#### MUTANTS OF ASPERGILLUS NIDULANS LACKING MALATE SYNTHASE

## Susan ARMITT, C.F. ROBERTS and H.L. KORNBERG

Departments of Genetics and Biochemistry, School of Biological Sciences, University of Leicester, Leicester LE1 7 RH, England

Received 8 December 1970

### 1. Introduction

The enzymes isocitrate lyase and malate synthase are unique to the operation to the glyoxylate cycle, which functions anaplerotically during growth on acetate [1]. Although these enzymes have been studied in a number of fungi [2-4], little is known of their regulation in these eukaryotic organisms.

We have previously described [5] mutants of Aspergillus nidulans lacking isocitrate lyase activity, and have shown that this enzyme is necessary for growth upon acetate. It is the purpose of this paper to describe mutants of A. nidulans that lack malate synthase activity and to show that malate synthase is also necessary for growth upon acetate as sole source of carbon. The malate synthase-less mutants have been allocated to a gene designated mas which is located in linkage group I of A. nidulans, whereas the structural gene for isocitrate lyase maps in linkage group V [5]. Thus the two genes are unlinked, although the enzymes show coincident regulation.

### 2. Experimental procedures

Media and routine procedures for genetic analysis in Aspergillus nidulans were those described by Pontecorvo et al. [6]. Cultures for the determination of enzyme activities were grown in a defined liquid minimal medium [7]. Carbon sources and magnesium sulphate were sterilised and added separately. Cultures were started by inoculation with suspensions of washed conidia to give 10<sup>6</sup> conidia/ml of medium, and incubated at 37° with vigorous rotation of a gyrotary shaker.

Mycelium was harvested by filtration, washed with distilled water and resuspended in buffer, pH 7,5, containing 20 mM tris, 2 mM MgCl<sub>2</sub> and 1 mM EDTA. Cell-free extracts for enzyme assays were prepared, and their protein contents were measured, as previously described [5]. Malate synthase activity was assayed as the rate of release of coenzyme A.SH when extracts were incubated with acetyl-coenzyme A and flyoxylate [8].

### 3. Results and discussion

# 3.1. Malate synthase activity in mycelium grown upon different carbon sources

Low malate synthase activity was found in wildtype A. nidulans grown upon sucrose whereas this enzyme was present in high activity after growth on acetate (table 1). Malate synthase, like isocitrate lyase [5], is thus induced by growth on acetate. Growth of mycelium upon a mixture of acetate and glucose results in a malate synthase activity as high as that found on acetate alone, but mycelium grown on acetate and sucrose has about half this amount. A similar response was also observed for isocitrate lyase in mycelium grown upon these mixtures [5], and both sets of data are compatible with the observation that A. nidulans utilises acetate preferentially from a mixture of acetate and glucose but not from acetate with sucrose [9]. The activities of these two enzymes of the glyoxylate cycle in A. nidulans are thus coincident, indicating a common control mechanism.

Table 1

Malate synthase activity after growth on different carbon sources.

Carbon source	Conen. (M)	Time of harvesting (hr after inoculation)	Specific activity*
Acetate	0.1	24	4.0
Sucrose	0.02	18	0.1
Acetate	0.1	18	1.4
and Sucrose	0.02		
Acetate and	0.1	18	3.7
Glucose	0.02	10	3.1

<sup>\*</sup> Malate synthase activity was measured as the rate of glyoxylate dependent release of CoA-SH from acetylcoenzyme A, in the presence of the enzyme and glyoxylate [8]. Specific activities are expressed as µmoles of -SH formed/mg of protein/hr.

#### 3.2. Mutants lacking malate synthase activity

Mutants unable to utilise acetate for growth were isolated by filtration enrichment and replica-plating following ultraviolet irradiation. Among 93 such mutants, which grew normally on sucrose but did not grow on acetate alone, 9 had no detectable malate synthase activity after growth on a mixture of acetate and sucrose. All of these mutants were non-complementary in heterokaryon tests, indicating loss of the same function; they all map very closely to the bi-1 (biotin) locus in linkage group 1 and identify a single gene (mas) which we interpret as the structural gene for malate synthase. The mas gene is unlinked to the structural gene for isocitrate lyase (icl), which is located in linkage group V [5]. Both genes are distinct from the fac A. fac B and fac C loci described by Apirion [10], which confer resistance to fluoroacetate; such fac mutants also grow very poorly on acetate. However, fac mutants contain both malate synthase and isocitrate lyase, albeit in low activity; mas mutants and icl mutants retain the wild-type sensibility of fluoroacetate.

The mas mutants from normal levels of isocitrate lyase when, grown upon acetate with sucrose, and similarly the icl mutants have normal malate synthase activity. This latter observation argues against a sequen-

tial induction of malate synthase by the glyoxylate formed by isocitrate lyase.

# 3.3. Reversion of mas mutants and the role of malate synthase

Spontaneous revertants, able to grow on acetate, were selected from 4 different *mas* mutants; of these, 26 were tested for malate synthase activity after growth on acetate. All were found to have regained the enzyme, though some had less activity than wild-type; this supports the view that *mas* specifies a structural gene for malate synthase.

Together with the results of studies on the rate of isocitrate lyase [5], the present observations on malate synthase confirm that both these component enzymes of the glyoxylate cycle are necessary for the growth of A. nidulans upon acetate. Two main differences are apparent between the genetic control of this anaplerotic sequence in E. coli and in A. nidulans. Whereas the bacterium forms two types of malate synthase [11], A. nidulans forms only one; whereas in E. coli, the structural genes for isocitrate lyase and one of these malate synthases are co-transducible [12] in A. nidulans there is no close genetic linkage.

## Acknowledgements

We gratefully acknowledge the financial support of this work by the Science Research Council, through Grant B/SR/5943, and a Research Fellowship to S.A.

## References

- [1] H.L. Kornberg, Biochem. J. 99 (1966) 1.
- [2] R.B. Flavell and J.R.S. Fincham, J. Bacteriol. 95 (1968) 1063.
- [3] J.F. Collins and H.L. Kornberg, Biochem. J. 77 (1960) 430.
- [4] W.S. Wegener and A.H. Romano, J. Bacteriol. 87 (1964) 156.
- [5] S. Armitt, C.F. Roberts and H.L. Kornberg, FEBS Letters 7 (1970) 231
- [6] G. Pontecorvo, J.A. Roper, L.M. Hemmons, K.D. MacDonald and A.W.J. Bufton, Advan. Genet. 5 (1953) 141.

- [7] C.F. Roberts, Biochim. Biophys. Acta 201 (1970) 267.
- [8] L.N. Ornston and M.K. Ornston, J. Bacteriol. 98 (1969) 1098.
- [9] A.H. Romano and H.L. Kornberg, Proc. Roy. Soc. London Ser. B. 173 (1969) 475.
- [10] D. Apirion, Genet. Res. (Camb.) 6 (1965) 317.
- [11] E. Vanderwinkel, P. Liard, F. Ramos and J.M. Wiame, Biochem. Biophys. Res. Commun. 12 (1963) 157.
- [12] C.B. Brice and H.L. Kornberg. J. Bacteriol. 96 (1968) 2185.