

Characterization of the Class I Major Histocompatibility complex of the *Macaca fascicularis*

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Abstract

In an attempt to establish *Macaca fascicularis* as a viable animal model for disease studies, characterization of the MHC class I genes is necessary. The necessity arises because the MHC class I molecules have a functional role in immune response. Pig-tailed macaques (*Macaca nemestrina*) and rhesus macaques (*Macaca mulatta*), two species closely related to *Macaca fascicularis* have been commonly used to model HIV infection and are well characterized in regards to their MHC class I molecules. As an initial step in establishing *M. fascicularis* as an animal model, we have cloned and characterized both classical and non-classical MHC class I genes and have identified 21 MHC class I alleles orthologous to rhesus and pig-tailed macaque MHC-B, -E, and -F genes. No MHC-C locus was detected in the *M. fascicularis*. The MHC-B alleles from *M. fascicularis*, *M. mulatta* and *M. nemestrina* form a single highly polymorphic group.

Figures

| Figure | | Page |
|------------|--|------|
| Figure 1. | Crystallized structure of HLA-A locus molecule. | 2 |
| Figure 2. | Crystallized structure of the binding groove in an HLA-A molecule. | 3 |
| Figure 3. | Crystallized structure of binding groove in an HLA-A molecule. | 4 |
| figure 4. | Haplotype map for Human and Macaque MHC class I region. | 6 |
| figure 5. | Nucleotide MSA for clones from <i>M. fascicularis</i> | 18 |
| figure 6. | Amino acid MSA for <i>M. fascicularis</i> sequences. | 26 |
| Figure 7. | Phylogenetic tree of of MHC class I sequences from Macaques. | 32 |
| Figure 8. | Phylogenetic tree of B locus MHC sequences from Macaques | 33 |
| Figure 9. | Phylogenetic tree of B and F binding pocket sequences from Macaques | 37 |
| Figure 10. | Pocket Extractor Query | 38 |
| Figure 11. | Pocket Extractor Results | 39 |
| Figure 12. | MSA of B and F binding pockets for HLA-B*27 alleles and 15-1 | 40 |

Tables

| Table | | Page |
|----------|---|------|
| Table 1. | Relationship between Animal ID numbers and clones obtained from that individual | 7 |
| Table 2. | Primers used for amplification and sequencing of MHC class I cDNAs from <i>M. fascicularis</i> | 11 |
| Table 3 | Amino acid positions in the mature protein contributing to the B and F binding pockets. | 16 |
| Table 4. | B and F binding pockets for B-locus alleles from <i>M. fascicularis</i> | 34 |
| Table 5. | B and F binding pockets for E and F locus alleles from <i>M. fascicularis</i> | 34 |
| Table 6. | <i>Synonymous (ds) and non-synonymous (dn) substitution rates in different regions of MHC Class I alleles</i> | 35 |

Table of Contents

| | |
|---|-----|
| Title Page | i |
| Abstract | ii |
| List of Figures | iii |
| List of Tables | iii |
| Table of Contents | iv |
| Introduction | 1 |
| Materials and Methods | 7 |
| Animals | 7 |
| cDNA Clones | 7 |
| PCR Experiments | 8 |
| Sequencing | 8 |
| Synonymous and non-Synonymous Substitutions | 12 |
| Nomenclature | 12 |
| Wisconsin GCG Package | 13 |
| Pocket Extraction | 16 |
| Peptide Binding | 17 |
| Results | 17 |
| Discussion | 41 |
| References | 45 |
| Appendix A – Peptide Binding Fragments | A1 |
| Appendix B – Pocket Extractor Code | B1 |