

Review

Gene database for the fission yeast *Schizosaccharomyces pombe*

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Summary. As an aid to the fission yeast genome project, we describe a database for *Schizosaccharomyces pombe* consisting of both genetic and physical information. As presented, it is therefore both an updated gene list of all the nuclear genes of the fission yeast, and provides an estimate of the physical distance between two mapped genes. Additionally, a field indicates whether the sequence of the gene is available. Currently, sequence information is available for 135 of the 501 known genes.

Key words: *Schizosaccharomyces pombe* – Gene list – Gene database – Fission yeast genome project

Introduction

With the advent of a fission yeast genome project {209}, it has become imperative to both collate and update what is known about the genes of this organism. Starting from the 1987 gene list published by Jürg Kohli along with the rules of *S. pombe* genetic nomenclature {145}, we have begun to collect such information in a database format. We have decided to focus only on the genes found on the three nuclear chromosomes of *S. pombe*, as these will be the focus of the genome project.

Methods

The database is run on a Macintosh using the Microsoft File application, and consists of six fields: gene symbol, location, description, sequence, synonyms, and literature references. These are briefly summarized as follows.

Gene symbols are generally as agreed upon by the *S. pombe* research community, and are designated by three lower case letters. Immediately following the three letters is a number indicating the exact locus being described.

The location of the gene is then indicated where known. If there is no information as to the location, the field is left blank. If the locus has been mapped to a chromosome, but not finer, the field

indicates either 1000, 2000, or 3000, to indicate chromosomes 1, 2, and 3, respectively. If the gene has been mapped relative to other mapped loci, then an estimate of the distance between the "upper" (or, left) chromosome telomere (as shown in Fig. 2, {216}) and the locus has been derived. These estimates are based on a combination of physical and recombinational distances, along with the assumption that physical distance is proportional to recombinational distance, and therefore should be used primarily to indicate ordering. This method of numerical encoding allows one to sort the database entries in order along the chromosome (and a printout with the entries in this order is available by request).

The locus description consists of information about either the gene product, or, the phenotypes exhibited by mutant alleles of this locus, or, characteristics of non-expressed DNA (such as origins of replication, centromeres, etc.). This field may also indicate when a gene has been physically localized to a *NotI* fragment of the yeast genome, but has not been genetically mapped relative to other loci.

The sequence field indicates whether DNA of the locus has been sequenced. Sequence data can usually be found in the GenEMBL sequence database; if not present there, check in the references listed.

The synonyms category indicates other names by which the locus may be known. Classically, loci have been identified as allelic to one another; more recently, genes have also been sequenced independently by two or more groups and have been given different names. Both categories have been combined in this database.

The reference field indicates some of the key references related to a given locus. It is not meant to be exhaustive, but merely to point the way to a key reference (one with sequence if possible).

Results and discussion

Of 501 unique loci identified to date, sequence information is available from 135. One interesting way to illus-

Table 1. Summary of *S. pombe* genes mapped or sequenced

	Mapped	
	No	Yes
Sequenced	No	173
	Yes	193
	No	82
	Yes	53

Table 2. *S. pombe* gene list

Gene	Loc.	Gene Description (Product or Phenotype)	Sequence	Synonyms	References
<i>act1</i>		Actin	y		{132}
<i>ade01</i>	2.2705	GAR synthetase (EC.6.3.1.3), allelic with <i>min4</i>	y	<i>min4</i>	{2,43,119}
<i>ade02</i>	1.4787	SAmP synthetase (EC.6.3.4.4), allelic with <i>min10</i>		<i>min10</i>	{85,50}
<i>ade03</i>	1.0973	FGAR amidotransferase (EC.6.3.5.3) allelic with <i>min11</i>		<i>min11</i>	{2,50}
<i>ade04</i>	1.5576	PRPP amidotr. (EC.2.4.2.12) allelic with <i>aza1, min13</i>		<i>aza1,min13</i>	{85,50}
<i>ade05</i>	3.3024	GAR formyltransferase (EC.2.1.2.2)			{85,50}
<i>ade06</i>	3.1566	AIR carboxylase (EC.4.1.4.21), allelic with <i>min1</i>	y	<i>min1</i>	{85,50,115}
<i>ade07</i>	2.0359	SAICAR synthetase (EC.6.3.2.6)			{85,50}
<i>ade08</i>	2.3905	Adenylosuccinate lyase(EC.4.3.2.2)			{85,50}
<i>ade09</i>	2.0000	Formyl THFA synthetase(EC.6.3.4.3), allelic with <i>min6</i>		<i>min6</i>	{85,43}
<i>ade10</i>	3.1323	ade10A:AICAR formyltransferase allelic with <i>min14, ade10B:IMP</i>		<i>min14</i>	{50,72}
<i>adh1</i>		Alcohol dehydrogenase	y		{150}
<i>ala1</i>		Lack of allantoicase			{41}
<i>all1</i>		Lack of allantoicase			{41}
<i>all2</i>		Hypoxanthine non utilisation			{17}
<i>ani1</i>		Anisomycine resistance			{154}
<i>ani2</i>		Anisomycine resistance, allelic with <i>cyh4, tri3</i>		<i>cyh4,tri3</i>	{154}
<i>arg01</i>	3.2147	Acetyl glutamyl aminotransferase (AGTase)			{42}
<i>arg02</i>	2.0000	Arginine requirement			{43}
<i>arg03</i>	1.1788	Ornithine carbamoyltransferase (OTCase)			{42}
<i>arg04</i>	2.4181	Carbamoylphosphate synthetase (CPSase A)			{42}
<i>arg05</i>	2.4154	Carbamoylphosphate synthetase (CPSase A)			{42}
<i>arg06</i>	2.0442	Arginine requirement			{43}
<i>arg07</i>		Arginine requirement			{43}
<i>arg08</i>		Arginine requirement			{43}
<i>arg09</i>		Arginine requirement			{43}
<i>arg10</i>		Arginine requirement			{43}
<i>arg11</i>	1.0000	Acetylglutamylphosphate reductase			{42}
<i>aro1</i>		DAHPh synthetase(try inhibited) (EC4.1.2.15)			{157}
<i>aro2</i>		DAHPh synthetase(phe inhibited) (EC4.1.2.15)			{157}
<i>aro3</i>	1.4826	Aromatic amino acid requirement, complex locus			{45,3,174}
<i>aro4</i>	3.2565	Aromatic amino acid requirement			{44}
<i>aro5</i>	1.3577	Aromatic amino acid requirement			{44}
<i>aro6</i>		Aromatic amino acid requirement			{44}
<i>aro7</i>		Aromatic amino acid requirement			{44}
<i>aro8</i>		Aromatic amino acid requirement			{44}
<i>ars01</i>		High frequency of transformation sequence, pFL20	y		{161,82}
<i>ars02</i>		High frequency of transformation sequence pFL20, pARS 727	y		{16,82}
<i>ars03</i>		High frequency of transformation sequence pARS 744	y		{16,82}
<i>ars04</i>		High frequency of transformation sequence pARS 745	y		{16,82}
<i>ars05</i>		High frequency of transformation sequence pARS 747	y		{16,82}
<i>ars06</i>		High frequency of transformation sequence pARS 756	y		{16,82}
<i>ars07</i>		High frequency of transformation sequence pARS 766	y		{16,82}
<i>ars08</i>		High frequency of transformation sequence pARS 767	y		{16,82}
<i>ars09</i>		High frequency of transformation sequence pARS 772	y		{16,82}
<i>ars10</i>	1.0000	High frequency of transformation sequence, next to <i>ura 1</i>			{16,82}
<i>ars17</i>	1.0000	High frequency of transformation sequence, next to <i>cdc 17</i>	y		{149}
<i>atb2</i>	2.0000	on 88kb Not I fragment "P"			{210}
<i>atp1</i>	1.0000	Mitochondrial ATPase, alpha subunit			{4,5}
<i>atp2</i>	1.0000	Mitochondrial ATPase, beta subunit	y		{4,5,214}
<i>aza1</i>	1.5576	Azaguanine resistance, allelic with <i>ade4</i>		<i>ade4,min13</i>	{85}
<i>aza2</i>	3.0000	Azaguanine resistance			{43}
<i>aza4</i>	2.1035	Azaguanine resistance			{43}
<i>ben1</i>	2.4278	Thiabendazole resistance, allelic with <i>nda3</i>		<i>nda3</i>	{155}
<i>ben2</i>	2.0000	Thiabendazole resistance			{155}
<i>ben3</i>	2.0000	Thiabendazole resistance			{155}
<i>ben4</i>	1.0000	Benomyl resistance			{48}
<i>bws1</i>		Bypass of <i>wee</i> suppression; type 1 protein phosphatase	y	<i>dis2,pp1</i>	{146}
<i>byr1</i>		Bypass of <i>ras</i>	y		{117}
<i>cam1</i>		Calmodulin	y	<i>cal1</i>	{123}
<i>can1</i>	2.1311	Canavanine resistance, arginine permease			{43,49}
<i>can2</i>	2.0000	Canavanine resistance			{43,49}
<i>cat1</i>		Catabolite repression, loss of glycolytic enzymes			{32}
<i>cdc01</i>	1.4260	Cell division cycle	y		{50}
<i>cdc02</i>	2.0745	Cell division cycle	y		{50,8}
<i>cdc03</i>	1.2249	Cell division cycle			{50}
<i>cdc04</i>	1.5602	Cell division cycle			{50}
<i>cdc05</i>		Cell division cycle.			{80}

Table 2. (continued)

Gene	Loc.	Gene Description (Product or Phenotype)	Sequence	Synonyms	References
<i>cdc06</i>	2.0000	Cell division cycle.			{43}
<i>cdc07</i>	2.0000	Cell division cycle.			{43}
<i>cdc08</i>	1.4497	Cell division cycle			{50}
<i>cdc09</i>	3.4970	Cell division cycle, allelic with <i>wee1</i> .		<i>wee1</i>	{81}
<i>cdc10</i>	2.2167	Cell division cycle; start gene	y		{50,11}
<i>cdc11</i>	3.2754	Cell division cycle			{50}
<i>cdc12</i>	1.0026	Cell division cycle			{50}
<i>cdc13</i>	2.0000	Cell division cycle; cyclin-related	y		{50,136}
<i>cdc14</i>	2.0000	Cell division cycle.			{43}
<i>cdc15</i>	1.0894	Cell division cycle			{50}
<i>cdc16</i>	1.2393	Cell division cycle	y		{50,208}
<i>cdc17</i>	1.0000	Cell division cycle; DNA ligase	y		{159,133,127}
<i>cdc18</i>	2.1814	Cell division cycle			{50,158}
<i>cdc19</i>		Cell division cycle.			{158}
<i>cdc20</i>		Cell division cycle.			{158}
<i>cdc21</i>		Cell division cycle.	y		{158}
<i>cdc22</i>		Cell division cycle.	y		{83}
<i>cdc23</i>		Cell division cycle.	y		{158}
<i>cdc24</i>		Cell division cycle.			{158}
<i>cdc25</i>	1.0184	Cell division cycle.	y	<i>sal2</i>	{50,33}
<i>cdc27</i>		Cell division cycle.	y		{158}
<i>cdc28</i>		Cell division cycle.			{158}
<i>cdc2L</i>	2.0000	Cell division cycle.			{78}
<i>cdr1</i>		Changed division response	y	<i>nim1</i>	{86,205}
<i>cdr2</i>		Changed division response			{86}
<i>cen1</i>	1.3892	Centromere sequence, chromosome I			{50,195}
<i>cen2</i>	2.1077	Centromere sequence, chromosome II			{50,195}
<i>cen3</i>	3.1458	Centromere sequence, chromosome III			{50,195}
<i>cho1</i>	2.0000	Choline requirement			{73}
<i>cho2</i>	2.0000	Choline requirement			{73}
<i>cid1</i>		Colcemid resistance			{29}
<i>cid2</i>		Colcemid resistance			{29}
<i>cid3</i>		Colcemid resistance			{29}
<i>cph</i>		Cyclophilin	y		{185}
<i>crm1</i>	1.2524	Cell division in absence of nuclear division	y		{114}
<i>cta3</i>		P-type ATPase gene	y		{40}
<i>cut01</i>	3.3392	Cell division in absence of nuclear division	y		{84,183}
<i>cut02</i>	2.1822	Cell division in absence of nuclear division	y		{84}
<i>cut03</i>		Cell division in absence of nuclear division			{84}
<i>cut04</i>		Cell division in absence of nuclear division			{84}
<i>cut05</i>		Cell division in absence of nuclear division			{84}
<i>cut06</i>		Cell division in absence of nuclear division			{84}
<i>cut07</i>	1.0000	Cell division in absence of nuclear division	y		{84,203}
<i>cut08</i>	1.4708	Cell division in absence of nuclear division			{84}
<i>cut09</i>		Cell division in absence of nuclear division			{84}
<i>cut10</i>		Cell division in absence of nuclear division			{84}
<i>cyc1</i>		Cytochrome c	y		{160}
<i>cyh1</i>	1.3932	Cycloheximide resistance, putative ribosomal protein			{152,153}
<i>cyh2</i>		Cycloheximide resistance			{152}
<i>cyh3</i>		Cycloheximide resistance			{152}
<i>cyh4</i>		Cycloheximide resistance, allelic with <i>ani2</i> , <i>tri3</i>		<i>ani2,tri3</i>	{152,154}
<i>cyr1</i>		adenylyl cyclase	y		{105,110}
<i>dap1</i>	1.3919	Diaminopurine resistance, adenine phosphoribosyl transferase			{85}
<i>deo1</i>	1.0000	Deoxyglucose resistance			{43}
<i>dis1</i>	3.0000	Mitotic chromosome disjunction block			{112}
<i>dis2</i>		Type 1 protein phosphatase	y	<i>bws1,pp1</i>	{112}
<i>dis3</i>		Mitotic chromosome disjunction block			{112}
<i>end1</i>	1.0000	DNA endonuclease			{9}
<i>ery1</i>	3.1350	Erythromycin resistance			{43}
<i>eth1</i>	2.0000	Ethionine resistance			{43}
<i>eth2</i>	1.1210	Ethionine resistance, allelic with <i>met1</i>		<i>met1</i>	{50}
<i>eth3</i>		Ethionine resistance			{50}
<i>fbp1</i>		Fructose-1,6-biphosphatase	y		{47,10,118}
<i>fur1</i>	3.1418	Fluorouracil resistance			{43}
<i>fur2</i>	2.0000	Fluorouracil resistance			{43}
<i>fur4</i>		Fluorouracil resistance, uracil permease			{161}
<i>fus1</i>		Sexual cell fusion			{162}
<i>g3pd</i>		Glycerol-3-phosphate dehydrogenase	y		{207}

Table 2. (continued)

Gene	Loc.	Gene Description (Product or Phenotype)	Sequence	Synonyms	References
<i>gdh1</i>		Glycerol dehydrogenase			{32}
<i>glu1</i>	2.0386	Glutamate requirement			{43}
<i>glu2</i>	2.2029	Glutamate requirement			{43}
<i>glu3</i>		Glutamate requirement			{43}
<i>glu4</i>		Glutamate requirement			{43}
<i>gs1</i>		Glutamine synthetase	y		{213}
<i>gua1</i>	2.1049	IMP dehydrogenase (EC.1.2.1.14)			{85,97}
<i>gua2</i>	1.3940	GMP synthetase (EC. 6.3.5.2)			{85,97}
<i>hcs</i>		Homolog of E. coli RNase III	y		{184}
<i>hfo1</i>		Histone H4, H4.1	y		{21}
<i>hfo2</i>		Histone H4, H4.2	y		{21}
<i>hfo3</i>		Histone H4, H4.3	y		{21}
<i>his1</i>	1.4497	Histidinol phosphate phosphatase (EC.3.1.3.15)			{85,50}
<i>his2</i>	2.1684	Histidinol dehydrogenase (EC.1.1.1.23)			{85,43}
<i>his3</i>	2.0759	Imidazole acetol phosphate transaminase (EC.2.6.1.9)			{85,43}
<i>his4</i>	2.3091	Histidine requirement			{85,43}
<i>his5</i>	2.1766	Imidazole glycerolphosphate dehydratase (EC.4.2.1.19)			{85,43}
<i>his6</i>	1.2485	Histidine requirement			{85,50}
<i>his7</i>	2.1546	Histidine requirement			{85,43}
<i>his8</i>		Histidine requirement			{85}
<i>his9</i>		Histidine requirement			{85}
<i>hsp1</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hsp2</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hsp3</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hsp4</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hsp5</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hsp6</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hsp7</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hsp8</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hsp9</i>		Hyperspeckled, suppressor of <i>smt</i>			{88}
<i>hta1</i>	3.1701	Histone H2A, H2A.1, H2A-a	y		{21,22}
<i>hta2</i>		Histone H2A, H2A.1,H2A-B	y		{21,22}
<i>htb1</i>	3.0000	Histone H2B, H2B.1,H2B-B	y		{21,22}
<i>hth1</i>		Histone H3, H3.1	y		{21}
<i>hth2</i>		Histone H3, H3.2	y		{21}
<i>hth3</i>		Histone H3, H3.3	y		{21}
<i>hyp1</i>		Hypoxanthine non-utilisation			{41}
<i>hyp2</i>		Hypoxanthine non-utilisation			{41}
<i>hyp3</i>		Hypoxanthine non-utilisation			{41}
<i>hyp4</i>		Hypoxanthine non-utilisation			{41}
<i>hyp5</i>		Hypoxanthine and xanthine non-utilisation			{41}
<i>kin1</i>		Protein kinase	y		{38}
<i>leu1</i>	2.1490	Isopropylmalate dehydrogenase	y		{43,144}
<i>leu2</i>	1.4603	Leucine requirement			{43}
<i>leu3</i>	2.2153	Leucine requirement			{43}
<i>lys1</i>	1.3919	Lysine requirement			{43}
<i>lys2</i>	1.1407	Lysine requirement (on 470kb NotI fragment "K")			{50}
<i>lys3</i>	1.0236	Lysine requirement			{50}
<i>lys4</i>	2.3008	Lysine requirement			{43}
<i>lys5</i>	1.0552	Lysine requirement			{50}
<i>lys6</i>	1.0000	Lysine requirement			{43}
<i>lys7</i>	1.4681	Lysine requirement			{50}
<i>lys8</i>		Lysine requirement			{43}
<i>lys9</i>		Lysine requirement			{43}
<i>mam1</i>	2.2098	Mating-type auxiliary (minus)			{163,43}
<i>mam2</i>		Mating-type auxiliary (minus)			{163}
<i>map1</i>		Mating-type auxiliary (plus)			{163}
<i>map2</i>		Mating-type auxiliary (plus)			{163}
<i>mat1</i>	2.1614	Mating-type expression locus	y		{52}
<i>mat2</i>	2.1628	Mating-type storage locus (plus), allelic with <i>mei1</i>	y	<i>mei1</i>	{52}
<i>mat3</i>	2.1642	Mating-type storage locus (minus)	y		{52}
<i>mcs1</i>		Mitotic catastrophe suppressor			{137}
<i>mcs2</i>		Mitotic catastrophe suppressor			{137}
<i>mcs3</i>		Mitotic catastrophe suppressor			{137}
<i>mcs4</i>		Mitotic catastrophe suppressor			{137}
<i>mcs5</i>		Mitotic catastrophe suppressor			{137}
<i>mcs6</i>		Mitotic catastrophe suppressor			{137}
<i>mei1</i>	2.1628	First meiotic division, allelic with <i>mat2</i>	y	<i>mat2</i>	{52}

Table 2. (continued)

Gene	Loc.	Gene Description (Product or Phenotype)	Sequence	Synonyms	References
<i>mei2</i>	1.4655	First meiotic division	y		{12,126}
<i>mei3</i>	2.0027	First meiotic division	y		{12,53,138}
<i>mei4</i>	2.0773	First meiotic division			{12}
<i>mes1</i>	1.1157	Second meiotic division			{12}
<i>mes2</i>		Second meiotic division			{69}
<i>met1</i>	1.1210	Methionine requirement, allelic with <i>eth2</i>		<i>eth2</i>	{50}
<i>met2</i>	1.1118	Methionine requirement			{50}
<i>met3</i>	2.2650	Methionine requirement			{43}
<i>met4</i>	2.0000	Methionine requirement			{43}
<i>met5</i>	1.0671	Methionine requirement			{50}
<i>min01</i>	3.1566	Methionine inhibited, allelic with <i>ade6</i>	y	<i>ade6</i>	{164}
<i>min02</i>		Methionine inhibited			{164}
<i>min03</i>	1.4800	Methionine inhibited			{164,43}
<i>min04</i>	2.2705	Methionine inhibited, allelic with <i>ade1</i>		<i>ade1</i>	{164}
<i>min05</i>	3.1620	Methionine inhibited			{164,43}
<i>min06</i>	2.0000	Methionine inhibited, allelic with <i>ade9</i>		<i>ade9</i>	{164}
<i>min07</i>		Methionine inhibited			{164}
<i>min08</i>		Methionine inhibited			{164}
<i>min09</i>		Methionine inhibited			{164}
<i>min10</i>	1.4787	Methionine inhibited, allelic with <i>ade2</i>		<i>ade2</i>	{164}
<i>min11</i>	1.0973	Methionine inhibited, allelic with <i>ade3</i>		<i>ade3</i>	{164}
<i>min12</i>		Methionine inhibited			{164}
<i>min13</i>	1.5576	Methionine inhibited, allelic with <i>ade4</i>		<i>ade4,aza1</i>	{164}
<i>min14</i>	3.1323	Methionine inhibited, allelic with <i>ade10</i>		<i>ade10</i>	{164}
<i>min15</i>		Methionine inhibited			{164}
<i>min16</i>		Methionine inhibited			{164}
<i>mut1</i>		Mutator			{165}
<i>mut2</i>	2.2539	Mutator			{43,165}
<i>mut3</i>	2.1849	Mutator			{43,165}
<i>nda01</i>	2.0400	Nuclear division arrest			{156}
<i>nda02</i>	2.3919	alpha 1-tubulin	y		{6,32}
<i>nda03</i>	2.4278	beta tubulin, allelic with <i>ben1</i>	y	<i>ben1</i>	{156,7}
<i>nda04</i>	1.2525	Nuclear division arrest			{94}
<i>nda05</i>	1.0000	Nuclear division arrest			{94}
<i>nda06</i>	1.0000	Nuclear division arrest			{94}
<i>nda07</i>	1.0000	Nuclear division arrest			{94}
<i>nda08</i>	1.0000	Nuclear division arrest			{94}
<i>nda09</i>	1.0000	Nuclear division arrest			{94}
<i>nda10</i>	3.0000	Nuclear division arrest			{94}
<i>nda11</i>	3.0000	Nuclear division arrest			{94}
<i>nda12</i>		Nuclear division arrest			{94}
<i>nim1</i>		Mitotic control element; protein kinase	y	<i>cdr1</i>	{192,205}
<i>nm11</i>		No message in thiamine	y		{100}
<i>nuc1</i>	2.2774	Alteration in nuclear structure; largest RNA pol I subunit	y		{84,196}
<i>nuc2</i>	1.4734	Alteration in nuclear structure	y		{94}
<i>orf54</i>		Strong promoter and unknown gene(s)	y		{211}
<i>pab1</i>		p-aminobenzoic acid requirement			{44}
<i>pac1</i>		RNase III homolog; suppressor of <i>pat1</i> temperature sensitive mul	y		{191}
<i>pap1</i>		AP-1-like transcription factor	y		{201}
<i>pat1</i>	2.0994	Sporulation of haploids, allelic with <i>ran1</i>	y	<i>ran1</i>	{54}
<i>pet1</i>		Respiration (nuclear gene)			{175}
<i>phe1</i>	1.0000	Phenylalanine requirement			{44}
<i>phe2</i>	2.0000	Phenylalanine requirement			{44}
<i>pho1</i>	2.3988	Acid phosphatase	y		{58,28}
<i>pho2</i>	2.2663	Alkaline phosphatase			{194}
<i>pho3</i>	2.3905	Alkaline phosphatase			{194}
<i>pho4</i>		Acid phosphatase, thiamine repressible	y		{18,35}
<i>php2</i>		Transcription activation complex subunit	y		{200}
<i>pma1</i>	1.3971	Plasma membrane ATPase	y		{25}
<i>pol1</i>	2.0000	DNA Polymerase alpha	y		{197}
<i>ppa</i>		Inorganic pyrophosphatase (E.C. 3.6.1)	y		{39}
<i>ppa1</i>		Type 2A Protein Phosphatase	y		{215}
<i>ppa2</i>		Type 2A Protein Phosphatase	y		{215}
<i>ppx1</i>		Phosphatase w/ homol. to <i>S. cerev.</i> SIT4 gene	y		{215}
<i>pro1</i>	1.0579	Proline requirement			{43,50}
<i>pro2</i>	1.1736	Proline requirement			{43,50}
<i>pur1</i>		Azathioxanthine resistance (EC.2.4.2.8)			{85}
<i>pyp1</i>		Protein tyrosine phosphatase (by homology)	y		{199}

Table 2. (continued)

Gene	Loc.	Gene Description (Product or Phenotype)	Sequence	Synonyms	References
<i>rad01</i>	1.5207	Radiation sensitivity; on NotI fragment E	y		{50,55,187}
<i>rad02</i>	1.5628	Radiation sensitivity			{50,55}
<i>rad03</i>		Radiation sensitivity			{55}
<i>rad04</i>		Radiation sensitivity			{55}
<i>rad05</i>		Radiation sensitivity			{55}
<i>rad06</i>		Radiation sensitivity			{55}
<i>rad07</i>		Radiation sensitivity			{55}
<i>rad08</i>	1.0000	Radiation sensitivity			{43,55}
<i>rad09</i>	1.1420	Radiation sensitivity	y		{50,55}
<i>rad10</i>	3.0621	Radiation sensitivity	y	<i>swi9,rad16,rad20</i>	{55}
<i>rad11</i>		Radiation sensitivity			{55}
<i>rad12</i>		Radiation sensitivity			{55}
<i>rad13</i>	1.0000	Radiation sensitivity	y		{55}
<i>rad14</i>		Radiation sensitivity			{55}
<i>rad15</i>	1.0329	Radiation sensitivity; homologous to <i>S. cerev.</i> rad3 gene	y		{50,55}
<i>rad17</i>		Radiation sensitivity			{55}
<i>rad18</i>		Radiation sensitivity			{55}
<i>rad19</i>		Radiation sensitivity			{55}
<i>rad21</i>	3.1593	Radiation sensitivity			{50,55}
<i>rad22</i>		Radiation sensitivity			{55}
<i>rad23</i>		UV radiation sensitive.			{96}
<i>ral1</i>		Ras-like			{113}
<i>ral2</i>		Ras-like	y		{113,103}
<i>ral3</i>		Ras-like			{113}
<i>ral4</i>		Ras-like			{113}
<i>ran1</i>	2.0994	See pat1	y	<i>pat1</i>	{56}
<i>ras1</i>	1.1762	Ras oncogene related	y	<i>ste5</i>	{57,121,128}
<i>rec01</i>		Recombination			{87}
<i>rec02</i>		Recombination			{13}
<i>rec03</i>		Recombination			{13}
<i>rec05</i>		Recombination			{13}
<i>rec06</i>		Meiotic recombination mutants			{107}
<i>rec07</i>		Meiotic recombination mutants			{107}
<i>rec08</i>		Meiotic recombination mutants			{107}
<i>rec09</i>		Meiotic recombination mutants			{107}
<i>rec10</i>		Meiotic recombination mutants			{107}
<i>rec11</i>		Meiotic recombination mutants			{107}
<i>rhp6</i>		<i>S. cerev.</i> rad6 homolog	y		{182}
<i>rpa01</i>		Acidic ribosomal protein gene 1	y		{188}
<i>rpa02</i>		Acidic ribosomal protein gene 2; SP-L40c	y	<i>rpl40c</i>	{188,131}
<i>rpa03</i>		Acidic ribosomal protein gene 3	y		{188}
<i>rpa04</i>		Acidic ribosomal protein gene 4	y		{188}
<i>rpa190</i>		RNA polymerase I, large (A190) subunit	y		{142}
<i>rpb1</i>		RNA polymerase II, largest subunit	y		{204}
<i>rpK37</i>		Ribosomal protein gene, homologous to <i>S. cerev.</i> L3	y		{130,125}
<i>rpl7</i>	1.1420	Homolog of rat ribosomal protein L7	y		{186}
<i>rpl7b</i>	2.0000	Ribosomal protein L7b	y		{198}
<i>rplK5</i>		Ribosomal protein gene K5	y		{212}
<i>rplKD4</i>		Ribosomal protein gene KD4	y		{212}
<i>rps6</i>		Ribosomal protein gene, small subunit	y		{78,143}
<i>rrf1</i>		5S ribosomal RNA gene, pSPr1, pYM116	y		{166,167}
<i>rrf2</i>		5S ribosomal RNA gene, pSPr11	y		{166}
<i>rrf3</i>		5S ribosomal RNA gene, pSPr36	y		{166}
<i>rrf4</i>		5S ribosomal RNA gene, pSPr41	y		{166}
<i>rrf5</i>		5S ribosomal RNA gene, pYM3	y		{167}
<i>rrf6</i>	2.0759	5S ribosomal RNA gene, close to <i>cdc2</i>			{59}
<i>rrf7</i>	3.2201	5S ribosomal RNA gene, close to <i>sup9</i>			{92}
<i>rrn1</i>	3.3051	5S ribosomal RNA gene repeats (nucleolar organizer)			{60,71,20}
<i>ryh1</i>		ras/rho/ypt homolog	y		{181}
<i>sal1</i>	1.0000	Allosuppressor			{50,51}
<i>sal2</i>	1.0184	Allosuppressor, allelic with <i>cdc25</i>		<i>cdc25</i>	{50,51}
<i>sal3</i>	3.2889	Allosuppressor			{50,51}
<i>sal4</i>		Allosuppressor			{51}
<i>sal5</i>		Allosuppressor			{90}
<i>scr1</i>		Suppressor of cycloheximide resistance			{151}
<i>scr2</i>		Suppressor of cycloheximide resistance			{151}
<i>sds21</i>		Suppressor of <i>dis2</i> ; Type 1 protein phosphatase	y		{112,202}
<i>sds22</i>	1.0000	Supp. of <i>dis2</i> ; on NotI fragment "H"	y		{112,202}

Table 2. (continued)

Gene	Loc.	Gene Description (Product or Phenotype)	Sequence	Synonyms	References
<i>sds23</i>	1.0000	Supp. of <i>dis2</i> ; on <i>NotI</i> fragment "H"			{112}
<i>sin01</i>	1.0000	Antisuppressor, loss of i6A in tRNA			{43,168}
<i>sin02</i>	3.1580	Antisuppressor			{43}
<i>sin03</i>	2.0000	Antisuppressor, loss of <i>mcm5s2U</i> in tRNA			{61}
<i>sin04</i>	3.1445	Antisuppressor, loss of <i>mcm5s2U</i> in tRNA			{43}
<i>sin05</i>	1.0000	Antisuppressor			{43}
<i>sin06</i>	1.0000	Antisuppressor			{43}
<i>sin07</i>	2.0000	Antisuppressor			{50}
<i>sin08</i>	1.0000	Antisuppressor			{43}
<i>sin09</i>	1.0000	Antisuppressor			{43}
<i>sin10</i>	2.0000	Antisuppressor			{43}
<i>sin11</i>	2.0000	Antisuppressor			{43}
<i>sin12</i>		Antisuppressor			{193}
<i>sin13</i>		Antisuppressor			{193}
<i>sin14</i>		Antisuppressor			{193}
<i>sin15</i>		Antisuppressor, loss of <i>ncm5U</i> in tRNA			{62}
<i>smt</i>	2.0000	Switching of mating-type sequence			{52}
<i>snm1</i>		defective in snRNA maintenance			{189}
<i>snu1</i>	2.0000	U1 small nuclear RNA	y		{106}
<i>snu2</i>	1.0000	U2 small nuclear RNA	y		{106,174}
<i>snu3A</i>	1.0000	U3A small nuclear RNA	y		{106}
<i>snu3B</i>	2.0000	U3B small nuclear RNA	y		{106}
<i>snu4</i>	2.0000	U4 small nuclear RNA	y		{106}
<i>snu43</i>	1.0000	Small nuclear RNA	y		{106}
<i>snu5</i>		U5 small nuclear RNA	y		{102}
<i>snu6</i>		U6 small nuclear RNA	y		{108}
<i>spk1</i>		Protein kinase conferring staurosporine resistance	y		{201}
<i>spo01</i>		Sporulation			{162}
<i>spo02</i>	2.3974	Sporulation			{162,27}
<i>spo03</i>	1.1670	Sporulation			{162,27}
<i>spo04</i>	2.4623	Sporulation			{162,27}
<i>spo05</i>	2.2084	Sporulation			{162,27}
<i>spo06</i>	2.2732	Sporulation			{162,27}
<i>spo07</i>		Sporulation			{162}
<i>spo08</i>		Sporulation			{162}
<i>spo09</i>		Sporulation			{162}
<i>spo10</i>		Sporulation			{162}
<i>spo11</i>		Sporulation			{162}
<i>spo12</i>		Sporulation			{162}
<i>spo13</i>	3.1080	Sporulation			{162,27}
<i>spo14</i>	2.1380	Sporulation			{162,27}
<i>spo15</i>	1.0289	Sporulation			{162,27}
<i>spo16</i>		Sporulation			{162}
<i>spo17</i>		Sporulation			{162}
<i>spo18</i>	2.0000	Sporulation			{162,27}
<i>spo19</i>	1.0000	Sporulation			{27}
<i>spo20</i>	1.0316	Sporulation			{27}
<i>stb1</i>	3.0000	Plasmid stabilisation	y		{24}
<i>ste01</i>	1.0000	Sterility, defective meiosis			{169}
<i>ste02</i>	2.2056	Sterility, defective meiosis			{63}
<i>ste03</i>	1.0407	Sterility, defective meiosis			{63}
<i>ste04</i>	1.0000	Sterility, defective meiosis			{63}
<i>ste05</i>	1.1762	Sterility mutant	y	<i>ras1</i>	{63}
<i>ste06</i>	3.1782	Sterility mutant			{63}
<i>ste07</i>	1.0000	Sterility, defective meiosis			{89}
<i>ste08</i>	2.1408	Sterility, defective meiosis			{89}
<i>ste09</i>	1.4839	Sterility, defective meiosis			{90}
<i>ste10</i>	2.3836	Partial sterility			{90}
<i>ste11</i>	2.0000	Sterility locus		<i>stex, aff1</i>	{116,101}
<i>ste12</i>	2.0000	Sterility locus			{101}
<i>ste13</i>	2.0000	Sterility locus			{101}
<i>stf1</i>		Suppressor of <i>cdc25</i>			{36}
<i>sts01</i>		Staurosporine sensitive			{201}
<i>sts02</i>		Staurosporine sensitive			{201}
<i>sts03</i>		Staurosporine sensitive			{201}
<i>sts04</i>		Staurosporine sensitive			{201}
<i>sts05</i>		Staurosporine sensitive			{201}
<i>sts06</i>		Staurosporine sensitive			{201}

Table 2. (continued)

Gene	Loc.	Gene Description (Product or Phenotype)	Sequence	Synonyms	References
<i>sts07</i>		Staurosporine sensitive			{201}
<i>sts08</i>		Staurosporine sensitive			{201}
<i>sts09</i>		Staurosporine sensitive			{201}
<i>sts10</i>		Staurosporine sensitive			{201}
<i>sts11</i>		Staurosporine sensitive			{201}
<i>suc1</i>		Suppressor of <i>cdc2</i>	y		{26,124}
<i>suc22</i>		Suppressor of <i>cdc22</i>	y		{83}
<i>suf01</i>	3.2457	Frameshift suppressor, group I			{64}
<i>suf02</i>	2.0000	Frameshift suppressor, group I			{64}
<i>suf03</i>	1.0000	Frameshift suppressor, group II			{64}
<i>suf04</i>	3.0000	Frameshift suppressor, group II			{64}
<i>suf05</i>	2.1049	Frameshift suppressor, group II			{64}
<i>suf06</i>	3.0000	Frameshift suppressor, Group II			{64}
<i>suf07</i>	3.0000	Frameshift suppressor, group II			{64}
<i>suf08</i>	2.1573	Frameshift suppressor, group II			{50,64}
<i>suf09</i>		Frameshift suppressor, group IV			{93}
<i>suf10</i>		Frameshift suppressor, group III			{93}
<i>suf11</i>	2.0000	Frameshift suppressor, group I			{64}
<i>sup01</i>	3.1917	Nonsense suppressor, omnipotent			{43,193}
<i>sup02</i>	1.4852	Nonsense suppressor, omnipotent			{50,193}
<i>sup03</i>	1.4445	Nonsense suppressor, opal, ochre, tRNA ^{ser} , tRNA ^{met}	y		{50,14}
<i>sup04</i>		Missense suppressor			{65}
<i>sup05</i>	2.2015	Missense suppressor			{50,65}
<i>sup06</i>		Missense suppressor			{65}
<i>sup07</i>	2.0000	Missense suppressor			{43,65}
<i>sup08</i>	2.0580	Nonsense suppressor, opal, ochre, tRNA ^{leu}	y		{43,66}
<i>sup09</i>	3.2187	Nonsense suppressor, opal, tRNA ^{ser} , tRNA ^{met}	y		{43,14}
<i>sup10</i>	1.2472	Nonsense suppressor, opal, tRNA ^{leu}			{50,62}
<i>sup11</i>	3.1755	Informational suppressor			{93}
<i>sup12</i>	1.0631	Nonsense suppressor, opal, tRNA ^{ser} , tRNA ^{met}	y		{50,14}
<i>sup13</i>		Nonsense suppressor, amber.			{15}
<i>sup14</i>		Nonsense suppressor, amber			{15}
<i>sup15</i>	3.1836	Nonsense suppressor			{217}
<i>swi01</i>	2.0166	Mating-type switching, class Ia			{67}
<i>swi02</i>	1.3853	Mating-type switching, class Ib			{67}
<i>swi03</i>	2.2705	Mating-type switching, class Ia			{67}
<i>swi04</i>	1.2485	Mating-type switching, class II			{67}
<i>swi05</i>	2.0276	Mating-type switching, class Ib			{67}
<i>swi06</i>		Mating type switching, class Ib			{67}
<i>swi07</i>	1.3524	Mating-type switching, class Ia			{67}
<i>swi08</i>	2.1932	Mating-type switching, class II			{67}
<i>swi09</i>	3.0621	Mating-type switching, class II, allelic with <i>rad10</i>	y	<i>rad10</i>	{67}
<i>swi10</i>	2.2208	Mating-type switching, class II			{67}
<i>tfIID</i>		TATA box binding-factor gene	y		{98}
<i>tnd1</i>		Aspartate tRNA, anticodon GTC, pYM116	y		{167}
<i>tne1</i>		Glutamate tRNA, anticodon TTC, pYM104	y		{173}
<i>tnf1</i>		Phenylalanine tRNA, anticodon AAG, pYM125	y		{173}
<i>tnh1</i>		Histidine tRNA, anticodon GTG, pYM7.2	y		{173}
<i>tnk1</i>		Lysine tRNA, anticodon CTT, pYM104	y		{173}
<i>tnr1</i>		Arginine tRNA, anticodon ACG, pYM104	y		{173}
<i>tnr2</i>		Arginine tRNA, anticodon ACG, lambda 805	y		{173}
<i>top1</i>	2.2857	DNA topoisomerase I	y		{9,122}
<i>top2</i>	2.1477	DNA topoisomerase II	y		{9,134}
<i>tpi1</i>		Triosephosphate isomerase	y		{19}
<i>tps12</i>		Temperature-sensitive lethal			{91}
<i>tps13</i>	2.1035	Temperature-sensitive lethal			{50}
<i>tps14</i>	3.1944	Temperature-sensitive lethal			{50}
<i>tps15</i>	2.1532	Temperature-sensitive lethal			{43,50}
<i>tps16</i>	3.1634	Temperature-sensitive lethal			{50}
<i>tps17</i>	1.0000	Temperature-sensitive lethal			{50}
<i>tps18</i>	1.0907	Temperature-sensitive lethal			{50}
<i>tps19</i>	1.5286	Temperature-sensitive lethal			{50}
<i>tps20</i>	2.1477	Temperature-sensitive lethal			{50}
<i>tps21</i>		Temperature-sensitive lethal			{91}
<i>tps22</i>		Temperature-sensitive lethal			{91}
<i>tps23</i>		Temperature-sensitive lethal			{91}
<i>tps24</i>	3.0000	Temperature-sensitive lethal			{50}
<i>tps25</i>	2.0000	Temperature-sensitive lethal			{50}

Table 2. (continued)

Gene	Loc.	Gene Description (Product or Phenotype)	Sequence	Synonyms	References
<i>tps26</i>	2.0000	Temperature-sensitive lethal			{8}
<i>tps27</i>		Temperature-sensitive lethal			{91}
<i>tps28</i>	3.2214	Temperature-sensitive lethal			{50}
<i>tri1</i>	2.1711	Trichodermine resistance			{43}
<i>tri2</i>	3.0000	Trichodermine resistance			{43}
<i>tri3</i>		Trichodermine resistance, allelic with <i>ani2</i> , <i>cyh4</i>		<i>ani2, cyh4</i>	{154}
<i>tri4</i>		Trichodermine resistance			{154}
<i>tri5</i>		Trichodermine resistance			{154}
<i>trp1</i>	2.3795	trp1A:PRA isomerase; trp1B:lnGP synth.; trp1C:anth. synthetase			{50,68}
<i>trp2</i>	1.2051	Tryptophan synthetase(EC.4.2.1.20)			{85,50}
<i>trp3</i>	3.2430	Anthranilate synthetase			{85,50}
<i>trp4</i>	2.3864	PR transferase(EC.2.4.2.20)			{85,50}
<i>tsl01</i>		Temperature-sensitive lethal			{170}
<i>tsl02</i>		Temperature-sensitive lethal			{170}
<i>tsl03</i>		Temperature-sensitive lethal			{170}
<i>tsl04</i>		Temperature-sensitive lethal			{170}
<i>tsl05</i>		Temperature-sensitive lethal			{170}
<i>tsl06</i>		Temperature-sensitive lethal			{170}
<i>tsl07</i>	1.1670	Temperature-sensitive lethal			{50,170}
<i>tsl08</i>		Temperature-sensitive lethal			{170}
<i>tsl09</i>		Temperature-sensitive lethal			{170}
<i>tsl10</i>		Temperature-sensitive lethal			{170}
<i>tsl11</i>		Temperature-sensitive lethal			{170}
<i>tws1</i>		Two-spored asci			{69}
<i>tyr1</i>	3.0000	Tyrosine requirement			{44}
<i>tyr2</i>		Tyrosine requirement			{44}
<i>ura1</i>	1.0381	Aspartate transcarbamylase			{50,171}
<i>ura2</i>	1.4576	Dihydroorotase (EC.3.5.2.3)			{85,50}
<i>ura3</i>	1.1026	Dihydroorotate dehydrogenase			{85,50}
<i>ura4</i>	3.0027	Orotidinephosphate decarboxylase	y		{172,120}
<i>ura5</i>	2.0442	Orotate phosphoribosyl transferase			{43}
<i>ure1</i>		Lack of urease			{41}
<i>ure2</i>		Lack of urease			{41}
<i>ure3</i>		Lack of urease			{41}
<i>ure4</i>		Lack of urease			{41}
<i>uro1</i>		Lack of uricase			{41}
<i>ver1</i>	3.0000	Verrucarine resistance			{43}
<i>vir1</i>	1.1486	Vegetative iodine reaction			{50,70}
<i>wee1</i>	3.4970	Cell division cycle, small cells	y	<i>cdc9</i>	{43,139}
<i>win1</i>		Wee interacting			{30}
<i>xan1</i>		Xanthine non-utilisation			{41}
<i>ypt1</i>		Related to <i>S. cerev.</i> YPT-1 gene	y		{180,111}
<i>ypt2</i>		also related to <i>S. cerev.</i> YPT-1 gene; GTP-binding	y		{190}
<i>ypt3</i>		also related to <i>S. cerev.</i> YPT-1 gene	y		{180,179}

trate the potential for correlating the physical and genetic data is shown in Table 1, which indicates the number of loci mapped (at a minimum, to a chromosome) in relation to the number sequenced. As filters containing genomic DNA in a known order become available, either from *NotI* or *SfiI* digests in relation to the *NotI/SfiI* macrorestriction map of the genome, or as arrays of cosmid DNAs spanning a completely mapped genome, it will become increasingly easy to determine where loci map. It is anticipated that this may lead, initially, to a decrease in the total number of known genes as a gene known primarily by sequence is mapped to a locus known primarily phenotypically.

The list of identified loci is presented alphabetically by gene symbol in Table 2. The 520 distinct entries describe

501 distinct (i.e. non-allelic) loci. This represents an increase of 89 loci as compared to the 1987 list previously published. This database is available in either printed or computer formats upon request; updates and corrections will be made periodically. As the yeast genome is thought to comprise between 5000 and 10000 genes, it is clear that much remains to be discovered.

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