication of how limited our knowledge is. Apart from their traditional importance in wine, bread and beer making, they are also used in many (agro)industrial and medicinal applications, and as workhorses in biological research. Suh and colleagues' studies on beetles show that efficient sampling of poorly explored habitats or geographical areas can yield an extraordinary extension to our knowledge of microbial biodiversity.

Since 1820, about 3,000 yeast species have been described (Fig. 1), many of which were later considered to be identical to previously described species, and consequently regarded as synonyms. Two recent monographs on yeasts accept only approximately 700 species<sup>2,3</sup>, but this figure has since risen closer to 1,000. Our present knowledge is heavily biased, however. The great majority of known species come from Western Europe, Japan and North America. Of the strains maintained in the collection of the Centraalbureau voor Schimmelcultures (CBS), which is the result of a century of work, 45% originated from clinical sources or from products such as wine, fermented foods, bread, fruit juices and dairy products, with 55% from natural substrates — plants, soil, fruits, animals and water<sup>4</sup>. Insect sources accounted for only 6% of the isolates in the CBS yeast collection. Clearly, this is only the tip of a very large iceberg: Suh *et al.*<sup>1</sup> consider that further sampling of beetles alone could result in the identification of another 350–500 yeast species.

In recent times, most researchers interested in yeast biodiversity have made effective

use of DNA-based taxonomic concepts<sup>5</sup>. Since the 1990s, a huge effort has been made with all accepted yeast species to sequence the specific regions of DNA that encode a cell component known as ribosomal RNA — these are standard sequences in systematics. The result is that comprehensive rDNA databases now exist for yeasts<sup>6,7</sup>. These molecular studies have produced an unparalleled increase in the number of yeast species described in the years 2000–05 (Fig. 1), even before we had news of the high biodiversity observed in beetle guts.

That news adds an extra dimension to our appreciation of yeast ecology. Suh *et al.* found that some clades of yeasts contain many insect-related species (a clade being a grouping consisting of an ancestor and all its descendants). Examples are the *Pichia guilliermondii*, *P. stipitis*, *Candida tanzawaensis* and *Stephanoascus–Arxula–Zygoascus* clades in the fungal phylum Ascomycota, and the *Trichosporon* clade within the phylum Basidiomycota. The *C. tanzawaensis* clade has expanded from a single strain of just one known species to 164 isolates representing

39 possible species. One wonders whether some of the insect-related species were described in the past, but traditional means of classification erroneously interpreted them as being identical to other known species. This may be true for some of the species in, for example, the *P. guilliermondii* clade, and it will be necessary to sequence the 'type' (reference) strains of all species considered to be synonyms.

Given the continuing development of molecular tools for the rapid identification of microbes, studies of yeast diversity in habitats and regions previously unexplored, or only scantily so, have become more feasible and will pay rich dividends. Large parts of Africa, Antarctica, Asia, Australia and Latin America are mainly virgin territory in this respect<sup>8</sup> — it could be that only 1% of yeast species have been described<sup>9</sup>. This endeavour will not just be for the education of biologists concentrating on biodiversity, but will also enhance our knowledge of ecological interactions — as, for instance, is the case in research<sup>10</sup> on xylose-fermenting yeasts in beetle guts, which may be involved in the breakdown of hemicellulose, a component of plants, and thus contribute to the decomposition of plant biomass. Moreover, some as-yet-undiscovered species are likely to be sources of useful compounds or as agents for biological control.

As far as the work of Suh *et al.*<sup>1</sup> is concerned, extra relevance stems from the fact that insects are also major vectors for the dispersal of yeasts, among them those involved

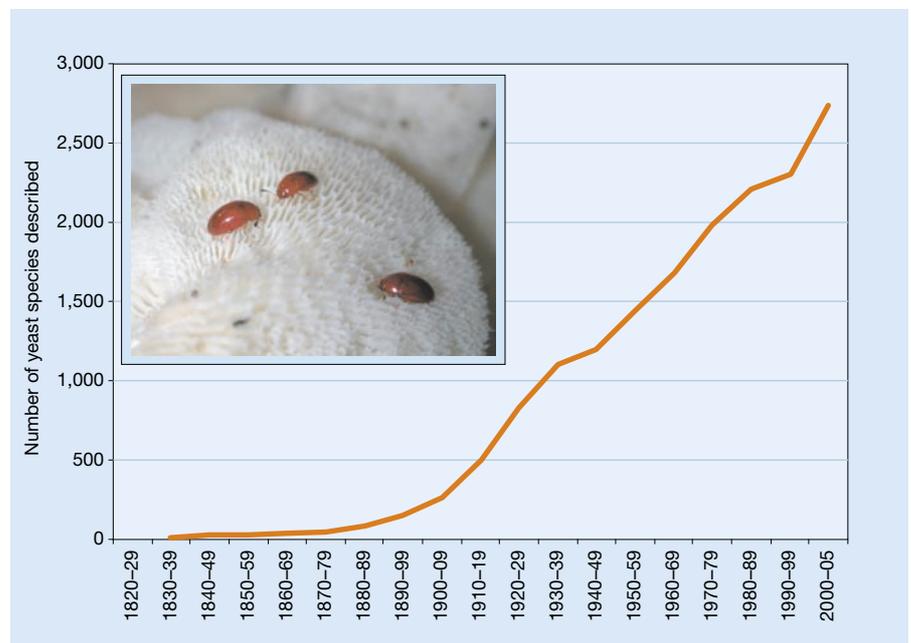


Figure 1 Yeast on the rise — the cumulative increase in yeast species described since 1820 (the total includes synonyms). Since 2000, application of DNA-based methods has produced a rapid increase in the yeast species recognized; the last time span covers only five years rather than ten, and includes the new identifications from the hyperdiverse guts of beetles. Blips in the increase in descriptions occurred during the Second World War and at the end of the twentieth century. Inset, beetles of the genus *Mycotretus*, family Erotylidae, one of the taxonomic groups of beetle sampled by Suh and colleagues<sup>1</sup>.

in fermentation and food spoilage. So a better understanding of yeast biodiversity in insects should help in controlling these processes. All in all, the new observations are a clear signpost to a highly promising route in the quest to identify hidden microbial biodiversity. ■

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