In all, 238 and 155 transfer (t)RNA genes were predicted from the genomes of *Phytophthora sojae* and *P. ramorum*, respectively. After omitting pseudogenes and undetermined types of tRNA genes, there remained 208 *P. sojae* tRNA genes and 140 *P. ramorum* tRNA genes. There were 45 types of tRNA genes, with distinct anticodons, in each species. Fourteen common anticodon types of tRNAs are missing altogether from the genome in the two species; however, these appear to be compensated by wobbling of other tRNA anticodons in a manner which is tied to the codon bias in *Phytophthora* genes. The most abundant tRNA class was arginine in both *P. sojae* and *P. ramorum*. A codon usage table was generated for these two organisms from a total of 9,803,525 codons in *P. sojae* and 7,496,598 codons in *P. ramorum*. The most abundant codon type detected from the codon usage tables was GAG (encoding glutamic acid), whereas the most numerous tRNA gene had a methionine anticodon (CAT). The correlation between the frequencies of tRNA genes and the codon frequencies in protein-coding genes was very low (0.12 in *P. sojae* and 0.19 in *P. ramorum*); however, the correlation between amino acid tRNA gene frequency and the corresponding amino acid codon frequency in *P. sojae* and *P. ramorum* was substantially higher (0.53 in *P. sojae* and 0.77 in *P. ramorum*). The codon usage frequencies of *P. sojae* and *P. ramorum* were very strongly correlated (0.99), as were tRNA gene frequencies (0.77). Approximately 60% of orthologous tRNA gene pairs in *P. sojae* and *P. ramorum* are located in regions that have conserved synteny in the two species.