**Table S4.** Comparison of evolutionary parameters of the *AvrPii* family among three *Mo* populations, of which parameters of the two populations previously reported were re-computed by the same approaches used in the current study

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Population** | ***S* a** | ***π* b** | ***D\** c** | ***F\**** | ***Ka* d** | ***Ks* e** | ***Ka/Ks*** |
| **All *AvrPii* (the current study)** |  |  |  |  |  |  |  |
| Entire coding region | 20 | 0.037 | 1.74 β | 2.65 β | 193.8 | 357.6 | 0.54 |
| Non-signal peptide region | 18 | 0.045 | 1.68 α | 2.59 β | 246.8 | 434.8 | 0.57 |
| Signal peptide region | 2 | 0.013 | 0.68 | 1.11 | 54.9 | 166.0 | 0.33 |
| **All *AvrPii* (Lu et al. 2019)** |  |  |  |  |  |  |  |
| Entire coding region | 15 | 0.013 | 1.58 α | 1.05 | 19.80 | 22.39 | 0.88 |
| Non-signal peptide region | 14 | 0.017 | 1.55 α | 1.04 | 24.97 | 31.48 | 0.79 |
| Signal peptide region | 1 | 0.003 | 0.54 | 0.34 | 5.98 | 0 | Ka>Ks |
| **All *AvrPii* (Sirisathaworn et al. 2017)** |  |  |  |  |  |  |  |
| Entire coding region | 11 | 0.003 | -3.81 β | -3.92 β | 3.71 | 0.88 | 4.23 |
| Non-signal peptide region | 5 | 0.002 | -2.20 | -2.48 | 3.07 | 0 | Ka>Ks |
| Signal peptide region | 6 | 0.004 | -3.90 β | -3.90 β | 5.49 | 3.33 | 1.65 |

a Number of segregating sites.

b Nei’s nucleotide diversity based on silent site.

cFu and Li’s *D*\*and *F*\*, and α, β represents statistical significance at *P* < 0.05, 0.02 level, respectively.

eNonsynonymous.

f Synonymous.