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Microbiology

## The polymorphic subtelomeric regions of *Plasmodium falciparum*

chromosomes contain arrays of repetitive sequence elements

(malaria/recombination/genome organization)

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620	Microbiology: de Bruin et al.	Proc. Natl. Acad. Sci. USA 91 (1994)
	RESULTS	a random clone isolated from the Malaysian CAMP strain
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	K3A K4HRP - GLARP - GLARP - MSA-2 - SERA	- wt70
Ĩ.		ID8 AA9 G FG9
	G7 ← FA3 ⊢ CB4 ← HG12	
	● DA12	4 BF4 4 CD12
·	FG9 CG7 CB4 Probe GC6 FA3	CHROMOSOME 2 YAC CONTIG CLONES HG12 DA12 ID8 GC1 HA11 BF4 AA9 CH4 DE12 CD12
	<b>R-CG7</b> + + + REP 20 +	
	- + + R-1A2 + - + +/_ R-FA3 +	+
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## FIG. 2. Southern analysis of PFG-separated parasite chromosomes identifies repetitive DNA elements. Parasite chromosomal DNA

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	vsis were carried out to localize the repetitive DNA elements	thereby preventing the silencing of transcriptional activity
	on the chromosome 2 telomere and subtelomere YAC clones.	(21-24). While the effect of <i>P. falciparum</i> subtelomeric
	GC6. CB4. and CG7. and on two additional. random telomere	sequences on either chromosome maintenance or transcrip-
	YAC clones. 1A3 and 2H1 (Fig. 3). The 60-kb telomere YAC	tional activity remains unclear, we propose a model whereby
	GC6	
	CB4	
}	CG7	
	2H1	H E N N N H A E   I I I I I I I
	YAC YAC Unique Unknown R- Left Arm Right Arm	-FA3 R-1A2 REP 20 R-CG7 Telomere

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FIG. 5. (A) Map of chromosome 2 subte-lomeric region. The left end of chromosome 2

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Construction of the second		16° ,
		contains ≈60-80 kb of repetitive DNA se-
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		These sequences display a conserved order
		between all chromosome ends examined.
		I ranscription units Hanking the KAHKP locus
		Transcription units flanking the KAHRP locus [the poly(A) <sup>+</sup> transcribed $K3A$ and $GLARP$ and the poly(A) <sup>-</sup> transcribed $KA^-$ ] are indi-
<u></u>	· · · · · · · · · · · · · · · · · · ·	and the poly(A) transcribed KA <sup>-1</sup> are indi-
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	*	cated (5). The approximate size range of the
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		zation of <i>P. falciparum</i> chromosome 2. The
F	N	chromosomal polymorphisms are restricted to
·······		within 100 kb at either end of the chromosome.
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for the second		The polymorphic ends are composed of con-
		The polymorphic enes are composed of com-
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		served arrays of repetitive DNA sequences
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