

Phylogenetic Relationships of Waders (Charadriiformes: Scolopacidae) in Sarawak Inferred from Cytochrome Oxidase I and Recombinant Activating Gene 1

(Hubungan Filogenetik Burung Laut (Charadriiformes: Scolopacidae) di Sarawak yang Tersimpul daripada Sitokrom Oksidase I dan Rekombinan Gen Pengaktif 1)

NURUL ASHIKEEN AB RAZAK*, MUSTAFA ABDUL RAHMAN & ANDREW ALEK TUEN

ABSTRACT

Family Scolopacidae includes the sandpipers, shanks, snipes, godwits and curlews. Systematic classifications of shorebirds at the higher level have been successfully resolved. Nevertheless, the phylogeny of shorebirds in the familial level is still poorly understood. Thus, this phylogenetic study on Scolopacidae was conducted upon the framework provided by the first sequence-based species-level phylogeny within the shorebirds to determine the phylogenetic relationships among family members of Scolopacidae in West Borneo, Sarawak using combined gene markers, mtDNA Cytochrome Oxidase I (COI) and nucDNA Recombinant Activating Gene 1 (RAG1). A total of 1,342 base pair (bp) were inferred from both COI and RAG1 gene from 45 sequences constituted of 15 species Scolopacidae sampled from Sarawak namely Xenus cinereus, Actitis hypoleucos, Tringa totanus, Tringa glareola, Tringa stagnatilis, Heteroscelus brevipes, Calidris alba, Calidris ruficollis, Calidris ferruginea, Calidris tenuirostris, Calidris alpina, Gallinago stenura, Gallinago megala, Numenius arquata, and Numenius phaeopus. The phylogenetic tree was constructed with Charadrius mongulus derived as an outgroup. The Bayesian Inference (BI) tree constructed supported grouping of species into several lineages of Numeniinae, Calidrinae, Scolopacinae and Tringinae. The groupings of species into several lineages correlate with morphological features that contribute to their adaptation and ability of the species to fit to their ecosystems.

Keywords: Cytochrome Oxidase I; phylogenetic; Recombinant Activating Gene 1; waders

ABSTRAK

Famili Scolopacidae merangkumi burung kedidi biasa, burung kedidi kaki merah, burung berkek dan burung kedidi kendi. Pengelasan sistematik burung laut pada peringkat lebih tinggi telah berjaya diselesaikan. Namun, filogeni burung laut pada peringkat famili masih belum difahami. Sehubungan itu, kajian filogenetik ke atas Scolopacidae telah dijalankan mengikut rangka kerja yang diberikan oleh filogeni berasaskan-urutan-pertama aras-spesies dalam kalangan burung laut untuk mengenal pasti hubungan filogenetik dalam kalangan famili Scolopacidae di barat Borneo, Sarawak, menggunakan penanda molekul berbeza; mtDNA Sitokrom Oksidase I (COI) dan nucDNA Rekombinan Gen Pengaktif 1 (RAG1). Sejumlah 1,342 pasangan asas (bp) diperolehi daripada kedua-dua jenis gen COI dan RAG1 daripada 45 jujukan merangkumi 15 spesies Scolopacidae yang disampel dari Sarawak iaitu Xenus cinereus, Actitis hypoleucos, Tringa totanus, Tringa glareola, Tringa stagnatilis, Heteroscelus brevipes, Calidris alba, Calidris ruficollis, Calidris ferruginea, Calidris tenuirostris, Calidris alpina, Gallinago stenura, Gallinago megala, Numenius arquata dan Numenius phaeopus. Pokok filogenetik telah dibina menggunakan Charadrius mongulus sebagai kumpulan luar. Pokok Bayesian Inference (BI) yang dibina menyokong perkumpulan spesies mengikut keturunan masing-masing iaitu Numeniinae, Calidrinae, Scolopacinae dan Tringinae. Perkumpulan spesies kepada beberapa keturunan berkait rapat dengan ciri morfologi yang telah menyumbang kepada adaptasi dan kebolehan spesies ini menyesuaikan diri dalam ekosistem mereka.

Kata kunci: Burung laut; filogenetik; Rekombinan Gen Pengaktif 1; Sitokrom Oksidase I

INTRODUCTION

Shorebirds are embedded in order Charadriiformes consisting more than 350 species and 19 families (Clements 2007). This falls into three sub-clades: Scolopaci (waders), Charadrii (plovers) and Lari (Baker et al. 2007; Mayr 2011; Paton & Baker 2006; Paton et al. 2003). Sub-clades Scolopaci consist of several families including Scolopacidae, Jacanidae, Rostratulidae, Thinocoridae and Pedionomidae. The largest of these families is the Scolopacidae with 90 species (Clements et al. 2010)

including the sandpipers, shanks, snipes, godwits and curlews. In family Scolopacidae, 65 species of waders were recorded worldwide (Clements et al. 2010), while 35 species were recorded in Borneo alone (Smythies 1999). Variation in life-histories, behavioral ecology and morphological traits makes this order a popular subject to study.

The study of order Charadriiformes were well established based on nuclear and mitochondrial DNA sequence by Ericson et al. (2003), Pereira and Baker