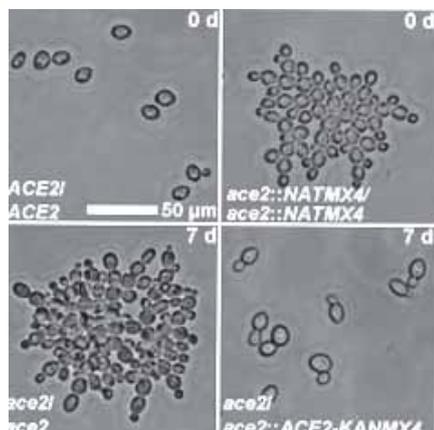


Mysteries of snowflake yeast may reveal clues to the evolution of multicellular life

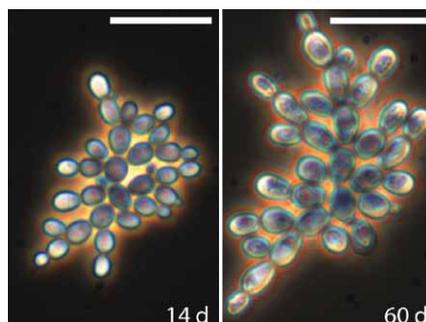


Saccharomyces cerevisiae (upper pair) normal unicellular morph (left) and snowflake (right), with and without transcription factor *ACE2*, respectively; and (lower pair) with the deletion snowflake is formed (left) and with it reinstated by complementation. Bar = 50 µm. Photo courtesy: William C. Ratcliff.

It is amazing how much can be gleaned from *Saccharomyces cerevisiae* about cellular processes and colony development. The yeast may present as a morph, not of separate single cells, but a multicellular agglomeration in which the mother and daughter cells fail to separate resulting in a cluster that has been nick-named “snowflake yeast”. The basis of this phenomenon has now been unraveled in a series of elegant genetic experiments by William Ratcliff of the Georgia Institute of Technology (Atlanta, GA) and colleagues (Ratcliff *et al.* 2015).

The group started with a diploid unicellular clone and selected for rapid settling through liquid media, within 60 daily transfers snowflake yeast evolved in ten out of ten populations, displacing the unicellular ancestors. The key to the change proved to be a single mutation disrupting transcription factor *ACE2* which is involved in the separation of mother and daughter cells after mitosis. This was established experimentally by constructing a diploid knock-out in the unicellular ancestor, and then complementing it with a single functional copy of the gene, on which multicellularity was regained. Conversely, when the functional gene was added to a snowflake colony, unicellularity returned and the snowflake morph was lost.

Another unexpected result was that the size of individual cells in the snowflakes



Comparison of the sizes of the snowflake cells at 14 d and 60 d in culture. Bars = 50 µm. Photo courtesy: William C. Ratcliff.

increased the longer they were grown, becoming 2.2-fold larger after 60 days of culture.

The authors modeled the process and found that the snowflake morphs developed through deterministic rules producing geometrically defined clusters. Further, multicellularity proved to be a heritable trait. The evolution of multicellularity is recognized as one of the major transitions in the development of more complex organisms, solitary ancestral cells becoming “collectives” and selection then starting to operate on the collectives rather than individuals. This might have been expected to be an extremely complex process, but this work shows that just a single gene can make all the difference and result in what are potentially major evolutionary events. *Saccharomyces cerevisiae* may not provide all the answers, but this trait demonstrates that at least the first steps on the route to organizational complexity do not necessarily involve the coordination of numerous genetic changes. Once more, this yeast has contributed to a better understanding of evolution in action pertinent to biology as a whole.

Ratcliff WC, Frankauer JD, Rogers DW, Greig D, Travisano M (2015) Origins of multicellular evolvability in snowflake yeast. *Nature Communications* 6: 6102. DOI:10.1038/ncomms7102.

Who else is having sex in American homes?

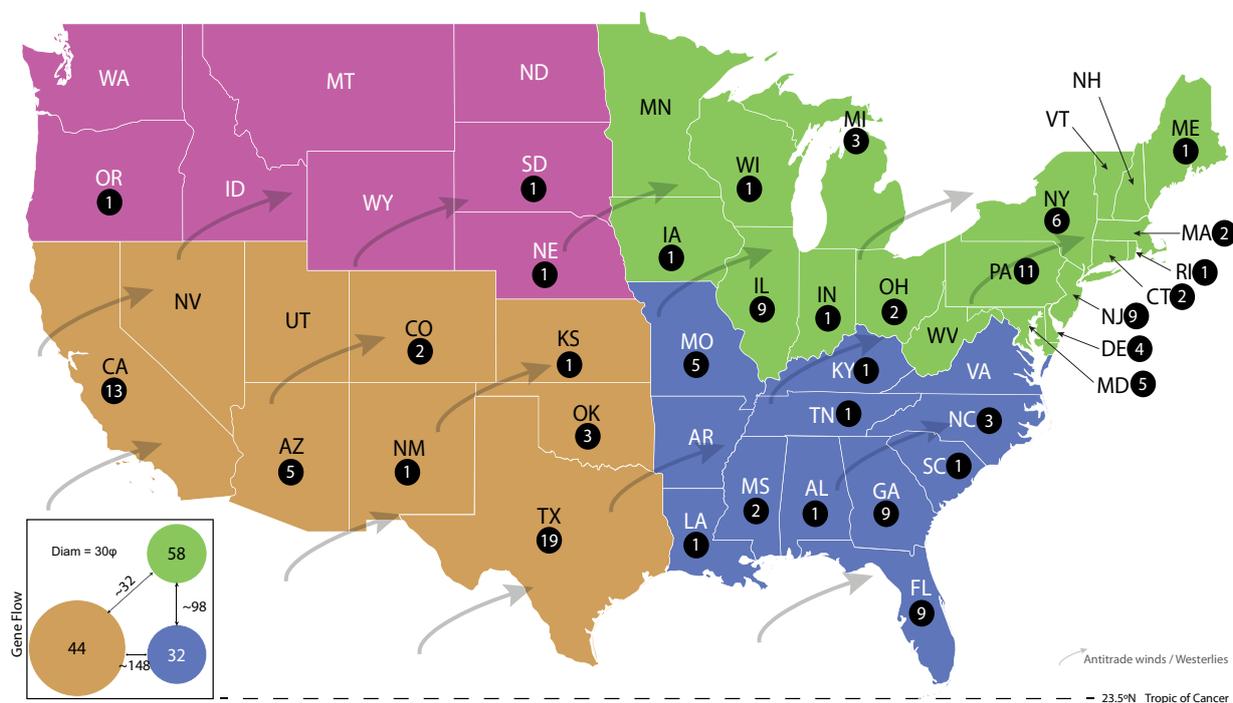
Alternaria species from section *Alternaria* are frequently associated with hypersensitivity pneumonitis, asthma and allergic fungal rhinitis and sinusitis. Since *Alternaria* is omnipresent in the outdoor environment, it is thought that the indoor spore concentration is mainly influenced by the outdoor spore concentration. Woudenberg *et al.* (2015) have investigated the molecular diversity of indoor *Alternaria* isolates in the USA, and tested for recombination. *Alternaria* isolates collected throughout the USA were identified using ITS, *gapdh* and *endoPG* gene sequencing. This was followed

by genotyping and population genetic inference of isolates belonging to *Alternaria* sect. *Alternaria* together with 37 reference isolates, using five microsatellite markers. Phylogenetic analyses revealed that species of *Alternaria* sect. *Alternaria* represented 98 % (153 isolates) of the indoor isolates collected throughout the USA, of which 137 isolates could be assigned to *A. alternata*. Population assignment analyses of these 137 *A. alternata* isolates suggested that subpopulations did not exist within the sample. The isolates were therefore divided into four artificial subpopulations

to represent four quadrants of the USA. Forty-four isolates representing the south-western quadrant displayed the highest level of uniqueness based on private alleles, while the highest level of gene flow was detected between the south-eastern and south-western quadrants. Genotypic diversity was high for all quadrants, and a test for linkage disequilibrium suggested that *A. alternata* has a cryptic sexual cycle. Woudenberg *et al.* hypothesize that this high genotypic diversity derives from Mexico/Central America, where many agricultural crops have evolved. From here

the fungi moved through the USA *via* the antitrade winds. This is the first report of such an observation in indoor samples of this fungus from homes in the USA.

Woudenberg JHC, van der Merwe NA, Jurjević Ž, Groenewald JZ, Crous PW (2015) Diversity and movement of indoor *Alternaria alternata* across the mainland USA. *Fungal Genetics and Biology* 81: 62–72.



Map of the mainland USA (Mercator projection) indicating the four artificially defined quadrants using different colours, and the general north-easterly direction of the antitrade winds over the subcontinent (grey arrows). Numbers in black solid circles are the numbers of isolates from each state. The boxed insert depicts gene flow estimations between the south-west, south-east and north-east quadrants. Diameters of the circles are proportionate to the level of uniqueness (ϕ) of each of the subpopulations. The north-west quadrant was excluded from these analyses due to lack of a sufficient number of isolates. Reproduced from Woudenberg *et al.* (2015).