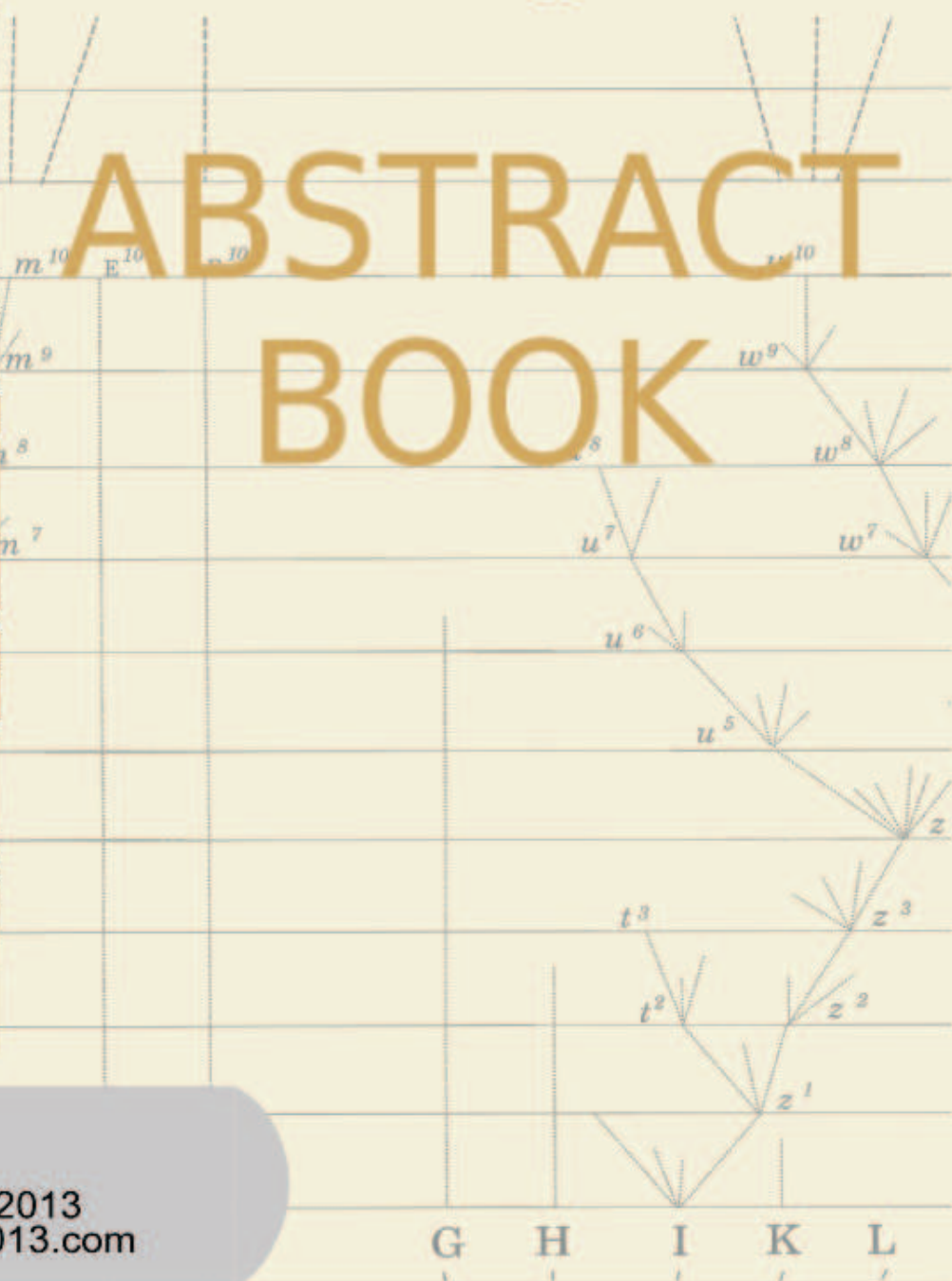


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ABSTRACT BOOK

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G H I K L

33. Population Ecology

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FREQUENT RECOMBINATION SHAPES THE EPIDEMIC POPULATION STRUCTURE OF A FRESHWATER CYANOBACTERIUM

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Based on increasing knowledge, cyanobacteria are prone to gene-flow, as are other prokaryotes. The planktonic genus *Planktothrix* showed remarkable signals of both homologous and non-homologous recombination. However, it is not yet clear how frequent recombination is and whether this phenomenon impacts population structuring. In the frame of a population genetics study, we characterized 290 *Planktothrix* strains isolated from seven neighbouring lakes in the subalpine Italian region with multi locus sequence typing. Four of six house-keeping loci analysed were polymorphic, resulting in 20 distinct multi-locus genotypes. Association indices among alleles at different loci were suggestive of a so called 'epidemic population structure', thus intermediate between clonal and panmictic structures. Further analyses carried out by using the software ClonalFrame, which is able to infer genealogies from multi-locus datasets impacted by recombination, supported this view by detecting: i) three major clades affected by three distinct recombination events, ii) a recombination rate about equal to the mutation rate and iii) the fact that recombination had an impact in introducing molecular diversity more than double the mutation rate. Furthermore, among-lake diversity, determined by the analysis of molecular variance and verified over an annual cycle in three of seven lakes, appeared as influenced by both recombination processes and local clonal expansions. Our observations suggest that microevolution of the cyanobacterium *Planktothrix* is frequently impacted by recombination, thus determining a reliable epidemic population structure.