# A gene from S. pombe with homology to E. coli RNAse III blocks conjugation and sporulation when overexpressed in wild type cells 

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We have screened the yeast $S$. pombe for genes capable of inhibiting conjugation and sporulation, two responses elicited by starvation. Haploid strain Sp870 (leul${ }^{-}$ura4- ) was transformed with Hind III partial digestion fragments of genomic DNA cloned into pWH5, a high copy shuttle vector expressing the S. cerevisiae LEU2 gene (1). $1.5 \times 10^{4}$ Leu + transformant colonies were stained with iodine vapor to identify colonies which did not contain spores (2). Plasmids were recovered from these colonies and retested. We thus identified three identical clones capable of efficiently inhibiting conjugation and spore formation upon retransformation into Sp870. Wild type haploid cells containing this plasmid have normal growth rate and morphology. Deletion analysis indicated that these biological effects are due to the expression of a single open reading frame, shown in Figure 1, capable of encoding a 363 amino acid protein. The first and last in frame stop codons are indicated in bold. We call this gene hcs for high copy sterile. Computer analysis revealed 24\% identity between hcs protein and E. coli RNAse III (see Figure 2), including an identical region of eleven amino acids. RNAse III has beeen implicated in the maturation of ribosomal RNA in E. coli, but may have other functions as well $(3,4,5)$. We speculate that hcs encodes a ribonuclease, that selectively degrades mRNAs encoding proteins essential for conjugation and sporulation in S. pombe. Regulation of the activity of hes may thus be one of the signal transduction events leading to conjugation and sporulation. Possibly similar RNAse might exist in higher organisms that coordinately regulate the expression of genes involved in differentiation. An S. pombe gene with identical coding potential has also been identified by M. Yamamoto and coworkers, University of Tokyo (personal communication).

## REFERENCES

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Figure 1. The nucleotide sequence of the region containing the hcs gene, and the encoded protein of 363 amino acids, are shown. Numbers on right are nucleotide coordinates and on left amino acid coordinates.

| hes | MGRFKRHHEGDSDSSSSASDSLSRGRRSLGHKRSSHIKNRQYYILEKKIRKLMFAMKALLEETKHSTKDD | 0 |
| :---: | :---: | :---: |
| n | VNLVIPGSTWSHIEGVYEMLKSRHDRQNEPVIEEPSSHPKNQKNQENNEPTSEEFEEGEYPPPLPPLRSE | 140 |
| RNAse 3 | MNPIVIN | 7 |
| $\cdots$ | KLKEQVFMHI SRAYEIYPNQSNPNELLDI HNERLEF LGDSFFNLFTTRIIFSKFPQMDEGSLSKLRAKFV | 210 |
|  |  |  |
| R | RLQRKLGYTFNHQ-ELLQQALTHRSASSKHNERLEFLGDSILSYVIANALYHRFPRVDEGDMSRMRATLV | 76 |
| : | GNESADKFARLYGFDKTLVLSY SAEKDQLRKSQKVIADTFEAYLGALI LDGQEETAFQWVSRLLQPKIAN | 280 |
|  | ...\|| ..... | I. .. .. ......||| || .|...||.. .|. . . . 1. |  |
| R | RGNTLAELAREFELGECLRLGPGELKSGGFRRESILADTVEALIGGVF LDSDIQTVEKLI LNWYQTRLDE | 146 |
| 8 | IT-VQRPIDKLAKSKLFHKYSTLGHIEYRWVDGAGGS-AEGYVIACIFNG-KEVARAWGANQKDAGSRAA | 347 |
|  | \|. ... | .. . . . .| |. |.. .....| | .| .| . . |.....|. || |  |
| 2 | :SPGDKQKDPKTRLQEYLQGRHLP LPTYLVVQVRGEAHDQEFTIHCQVSGLSEPVVGTGSSRRKAEQAA | 216 |
| \% | MQALEVLAKDYSKFAR | 363 |
|  | 1. |  |
|  | EQALkKlele | 22 |

Figure 2. The comparison of hcs protein with E. coli RNAse III. Amino acid identities between these two proteins are indicated by lines and conservative amino acid differences are indicated by dots.

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