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Scientists trace yeast's gene shuffle

By Branwen Morgan

The humble baker's yeast has had its history of evolution uncovered by Irish researchers.

Dr Jonathan Gordon and colleagues at Trinity College Dublin in Ireland have traced the ancestry of 13 related yeast species by studying the middle and ends (telomeres) of their chromosomes.

Their findings, published in the online journal PLoS Genetics, show five of the yeasts had evolved from a family member that doubled its number of chromosomes from 8 to 16 approximately 150 million years ago.

Subsequent generations have either retained or offloaded this additional genetic material in a manner which has relevance for cancer development.

"The ancestral reconstruction has allowed us to trace the genomic rearrangements that gave rise to the genome structures of extant species," the authors write.

Gordon says they identified nine rearrangements in the yeast species for which whole genome sequences were available.

Rising to the occasion

Since the whole genome duplication (WGD) event that increased the number of yeast chromosomes to 16, subsequent rearrangements have all lead to a decrease in chromosome number.

Today's post-WGD species contain between 10 and 16 chromosomes.

Gordon says they found the decrease in chromosome number was due to the loss of centromeres, specialised structures essential for accurate replication.

"In eight of the nine cases, chromosome loss was due to the telomere-to-telomere fusion of two chromosomes and the removal of one of the centromeres," explains Gordon.

One exception to this mechanism was the breakage of a chromosome and the subsequent fusion of the two broken edges to two different chromosome ends. These events lead to a change in the order of the organism's genes.

Yeasts are simple organisms that are often used for studies of cell replication and division because they yield insights into how these processes go awry in cancer.



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Evolution and cancer

"In cancer, you can lose a whole chromosome or parts of a chromosome," explains Associate Professor David Thomas of the Peter MacCallum Cancer Centre in Melbourne. "In some circumstances you can actually end up with a shuffling of bits of chromosomes around creating a new chromosome."

"These accessory or neo [new] chromosomes are clearly important in the development of some types of cancer. So the question arises ... how do they form? This is where this paper comes in because it talks about the role of structures that are absolutely required for chromosome transmission."

Changes in chromosome number also have an important place in the evolution of plants and animals.

"This paper tells us that the mechanism of shuffling DNA around doesn't just occur in an aberrant way in cancer cells, but it may actually be a way in which genomes evolve in an evolutionary sense," says Thomas.

Gordon says a notable example is the fusion of two great ape chromosomes, which led to us having a chromosome count of 23 pairs compared with 24 pairs in great apes.

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