The genetic diversity in *P. vivax* populations is a major obstacle to the control and elimination of the parasite. This diversity influences the stability of transmission, the development of immunity and has consequences for the emergence and spread of virulent or drug-resistant mutations. A greater understanding of the *P. vivax* genetic populations could be critical for the control and elimination of malaria. Currently our ability to study these parasite populations is inhibited by a lack of standardised methodologies, which lag behind far behind those available for *P. falciparum*.

APMEN’s vivax working group (VxWG) had its inaugural meeting in February 2011 in Sri Lanka. At this meeting the harmonisation of *P. vivax* genotyping methods across the Asia Pacific was identified as a major research priority.

Potential applications of parasite genotyping include:
- Defining the origin and migratory patterns of clinically important parasite populations (eg outbreaks)
- Distinguishing between reinfection, relapse and recrudescence
- Improving the quality of data derived from epidemiological and clinical studies of *P. vivax*
- Investigation of molecular mechanisms of antimalarial drug resistance
- Monitoring the impact of control efforts in reducing parasite diversity

The first round of grants in the APMEN Research Grant Program includes five projects which focus on *P. vivax* genotyping. Most Country Partners have either already developed capacity for molecular malaria research or expressed an interest in developing such technology. The VxWG plans to develop a framework to share methods and findings describing the diversity of *P. vivax* across the region.

The objective of this one day workshop is to bring together researchers who are working on various aspects of *P. vivax* genotyping in order to:
- Review current status of the available *P. vivax* genotyping techniques
- Discuss the range of practical applications of *P. vivax* genotyping techniques
- Discuss a potential consensus protocol
- Discuss opportunities for collaborative studies

The workshop will bring together representatives from APMEN Country Partners, Partner Institutions, the WHO, recently awarded grantees, and four guest speakers recognised as international experts in molecular parasitology.
# Agenda

**Vivax Working Group: Plasmodium Vivax Genotyping Workshop**

<table>
<thead>
<tr>
<th>Time and Session</th>
<th>Session</th>
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<tbody>
<tr>
<td>10:00 – 10:30</td>
<td>Morning Tea</td>
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| 10:30 – 10:40    | Welcome and Introductions  
Prof Ric Price / Dr. Lorenz von Seidlein |
| 10:40 – 11:10    | Genotyping lessons learnt from *P. falciparum* and their application to *P. vivax*  
Dr Georges Snounou |
| 11:10 – 11:40    | Genotyping opportunities in *P. vivax*  
Dr Qin Cheng |
| 11:40 – 12:10    | *P. vivax* Genotyping for population genetic characterisation  
Dr John Reeder |
| 12:10 – 12:30    | Discussion on genotyping applications |
| 12:30 – 13:30    | Lunch |
| 13:30 – 14:10    | Practical aspects of genotyping  
Dr Sarah Auburn |
| 14:10 – 14:30    | Discussion on practical aspects of genotyping |
| 14:30 – 14:35    | Introduction to project presentations  
Dr Lorenz von Seidlein |
| 14:35 – 14:50    | Dr Gao Qi |
| 14:50 – 15:05    | Dr Rintis Noviyanti |
| 15:05 – 15:20    | Dr Noor Rain Abdullah |
| 15:20 – 15:35    | Dr Gawrie Nirdoshi Gallapaththy |
| 15:35 – 15:50    | Dr Preethi Udagama-Randeniya |
| 15:50 – 16:00    | Discussion on project presentations |
| 16:00 – 16:30    | Afternoon Tea |
| 16:30 – 17:00    | Introduction to whole genome sequencing in *Plasmodium*  
Dr Olivo Miotto |
| 17:00 – 17:20    | Discussion on whole genome sequencing |
| 17:20 – 17:50    | Summary and Discussion  
Prof Ric Price / Dr Lorenz von Seidlein |