

A quantitative and representative method to delineate freshwater regions for biodiversity conservation

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Abstract

Abstract: Effective biodiversity conservation requires reasonable targeted regionalization, and insufficient data and unclear targets often lead to conservation biases and deficiencies. So, we explored quantitative and representative methods to delineate freshwater biodiversity regions. We established a river-lake network model as the mask of the Yangtze River Basin. Based on field samplings and the literatures, we filtered the environmental variables by principal component analysis, and identified key factors to distribution of fish functional group and macroinvertebrate taxonomic group by Mantel test, then conducted species distribution models using maximum entropy modeling. We delineated biodiversity regionalization using the binary data of high suitability in the hydrological units (HUs) by spatial cluster analysis, then calculated Jaccard dissimilarity index (β dissim) among all HUs. Proportion of vegetation and waterbody type are key to the distribution of annelids and mollusks, while distribution of arthropods depend more on bioclimatic and topographic variables. For fish, topographic and hydrological variables were more important. We have delineated seven freshwater biodiversity regions (HWR, HDR, WSR, DQR, QWR, LXR and FPR). The β dissim of fish is the highest in LXR and FPR, while for macroinvertebrates, it is the highest in HWR. Species distribution models could compensate for the scarce and uneven data. Single target, and region delineation based on provincial administration or subbasins are insufficient for biodiversity conservation. Transition zones and confluent regions exhibit higher species richness and beta diversity, while these regions are often overlooked. We hope the method could serve as a reference to realize comprehensive of systematic conservation planning for biodiversity conservation.

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