Saccharomyces cerevisiae

SGD (*Saccharomyces* Genome Database)
http://genome-www.stanford.edu/Saccharomyces/

Saccharomyces cerevisiae – Overview

Genes (loci)

Gene symbols comprise three italic lowercase letters, and an Arabic number (full gene names are not controlled by the nomenclature system).
Symbols are styled according to the phenotype of the identifying mutation or for the function of the wild-type gene (see 'Genes' and 'Alleles' for more details): lowercase italic for recessive, uppercase italic for dominant.

Alleles

Allele designations consist of the gene symbol, a hyphen and an italic Arabic number.

Proteins

Proteins are referred to by the relevant gene symbol, non-italic, initial letter uppercase and with the suffix 'p' (to avoid confusion with the phenotype, see below). If unambiguous, the suffix can be omitted e.g. 'the Ade5 protein'.

Phenotypes

Phenotypes are designated by a non-italic three-letter abbreviation corresponding to the gene symbol, initial letter uppercase.
Wild-type or **mutant status** is indicated by a superscript plus or minus sign, respectively, e.g. a strain requiring arginine.

Examples

eg *ade5 cdc28 CUP1 SPC105*

eg *act1-606 his2-1*

eg Ade5p Cdc28p Cup1p Spc105p

eg Arg^- (cf. wild type Arg^+)

Saccharomyces cerevisiae – Details

Genes

As mentioned above, for genes defined by mutation, upper- and lowercase designations are used for **dominant** and **recessive** alleles, respectively. However, because a given allele can be dominant in one cross and recessive in another, this can lead to some difficulty. On the genetic and physical maps, the convention is to use the mapped allele to decide which form of the name is used.
Genes with related properties are usually given the same three-letter name and different numbers, e.g. there are multiple genes that have functions in mating-type switching.
Open reading frame (ORF) designations are not gene names but 'location holders' on the genetic map until a gene name is assigned. ORF names are always three non-italic uppercase letters, a number and a letter: Y (for yeast unknown sequence); A, B to P (for chromosome I, II through XVI); R or L (for right or left arm); a number corresponding to the order of the ORF (counting from the centromere), and W or C to designate Watson or Crick strand (the Watson strand is 5′→3′ left telomere to right telomere), e.g. the 25th ORF on the left arm of chromosome XI.
Mitochondrial mutations should, in general, be designated following the rules outlined above, but well-known symbols, such as ρ^+, ρ^-, ψ^+ and ψ^-, have been retained. Detailed designations have been published for **mitochondrial mutants**[1] and **killer strains**[2].

Alleles

Alleles created by recombinant DNA technology should be named by use of the symbol for the gene that is altered, followed by a symbol to indicate the nature of the alteration: **disruption** (::); **deletion** (-Δ); **replacement** (Δ::).
e.g. (a) **Disruption** of the *ade6* gene by integration by the functional *URA4* gene. (b) **Deletion** number 1 of the *ade6* gene. (c) **Replacement** of *ade6* by the *URA4* gene.
Dominant and **recessive suppressors** are designated by three upper- or lowercase letters, respectively, and a locus number.
Frameshift suppressors are normally designated in upper- or lowercase.
Metabolic suppressors can be designated in various ways, e.g. (a) a suppressor of *snf1*; (b) a suppressor of *rna1-1*; (c) a suppressor of *his2-1.*
Ochre and **amber suppressors** are sometimes distinguished by a bold-face suffix **-o** or **-a**.
Intragenic mutations that inactivate suppressor function are designated by the same rules as other mutant alleles.

Examples

eg (a) *ade6::URA4* (b) *ade6-Δ1* (c) *ade6Δ::URA4*

eg *SUP4 SUF1 sup35 suf11*

eg *SUF1* or *suf1*

eg (a) *ssn1* (b) *srn1* (c) *suh1*

eg *SUP4-o SUP4-a*

eg *sup4-o-1*

Saccharomyces cerevisiae – Details

Mating-type loci. Special rules apply: (a) **wild-type alleles** of the mating-type (*MAT*) locus; (b) **the two complementation groups** of the *MAT*α locus; (c) **mutations of the *MAT* genes** are lowercase italic; (d) **the two wild-type homothallic alleles** at the *HMR* and *HML* loci; (e) **mutations at the *HMR* and *HML*** loci.
Alleles resulting from transposon insertion are designated by the same rules as alleles created by recombination technology; the name of the transposon does not normally form part of the allele designation.

GENOTYPES

The mating-type loci are typically listed first. If the cell is **haploid**, just one copy of each gene is listed.
If the cell is **diploid** then two copies of each gene are listed, separated by a slash.
Nonmendelian genotypes (e.g. those conferred by **plasmids** and **mitochondrial** DNA elements) can be distinguished by square brackets[2].

CHROMOSOMES

The 16 chromosomes are designated by Roman numerals.
(a) Chromosome arms are designated left (L, short arm) and right (R, long arm); (b) *CEN*, centromeres (no specific rule for telomeres).

MOBILE ELEMENTS

A new genetic nomenclature[3] for *S. cerevisiae* transposons, called **Ty elements** (originally designated Ty1, Ty2, Ty3 and Ty4), has been created. The initial letter of the designation is Y, followed by the single letter for the chromosome containing the Ty element, L or R to denote which chromosome arm, C or W for the strand (as in ORF designations, see above), Ty1 or Ty2, etc., a hyphen and a number to make it unique. e.g. (a) The first Ty1 on chromosome V, right of the centromere, in the Crick strand; and (b) the first Ty5 on chromosome III, left of the centromere, in the Watson strand.
The LTR sequences of Ty1 and -2, Ty3 and Ty4 are designated δ, σ and τ, respectively.

Examples

eg (a) *MATa* and *MATα* (b) *MATα1* and *MATα2* (c) *mata-1* and *matα1-1* (d) *HMRa* *HMRα* *HMLa* *HMLα* (e) *hmra-1* *hmlα-1*

eg *ura3::Ty2*

eg *MATα act1-1 URA3 ADE2*

eg *MATα/MATa act1-1/ACT1 ura3Δ/URA3 ADE2/ADE2*

eg *[KIL-0] MATα trp1-1*

eg I to XVI

eg (a) L and R (b) *CEN1* to *CEN16*

eg (a) YERCTy1-1 (b)YCLWTy5-1

Saccharomyces cerevisiae – Resources

NOMENCLATURE INFORMATION

The nomenclature rules for *S. cerevisiae* were compiled by the Committee for Genetic Nomenclature, chaired by Robert Mortimer. Queries about *S. cerevisiae* nomenclature should be addressed to: the SGD curators (yeast-curator@genome.stanford.edu).

WEBSITES

The *Saccharomyces* Genome Database (SGD) contains genetic maps, physical maps, DNA sequence data, functional analysis results, and a large collection of biological information gathered from the literature and the community. SGD also serves as the S. *cerevisiae* community's repository for genetic nomenclature and maintains the **Gene Name Registry**. The genomic sequence and tables of useful information can also be obtained from the SGD FTP site. **The MIPS Yeast Genome Project** contains yeast genomic sequence and protein infromation. This site also includes database search features, a catalogue of protein functions and a growing number of reviews written for the MIPS website. Other topic areas of the MIPS site include transcription, lists of intron-containing genes, centromeres, and tables and graphics describing a large variety of results determined at MIPS. **The Yeast Protein Database (YPD™)** provides a web database on the literature and characteristics of yeast proteins.

GENOME PROJECT

The complete genomic sequence was released in April 1996 (Ref. 4). See also Dujon[5]. Minor updates to the sequence can be obtained from the GenBank/EMBL/DDBJ sequence databases or from the SGD and MIPS yeast databases.

STOCK CENTRE

ATCC (American Type Culture Collection) contact: help@atcc.org (The YGSC has closed and all of its stocks will be available from the ATCC in the very near future.)

CONTRIBUTOR

J. Michael Cherry (cherry@genome.stanford.edu) Department of Genetics, School of Medicine, Stanford University, USA.

References and URLs

1 Grivell, L. (1993) Mitochondrial DNA in the yeast *Saccharomyces cerevisiae* in *Genetic Maps*, 6th edn (O'Brien, S.J., ed.) pp. 3.57–3.65, Cold Spring Harbor Laboratory Press
2 Wickner, R.B. (1991) Yeast RNA virology: the killer systems in *Molecular and Cellular Biology of the Yeast Saccharomyces* (Vol. 1), (Broach, J.R., Pringle, J.R. and Jones, E.W., eds), pp. 263–296, Cold Spring Harbor Laboratory Press
3 Kim, J.M. *et al.* (1998) Transposable elements and genome organization: a comprehensive survey of retrotransposons revealed by the complete *Saccharomyces cerevisiae* genome sequence *Genome Res.* 8, 464–478
4 The yeast genome directory, *Nature* 387, issue 66325S
5 Dujon, B. (1996) The yeast genome project: what did we learn? *Trends Genet.* 12, 263–270

SGD
http://genome-www.stanford.edu/Saccharomyces/

SGD ftp site
ftp://genome-ftp.stanford.edu/yeast/

MIPS
http://speedy.mips.biochem.mpg.de/mips/yeast/index.html

YPD
http://www.proteome.com/YPDhome.html