SHORT COMMUNICATION

Isolation of a fragment homologous to the *rp49* constitutive gene of *Drosophila* in the Neotropical malaria vector *Anopheles aquasalis* (Diptera: Culicidae)

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The constitutive ribosomal gene rp49 is frequently used as an endogenous control in Drosophila gene expression experiments. Using the degenerate primer PCR technique we have cloned a fragment homologous to this gene in Anopheles aquasalis Curry, a Neotropical vector of malaria. In addition, based on this first sequence, a new primer was designed, which allowed the isolation of fragments of rp49 in two other species, Aedes aegypti (Linnaeus) and Culex quinquefasciatus Say, suggesting that it could be used to clone fragments of this gene in a number of other mosquito species. Primers were also designed to specifically amplify rp49 cDNA fragments in An. aquasalis and Ae. aegypti, showing that rp49 could be used as a good constitutive control in gene expression studies of these and other vectorially important mosquito species.

Key words: Anopheles aquasalis - Aedes aegypti - Culex quinquefasciatus - Drosophila constitutive gene - rp49 - rpL32 - mosquitoes

The ribosomal protein 49 gene (rp49) of the fruitfly *Drosophila* (O'Connell & Rosbash 1984), also known as rpL32 (http://flybase.bio.indiana.edu), has been widely used as an endogenous constitutive control in gene expression studies (e.g. Glossop et al. 1999, Goodwin et al. 2000, Kurapati et al. 2000, Stanewsky et al. 2002). The sequence of rp49 is also available for the mosquito *Anopheles gambiae* (Holt et al. 2002), the most important Afrotropical malaria vector, but until recently this gene had not been sequenced from other species of mosquitoes. As part of our molecular studies of insect vectors of tropical diseases, we attempted to clone a rp49 homologous fragment in *An. aquasalis*, a widespread Neotropical malaria vector that is associated with coastal habitats (Consoli & Lourenço-de-Oliveira 1994, Fairley et al. 2002, Forattini 2002).

Specimens used in this work were derived from a laboratory colony of *An. aquasalis* established in 1993 with around 200 females collected in a farm in Paracambi, Rio de Janeiro, Brazil (Carvalho et al. 2002). Using kits supplied by Amersham Biosciences, genomic DNA was isolated by means of the GenomicPrepTM Cells & Tissue DNA isolation kit; mRNAs with the QuickPrepTM Micro mRNA purification kit and cDNAs were synthesized using the First-Strand cDNA synthesis kit. PCR was performed in 40 µl using Tth DNA polymerase (Biotools) according

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to manufacturer's directions using various cycling conditions (see below) and the primers listed in the Table. PCR products were purified using either the Micro Spin S-400 HR Column (Amersham Biosciences) or the Wizard SV Gel and PCR Clean-up System (Promega), and cloned using the pGEM-T Easy Vector Kit (Promega). DNA sequencing was carried out in an ABI377 Sequencer using the Big Dye 3.1 Kit (Applied Biosystems).

The first rp49 fragment from An. aquasalis was obtained using cDNA as template and degenerate primers based on conserved regions identified by comparison between the putative protein sequences of D. melanogaster and An. gambiae. Initially, we conducted PCR using primers 5rp49deg1 and oligo-d(T)20 and the following cycling conditions: 94°C for 5 min; 15 cycles at 94°C for 1 min, 55°C (minus 1°C each cycle) for 1 min and 72°C for 2 min; then 20 more cycles at 94°C for 1 min, 50°C for 1 min and 72°C for 2 min. Although no amplification products could be detected by 2% agarose gel electrophoresis, a fragment of ~320 base pairs was observed after reamplification of 1 μ l of the first reaction using primers 5rp49deg1 and 3rp49deg3 (Fig. 1, Table), and 35 cycles at 94°C for 1 min, 50°C for 1 min, and 72°C for 2 min. This product was purified, cloned and sequenced as described above. Homology to rp49 was confirmed by comparison to the Drosophila sequence database using BlastX (http:// www.ncbi.nlm.nih.gov/).

Based on the *An. aquasalis rp49* cDNA sequence obtained, a specific primer (5aquaRP1, Fig. 1, Table) was designed and used with degenerate primer 3rp49deg3 in a new PCR (94°C for 5 min, followed by 35 cycles of 94°C for 30 s, 50°C for 30 s, and 72°C for 1 min) to amplify an *An. aquasalis rp49* 400 bp genomic sequence. This fragment was cloned and sequenced. Comparison with the

cDNA sequence confirmed the presence of an 88 bp intron, located in the same position as that of *D. melanogaster*.

Because primer 5aquaRP1 is in a conserved region, we tried to see if it could be used to isolate fragments of rp49 in other mosquito species. Aedes aegypti is a highly competent vector of dengue and urban vellow fever in Brazil and elsewhere (Lourenco-de-Oliveira et al. 2004); this mosquito originated from Africa and is now synanthropic (Alonso et al. 2003, Braga et al. 2004, Cunha et al. 2005) throughout the tropics (within the 20°C isotherm) between latitudes 45° N and 35° S approximately (Christophers 1960, Forattini 2002). The tropical house mosquito Culex *quinquefasciatus* is the urban vector of lymphatic filariasis (White & Nathan 2002) and transmits arboviruses such as St. Louis and West Nile (Service 2001). The primer 5aguaRP1 was used, together with oligo-d(T)20, to amplify rp49 cDNA sequences from these two species as described above. As before, products were observed only after a reamplification reaction, using primers 5aguaRP1 and 3rp49deg3. Fragments of \sim 300 bp obtained from Ae. aegypti and Cx. quinquefasciatus were purified, cloned and sequenced. Homology to rp49 was again confirmed by comparison to the Drosophila sequence database.

Fig. 1 gives the alignment of RP49 proteins from *D. melanogaster* and *An. gambiae* compared to the deduced amino acid sequences obtained from the fragments we isolated from *An. aquasalis, Ae. aegypti* and *Cx. quinquefasciatus* (sequences submitted to the GenBank, accession numbers AY539746 to AY539748). As shown, the amplified region is highly conserved with only a few substitutions observed among the five sequences.

To illustrate the use of *rp49* as an endogenous control in mosquitoes we designed a primer (5aquaexpRP) across the intron-exon boundary to specifically amplify cDNA sequences of An. aquasalis (Fig. 1, Table). Fig. 2 shows the results of PCR carried out using this and other primers. Lanes 1 and 2 show the amplification products obtained for An. aquasalis cDNA and genomic DNA, respectively, using the primers 5aquaRP1 and 3aeaquaRP1, flanking the intron that accounts for the size difference between the two fragments. Lane 3 is the negative control for these reactions. Lanes 4 and 5 show the results of PCR using primers 5aquaexpRP and 3aeaquaRP1 with the same templates and lane 6 is their respective negative control. Note that although some primer-dimer formation is observed in all three lanes, a 190 bp fragment corresponding to the expected size is amplified when cDNA, but not

TABLE

Degenerate and specific primers used to amplify the rp49 fragments of Anopheles aquasalis, Aedes aegypti, and Culex quinquefasciatus

Name	Sequence (5' — 3')			
5rp49deg1	GNCCNAARATHGTNAARAA			
3rp49deg3	TCYTTNGCNCKYTCNACDAT			
5aquaRP1	GTGAAGAAGCGGACGAAGAAGTT			
5aquaexpRP	GCTATGATAAGCTCGCTCCTGC			
3aeaquaRP1	TGCATCATCAGCACCTCCAGC			
5aeexpRP	GCTATGACAAGCTTGCCCCCA			
3aeaquaRP1b	TCATCAGCACCTCCAGCTC			
5aquaexpRP 3aeaquaRP1 5aeexpRP 3aeaquaRP1b	GCTATGATAAGCCGCTCCTGC TGCATCATCAGCACCTCCAGC GCTATGACAAGCTTGCCCCCA TCATCAGCACCTCCAGCTC			

	5rp49deg1	5aquaRP1	5aquaexpR 5aeexpRP	P		
D.melanogaster	MTIRPAYRPKIVKKR	TKHFIRHOSE	RYAKLSH	• WRKPKGIDNRVI	RRFKGOYLMPNIGY	G
An.gambiae	MAVRPAYKPKIVKKR	TKKFIRHOSE	RYDKLAPI	WRRPKGIDNRVI	RRFKGOYLMPNIGY	G
An.aquasalis	R	TKKFIRHOSE	RYDKLAP	WRRPKGIDNRV	RRFKGOYLMPNIGY	G
Ae.aegvpti		IRHOSE	RYDKLAPI	WRKPKGIDNRVI	RRFKGOYLMPNIGY	G
Cx.quinquefasciatus		IRHOSE	RYDKLAPN	WRKPKGIDNRVI	RRFKGOYLMPNIGY	G
		*****	** **:	** *******	****	*
		3aeaquaR	P1b			
		4	3aea o	uaRP1	3rp49deg3	
D.melanogaster	SNKRTRHMLPTGFKK	FLVHNVRELE	VLLMQNRV	YCGEIAHGVSS	KKRKEIVERAKQLSV	R
An.gambiae	SKKSTRHMLPTGFKK	FLVHNVRELE	VLMMQNRV	/YCAEIAHAVSSE	KKRKAIVERAKQLAI.	A
An.aquasalis	SNKRTRHMLPCGFKK	FLVHNVRELE	VLMMQNR	/YCAEIAHAVSSE	KKRKA	_
Ae.aegypti	SNKRTRHMLPNGFKK	FLVHNVRELE	VLMMQNRV	/YCAEIAHAVSSH	KKRKQ	_
Cx.quinquefasciatus	SNKRTRHMLPNGFKK	FLVHNVRELE	VLLMQNRV	/YCAEIAHGVASH	KKRKL	_
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D.melanogaster	LTNPNGRLRSQENE					
An.gambiae	VTNPNARLRAQEME					
An.aquasalis						
Ae.aegypti						
Cx.quinquefasciatus						

Fig. 1: alignment of the RP49 proteins from *Drosophila melanogaster* and *Anopheles gambiae* compared to the amino acid sequences encoded by the fragments obtained from *An. aquasalis, Aedes aegypti,* and *Culex quinquefasciatus.* Arrows point to the approximate location of the different primers used. The position of the intron found in the genomic sequences of *D. melanogaster, An. gambiae,* and *An. aquasalis* is indicated by an inverted triangle (∇) .

genomic DNA, is used as template. Similar results were obtained with *Ae. aegypti* using primers 5aeexpRP and 3aeaquaRP1b (data not shown).

Since *rp49* has been frequently used as an endogenous constitutive control in gene expression studies in *Drosophila*, its homologues from *An. aquasalis*, *Ae. aegypti*, *Cx. quinquefasciatus*, and other vector species might provide useful tools in molecular studies of these medically important mosquitoes.



Fig. 2: electrophoresis (agarose 2%) of the *Anopheles aquasalis rp49* PCR products. M- 100 bp ladder; 1: cDNA, primers 5aquaRP1 and 3aeaquaRP1; 2: genomic DNA, primers 5aquaRP1 and 3aeaquaRP1; 3: negative control, primers 5aquaRP1 and 3aeaquaRP1; 4: cDNA, primers 5aquaexpRP and 3aeaquaRP1; 5: genomic DNA, primers 5aquaexpRP and 3aeaquaRP1; 6: negative control, primers 5aquaexpRP and 3aeaquaRP1.

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