Table S1. Genetic regions used in the phylogeny, with primers, source of primers, length of the aligned sequence plus simple indel characters, and number and percent of variable sites and parsimony-informative sites, with and without the outgroups.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  | **With Outgroups** | | ***Amaranthus* Alone** | |
| **Region** | **Primer Name** | **Primers (5'-3')** | **Source** | **Aligned basepairs + indel characters included** | **#/% omitted sites** | **#/% variable sites** | **#/% parsimony-informative sites** | **#/% variable sites** | **#/% parsimony-informative sites** |
| **A36** | A36F | TGGTTATCCGTGCCTTTCTC | Beard 2014 | 764 | 0 | 143 (19%) | 92 (12%) | 81 (11%) | 58 (7%) |
|  | A36R | CAGGACCTGGATTCTTTCCA | Beard 2014 |  |  |  |  |  |  |
|  | A361F | GCAACCTGTGCCACAGGACCTG | This paper |  |  |  |  |  |  |
|  | A361R | CAGGTCCTGTGGCACAGGTTGC | This paper |  |  |  |  |  |  |
| **G3PDH** | G3F | AGGGTCTCATGACAACTGTTCACTCT | modified from Strand et al., 1997 | 943 | 33 (3%) | 333 (35%) | 206 (22%) | 299 (32%) | 200 (21%) |
|  | G3R2 | TCACCAACGAAGTCGGTGGAA | modified from Strand et al., 1997 |  |  |  |  |  |  |
|  | G3BIF | CACTGGAGCAGCCAAGGTAT | This paper |  |  |  |  |  |  |
| **ITS** | ITS4 | TCCTCCGCTTATTGATATGC | White et al., 1990 | 749 | 0 | 216 (29%) | 159 (21%) | 128 (17%) | 90 (12%) |
|  | ITS5 | GGAAGTAAAAGTCGTAACAAGG | White et al., 1990 |  |  |  |  |  |  |
| **Waxy** | WXF12 | GGTCTTGGTGATGTCCTTGG | designed from Park et al., 2010 | 1448 | 0 | 565 (39%) | 320 (22%) | 455 (31%) | 300 (21%) |
|  | WXR7 | AGGCAAATCTTCCTTGATATACAATA | from Park et al., 2010 |  |  |  |  |  |  |
|  | WXF5 | TAATATGTGCTTCAGGCAGCT | This paper |  |  |  |  |  |  |
|  | WXR5 | GAAGTTCGGATTGTTGTTGAGA | This paper |  |  |  |  |  |  |
| **matK/trnK** | TrnKF1 | ATCATGGGGTTGCTAACTCA | Müller and Borsch, 2005 | 2536 | 0 | 396 (16%) | 248 (10%) | 205 (8%) | 132 (5%) |
|  | TrnKR1 | AACTAGTCGGATGGAGTAG | Müller and Borsch, 2005 |  |  |  |  |  |  |
|  | TrnKR31 | GGCATCTTTCAACCAATAGCGAAGAG | This paper |  |  |  |  |  |  |
|  | MatKF | CGATCTATTCATTCAATATTTC | Cuenoud et al., 2002 |  |  |  |  |  |  |
|  | MatKR | TCTAGCACACGAAAGTCGAAGT | Cuenoud et al., 2002 |  |  |  |  |  |  |
|  | MatK1F | AAGAACCTTTTCTGCATTATGTTCGG | This paper |  |  |  |  |  |  |
| **trnL5’-trnL3’** | trnL5’F (TabC) | CGAAATCGGTAGACGCTACG | Shaw et al., 2005 | 680 | 23 (3%) | 95 (14%) | 58 (9%) | 54 (8%) | 33 (5%) |
|  | 3’trnLR (TabD) | GGGGATAGAGGGACTTGAAC | Shaw et al., 2005 |  |  |  |  |  |  |
| **Nuclear concatenated** |  | N/A | N/A | 3875 | 33 (<1%) | 1156 (30%) | 712 (18%) | 840 (22%) | 590 (15%) |
| **Chloroplast concatenated** |  | N/A | N/A | 3216 | 23 (<1%) | 491 (15%) | 306 (10%) | 259 (8%) | 165 (5%) |

Table S2. Molecular models of evolution chosen for each dataset as the best fit by jModeltest 2.1.6, using the Akaike information criterion (AIC), and closest approximate model implemented in MrBayes.

|  |  |  |
| --- | --- | --- |
| **Dataset** | **AIC** | **MrBayes** |
| ***A36*** | TrN+Γ | GTR+Γ |
| ***G3PDH*** | TIM2+I+Γ | GTR+I+Γ |
| ***ITS*** | GTR+I+Γ | GTR+I+Γ |
| ***Waxy*** | TPM3uf+Γ | GTR+Γ |
| ***trnL5’-trnL3’*** | TPM1uf+Γ | GTR+Γ |
| ***matK/trnK*** | GTR+I+Γ | GTR+I+Γ |