Supplementary Table 1. The isolates list, country, mating types, genotypes and multilocus haplotype of mitochondrial genome in *Phytophthora infestans*

| Isolate | Country      | Alternate culture accession | Mating type | RFLP-based haplotype | Genotype<sup>b</sup> | Locus 1 | Locus 2 | Locus 3 | Locus 4 | Locus 5 | Multilocus haplotype | Haplotype abbreviation |
|---------|--------------|-----------------------------|-------------|----------------------|----------------------|---------|---------|---------|---------|---------|----------------------|------------------------|
| P12021  | Russia       | N-6-02                      | A2          | IIa                  | -                    | 3       | 3       | 2       | 2       | 3       | IIa-3-3-2-2-3         | IIa-1                  |
| P10110  | USA          | US940604                    | A2          | IIa                  | US-13                | 2       | 3       | 2       | 2       | 3       | IIa-2-3-2-2-3         | IIa-2                  |
| P10257  | Hungary      | H-24/02                     | A1          | IIa                  | -                    | 2       | 4       | 2       | 2       | 3       | IIa-2-4-2-2-3         | IIa-3                  |
| P15149  | South Korea  | KN-2                        | A2          | IIa                  | -                    | 2       | 5       | 2       | 1       | 3       | IIa-2-5-2-1-3         | IIa-4                  |
| P12043  | Russia       | -                           | A1          | IIa                  | -                    | 2       | 5       | 2       | 2       | 3       | IIa-2-5-2-2-3         | IIa-5                  |
| P15101  | South Korea  | HC-1                        | A1          | IIa                  | -                    | 2       | 3       | 2       | 2       | 4       | IIa-2-3-2-2-4         | IIa-6                  |
| P12203  | UK           | C3 SC97,38,2.2              | A1          | IIa                  | EU_8_A1              | 2       | 5       | 2       | 2       | 4       | IIa-2-5-2-2-4         | IIa-7                  |
| P6750   | Mexico       | Goodwin 586                 | A1          | IIa                  | -                    | 2       | 5       | 3       | 2       | 4       | IIa-2-5-3-2-4         | IIa-8                  |
| P10122  | USA          | US970018                    | A1          | IIb                  | US-11                | 1       | 2       | 1       | 1       | 2       | IIb-1-2-1-1-2         | IIb-1                  |
| P9464   | USA          | 035-96G                     | A1          | IIb                  | US-11                | 1       | 2       | 1       | 1       | 1       | IIb-1-2-1-1-1         | IIb-2                  |
| P7629   | USA          | Varoujan Pi65, Shaw Ca65    | A1          | IIb                  | US-6                 | 1       | 1       | 1       | 1       | 1       | IIb-1-1-1-1-1         | IIb-3                  |
| AY898628| USA          | 94-52                        | A1          | IIb                  | -                    | 1       | 1       | 1       | 3       | 1       | IIb-1-1-1-3-1         | IIb-4                  |
| MH286884| South Korea  | Kpi16-9                     | A1          | IIa                  | KR_1_A1              | 2       | 3       | 2       | 2       | 4       | IIa-2-3-2-2-4         | IIa-6                  |
| MH286885| South Korea  | Kpi15-4                     | A1          | IIb                  | US-11                | 1       | 2       | 1       | 1       | 1       | IIb-1-1-1-1-1         | IIb-2                  |
| MH286886| South Korea  | Kpi15-3                     | A2          | IIa                  | KR_2_A2              | 2       | 5       | 2       | 2       | 3       | IIb-2-5-2-2-3         | IIa-5                  |
| MH286887| South Korea  | Kpi15-10                    | A1          | IIa                  | SIB-1                | 2       | 3       | 2       | 2       | 4       | IIa-2-3-2-2-4         | IIa-6                  |

<sup>a</sup>Culture accession numbers starting with “P” are from the World Oomycete Genetic Resource Collection (http://phytophthora.ucr.edu).

<sup>b</sup>Genotype determined with RG-57 restriction fragment length polymorphism (RFLP) analysis as described in Martin and Tooley’s study (2004) and simple sequence repeat data in this study.

Reference

Martin, F. N. and Tooley, P. W. 2004. Identification of phytophthora isolates to species level using restriction fragment length polymorphism analysis of a polymerase chain reaction-amplified region of mitochondrial DNA. *Phytopathology* 94:983-991.
Supplementary Table 2. The SNPs and InDels of mitochondrial genome sequences among four Korean *Phytophthora infestans* isolate

| Type       | Location | Gene       | AY898627_Il1 | AY898628_Il2 | KR_1_A1 (SIB-1) | KR_2_A2 | US-11 | Remark                          |
|------------|----------|------------|--------------|--------------|-----------------|---------|-------|---------------------------------|
| InDel      | Genic    | *orf170*   | -            | ATT          | -               | -       | ATT   |                                 |
|            |          | *orf198*   | -            | A            | -               | -       | A     |                                 |
|            |          | *orf199*   | -            | A            | -               | -       | A     |                                 |
| Intergenic |          | *orf79-cox2* | -            | (ATCTATTTAAAT-TAACTGTTTATA-ATTTTTTTTTC)₂ | (ATCTATTTAAAT-TAACTGTTTATA-ATTTTTTTTTC)₂ | (ATCTATTTAAAT-TAACTGTTTATA-ATTTTTTTTTC)₂ | (ATCTATTTAAAT-TAACTGTTTATA-ATTTTTTTTTC)₂ | Variation number of tandem repeats |
| SNP        | Genic    | *nad3-nad5*| A            | -            | A               | A       | -     |                                 |
|            |          | *cob*      | G            | -            | G               | G       | -     |                                 |
|            |          | *atp1*     | G            | A            | G               | A       | -     |                                 |
|            |          | *atp1*     | C            | T            | C               | C       | T     |                                 |
|            |          | *nad2*     | A            | G            | A               | A       | G     |                                 |
|            |          | *rps7*     | A            | G            | A               | A       | G     |                                 |
|            |          | *cox3*     | T            | C            | T               | T       | C     |                                 |
|            |          | *nad5*     | T            | C            | T               | T       | C     |                                 |
|            |          | *nad6*     | T            | C            | T               | T       | C     |                                 |
|            |          | *nad11*    | A            | G            | A               | A       | G     |                                 |
|            |          | *nad11*    | A            | G            | A               | A       | G     |                                 |
|            |          | *nad11*    | A            | G            | A               | A       | G     |                                 |
|            |          | *nad11*    | A            | G            | A               | A       | G     |                                 |
|            |          | *tRNA_Leu* | C            | T            | C               | T       | T     |                                 |
|            |          | *ymf16*    | G            | A            | G               | G       | A     |                                 |
|            |          | *rps3*     | T            | C            | T               | T       | C     |                                 |
|            |          | *atp8*     | A            | A            | A               | G       | A     |                                 |
|            |          | *rps8*     | A            | G            | A               | A       | G     |                                 |
|            |          | *orf100*   | T            | C            | T               | T       | C     |                                 |
|            |          | *orf99*    | T            | C            | T               | T       | C     |                                 |
|            |          | *orf198*   | A            | C            | A               | A       | C     |                                 |
|            |          | *orf198*   | T            | C            | T               | T       | C     |                                 |
|            |          | *rms*      | G            | A            | G               | G       | A     |                                 |
|            |          | *ms*       | A            | G            | A               | A       | G     |                                 |
| Intergenic |          | *atp9-nad9*| T            | A            | T               | T       | A     |                                 |
|            |          | *atp9-nad9*| T            | A            | T               | T       | A     |                                 |
|            |          | *tRNA_Arg-nad4L* | G         | A            | G               | G       | A     |                                 |
|            |          | *tRNA_Arg-nad4L* | T       | A            | T               | A       | T     |                                 |
|            |          | *tRNA_Pro-rRNA_Met* | G    | A            | G               | G       | A     |                                 |
|            |          | *orf198-rms* | G           | A            | G               | G       | A     |                                 |

SNP, single nucleotide polymorphism; InDel, insertion and deletion.
Supplementary Data 1. The 16 *Phytophthora infestans* DNA FASTA sequences of five loci from mitochondrial genome sequences for haplotyping; loci 1 (*rpl5-rns*), loci 2 (*rns-cox2*), loci 3 (*cox1-nad9*), loci 4 (*nad3-nad5*), and loci 5 (*nad6-nad4L*).