Genetic characterization of mating system and population diversity in *Ustilago esculenta*, a smut fungus associated with an oriental vegetable

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*Zizania latifolia* is a perennial aquatic plant that belongs to the family Poaceae. On infection with the smut fungus *Ustilago esculenta*, swollen gall is developed at the basal part of the plant and becomes a favorable vegetable known as “water bamboo, water oat, or jiaobai”. Development of edible galls is affected significantly by *U. esculenta*; however, studies related to its genetic features and infection-related processes are limited. To reveal the mating and population features of *U. esculenta*, we have extensively isolated strains from the field materials in Taiwan and Japan. By conducting molecular and genomic studies, we identified three idiomorphs of the mating type locus among collected strains. Screening of meiotic offspring and field strains by multiplex PCR and mating assay, we confirmed the bipolar heterothallic mating system in *U. esculenta*. The MAT-1 locus of *U. esculenta* is 552,895 bp, the largest mating type locus reported so far in fungi, and contains 44% repeated sequences. Sequence comparison revealed that *U. esculenta* MAT-1 shares great gene synteny with other smut fungi and may evolve from a common ancestor with *S. reilianum* due to the chromosomal translocation of P/R and HD loci with an identified intermediate. To further reveal the genetic diversity of *U. esculenta* population, 13 simple sequence repeat markers have been developed to screen for field strains. The results revealed that *U. esculenta* strains are separated into two major clustering groups, i.e. T and MT strains. Additionally, T strains showed higher genetic polymorphism as compared to MT strains. In conclusion, our findings have revealed genetic features of *U. esculenta* population and sexual production and the information will be utilized for commercial breeding and further studies of detailed mechanism of gall formation.