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The highly pathogenic H5N1 avian influenza virus is a real threat to humans

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The highly pathogenic H5N1 avian influenza virus is the strongest candidate for next pandemic. H5N1 viruses emerged in Hong Kong in 1997 and continuously evolve and threaten humans. H5N1 viruses have broad host ranges to infect cats, dogs, chicken and humans. The worldwide efforts have been put into controlling these viruses. So far, no effective vaccine and antiviral agents are available. When we compared the stimulatory response to human dendritic cells between H5N1 vaccines and epidemic H3N2 vaccines, H5N1 vaccines are less immunogenic to human dendritic cells than are epidemic H3N2 vaccines. When we compared IL-2 production in human dendritic cells, the amount of IL-2 production in human dendritic cells treated with H5N1 vaccines were significantly lower than that in human dendritic cells treated with epidemic H3N2 vaccines. In addition, the stimulatory effects on MHC class II and B7-1 molecules on the surfaces of human dendritic cells is less in the dendritic cells treated with H5N1 vaccine than in the dendritic cells treated H3N2 vaccines. These data suggest that more efforts are needed to develop the effective vaccines against the highly pathogenic H5N1 viruses.

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Rice retroposon *p-SINE1* and origin of *Oryza* species

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Short interspersed elements (SINEs) are 70–500 bp repetitive DNA sequences that have proliferated via transcription, followed by reverse transcription. SINEs are found in a wide variety of eukaryotes, including animals, fungi and plants. SINEs have been used as useful markers for phylogenetic studies owing to their specific characters: once inserted, SINE remains in that genomic locus; the probability of insertion occurring more than once at any single site presumed to be extraordinarily low. In particular, the presence or absence of a SINE at a locus is easy to assay by PCR, thus they have found increasing use as phylogenetic markers to study relationships among species of primates, whales and even-toed ungulates, salmonid fish, and plants. *p-SINE1* (122 bp) is the first plant SINE identified in the *Waxy* gene in *Oryza sativa*, the cultivated rice, and is present in strains of *Oryza* species with various genome type. Some *p-SINE1* members show "interspecific" insertion polymorphism among the rice strains, indicating that they are suitable genetic markers for classifying them for inferring their phylogenetic relationships. Based on the presence or absence of the members at the corresponding loci, *p-SINE1* subfamily members show insertion polymorphism among the *O. sativa*-*O. rufipogon* population. *O. rufipogon*, the wild rice species, which displays wide "intraspecific" variation, is considered to be the progenitor of the cultivated rice species *O. sativa* with two ecotypes, japonica and indica. To determine the origin of cultivated rice, we used fifty-one *p-SINE1* members to bar-code each of 101 cultivated and wild rice strains based on the insertion polymorphism at the respective loci. A phylogenetic tree constructed using the bar codes, given to all the rice strains, showed that *O. sativa* japonica strains were closely related to the *O. rufipogon* perennial strains, whereas the indica strains to the *O. rufipogon* annual strains, indicating that *O. sativa* had been derived polyphyletically from *O. rufipogon*. We, here, propose the "SINE Code" which represents the name of the species determined by the insertion polymorphism of *p-SINE1* at the several representative loci of rice genome. In SINE Code, (1) or (0) stands for the "presence" or "absence" of insertion of *p-SINE1*. Now, each wild rice species can be encoded into (1, 0) pattern according to the "SINE Code" we developed.