## Sequence and length polymorphism of a major malaria vaccine candidate analysed following DNA amplification

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We have applied polymerase chain reaction (1) combined with DNA sequence analysis to determine the structure of the variable region of the p190 allele from two *P.falciparum* isolates, Bandia-Senegal (2) and Palo Alto FUP-Uganda (3). This analysis revealed that both p190 alleles belong to the MAD20/Wellcome dimorphic group (4). The Bandia sequence is almost identical to that of the Wellcome strain except that it contains an additional tripeptide repeat (Figure 1). The Palo Alto sequence however, appears to have been generated by a crossover between the Wellcome and MAD20 alleles (indicated by arrow). Interestingly, the Palo Alto p190 sequence presented here, differs from that recently described for the Palo Alto FUP-Uganda isolate (5), implying that the isolate contains more than one *P.falciparum* strain; the individual culture conditions probably favouring the growth of one strain over another.

Bandia

WELL <u>GAATTCTTGTCAAAAAACTAGAAGCTTTA</u>GAAGATGCAGTATTGACAGGTTATAGTTTATTTCAAAAAGGAAA PA Bandia G WELL ARATGGTATTARATGARGGRACAAGTGGAACAGCTGTTACAACTAGTACACCTGGTTCAAAGGGTTCAGTTG PA. A G Bandia G TTCAGGTGGT WELL CTTCAGGTGGTTCAGGTGGCTCAGTTGCTTCAGGTGGC-----TCAGTTGCTTCAGGTGGCTCAGTTG PA Bandia WELL CTTCRGGTGGCTCRGTTGCTTCRGGTGGTTCRGGTRATTCRRGRCGTACRHATCCTTCRGATRATTCRRGTG F'A -----Bandia HELL ATTCAGATGCTARATCTTACGCTGATTTARAACACCAGAGGTACGARATTACTTGTTAACTATCAAAGAACTCA PA Bandia HELL ARTATCCTCRACTCTTTGATTTARCTRATCATATGTTARCTTTGTGTGATAATATTCATGGTTTCAAATATT PA Ξ> CCCGC G ACAA G G Bandia WELL TTAATTGATGGATCC PA

Fig.1 The N-terminal regions of the p190 alleles from isolates Bandia and Falo Alto (PA) and their comparison with the previously described Wellcome (WELL) sequence. The dotted lines indicate deletions and only base differences are shown. The oligomers used are underlined.

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