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PUBLICATIONS

ALDERSON, T. and C. SCAZZOCHIO. A system for the study of interlocus specificity for both forward and reverse mutation in at least eight gene loci in Aspergillus nidulans.
Mutation Res. 4: 567 - 577.

ARST, H.N., jun. Genetic analysis of the first steps of sulphate metabolism in Aspergillus nidulans.
Nature 219: 268 - 270

BALL, C. Chromosome instability related to gene suppression.
Genet. Res. 10: 173 - 183.

GAJEWSKI, W., and J. LITWINSKA. Methionine loci and their suppressors in Aspergillus nidulans.
Molec. Gen. Genetics in print.

LANIER, W.B., R.W. TUVESON and J. E. LENNOX. A radiation sensitive mutant of Aspergillus nidulans.
Mutation Res. 5: 23 - 31.

MacDONALD, K.D. The selection of auxotrophs of Penicillium chrysogenum with nystatin.
Genet. Res. 11: 327 - 330

MILLINGTON-WARD, A.M. A vegetative instability in Aspergillus nidulans.
Genetica 38: 191 - 207.

MORPURGO, G. and L. VOLTERRA. The nature of mitotic recombination in Aspergillus nidulans.
Genetics 58: 529 - 541.

MORPURGO, G. and L. VOLTERRA. Sulla natura della recombinazione mitotica intracistronica in Aspergillus.
Atti Assoociazione Genetica Italiana 13: 289 - 290.

NGA, B.H. and J. A. ROPER. Quantitative intrachromosomal changes arising at mitosis in Aspergillus nidulans.
Genetics 58: 193 - 209.

PUTRAMENT, A. On the mechanism of mitotic recombination in Aspergillus nidulans. I. Intragenic recombination and DNA replication.
Molec. Gen. Genetics 100: 307 - 320.

PUTRAMENT, A. On the mechanism of mitotic recombination in Aspergillus nidulans. II. Simultaneous recombination within two closely linked cistrons.
Molec. Gen. Genetics 100: 321 - 336.

TUVESON, R.W., and J. E. LENNOX. A UV-sensitive mutant of Aspergillus rugulosus unrelated to intergenic crossing over.
Can. J. Genet. Cytol. 10: 50 - 53.

CURRENT RESEARCH PROJECTS

C. BALL. The genetics of Penicillium chrysogenum

C. TAKEICHI. Cytological studies of a pathogenic fungus: effect of antibiotics on Trichophyton.

C. BALL

Chromosome Instability related to Gene Suppression

A number of additional observations related to this work (see publications) that were made with a view to further study are worth mentioning here, since they may be of value to others.

1. Possible Interference

In a cross between a strain carrying a non-reciprocal III - V translocation and a normal strain, both carrying markers for the translocated region (i.e. gal_1 and arg_2 respectively) negative interference was detected. This could reflect on pairing in such regions.

2. Possible Meiotic Non-Disjunction

Abnormal colonies which readily sectored more normal growth were observed at meiosis in crosses between translocated and normal strains and between duplicated and normal strains. However, they occurred in lower frequency than the types observed by Pollard and Käfer in their studies on crossing chromosomally re-arranged strains to normal. (Canadian Journal of Genetics & Cytology, Vol. 9, 1967).

3. Possible Recombination in a Heterokaryon

A heterokaryon was established between a white unstable strain ("US") and yellow stable strain ("S") carrying the chromosome I markers pro_1 $paba_6$. It was found that abnormal sectors could arise in the heterokaryons. Subculture from such areas enabled isolation of y pro_1 $paba_6$ types which were "US" in morphology. Since the transition of "S" → "US" has not been observed to take place spontaneously, this result could readily be explained in terms of diploid formation in the heterokaryon followed by subsequent breakdown to yield the recombinant genotypes observed.

C. E. CATEN

The genetic compositon of single cleistothecia of Aspergillus heterocaryoticus

Aspergillus heterocaryoticus is a homothallic species

belonging to the A. glaucus group. It has been isolated from nature in two colour forms, one with white conidia and the other with brown (Christensen et al. 1965. Mycologia 57, 535 - 542). When crosses were made between these forms a third type with green conidia was recovered among the progeny. Using the production of such green recombinants as a criterion of hybrid origin, approximately 50% of cleistothecia sampled from heterokaryotic areas proved to be hybrid.

Analysis of the segregation of the white, brown and green phenotypes in the progeny of single hybrid cleistothecia, revealed marked heterogeneity between cleistothecia. Approximately 25% of the hybrid cleistothecia produced the three phenotypes in the ratio 2 white : 1 brown : 1 green, suggesting that spore colour is determined by two unlinked genes, with white epistatic to brown. The remaining 75% showed an excess of one, or the other, or both parental types. Assuming the above genetical interpretation to be correct, these "anomalous" segregations can be accounted for by the occurrence of more than one type of ascus within a cleistothecium, i.e. they are partially hybrid. The segregation ratios of 75% of the "anomolous" cleistothecia are consistent with the presence of two types of asci, one hybrid and the other selfed. The remaining 25% require the occurrence of all three possible fusions. This interpretation of the heterogeneous segregation ratios is supported by the formation of cleistothecia which segregate for the two parental types but fail to produce recombinants, and by a reduction in the frequency of hybrids when smaller cleistothecia are selected for analysis.

The origin of many of the cleistothecia from more than one dikaryotic initial, in part accounts for the high frequency of hybrid cleistothecia produced in mixed cultures of this fungus.

A.J. CLUTTERBUCK

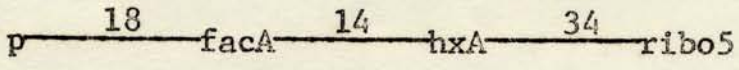
New Conidial Colour mutants in Aspergillus nidulans

w-White Four new mutants of this phenotype have been picked up: w5 is a white mutant induced simultaneously with an inositol mutant in the bi1 strain. w6 is slightly temperature sensitive, i.e. it is white at 37° but pale green at room temperature. w7 is a leaky mutant, pale green at all temperatures. w8 was isolated by N. Glansdorff in a homozygous green diploid treated with NTG (Clutterbuck & Sinha, ANL 7). Haploid segregants bearing the mutant are white spored and a diploid made with the green master strain MSG is pale coloured like the original diploid, i.e. the mutant is semi-dominant. w8 does not complement with w3 in diploids, while w7 has been shown to be closely linked to w3.

y-yellow Thirty-eight new mutants of this type, thirteen of them leaky or temperature sensitive, have been tested in diploids with MSF. All of them fail to complement with y1.

yg-yellow-green The mutant yg1 was reported by Dorn 1967 (Genetics 56, 619) Dorn's mutant mapped 0.1 from ad1 on chromosome II. I have isolated a second mutant yg6 which similarly maps 0.1 units from ad3. Colonies bear a mixture of yellow and green conidia, green predominating at low pH and yellow at high pH. A second feature of the phenotype is the colour of the conidiophore and sterigmata, which is a paler brown than in the wild-type. Five mutants isolated on the basis of this feature failed to complement with yg6 in diploids.

p-pale A new mutant p3, closely linked to p2, has been mapped on chromosome VII. There is no linkage with meth3 or nic2, and the results suggest a different arrangement of hxA, facA and ribo5 from that given in Dorn 1967:



P. R. da CUNHA and B. H. NGA

Preliminary studies of a temperature sensitive mutant of A. nidulans.

Following U.V. irradiation of a translocation-free bi_1 strain, a number of morphologically normal, biotin requiring,

temperature sensitive mutants was isolated. These mutants do not grow on CM at 42° but will grow at 34° or 37°. Preliminary analysis of one of these is given below.

Results of haploidisation analysis of the diploid with master strain E indicated the presence of a tsl on linkage group IV and a III; V translocation.

From meiotic analysis of the same cross, one third of the viable meiotic segregants had abnormal morphology suggesting that the translocation was non-reciprocal. There was also a 1 : 1 segregation of tsl : tsl^{+} among a random sample of the segregants.

The tsl is recessive in heterozygote.

J. A. HOUGHTON

Krebs Cycle Mutants in Aspergillus nidulans

Apirion (1965) described a class of mutants in Aspergillus nidulans unable to utilize acetate as sole carbon source, and showing resistance to fluoroacetic acid. These mutants showed normal growth on glucose but grew better on Krebs Cycle intermediates than wild type strains.

Using ultra-violet irradiation as mutagen 6 mutants have been isolated by replica-plating which do not grow on acetate medium. They differ from Apirion's mutants in showing no resistance to fluoroacetic acid and an inability to utilize any substrate of the Krebs Cycle. On glucose they have a growth rate of 0.4 that of wild type and have only scanty conidiation and no perithecial production. They fall into four functional classes, which produce mature perithecia when crossed. Genetic evidence suggests that four unlinked loci are involved.

Electron microscopy reveals no gross mitochondrial abnormalities, as in petite yeast and poky Neurospora. Radiorespirometry using ^{14}C labelled glucose and succinate is being used to investigate the enzymology of these strains.

References: D. Apirion (1965). Genet. Res. Camb. 6, 317-329.
J. A. Houghton (1967). Aspergillus News Letter No. 8.

B. H. NGA

Production and analysis of new translocations in *A. nidulans*.

Fifty-eight biotin requiring, morphologically normal isolates were made following plating, on CM, of conidia of an untranslocated, haploid *bi*$_1$ strain which had been subjected to a total of 100,000r of γ-irradiation with a Co^{60} source and which gave 0.5% viability. These were tested for translocations.

Haploidisation analysis of diploids of each of the isolates with master strain F, showed that 35 of the 58 isolates carried translocations of varying complexity, in some instances, as many as four linkage groups were involved.

Casual inspection of the morphology and mitotic instability of the translocation haploids and diploids revealed the following. The haploid translocation strains were morphologically normal and vegetatively stable. Their diploids with master strain F, like the diploid of the untranslocated *bi*$_1$ and master strain F, were morphologically normal and stable at mitosis apart from relatively rare mitotic crossing over and haploidisation. Thus the translocations had no detectable effect on mitotic stability (cf NGA, this issue).

Translocations induced by γ- irradiation

Isolate number	*Linkage groups involved
34	I - II
35	I - III
27	I - VII
1, 9, 22, 25, 28, 32	I - VIII
11	II - III
10, 29	III - IV
15, 17	III - V
3, 6	III - VII
30	IV - V
2	IV - VI
4, 5, 8	IV - VII
18, 19	V - VII
13, 16	VI - VII

7	VI - VIII
14	VII - VIII
20	I - II - IV
24, 26, 33	I - II - VIII
31	III - IV - VIII
12	VI - VII - VIII
23	I - II - IV - V
21	I - II - IV - VI

*The direction of translocation and reciprocity or non-reciprocity are not implied.

B. H. NGA

High rate of spontaneous vegetative sectoring of diploids between a duplication strain and normal haploid strains in A. nidulans: lethal deletion

A newly purified green diploid between master strain F and a strain with a segment of the right arm of chromosome I in duplicate, when stabbed (or plated at low density) on to CM plates and incubated at 37° for 3 (or 5) days gave about 7 faster-growing yellow diploid sectors per colony. Also observed were rare deteriorated brown pigmented green or yellow conidiating and faster-growing green

I	su_{1} ad_{20} y ad_{20}	pro_{1} $paba_{6}$ y $ad_{20}^{\dagger}$ $bi_{1}^{\dagger}$
II	Acr_{1}	$y^{\dagger}$ ad_{20} bi_{1}
III	gal_{1}	
IV	$pyro_{4}$	
V	fac A_{303}	
VI	s_{3}	
VII	nic_{8}	
VIII	$ribo_{2}$	

Master strain F Duplication strain

sectors and yellow patches of growth amongst the original diploid colonies.

A preliminary analysis of 8 out of 9 faster growing

yellow diploid sectors, via haploidisation, suggested that they arose as a result of loss, or partial loss, of the translocated segment in the II - I complex of the duplication strain. In the remaining case, linkage group II of the duplication strain was not recovered among 30 haploid segregants classified. This result can be explained most plausibly on the basis of a single deletion of part (perhaps all) of the translocated segment together with part of the linkage group II. Analysis of other diploid sectors is in progress.

Preliminary results from observation of vegetative sectoring of other diploids between the duplication strain and other normal haploid strains and between translocation strains and normal haploid strains showed that diploids with a duplicate segment generally have a much higher rate of spontaneous vegetative sectoring under similar conditions of culture. These results suggest an active role of the duplication in causing high vegetative instability in diploids.

M. PIOTROWSKA

A new type of proline suppressor in Aspergillus nidulans

Mutant pro6 in A. nidulans is blocked in major route of proline synthesis (glutamate → glutamic-γ-semialdehyde (GSA) → Δ'-pyrroline carboxylic acid → proline) between glutamate and GSA.

The frequently occurring proline suppressors act through opening the alternative pathway of proline synthesis (arginine → ornithine → GSA). (Weglenski, P., J. Gen. Microbiol. 47, 77, 1967).

A new mutant, otaI, showing no ornithine-transaminase activity was isolated. Thus pro6 otaI strain is blocked in both major and alternative pathways of proline synthesis. Using pro6 otaI strain several spontaneous and UV-induced proline-independent revertants were obtained. They were tested in heterokaryons and diploids against the pro6 strain and crossed with the wild strain.

All revertants obtained after UV treatment appeared to be semidominant; they are mutations within the pro6 locus itself.

Spontaneous revertants are dominant or semidominant. Some of them appeared to result from suppressor mutations unlinked to the pro6 locus.

The presence of these suppressors suggests the possibility of a third pathway of proline synthesis in A. nidulans.

These suppressors could be similar to that obtained by Baumberg (Heredity, 23, 168, 1968) in E. coli, which are partially blocked in N-acetylornithine-6-transaminase. Accumulated N-acetylglutamic-γ-semialdehyde could be de-acetylated to GSA, a proline precursor.

In order to check this hypothesis further genetical and enzymatical analysis of suppressor strains is now being carried out.

A.P.J. TRINCI and G. GIFBON

Carbon dioxide fixation by Aspergillus nidulans and its influence on growth

In a recent communication (Trinci & Whittaker, A.N.L. 7) we reported that both CO_2 and (HCO_3^-) stimulated the germination of A. nidulans conidia. We have continued this investigation using a prototrophic strain of A. nidulans (BWB 224 (Glasgow) recombinant ve y).

$^{14}CO_2$ fixation by germinating conidia was followed (Table 1). Viable spores started to fix $^{14}CO_2$ as soon as they were suspended in a nutrient medium containing glucose although the conidia did not start to form germ tubes until c. 3.5 h later. Conidia suspended in a medium lacking glucose did not swell or form germ tubes during the course of the experiment but nevertheless, they fixed a significant amount of $^{14}CO_2$. There was no significant $^{14}CO_2$ uptake by killed conidia. In addition, we have demonstrated $^{14}CO_2$ fixation by vegetative hyphae.

Table 1

Carbon dioxide fixation by A. nidulans conidia

Treatment	Spore density (conidia/ml of medium)	$^{14}CO_2$ uptake in counts/minute/ 1×10^7 conidia	
		After 2 h	After 6.7 h
1. U.V. killed conidia	5×10^7	276	280
2. Conidia suspended in medium lacking glucose	6×10^7	844	1,629
3. Conidia suspended in medium containing glucose	6×10^7	2,443	13,370

The experiment was carried out in sealed 50 ml Katz flasks containing 0.1% carbon dioxide in the gaseous phase. The flasks were shaken at 37°C and each contained 2 μC of ^{14}C.

We have also found that the CO_2 concentration in the atmosphere above a culture influences its radial growth rate (Table 2), the optimal concentration being 0.8%.

Table 2

Influence of carbon dioxide concentration on the radial growth rate of A. nidulans colonies

% CO_2 (v/v air) in gaseous phase above colony	0	0.2	0.4	0.8	1.5
Radial growth rate (μ/h)	273	286	295	301	288

Colonies were grown on a medium containing 1% glucose at 37°C. The CO_2 concentrations were maintained by Pardee's diethanolamine buffers.

We intend to continue this work by studying the metabolic fate of the $^{14}CO_2$ fixed and the effect of CO_2 on differentiation.

M. TYC

An attempt to produce interspecific hybrids between Aspergillus nidulans and Aspergillus rugulosus.

To obtain crosses between A. nidulans and A. rugulosus the nutritional mutants with different coloured conidia were employed. More than 20 different combinations of auxotrophs of mentioned strains were tried to synthesize heterokaryons. It was observed that one combination: A. nidulans ribo y nic

and A. rugulosus an formed a mixed culture on minimal agar. The heterokaryons were formed by the following technique: approximately equal number of conidia of the two strains were placed in 2 ml of liquid MM enriched with 2% liquid CM. This mixed suspension was incubated for two days at a temperature of 37°C. The mat formed on the surface was teased out onto solid MM and small fragments from the edge of the mat were detached with a nichrome wire and transferred to plates of MM. Heterokaryotic growth usually developed after a few days at 37°C.

All attempts to obtain a heterozygous diploid failed. The analysis of perithecia produced by mixed culture involved difficulties also. In order to prove that nutritional co-operation had been established between diverse nuclei in the same hypha, conidia were isolated from a single mixed head, which gave rise to both parental strains. Furthermore, pieces of putative heterokaryotic mycelium isolated by micromanipulation showed ability to grow on MM agar and to produce conidial heads of both component strains.

From heterokaryotic culture more than 50 perithecia were isolated and examined. Some perithecia yielded progeny resembling both parents and progeny decidedly different from either parents (resembling the aneuploids described by Käfer). The perithecia contained extremely few viable ascospores (1-30) although the estimation by haemocytometer count showed several thousand. The ascospores derived from the hybrid perithecia were of abnormal shapes.

It was observed that the heterokaryotic culture yielded conidial heads of both component strains at a temperature of 37°C. At 30°C only conidial heads of A. rugulosus appeared. The results suggest that the temperature of 30°C gave a selective advantage to the nuclei of A. rugulosus.

S. H. WEISBERG

Karyokinesis in Aspergillus nidulans

In Aspergillus News Letter No. 8, 1967, there appeared an article by Robinow and Caten titled, "Mitosis in Aspergillus nidulans." These authors omitted reference to a previous published paper entitled, "Karyokinesis of the Somatic Nucleus of Aspergillus nidulans. I. The Juvenile Chromosome

cycle (Feulgen Staining)", (Weijer and Weisberg, 1966. Can. J. Genet. Cytol. VIII, p. 361 - 374). In this study nine Feulgen-positive bodies were found attached end to end in a linear arrangement with the terminal body a triangular shaped centriole. This Feulgen-positive triangular centriole has been demonstrated previously in the hyphal nuclei of Neurospora crassa (Weijer et al., 1965, Can. J. Genet. Cytol. VII. p. 140 - 163).

This nuclear chain of chromosomes may be seen in a rod shape, or it may become crescent or ring shaped around a Feulgen-negative central body. These different nuclear configurations were not considered to be different stages in the division cycle but the result of cytoplasmic currents wrapping the linear nucleus around the Feulgen-negative central body (probably the nucleolus). The nuclear chain divided longitudinally (transversely) and the division was preceded by the division of the centriole. Cytoplasmic streaming was believed to aid in the separation of the daughter nuclei. Hyphal nuclear division proceeded rapidly until the medium was exhausted. At this stage the nuclei became spherical shaped (as in resting conidia) and the centriole was often seen outside the sphere but attached to it by a weakly Feulgen-positive thread. Upon further incubation and nutrition these resting nuclei enlarge into a large nuclear chain of chromosomes which belongs to the second chromosome cycle (Maturation Cycle.)

The Maturation Cycle, which gives rise to the conidiophore, has recently been investigated using a 5N HCl hydrolysis, Feulgen technique (Weisberg and Weijer, 1968, in press). In this cycle the chromosomes become much larger (polytenic) and spread out along the connecting thread. Chromosomes spread out along a thread 119 μ long have been photographed. This thread may be stained with acid fuchsin but is also commonly seen in Feulgen preparations under phase contrast.

Somatic nuclear division in Aspergillus was found to be closely related to the mode of division demonstrated in Neurospora by Weijer et al. (loc. cit.). Laane (Can. J. Genet. Cytol. IX, p. 342 - 351) in a study of nuclear division

in Penicillium expansum states that nuclear structures found in P. expansum have much in common with those found in A. nidulans and that "the interpretation of somatic nuclear division, as proposed by Weijer and co-workers, remains extremely attractive as a working hypothesis for the mode of karyokinesis in P. expansum" (p. 350).

GENE SYMBOLS IN ASPERGILLUS NIDULANS

J. A. ROPER

Professor Sermonti has expressed concern at the diversity of symbols used in microbial genetics and wonders whether Aspergillus workers might prefer to conform to the proposals made by Demerec et al. for bacteria. Professor Dorn is sympathetic to this idea and there follows a list of suggested symbols based on the Demerec system.

There has been little oppotunity to consult the views of other workers but some comments and suggestions by Dr. Clutterbuck follow those of Sermonti and Dorn.

I am rather reactionary and would prefer to keep at least most of the symbols at present in use. I fear that a substantial change might create difficulty in reading the earlier literature.

Views of other workers would be welcomed and can be given in summary or in detail, as required, in the next number of A.N.L.

If Dr. Clutterbuck's suggestion is adopted A.N.L. could act as a clearing house for the distribution of allele numbers.

G. SERMONTI

List of proposed symbols

A) metabolic mutations

(According to the proposal for a uniform bacterial genetics nomenclature by M. Demerec, E.A. Adelberg, A.J. Clark and Philip E. Hartman, Genetics, 54: 61 - 76, July 1966).

(genes determining and regulating ...)

aac	(aa)	allantoic acid biosynthesis (urea/ammonium requirement)
abt	(ab)	α-aminobutirate utilization
ade	(ad)	adenine biosynthesis
ane	(an)	aneurine biosynthesis
arg		arginine biosynthesis

bio	(bi)	biotin biosynthesis
cho		choline biosynthesis
cys		cysteine biosynthesis
fru	(fr)	fructose utilization
gal		galactose utilization
his		histidine biosynthesis
hyx	(hx)	hypoxanthine biosynthesis
ile		isoleucine biosynthesis
lac		lactose utilization
leu	(lu)	leucine biosynthesis
lys		lysine biosynthesis
mal		maltose utilization
met	(meth)	methionine biosynthesis
nic		nicotinic acid biosynthesis
nit	(ni)	nitrate reduction
orn		ornithine biosynthesis (see arg)
pab	(paba)	p-aminobenzoic acid biosynthesis
pan	(panto)	pantothenic acid biosynthesis
phe	(phen)	phenylalanine biosynthesis
pro		proline biosynthesis
put	(pu)	putrescine biosynthesis
pyr	(pyro)	pyridoxine biosynthesis
rib	(ribo)	riboflavine biosynthesis
slp	(s)	sulphate reduction
srl	(sb)	sorbitol utilization
thi		thiazole biosynthesis
trp	(tryp)	tryptophane biosynthesis
uac	(ua)	uric acid biosynthesis
ure	(u)	urea biosynthesis

B) Miscellaneous mutations

(Genes determining ...)

act		actidione biosynthesis
adr		response to actidione (resistance or sensitivity)
amm	(am)	glutamic dehydrogenase (α-aminonitrogen requirement when mutant)
azg		response to 8-azaguanine (resistance or sensitivity)
bla	(bl)	non-autonomous ascospore colour (blue or normal)

brw	(br)	conidial colour (brown or normal)
cha		conidial colour ("chartreuse" or normal)
cla	(cl)	non-autonomous ascospore colour (colourless or normal)
com	(c, co)	growth habit (compact or normal)
dil		conidial colour (dilute or normal)
dwf	(dw)	growth habit (dwarf or normal)
fac	(fl)	response to fluoro-acetic acid (resistance or sensitivity)
fan		response to fluoro-acetic acid (resistance or sensitivity) and acetate utilization.
fpa	(pfp, fp)	response to p-fluorophenylalanine (resistance or sensitivity)
fwn	(f, fw, a)	conidial colour (fawn or normal)
mag	(mg)	response to malachite green (resistance or sensitivity)
olv	(o)	conidial colour (olive or normal)
pal	(p)	colour of conidia (pale or normal)
pba	(palc)	alkaline and acid phosphatase
pbl		colour of conidia (pale blue or normal)
pea		colour of conidia (peach or normal)
pha	(pac, r?)	acid phosphatase
phb	(pal, pho, p, r?)	alkaline phosphatase
rst	(r)	growth habit (restricted or normal)
sml	(sm)	colonial size (small or normal)
sup-	(su-)	suppression of the mutant phenotype due to a mutation (to be indicated after the symbol sup-) in another gene
teo	(te)	response to teoquil (resistance or sensitivity)
whi	(w)	conidial colour (white or normal)
xdh		xanthine dehydrogenase
ylg	(yg)	conidial colour (yellow-green or normal)
ylo	(y)	conidial colour (yellow or normal)

A.J. CLUTTERBUCK

Gene symbols and nomenclature: proposals and notes on them

It has been suggested that the nomenclature of Aspergillus nidulans genetics should conform to that proposed for bacteria by Demerec et al. (Genetics 54, 61, reprinted in J. Gen.

Microbiol. 50, 1). The proposals below are intended as a move in this direction.

Proposals

1. New loci should be designated by three-letter, lower case symbols (using the symbols proposed for bacteria, where available).
2. Symbols in current use should not be changed except where conflicting symbols have been used for the same locus.
3. Wild-type alleles should be written xyz^{+} (not XYZ).
4. Different loci of similar phenotype, and bearing the same symbol, should be distinguished by an italicised capital letter following the symbol. If it is not known at which of several such loci a mutation has occurred, the capital letter should be replaced with a hyphen.
6. Strains should have a simple serial number preceded by an initial letter denoting the laboratory of origin.
7. There should be a clearing house for gene symbols and allele numbers.

Notes

1. The gene symbols should not indicate degree of dominance since alleles differing in dominance may be isolated at one locus. All new symbols should be submitted to the clearing house (see proposal and note 7) to prevent any conflict or ambiguity.
2. Relatively few conflicting gene symbols are in use and it is, therefore, considered that the gain in neatness obtained by change to a three-letter system would be more than offset by the confusion created when any reference is made to work using the old system.

   An important point of Demerec's proposals is that the symbols should not attempt an exact description of the function of the locus and, therefore, should not be changed when further information is obtained on the locus. A gene symbol should only be changed when it is discovered that the mutant concerned is allelic with a previously known mutant: in this case priority of symbols should be observed.

For the cases of conflict known to me I would propose the following:

fpa (pfp, fp) fluorophenylalanine resistance/ sensitivity (see Sermonti, this issue).

nia (ni, nia, cnx) nitrate utilization (as nitrogen source)

nii (ni, nii) nitrite utilisation (as nitrogen source)

3. -

4. Capital letters have been used for many loci in recent publications. These should also be applied retrospectively, therefore the following suggestions are made (the old locus number being shown here after the proposed capital letter).

AcrA1 acrB2

adC1 adD3 adE8 adF9 adG14 adH23 adI50

anA1 anB2

argA1 argB2 argC3

c1A4 c1B6

galA1 galB3 galC4 galD5 galE9

hisJ122

lacA1 lacB3

lysA1 (=lysA2) lysB5 lysC6 lysD7 lysE10 lysF51 (see Pees ANL 7)

methF1 methG2 methH3 (these are additions to the series proposed by Gajewski and Litwinska, ANL 8)

nicA2 nicB8 nicC10

ornA4 ornB7

pabaA1 pabaB22

phenA2 phenB6

proA1 proB3

riboA1 riboB2 riboC3 riboD5 riboE6 riboF7

sA1 sB3 sC12 sD50

For the location of these loci and for already accepted symbols, see Dorn(Genetics, 56, 619.)

In future if a second locus is found giving a phenotype shown by only one locus previously, the original locus should be given the letter A and the additional one the letter B.

5. See proposal and notes 7.

6. A suitable laboratory identification letter should be

worked out by collaboration with the clearing house (see 7). For strains obtained from Glasgow, it is hoped that a set of numbers can be worked out by agreement with the major centres holding Glasgow stocks within the near future. Such strains in other laboratories should then be given the same strain number, but recombinants or mutants obtained in other laboratories should bear a number in the series of that laboratory. (All these proposals apply only to stocks ultimately derived from the single wild-type which is the origin of all the Glasgow strains. All other Aspergillus nidulans strains should be kept completely separate.)

7. Professor Roper has said that he would be willing to provide a clearing house of the type proposed, and it would I am sure be appreciated as a very valuable service to all Aspergillus workers if he would do this. I therefore propose that anyone isolating mutants should ask Professor Roper to allocate a batch of isolation numbers, according to the number of mutants isolated or expected to be isolated. All new locus symbols should also be checked with Professor Roper.

This system will only work satisfactorily if workers describing new loci are willing to make strains available to other laboratories for testing for allelism. The most convenient method of doing this is by making use of the Fungal Genetics Stock Centre (Barratt, Johnson & Ogata, Genetics 52, 233).

Comments on these proposals and suggestions are welcome. If such a scheme is agreed to, the first step will be to inform the clearing house of all the locus symbols and isolation numbers at present in use in the various laboratories. It is hoped that this can be done before the publication of the next News Letter so that any necessary changes can be reported there.