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Efficiency of DNA Mini-barcode for Identification of Insect Foreign Matters in Food

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Insect pests that are found in food are of great economic and hygienic significance. In recent years, DNA barcoding has emerged as a powerful tool for species identification. Conventional DNA barcoding uses a 650 bp DNA barcode of the mitochondrial gene COI for species identification in animal groups. However, PCR amplification and sequencing of a 650 bp fragment is difficult to obtain in old specimens and samples which have been processed with DNA-unfriendly preservatives. In this study, we tested the efficiency of shorter barcode sequences, termed as 'DNA mini-barcode', for identification related to insect foreign matters in food. We used full length COI barcode sequences of 45 species, 120 individuals of insect food pest and calculated the probability of having species-specific barcodes for varied size fragments. Pairwise sequence divergence was calculated using the Kimura two-parameter model, and a neighbor-joining tree based on calculated generic differences among and within species was constructed. As a result, both the full-length and mini-barcodes of 130 bp from the standard barcode region were shown to be effective for identifying majority of insect food pest specimens.

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The Complete Mitochondrial Genome Sequences of *Trinorchestia longiramus* (Crustacea: Amphipoda: Talitridae)Ye-Seul Baek¹, Sanghee Kim¹, Gi-Sik Min², Han-Gu Choi¹¹Division of Life Sciences, Korea Polar Research Institute, Incheon 406-840; ²Department of Biological Sciences, Inha University, Incheon 402-751

The talitrid amphipods are common in sand beaches, estuarine marshes, shores of lakes and rivers around the world. They are detritivores and preys for birds and other animals, and play an important role in the food chain of ecosystem. Despite of their significance and vast diversity, no complete mitochondrial genome data have been available so far. Mitochondrial genomes contain the most informative sequences and gene arrangement for deeper phylogenetic analyses and they reflect evolutionary relationships and biogeography in the metazoans. In the present study, we describe the mitochondrial genome (mitogenome) sequences of two talitrid species: *Trinorchestia chilensis* and *Trinorchestia longiramus*. *Trinorchestia chilensis* was collected in the subantarctic area and *T. longiramus* was collected from the east coastal area in Korea. To analyze the mitogenome of the talitrids, we obtained the sequences of COI, 12S, 16S, CO3 and Cytb in each talitrid using universal primers published or newly designed in our group and then, amplified the complete mitogenome of using long-PCR and genome walking techniques. As it has been reported that some species in extreme environment show unusual mt genome composition and structure, we attempted to compare mitochondrial genome features of two species inhabiting in the Subantarctic South Korea. Also, we attempted to solve the ordinal relationships of Amphipoda in Class Malacostraca of Subphylum Crustacea by phylogenetic analysis using sequence data from mitochondrial protein-coding genes. Our result would provide a useful information for studying phylogenetic relationships of talitrid and be helpful in the further crustacean phylogenetic study.

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The Complete Mitochondrial Genome of the Arctic Calanoid Copepod, *Calanus hyperboreus* (Copepoda, Calanoida)Sanghee Kim¹, Gi-Sik Min², Han-Gu Choi¹¹Division of Life Sciences, Korea Polar Research Institute, Incheon 409-840; ²Department of Biological Sciences, Inha University, Incheon 402-751, Korea

Copepods are the most diverse and abundant groups in aquatic ecosystems and also dominate in polar ecosystem. Despite of their abundance and vast diversity, few complete mitochondrial genome data have been reported so far. Mitochondrial genomes contain the most informative sequences and gene arrangement for deeper phylogenetic analyses and they reflect evolutionary relationships and biogeography in the metazoans. In an attempt to get more mt genome data of polar organisms, we selected two calanoid copepod species: *Boeckella poppei* and *Calanus hyperboreus*. *Boeckella poppei* and *Calanus hyperboreus* are considered being endemic species in Antarctic and Arctic, respectively. Firstly, we obtained the sequences of COI, 12S, 16S, CO3 and Cytb in each copepod using universal primers published or newly designed by our group. The long-PCR fragments in various combinations were amplified and sequences were analyzed. In our result, the gene arrangement of *C. hyperboreus* is very distinctive compared to the pan-crustacean ground pattern. The interaction between adaptation in the harsh environment and mt genome rearrangement has been postulated in several studies. Therefore, we attempted to compare mt genome of Arctic *C. hyperboreus* with non-polar habiting *Calanus sinicus* previously published. Also, we compared mt genomes between Arctic *C. hyperboreus* and Antarctic *B. poppei* to investigate the possible correlation between environment and mitogenomic features. In addition, we attempted to solve the ordinal relationships of copepods in Subphylum Crustacea by phylogenetic analyses using sequence data from mitochondrial protein-coding genes.

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다래(*Actinidia arguta*)의 품종간 유전적 변이와 유연관계 분석

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다래 (*Actinidia arguta*) 12품종과 백제 고분 유래 다래 종자 품종의 유전적 다양성을 비교분석하고자 Barcode DNA인 NADH dehydrogenase 유전자 (*ndh1*)의 primer를 이용하여 PCR을 수행하였다. 다래 12품종과 백제 고분 유래 다래 종자에서 확인된 *ndh1* 유전자는 425 bp의 크기였다. 백제 고분에서 발견된 다래로 추정되는 2개의 종자의 *ndh1* 유전자 서열은 다래의 공통서열과 정확히 일치하여 다래 종자임을 알 수 있었다. 다래 12 품종과 고대 다래의 *ndh1* 서열의 비교분석에서 1-188번, 336-425번까지의 서열은 모두 일치하였다. 다래 12품종에서도 제주 섬 다래 품종의 경우 16개의 변이를 보였고 이 중에는 염기가 변이 되거나 없어진 것도 있었다. 또한 광산, 다용 품종도 각각 하나씩의 염기 변이를 보였으나 다래 품종의 유전자원은 잘 보존되고 있음을 알 수 있었다. 이상에서 다래의 품종간 유전자 분석에 primer *ndh1*가 유용할 수 있었다.

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Genetic (Scrophular) Sequence

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Genus Ps which include very In addition genus are examined DNA (nrDNA) taxa of P relationship of the nrDNA giving an characters, parsimony both neighbor methods. data were sequence currently kiusianum infragener