High Connectivity Among Synedrella nodiflora Populations in Java Island Based on Intergenic Spacer atpB-rbcL

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Abstract	Synedrella nodiflora (L.) Gaertn has taxonomically been the only species of genus Synedrella, which spreads over many tropical countries. In spite of its wide range of distribution, the genus remains monospecific. This leads to assumption of the very low genetic diversity among S. nodiflora populations worldwide. It may also be the case in Java Island, though rapid changes in ecosystem condition occurs. Here we report our study on S. nodiflora population genetics in Java Island using intergenic spacer (IGS) atpB Ãƒ Â¢Ã‚Â€Ã‚Â“Ãƒ Â‚Ã‚Â rbcL as a molecular marker, since it has been well known as one of the most variable chloroplast genome regions in a wide range of plant species so far. As many as 58 individuals were collected randomly from ten different locations in the island. Based on IGS atpB Ãƒ Â¢Ã‚Â€Ã‚Â“ rbcL sequences of 860 bp length, only two haplotypes were observed. Both show only one polymorphic site (0.12%) and one transversion, where T is substituted by G at position 790, indicating that high connectivity among populations of S. nodiflora in Java Island is observed. This results in a low genetic differences among the populations, which at the same time provides a fact of nearly no variation among the IGS atpB Ãƒ Â¢Ã‚Â€Ã‚Â“ rbcL sequences.
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