

Y CHROMOSOMAL DNA VARIATION OF THE FILIPINO POPULATION AT 34 Y CHROMOSOME SPECIFIC SHORT TANDEM REPEAT (STR) MARKERS

Jazelyn M. Salvador¹, Jae Joseph Russell B. Rodriguez², Altair B. Agmata¹, Maria Lourdes D. Honrado¹, Gayvelline C. Calacal¹, Maria Corazon A. De Ungria¹

¹DNA Analysis Laboratory, Natural Sciences Research Institute, University of the Philippines

²Genetics and Molecular Biology Division, Institute of Biological Sciences, College of Arts and Sciences, University of the Philippines Los Baños, College

Male-specific polymorphisms on the non-recombining portion of the Y-chromosome, specifically short tandem repeat (STR) markers, have become an important tool for forensic investigations. In the Philippines, currently available Y-STR sets (8-11 Y-STRs) are used in deficient paternity testing cases; in the detection of the male DNA fraction in vaginal smears/swabs collected in sexual assault cases; and in the identification of disaster victims and missing persons by direct comparison with the Y-STR DNA haplotype of patrilineal male relatives. However, the current Y-STR sets provide limited resolution to paternally-related males and inbred communities. In the past two years, a set of 13 Y-STR markers termed as '*rapidly mutating (RM) Y-STR*' were identified which have a 6.5-fold higher mutation rate than the standard Y-STR markers. In addition, a new Y-STR multiplex system from Promega, known as PowerPlex® Y23, was launched which combines the markers included in the PowerPlex® Y (Promega) and AmpF/STR® YFiler® (Applied Biosystems) kits with six additional Y-STR markers, two of which are RM Y-STR markers. Because of the potential use of an expanded panel of conventional Y-STR and RM Y-STR markers in forensics, there is a need to further expand the existing Philippine Y-STR database across these markers. We report here the analysis of additional Filipino samples (n=155) using the PowerPlex® Y23 and RM Y-STR protocol (International RM Y-STR Study group, unpublished). Allele and haplotype frequencies and, gene and haplotype diversities will be calculated. Likewise, application of the use of this database on assessing sibling relationships will be reported.