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Taxonomy and phylogeny of *Golovinomyces* (Erysiphaceae) in China

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Purpose: *Golovinomyces* is an important genus of Erysiphaceae. They can cause powdery mildew diseases by infecting a wide range of host families, such as Asteraceae, Solanaceae, Cucurbitaceae, which make them economical value. Few researches were conducted on taxonomy and molecular phylogeny of *Golovinomyces* in China. We collected specimens all over China and tried to clarify their distribution, diversity and phylogeny in China.

Methods: Fresh samples were mounted in sterile water, and dried specimens were scraped from the leaf surface with a clean scalpel, and were mounted in a drop of lactic acid on a microscope slide.

Results: More than 1000 specimens were collected all over the China. And twenty-two species and one variety were identified belonging to *Golovinomyces*. Among them there is one new combination, *G. latisporum* comb. nov., five new records to China, *G. tabaci*, *G. bolay*, *G. monardae*, *G. asperifolii*, *G. macrocarpus*, one new records host family, Boraginaceae, three new record host genera, *Lagopsis*, *Rubia* and *Picris*. The host plants of *Golovinomyces* scattered among 16 families, 46 genera, 78 species. These fungi distributed in 12 provinces, 2 autonomous regions and 1 municipality. Molecular phylogeny results based on ITS and 28S rDNA sequences showed that all these species of *Golovinomyces* formed twelve groups. But some plurivorous species need more molecular evidence. The circumscriptions of *G. ambrosiae*, *G. spadiceus* and *G. circumfusus* were conducted based on the morphology and multigene (ITS, 28S rDNA, IGS, TUB2, CHS1) phylogeny.

Conclusions: The biodiversity of *Golovinomyces* in China was clarified and it is still need further investigation to try to find more species. The results provided some scientific evidences for evaluating the phylogeny of powdery mildews.