A resource of genome-wide single-nucleotide polymorphisms generated by RAD tag sequencing in the critically endangered European eel - DTU Orbit (11/12/2018)

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Reduced representation genome sequencing such as restriction-site-associated DNA (RAD) sequencing is finding increased use to identify and genotype large numbers of single-nucleotide polymorphisms (SNPs) in model and nonmodel species. We generated a unique resource of novel SNP markers for the European eel using the RAD sequencing approach that was simultaneously identified and scored in a genome-wide scan of 30 individuals. Whereas genomic resources are increasingly becoming available for this species, including the recent release of a draft genome, no genome-wide set of SNP markers was available until now. The generated SNPs were widely distributed across the eel genome, aligning to 4779 different contigs and 19 703 different scaffolds. Significant variation was identified, with an average nucleotide diversity of 0.00529 across individuals. Results varied widely across the genome, ranging from 0.00048 to 0.00737 per locus. Based on the average nucleotide diversity across all loci, long-term effective population size was estimated to range between 132 000 and 1 320 000, which is much higher than previous estimates based on microsatellite loci. The generated SNP resource consisting of 82 425 loci and 376 918 associated SNPs provides a valuable tool for future population genetics and genomics studies and allows for targeting specific genes and particularly interesting regions of the eel genome

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