Parauncinula septata has been known as a powdery mildew species infecting Quercus spp. in China and Japan. We determined the nucleotide sequences of ITS and 28S rRNA gene of P. septata on Quercus spp. Phylogenetic analyses indicated that P. septata divided into three distinct genotypes. Genotype I consists of collections on Q. cuspidata var. horikawae, Q. serrata and Q. aliena. Genotype II consists of collections on Q. robur and Q. serrata. Genotype III is composed of collections on Q. variabilis. The sequence similarities between the three genotypes were less than 95%, suggesting species level differences among the genotypes. Morphological observations showed that there are differences in morphology among genotypes. Genotype III has chasmothecia and appendages larger and slightly longer than those of other two genotypes. Apices of appendages are uncinate in genotype III while they are often sub-helicoid in genotypes I and II. Septa of appendages present at the tip in genotypes I and II, whereas they are not found in the tip in genotype III. Number of ascospores per ascus is mainly 8 in genotype I, while it is mainly 6 in genotype II. Ascospores are usually immature in genotype III. These results suggest that P. septata is a species complex composed of at least three cryptic species. Quercus aliena is the first host record of P. septata.

Cryptic species found in Parauncinula septata (Erysiphales) on Quercus spp.

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