Severe plasmodium vivax infections in children

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**Background:** Severe clinical cases exclusively associated with *Plasmodium vivax* are increasingly being reported worldwide with complications like renal failure, jaundice, acute respiratory distress syndrome, cerebral malaria, seizures, anemia, thrombocytopenia, pulmonary edema, splenic rupture and death. Recently vivax severity has been on the rise in India where *P. vivax* contributes in equal ratio with *P.falciparum* to the disease. Two main transporters studied with regard to chloroquine resistance (CQR) are chloroquine resistance transporter (*pvcrt-o*) and the multidrug resistance transporter (*pvmdr1*) orthologous to the *pfcr* and *pfmdr1* genes respectively. Even though these transporters are not established as molecular markers for CQR, they have a speculated role in CQR of *P. vivax*. Further, it has been demonstrated that the clinical severity in *P. vivax* could be associated with increased expression levels of *pvcrt-o* and *pvmdr1* genes.

We report here two cases of vivax malaria- a severe and non-severe case, diagnosed and confirmed by microscopy, rapid diagnostic tests and 18S rRNA PCR assay.

**Methods & Materials:** Relative quantification was carried out to find the expression levels of five *vir* genes (*vir 14-related, vir 12, vir 17-like, putative vir 14 and vir 10-related*) and two *P. vivax* speculated drug resistance genes viz. *P. vivax* chloroquine resistance transporter (*pvcrt-o*) and *P. vivax* multidrug resistance transporter (*pvmdr1*) gene. These genes were selected on the basis of their in silico data and a previous understanding of their speculated role in the pathogenesis of *P. vivax*.

**Results:** Expression *pvcrt-o* and *pvmdr1* genes and five *vir* genes (*vir 14-related, vir 12, vir 17-like, putative vir 14 and vir 10-related*), were measured simultaneously in these two cases for comparison. It was found that the expression levels of *pvcrt-o* and *pvmdr1* genes and *vir* genes (*vir 14-related, vir 12, vir 17-like and vir 10-related*), was much higher in the severe vivax isolate as compared to the uncomplicated case. Putative *vir14* gene was not expressed in the test and control isolates.

**Conclusion:** It brings to light how genes linked to the emerging CQR in *P. vivax* might impart virulence to vivax malaria making them excellent genetic markers for disease severity.

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