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Diversity and distribution of mating types in *Lentimula edodes* and mating type preference in domesticated strains

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Mating type of *Lentimula edodes* is determined by two unlinked genetic loci, *A* and *B*. To better understand mating behavior of *L. edodes*, we investigated variations in mating type genes in 129 dikaryotic strains collected from East Asia. Through sequence analysis of *A* locus, we discovered that hypervariable region spanning N-term of *HD2*-intergenic region-N-term of *HD1* could represent *A* mating type. Mating and hypervariable region analyses revealed 70 unique *A* mating types: 27 from 98 cultivated strains, 53 from 31 wild strains, and 10 commonly found. It was also revealed that only a few *A* mating type alleles such as *A1*, *A4*, *A5*, and *A7* were prevalent in cultivated strains. Contrarily, *A* mating type in wild strains was highly diverse: 23 unique *A* alleles were discovered in small mountainous area in Korean peninsula, suggesting rapid evolution of *A* mating type in nature. The *B* locus was assessed by allelic variations in pheromone (PHB) and pheromone receptor (RCB) pairs which constituted subloci *Ba* and *Bb*. Sequence analyses and mating assay revealed 5 alleles of RCB1 with 9 associated PHBs in *Ba* sublocus and 3 alleles of RCB2 with 5 associated PHBs in *Bb* sublocus. Each RCB was primarily associated with two PHBs. Each PHB-RCB pair was always discovered as a distinct unit. This allowed us to propose 15 *B* mating types via combinations of five *Ba* and three *Bb* subloci. Further investigation on 129 strains confirmed that the *B* locus, unlike the *A* locus, was indeed restricted to 15 mating types. Thus, the total number of mating types became 1,050 in *L. edodes* through a combination of 70 *A* and 15 *B*. This number will further increase because of rapid diversification of *A* mating type. Our findings provide a comprehensive and practical knowledge on mating behaviors of *L. edodes*.