**Supplementary Table 3 Partial list of candidate orthologs under positive selection between *E. fischeriana* and *E. ehracteolata*.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GO id | GO term | *P*-value | Frequency in test set | Frequency in reference set | Orthologous gene | Descriptions | Function |
|  | **Biological Process** |  |  |  |  |  |  |
| GO:0015031 | protein transport | 0.02 | 9 | 218 | OG14664, OG06839, OG07794, OG14692, OG17196, OG07291, OG13657, OG07602, OG03030 | *AtPES1* (Lippold et al., 2012),*AtGCN1* (Wang et al., 2017),*TatA* (Walker et al., 1999),*AtVTI13* (Larson et al., 2014), *PPR* (Li et al., 2021)  | Fatty acid metabolism, cold stress tolerance, root hair development |
| GO:0015886 | heme transport | 0.02 | 3 | 9 | OG13992, OG16428, OG14718 | *At**YLS9* (Griebel et al., 2022) | Cold stress tolerance |
| GO:0051181 | cofactor transport | 0.00 | 3 | 9 | OG13992, OG14718, OG16428 | *AtYLS9* (Griebel et al., 2022) | Cold stress tolerance |
| GO:0071705 | nitrogen compound transport | 0.00 | 4 | 52 | OG16428, OG14718, OG16391, OG13992 | *AtWER1* (Wang et al., 2019),*AtYLS9* (Griebel et al., 2022) | Root hair development, cold stress tolerance |
| GO:0071702 | organic substance transport | 0.02 | 34 | 314 | OG14150, OG07253, OG04859, OG07737, OG16515, OG14718, OG17219, OG07175, OG07288, OG03647, OG03030, OG13754, OG13657, OG14692, OG07354, OG16702, OG01365, OG07060, OG13992, OG17193, OG16428, OG14664, OG11159, OG06839, OG07602, OG09743, OG04971, OG07794, OG07291, OG02209, OG17196, OG15862, OG04844, OG07033 | *AtPOLD4* (Shultz et al., 2007),*AtCCDC* (Lohmeier-Vogel et al., 2008), *AtHSPBP1* (Zhang et al., 2010)*,* *AtFRL* (Michaels et al., 2004)*,* *ABC* (Kretzschmar et al., 2011),*AtLIP1* (Wang et al., 2022), *AtOST1* (Assmann, 2003), *AtYLS9* (Griebel et al., 2022), *AtPES1* (Lippold et al., 2012), *AtGCN1* (Wang et al., 2017)*,* *PPR* (Li et al., 2021), *AtSRP19* (Wang et al., 2008), *TatA* (Walker et al., 1999)*AtVTI13* (Larson et al., 2014), *CPRF2*, *ELIP* (Hayami et al., 2015), *AtBASS2* (Furumoto et al., 2011; Mueller et al., 2014; Lee et al., 2017) | Starch metabolism, heat, cold and drought stresses tolerance,abiotic and biotic stresses tolerance, glycerolipid metabolism, fatty acid metabolism, root hair development, pyruvate transport |
| GO:0051240 | positive regulation of multicellular organismal process | 0.01 | 2 | 2 | OG06917, OG07011 | *BrRZFP* (Jung et al., 2013)*,* *TSA1* (Geem et al., 2019) | Cold, salt and dehydration stresses tolerance |
| GO id | **GO term** | ***P*-value** | **Frequency** **in test set** | **Frequency** **in reference set** | **Orthologous gene** | **Descriptions** | **Function** |
| GO:0030522 | intracellular receptor signaling pathway | 0.05 | 2 | 5 | OG07015, OG01198 | *AtPFD* (Perea-Resa et al., 2017)*,**VPS54* (Xiang et al., 2013) | Cold stress tolerance, vesicular trafficking |
| GO:0065004 | protein-DNA complex assembly | 0.03 | 5 | 24 | OG07214, OG15660, OG15240, OG17052, OG16125 | *AtBLT* (Kasili et al., 2011; Mazie and Baum, 2016), *AtSMH* (Hofr et al., 2009), *BrRZFP* (Jung et al., 2013), *AtNRP2* (Zhu et al., 2017) | TRICHOME development,cold stress tolerance,Root hair development |
| GO:0006461 | protein complex assembly | 0.04 | 12 | 93 | OG16702, OG14718, OG07878, OG13992, OG07214, OG02759, OG16428, OG16819, OG13999, OG09743, OG13590, OG15659 | *AtBLT*(Kasili et al., 2011; Mazie and Baum, 2016), *AtEML3* (Milutinovic et al., 2019),*AtMAIL* (de Luxan-Hernandez et al., 2020), *AtPSKR2* (Kaufmann et al., 2021),*SMH* (Marian et al., 2003) | TRICHOME development,seed and root development |
| GO:0033014 | tetrapyrrole biosynthetic process | 0.04 | 2 | 30 | OG00941, OG07442 | *AtTIC32* (Hormann et al., 2004), *AtHPPR3* (Xu et al., 2018) | Tyrosine metabolism |
| GO:0019521 | D-gluconate metabolic process | 0.00 | 1 | 11 | OG07442 | *AtHPPR3* (Xu et al., 2018) | Tyrosine metabolism |
| GO:0051188 | cofactor biosynthetic process | 0.04 | 4 | 85 | OG07442, OG13865, OG00941, OG13581 | *AtHPPR3* (Xu et al., 2018), *AtSAM1* (Sekula et al., 2020),*AtTIC32* (Hormann et al., 2004),*AtNAD5* (Qiu et al., 2021) | Tyrosine metabolism, amino acid biosynthesis, abiotic and biotic stresses tolerance |
| GO:0006354 | DNA-dependent transcription, elongation | 0.00 | 1 | 3 | OG16324 | *ABC* (Kretzschmar et al., 2011) | abiotic and biotic stresses tolerance |
| GO:0042157 | lipoprotein metabolic process | 0.01 | 5 | 19 | OG14150, OG04859, OG16372, OG07175, OG17193 | *-* | *-* |
| GO:0031123 | RNA 3'-end processing | 0.04 | 3 | 11 | OG04052, OG01293, OG07356 | *AtCSTF64* (Yao et al., 2002)*,* *AtCPRF1* (Satou et al., 2014)*, AtCFIS1* | Seedling development, amino acid metabolism |
| GO:0009890 | negative regulation of biosynthetic process | 0.04 | 3 | 11 | OG07740, OG14055, OG15499 | *MUS81* (Enderle et al., 2019),*RIP* (Zhu et al., 2018),*NET2A* (Duckney et al., 2021) | DPC repair, biotic stress tolerance, pollen development |
| GO:0007050 | cell cycle arrest | 0.03 | 1 | 3 | OG07187 | *AtKRP3*(Jun et al., 2013) | Organ development |
| GO:0044419 | interspecies interaction between organisms | 0.02 | 6 | 134 | OG07349, OG16562, OG07291, OG02170, OG15907, OG06925 | *AtRIE1* (Xu and Li, 2003), *AtVTI13* (Larson et al., 2014), *DPB3* (Sato et al., 2015; Sato et al., 2016) | Seed development, root hair development,heat stress tolerance |
| GO id | **GO term** | ***P*-value** | **Frequency** **in test set** | **Frequency** **in reference set** | **Orthologous gene** | **Descriptions** | **Function** |
|  | **Molecular function** |  |  |  |  |  |  |
| GO:0031490 | chromatin DNA binding | 0.00 | 1 | 1 | OG07565 | *SelH* (Van Hoewyk, 2013) | Selenoproteins and oxidative stresses tolerance |
| GO:0016627 | oxidoreductase activity, acting on the CH-CH group of donors | 0.05 | 3 | 66 | OG00941, OG07822, OG07442 | *AtTIC32* (Hormann et al., 2004),*HSP,* *At**HPPR3* (Xu et al., 2018) | Chloroplast development, tyrosine metabolism |
| GO:0019210 | kinase inhibitor activity | 0.03 | 1 | 6 | OG07187 | *At**KRP3* (Jun et al., 2013) | Organ development |
| GO:0005319 | lipid transporter activity | 0.05 | 1 | 3 | OG07253 | *At**POLD4* (Shultz et al., 2007) | DNA replication |
| GO:0003955 | NAD(P)H dehydrogenase (quinone) activity | 0.01 | 1 | 1 | OG02575 | *At**NQR* (Biniek et al., 2017) | Oxidative stress tolerance |
| GO:0004721 | phosphoprotein phosphatase activity | 0.03 | 1 | 11 | OG01773 | *AtPTP1* (Liu et al., 2016) | Cold stress tolerance |
| GO:0016773 | phosphotransferase activity | 0.03 | 2 | 4 | OG07060, OG07737 | *AtCCDC* (Lohmeier-Vogel et al., 2008) | Starch metabolism |
|  | **Cellular Component** |  |  |  |  |  |  |
| GO:0000428 | DNA-directed RNA polymerase complex | 0.02 | 2 | 16 | OG03552, OG16324 | *AtSCL22* (Ma et al., 2014), *ABC* (Kretzschmar et al., 2011) | Branch bud formation,abiotic and biotic stresses tolerance |
| GO:0000347 | THO complex | 0.05 | 1 | 6 | OG07214 | *AtBLT* (Kasili et al., 2011; Mazie and Baum, 2016) | TRICHOME development |
| GO:0031082 | BLOC complex | 0.00 | 1 | 3 | OG07291 | *AtVTI13* (Larson et al., 2014) | Root hair development |
| GO:0030054 | cell junction | 0.00 | 1 | 6 | OG07702 | *EYA* (Musharraf et al., 2008) | *-* |
| GO:0044463 | cell projection part | 0.00 | 2 | 6 | OG16747, OG07793 | *SHY* (Guyon et al., 2004; Wang et al., 2018)*, VPS52* (Xiang et al., 2013) | Pollen development |
| GO:0009357 | transmembrane transporter complex | 0.03 | 2 | 4 | OG07737, OG07060 | *AtCCDC* (Lohmeier-Vogel et al., 2008) | Starch metabolism |

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