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FEATURE ARTICLES

MULTIPLE GENE EVIDENCE FOR PARALLEL EVOLUTION AND RETENTION OF ANCESTRAL MORPHOLOGICAL STATES IN THE SHANKS (CHARADRIIFORMES: SCOLOPACIDAE)

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Abstract. Because systematic studies based on morphology have failed to fully resolve phylogenetic relationships of shanks (Charadriiformes: Scolopacidae), we obtained mitochondrial DNA (6349 bp) and nuclear DNA (1315 bp) sequences from 15 taxa. Using maximum parsimony and Bayesian analysis we show that *Catoptrophorus* and *Heteroscelus* are embedded within *Tringa*, and thus these genera should be merged in *Tringa*. Phylogenetic analyses of 18 morphological characters resulted in a partly resolved tree, so we mapped them on the molecular phylogeny and reconstructed ancestral states by maximum likelihood. Twelve of the morphological characters are homoplastic or plesiomorphic, and only six are phylogenetically informative, placing *Xenus* and *Actitis* outside the remaining genera. The bright yellow and red leg coloration of yellowlegs and redshanks are, respectively, a retained ancestral state and a parallel acquisition. Using a semi-parametric penalized-likelihood approach to correct for rate variation among lineages we estimated that speciation occurred in the Early Miocene-Pliocene.

Key words: *ancestral states, divergence time, parallel evolution, plesiomorphy, Scolopacidae, shanks, systematics.*