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Searching Genes for Endocellular Lifestyle of X-bacteria in *Amoeba proteus*: A Comparative Genomic Analysis

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The X-bacteria in *Amoeba proteus* are in symbiosis with their host and could not be cultivated in vitro. The lifestyle of the bacteria is similar to Legionella as they enter amoebae through phagocytic pathway and survive in symbiosomes. In order to understand the mechanism for intracellular survival and integration to the host we performed comparative genomic analysis of the X-bacteria. A total of 291 non-redundant plagues from the genomic DNA library of 3106pfu was tagged by nucleotide sequencing. In summary, we tagged 593 genes in 461,748 bp. The average G+C content was 39.91%. The AT richness is a feature of endo-cellular symbiotic and parasitic prokaryotes. In a similarity search we identified 207 tags for genes of known functions and 99 tags for genes of unknown functions. The rest 217 tags had low homology. We completed 20 ORFs by subcloning and additional sequencing. Identified genes to be related with infection and endocellular lifestyle of X-bacteria were *dpsA*, a GTP-binding protein, *mazEF*, multidrug efflux systems (*oprN, norM*), *dnaK, dnaJ*, virulence system (*icm, dot*), type ? secretion system (*lvhB, lvrC*), intracellular infection related genes (*rcp, trpC*), mating system (*tra, trb*), sensor kinase, chemiosmotic efflux system protein A-like protein, Na+/Ca+ exchanger family (*necA*) and several transporter related genes. A comparative genomic analysis of non-cultivatable symbiotic x-bacteria would promote our understanding for the mechanism of endocellular lifestyle of the obligate symbionts.

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Y-chromosomal DNA Haplogroups and their Implications for the Dual Origins of the Koreans

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We have analyzed eight Y-chromosomal binary markers (YAP, RPS4Y711, M9, M175, LINE1, SRY+465, 47z, and M95) and three Y-STR markers (DYS390, DYS391,and DYS393) in 738 males from 11 ethnic groups in east Asia to study the male lineage history of Korea. Haplogroup DE-YAP was found at a high frequency only in Japan but was also present at low frequencies in northeast Asia, including 2.5% in Korea, suggesting a northern origin for these chromosomes. Haplogroup C-RPS4Y711 was present in Korea and Manchuria at moderate frequencies: higher than in populations from southeast Asia, but lower than those in the northeast, which may imply a northern Asian expansion of these lineages, perhaps from Mongolia or Siberia. The major Y-chromosomal expansions in east Asia were those of haplogroup O-M175 (and its sublineages). This haplogroup is likely to have originated in southern east Asia and subsequently expanded to all of east Asia. The moderate frequency of one sublineage in the Koreans, haplogroup O-LINE1 (12.5%), could be a result of interaction with Chinese populations. The age of another sublineage, haplogroup O-SRY+465, and Y-STR haplotype diversity, provide evidence for relatively recent male migration, originally from China, through Korea into Japan. In conclusion, the distribution pattern of Y-chromosomal haplo-groups reveals the complex origin of the Koreans, resulting from genetic contributions involving the northern Asian settlement and range expansions mostly from southern-to-northern China.

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Population Genetics of Twelve STR loci - D3S1358, vWA, FGA, TH01, TPOX, CSF1PO, D5S818, D13S317, D7S820, FESFPS, F13A01 and D16S539 in a Korean Population

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Allele frequencies for twelve STR loci(D3S1358, vWA, FGA, TH01, TPOX, CSF1PO, D5S818, D13S317, D7S820, FESFPS, F13A01, D16S539) obtained from a sample of 300 unrelated individuals living in Chungcheong-do, South Korea were studied. Genotypes for twelve STR loci were determined usingcommercial PCR amplification kits. Allele frequencies, heterozygosity, power of discrimination, power of exclusion typical paternity index, and polymorphism information content of each locus were calculated by statistical analysis. For forensic testing, The power of discrimination(PD) index ranged from 0.801 at TPOX to 0.961 at FGA. The combined probability of match(PM) calculated from twelve STR loci was 2.10 X 10-12, which is highly informative. The Exact Test demonstrated that all loci were found to be no deviations from Hardy-Weinberg expectations(P >0.05). In addition, the results demonstrate the assumption of independence within and between the loci analyzed.

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Isolation of Microsatellite Loci in the Pacific Abalone, *Haliotis discus hannai*

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The Pacific abalone, *Haliotis discus hannai*, is distributed along the coastal waters of Korea, where it is one of the most valuable and popular fisheries resources.To find genetic markers associated with loci that control economically important traits to assist in selective breeding programs, the development of molecular markers is needed. Microsatellites are tandemly repeated arrays of short nucleotide motifs found in all prokaryotic and eukaryotic genomes analyzed to date. Recently, various approaches have been developed to enrich for microsatellites. In this research we used the magnetic bead hybridization selection method, a protocol that is commonly used in enrichment procedures. An enriched library of about 800 white colonies was screened using the PCR-based technique, and 308 clones were identified by the presence of two or more bands on the agarose gel. Now, from the sequencing of the 308 clones, primer pairs are designing for sequences with long, uninterrupted repeats and adequate unique regions flanking the microsatellite array.