The abundance of approximately 1200 new mRNAs increases dramatically during asexual reproduction (conidiation) in *Aspergillus nidulans* (1). About 200 of these RNAs are conidium-specific and the majority (85%) of the genes encoding these latter mRNAs are organized into tightly-linked clusters (2). The SpoC1 cluster comprises a 38 kb domain that includes 14 conidium-specific genes (3, 4) whose regulated expression appears to be controlled by a combination of regional depression via alterations in chromatin structure and trans-activation by conidium-specific transcriptional factors (5). Specific functions of gene products encoded by the SpoC1 cluster are unknown but are believed to be structural components of the conidium or to function in conidium maturation. The SpoC1-CID gene is one of the most highly regulated genes of this cluster and encodes a 794 nt mRNA that is present at 40 copies per conidium (3). Translation will yield a 151 amino acid, 15.8 kd polypeptide. Nucleotides are numbered on the left and amino acids on the right. Underlining indicates a potential promoter element (CAAT, TATA) or polyadenylation signal (AATAAA). Transcribed sequences are indicated by capital letters; > = transcriptional start site.

REFERENCES


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| ATACCGCGCTTGGTAGACGATGGTAGCAGCCAGTCCGATTTCACATCACAGGACATGCATTAGCTCATCCGGCCGCTGGTGATACAGCTGGGAAATCCACCGCAAGGCAATTCGCCGATA | 1 |
| ATCTGTCAGTCTGCGCGCGCTATAAACCCCGCTGATTACACATGCTATTCGCCGCTGGTGATACAGCTGGGAAATCCACCGCAAGGCAATTCGCCGATA | 101 |
| AAGGGAGACATCTCTGCGCGGTATCTAGTGGGACATCTGCTAGCTGGCCGCTGGTGATACAGCTGGGAAATCCACCGCAAGGCAATTCGCCGATA | 201 |
|  | 301 |
| MKPHCSSRSSGGLLALPRGGS | 401 |

**Amino Acid Sequences**

- **SpoC1-CID**
  - Translation will yield a 151 amino acid, 15.8 kd polypeptide. Nucleotides are numbered on the left and amino acids on the right. Underlining indicates a potential promoter element (CAAT, TATA) or polyadenylation signal (AATAAA). Transcribed sequences are indicated by capital letters; > = transcriptional start site.

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