

ABSTRACT #99 **The use of PCR-SSP to determine the frequency of MHC class I alleles in Chinese rhesus macaques** Daniel Wambua, Christopher Solomon¹, Sergio Itai, Alessandro Sette², Bianca Mothe¹ Department of Biological Sciences, California State University San Marcos, San Marcos, CA 92096-0001², Vaccine Discovery, La Jolla Institute for Allergy and Immunology, La Jolla, CA 92037 Background: Relatively little is known about MHC class I allele frequency within the Chinese rhesus macaque population. This study is therefore one of the first efforts to discover the frequency of several alleles within a cohort of rhesus macaques obtained from different sources. In this study, we performed PCR-SSP to examine the frequency of three alleles namely: MamuA1*2601, Mamu-B*3901 and Mamu-B*9001. With the knowledge of MHC class I composition, vaccine researchers may better design their studies, as well as gain insight into viral pathogenesis. PCR-SSP also helps identify high frequency alleles, and is a quick and effective genotyping technique for screening large cohorts of rhesus macaques. Methods: Whole blood was collected from several primate research centers. mRNA was extracted from these samples and was used to generate cDNA which served as a template in PCR-SSP using previously published primers (Karl et al. Immunogenetics 2008). 101 samples were tested for A1*2601, 92 for B*3901 and 91 for B*9001. Gel electrophoresis was performed on the PCR products, and appearance of a 500 base pair amplification product was used to score samples as positive. Results: We observed that 8 of 101 samples were positive for A1*2601, (7.92%), 9 of 92 were positive for B*3901 (9.78%) and 7 of 91 were positive for B*9001, (7.69%). Conclusion: We observed that alleles: Mamu-A1*2601, Mamu-B*3901 and Mamu-B*9001 are at lower frequency compared to previously reported Indian rhesus macaque alleles (Kaizu et al. Immunogenetics 2007). Knowing which alleles prevail in rhesus macaques will help vaccine researchers to better design their studies. This information also helps in designing studies aimed at looking at the immunologic effect of certain alleles in viral pathogenesis as well as identifying high frequency alleles which become potential candidates for further characterization. [Supported by 1R01AI070902-01A2 to BRM and AS and 2R15AI064175-02 to BRM]