CORRIGENDUM

Domain structure and function within the QUTA protein of *Aspergillus nidulans*: implications for the control of transcription

Ian Levesley, Giles H. Newton, Heather K. Lamb, Evert van Schothorst, Raymond W. M. Dalgleish, Anthony C. R. Samson, Clive F. Roberts and Alastair R. Hawkins

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Owing to a printer's error, some of the numbers in parentheses in Table 1 (p. 89) were omitted. The correct version of the table is given below.

Table 1. Genetic mapping of the *qutA* activator gene locus in *A. nidulans*

The numbers in the table represent the frequency (per 10⁶ ascospores plated in selective medium) of quinic-acid-utilizing recombinants (*qut*⁺) in crosses between the *qutA* mutants indicated. The arrows show on which side of the sign-post marker particular alleles are located, thereby defining the interval to which the mutation was allocated based upon the distribution of the *qutR16* flanking marker. Numbers in parentheses indicate very close linkage where the mutation could not be ordered with confidence. The phenotypes of heterozygous diploid strains with the *qutA*⁺ wild-type allele in combination with each mutant allele are shown based upon growth on quinic acid plates: diploids with a dominant *qutA* allele (D) produced no growth; recessive *qutA* alleles (R) full normal wild-type growth (identical with that of a *qutA*⁺/*qutA*⁺ homozygote); semi-dominant *qutA* alleles (SD) a marked decrease in growth, both in the density of the mycelium and amount of conidiation, their growth appearing roughly 75% of that compared to wild-type (100%) or the dominant mutants (0%).

R153 <i>qutA</i> strain	Phenotype	R21 <i>qutA</i> 552/633/506/636; <i>qutR16</i> strain			
		R153 <i>qutA</i>	R153 <i>qutA</i>	R153 <i>qutA</i>	R153 <i>qutA</i>
		× 552 (r)	× 633 (r)	× 506 (r)	× 636 (r)
380	R	417←		436←	
404	SD	133←		369←	
402	SD	172←		242←	
422	SD	63←		232←	
423	SD	70←		458←	
400	SD	19←		174←	
394	SD	(3)	88←	245←	106←
341	SD	→6	84←		165←
393	R	→10	136←	193←	214←
386	SD	→17	34←	151←	55←
4	SD	→23	22←	99←	127←
384	SD	→28	21←	83←	117←
399	R	→114	11←	47←	64←
385	R	→104	(0)	41←	10←
379	R	→141	(2)	32←	18←
324	R	→371	→33	(3)	
361	R	→163	→6	(2)	5←
389	SD			(2)	10←
390	SD	→868	→20	(1)	7←
303	R	→168	→66		(1)
444	R	→218	→39	→19	
382	D		→132	→23	→17
214	D	→286	→221	→144	→38