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SHORT COMMUNICATION

M. Bibbins · N. J. Cummings · I. F. Connerton

DAB1: a degenerate retrotransposon-like element from *Neurospora crassa*

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Abstract A repeated DNA sequence in the genome of *Neurospora crassa* has been identified as a family of degenerate retroelements. Retroelements encode protein sequences with clear homology to the reverse transcriptase, RNase H and endonuclease products of the *pol* genes common to retroviruses and retrotransposons. These sequence comparisons place the *N. crassa* element within the *gypsy* group of retrotransposons, akin to other elements found in filamentous fungi. However, the *Neurospora* element is defective, as no flanking long terminal repeats (LTRs) could be distinguished and the *pol* gene homologues contain numerous stop codons as a result of multiple base substitutions. The base composition of the element displays significant under-representation of the dinucleotide CpA, the preferred target site of repeat-induced point mutation (RIP). The genomic sequences exhibit G:C to A:T transitions between copies which are diagnostic of RIP. The degenerate retroelement has accordingly been designated by the acronym *dab-1* (dead and buried).

Key words Transposon · *Neurospora crassa* · Repeat-induced point mutation (RIP) · Fungi

Introduction

Transposable elements constitute a major source of genetic variation in nature. Transposons found in a variety of eukaryotic organisms fall into two classes depending on their mode of replication: those that replicate via RNA intermediates, the retrotransposons, and those that replicate via DNA excision and reintegration. Transposon-like sequences are often identified as repeated sequences, with positional polymorphism reflecting their latent mobility functions. This is particularly true of the *gypsy* class (Doolittle et al. 1989) of retrotransposon-like elements in filamentous fungi. The genomes of the following species have been shown to contain such sequences: *Cladosporium fulvum* (*Cf*T-1; McHale et al. 1992), *Fusarium oxysporum* [*Fret 1* (Julien et al. 1992) and *skippy* (Anaya and Roncero 1995)], *Magnaporthe grisea* [*grasshopper* (Dobinson et al. 1993) and MAGGY (Farman et al. 1996)], *Botrytis cinerea* (Boty; Diolez et al. 1995), *Aspergillus nidulans* (*ans1*; Cullen et al. 1987; Britten et al. 1995), *Aspergillus fumigatus* (*Afut1*; Neuveglise et al. 1996) and *Ascobolus immersus* (*Mars* 4; Goyon et al. 1996). At present only the elements from *Magnaporthe grisea* exhibit evidence of active transposition (Valent and Chumley 1994). Whereas others clearly have the potential to transpose (*Cf*T-1, for example, has been shown to be transcribed and the RNA packaged into virus-like particles that contain reverse transcriptase; McHale et al. 1992), the elements *Fret1*, *ans1* and *Afut1* are almost certainly defective, as their coding regions are peppered with stop codons.

Repeated sequences in *Neurospora crassa* are subject to at least three mechanisms which lead to gene silencing. The RIP (Repeat-Induced Point mutation) effect in *Neurospora crassa* results in premeiotic disruption of repeated sequences by base pair changes which are often accompanied by cytosine methylation (Selker et al. 1987; Selker and Garrett 1988; Fincham et al. 1989). The base changes are exclusively G:C to A:T transitions, an observation which is consistent with a mechanism of deamination of the 5-methyl cytosine residues to generate thymine (Cambereri et al. 1989). In contrast to RIP, which occurs in the sexual phase, quelling occurs in vegetative cells and can often be observed post-transformation (Pandit and Russo 1992; Romano and Macino 1992). In addition to the nucleus carrying the triggering duplication, quelling also affects neighbouring nuclei in heterokaryons that lack the duplication.

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M. Bibbins · N. J. Cummings · I. F. Connerton (✉)
Department of Food Macromolecular Science,
Institute of Food Research, Earley Gate,
Whiteknights Road, Reading RG6 6BZ, UK
Fax: +44-1189-267917; E-mail: ian.connerton@bbsrc.ac.uk