

SUPPLEMENTARY MATERIAL

Table S1. Description of protein ORFs and tRNA genes identified in the genomic DNA surrounding *rac* genes

Gene	Locus	Description	EST clones /accession no.
<i>Ia/3-1</i>	–	Putative, incomplete	
<i>Ic/5-1</i>	–	Putative, incomplete	Weak similarity to SLE870, SLE392, SSD121
<i>A/3-1</i>	–	Sequence available too short	SSH551
<i>B/3-1</i>	–	Incomplete. No similarities	SLB253
<i>C/3-1</i>	–	Putative, incomplete	
<i>D/5-1</i>	–	Incomplete. Similarity to mouse SH3-domain containing adaptor protein (central part; 55%) and rat L-glutamine aminohydrolase (C-terminal part; 43%)	
<i>D/3-1</i>	–	Putative, incomplete	
<i>E/5-1</i>	<i>pcmA</i>	Similarity (60–69%) to PIMT or PCMT (L-isoaspartyl/D-aspartyl protein carboxyl methyltransferase or protein-L-isoaspartate (D-aspartate) O-methyltransferase) from several eukaryote species	SSE195, SSJ632, SSC895, SLB777, FC-BG10
<i>Phe-tRNA</i>	–	Accompanied by 240 nt of a TRE3-A, a non-LTR retrotransposable element that inserts downstream of tRNA genes. The full-length TRE3-A is 5.2 kb, therefore the element downstream of the Phe-tRNA could have undergone recombination	
<i>E/3-1</i>	–	Incomplete. Similarity (68–70%) to mammalian organic anion transporter/multidrug resistance-associated protein	Similar to SSM455
<i>F1/5-1</i>	–	Incomplete. Similarity (up to 50%) to diverse ABC transporter proteins	Similar to SSB583, SLD548, SLD691, SSA850
<i>Glu-tRNA</i>	–	Lacks a TRE5-A (DRE) repetitive element upstream, but there is instead a 730 nt region with 80–85% sequence similarity to other genomic clones, possibly a repetitive element not described so far	
<i>F1/3-1</i>	–	Putative, incomplete	
<i>F2/5-1</i>	<i>glTA</i>	Incomplete. Similarity (70–80%) to citrate synthase genes of various species	SLH712, SSC167, SSG229, SSD179. Similar to SSF821, SSG330, SSK530, SSL893, SLD239
<i>F2/3-1</i>	–	C-terminal part 60% similar to <i>A.thaliana</i> plant adhesion molecule 1, <i>D.melanogaster</i> extracellular matrix adhesion protein Pollux and human rab6 GTPase activating protein GAPCENA	SSK211. Similar to SSC437, SSB224, SLB536, SSG520, SLE119
<i>F2/3-2</i>	<i>lipB</i>	Similar to U12735 (aminoalcohol phosphotransferase)	AF019108
<i>G/5-1</i>	–	Similarity (59%) to AK000803 (unknown) and several human and mouse EST clones	SSK818
<i>G/3-1</i>	–	Incomplete. Similarity (60–66%) to <i>S.pombe</i> chromosome II cosmid c24C6, several mammalian EST clones and one <i>Botrytis cinerea</i> cDNA clone (unknown)	SSF876
<i>H/5-1</i>	<i>pspC</i>	Prespore-specific protein	AF104350
<i>H/3-1</i>	<i>bopA</i>	Incomplete. Central part 48% similar to mouse BOP, a zinc finger protein	AF104350; SSI618
<i>I/5-1</i>	–	C-terminal part contains PPOQPYGA repeats with similarity to <i>Neurospora crassa</i> annexin XIV and <i>D.discoideum</i> annexin VII repeats	SSB143, SLE552, SSB142, SSB172
<i>I/5-2</i>	–	Putative	
<i>I/5-3</i>	<i>rimA</i>	Similarity (62%) to <i>S.cerevisiae</i> RIM2, an internal membrane protein with similarities to mitochondrial ADP/ATP translocases	
<i>I/3-1</i>	Ψ <i>hirB</i>	Pseudogene. Contains stops and frameshifts due to insertions and deletions, and one putative intron with the donor site mutated, as deduced by comparison with similar EST clones and orthologues in mammals. The reconstructed amino acid sequence displays 40–50% similarity to eukaryotic HIRA, a nuclear protein, regulator of histone gene transcription in yeast	Similar to SSE152, SSA889
<i>J/5-1</i>	–	Similar (56%) to human CGI-128 or HSPC118 and orthologues in <i>S.cerevisiae</i> , <i>S.pombe</i> , <i>C.elegans</i> , <i>D.melanogaster</i> and <i>A.thaliana</i> . Similar (up to 68%) to numerous EST clones of animal and plant species	
<i>J/5-5</i>	–	Putative, incomplete	
<i>J/3-1</i>	<i>lagC3</i>	Incomplete. Similar to <i>Dictyostelium</i> lagC (54%) and lagC2 (59%)	SSL841, SLA 871
<i>K/3-1</i>	–	Weak similarity to AK000218 (unknown) and several mammalian EST clones	FC-BE14
<i>K/3-2</i>	–	Putative, incomplete	Similar to FCL-AC15, SSI371
<i>L/3-1</i>	–	Putative	

The genes have been named according to their position with respect to the *rac* gene of the contig where they are located (see Fig. 1). Except for the cases of already annotated genes (*lipB* and *pspC*) or genes represented by EST clones, all other ORFs have been identified by visual inspection. A locus name has been assigned when orthologues or paralogues could be reliably identified in the available databases. ORFs not represented by EST clones and with no homologues in the databases are designated as putative. Less than half of the protein ORFs identified correspond to genes whose function is known in *Dictyostelium* or in other species. Information on EST clones is available at <http://www.csm.biol.tsukuba.ac.jp/cDNAproject.html>.