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Multigene family encoding malarial variance

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Plasmodium vivax is the most prevalent of the species of malarial parasite and causes severe disease, but unlike *P. falciparum* it is rarely fatal. In the 12 April [Nature](#), Hernando del Portillo and colleagues of the [Universidade de Sao Paulo](#), Brazil suggest a possible explanation for the difference in virulence between the two parasites.

Sequence analysis of a 155 kb yeast artificial chromosome clone from a *P. vivax* genomic library revealed a multigene family that is unique to *P. vivax* (*Nature* 2001, **410**:839-842). Southern blotting showed that the genes - designated *vir* (*P. vivax* variant genes) - are present in 600-1,000 copies on possibly all 14 *P. vivax* chromosomes. Analysis of sera isolated from *P. vivax* patients indicated that each patient was infected with a parasite expressing a different VIR protein variant. This suggests that *P. vivax* is able to establish chronic infections by varying its appearance to the immune system.

References

1. del Portillo HA, Fernandez-Becerra C, Bowman S, Oliver K, Preuss M, Sanchez CP, Schneider NK, Villalobos JM, Rajandream MA, Harris D: A superfamily of variant genes encoded in the subtelomeric region of *Plasmodium vivax*. *Nature* 2001, 410:839-842., [<http://www.nature.com/nature>]
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