Title: Combined QTL and GWAS analysis to identify the growth-related gene in *Rhopilema esculentum* with the help of 2b-RAD sequencing

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Table S1 Statistical analysis of body weight and umbrella diameter in *R. esculentum* F1 offspring

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phenotype | Min | Max | Mean | STDEV | C.V (%) |
| Body weight | 2.70 | 33.50 | 9.14 | 4.55 | 49.79 |
| Umbrella diameter | 3.20 | 7.00 | 4.47 | 0.75 | 16.82 |

Table S2 Summary of the consensus genetic linkage map in *R. esculentum*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Linkage group | Mapped markers | Distinct positions | Genetic length (cM) | Marker interval (cM) |
| LG1 | 150 | 140 | 88.02 | 0.59 |
| LG2 | 130 | 118 | 70.54 | 0.54 |
| LG3 | 137 | 127 | 70.37 | 0.51 |
| LG4 | 148 | 142 | 82.38 | 0.56 |
| LG5 | 94 | 86 | 53.43 | 0.57 |
| LG6 | 129 | 119 | 78.95 | 0.61 |
| LG7 | 158 | 144 | 81.98 | 0.52 |
| LG8 | 146 | 138 | 65.23 | 0.45 |
| LG9 | 122 | 113 | 67.6 | 0.55 |
| LG10 | 140 | 130 | 68.86 | 0.49 |
| LG11 | 128 | 122 | 56.78 | 0.44 |
| LG12 | 75 | 70 | 50.89 | 0.68 |
| LG13 | 131 | 120 | 87.66 | 0.67 |
| LG14 | 120 | 105 | 88.9 | 0.74 |
| LG15 | 130 | 121 | 66.32 | 0.51 |
| LG16 | 159 | 149 | 57.61 | 0.36 |
| LG17 | 115 | 109 | 82.17 | 0.71 |
| LG18 | 83 | 76 | 61.3 | 0.74 |
| LG19 | 114 | 109 | 56.78 | 0.5 |
| LG20 | 58 | 56 | 52.04 | 0.9 |
| LG21 | 41 | 37 | 68.53 | 1.67 |
| Total | 2508 | 2331 | 1456.34 | 0.58 |
| Ge | 1475.89 |  |  |  |
| Coverage | 98.68% |  |  |  |

Table S3 Candidate genes related to umbrella diameter and body weight in in *R. esculentum* by GWAS analysis

|  |  |  |  |
| --- | --- | --- | --- |
| Gene name | Annotation | Conserved domain | Blast result  (Per. Ident) |
| *RE13677* | Myb-like protein X | SGNH\_hydrolase | [myb-like protein X [*Hydra vulgaris*]](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_XP_004206580) (58.48%) |
| *RE13676* | CSC1-like protein At3g21620 | COG5594 super family | PREDICTED: CSC1-like protein At3g21620 [*H. vulgaris*] (41.45%) |
| *RE13675* | - | - | - |
| *RE13674* | CREB-binding protein-like | zf-TAZ super family | Histone lysine acetyltransferase CREBBP-like [*Myotis myotis*] (35.11%) |
| *RE13673* | Gem-associated protein 8 | GEMIN8 super family | [Gem-associated protein 8 [*Cricetulus griseus*]](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_EGV98470) (42.86%) |
| *RE13672* | Transmembrane 9 superfamily member 3 | Endomembrane protein 70 | PREDICTED: transmembrane 9 superfamily member 3-like [*Octopus bimaculoides*] (79.89%) |
| *RE13671* | Transcription factor IIIA | FOG | transcription factor IIIA [*Anas platyrhynchos*] (40.00%) |
| *RE13670* | sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1-like | Ephrin\_rec\_like; DUF5011 super family; IG\_like; PLAT; FXa\_inhibition; EGF\_CA; Ephrin\_rec\_like super family | PREDICTED: sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1-like [*Acropora digitifera*] (30.36%) |
| *RE13669* | Uncharacterized protein LOC107332770 | CAP\_ED | uncharacterized protein LOC113664578 isoform X3 [*Pocillopora damicornis*] (42.99%) |
| *RE13668* | Low quality protein: eukaryotic translation initiation factor 5B | InfB super family | eukaryotic translation initiation factor 5B-like isoform X1 [*Acropora millepora*] (73.45%) |
| *RE03622* | Eukaryotic translation initiation factor 4 gamma 1-like, partial | PTZ00184; MIF4G; MA3 domain | eukaryotic translation initiation factor 4 gamma 1-like [*Actinia tenebrosa*] （42.25%） |
| *RE03621* | Nucleotide-binding oligomerization domain-containing protein 1-like | - | uncharacterized protein LOC114965363 [*Acropora millepora*] (53.79%) |
| *RE03620* | Hypothetical protein CICLE\_v10024023mg | MIF4G; CIDE-N; Med15 super family | PREDICTED: eukaryotic translation initiation factor 4 gamma 1-like [*Gavia stellata*] (50.98%) |
| *RE03619* | A-kinase anchor protein 7 isoform X3 | AKAP7\_NLS | AKA7G protein [*Cnemophilus loriae*] (37.93%) |
| *RE03618* | - | CIDE\_N super family  at the N-terminus of the CIDE (cell death-inducing DFF45-like effector) | DNA fragmentation factor subunit alpha [*Nematostella vectensis*] (40.00%) |
| *RE03617* | uncharacterized protein LOC101847362 | - | uncharacterized protein LOC115217646 [*Octopus sinensis*] (59.26%) |
| *RE03616* | Wnt4 | Wnt super family | Wnt4 [*Rhopilema esculentum*] (100%) |
| *RE03615* | Protein Wnt-4-like isoform X1 | wnt | Protein Wnt-4a [*Bagarius yarrelli*] (41.38%) |
| *RE03614* | 6-phosphogluconate dehydrogenase, decarboxylating-like | PRK09287 | 6-phosphogluconate dehydrogenase, decarboxylating-like [*Anneissia japonica*] (85.03%) |
| *RE03613* | Serine/arginine-rich splicing factor 6-like isoform X1 | RRM\_SF super family | serine/arginine-rich splicing factor 6-like isoform X1 [*Orbicella faveolata*] (64.09%) |
| *RE03612* | Hypothetical protein TRIADDRAFT\_57615 | RRM\_SF super family; SF-CC1 super family | protein gar2-like [*Dendronephthya gigantea*] (48.22%) |
| *RE03611* | Reduced wall acetylation 1-like | Cas1\_AcylT super family | predicted protein [*Nematostella vectensis*] (64.83%) |
| *RE03610* | Prohibitin-2-like | SPFH\_prohibitin | PREDICTED: prohibitin-2-like [*Acropora digitifera*] (80.25%) |
| *RE03609* | - | ICAT  Beta-catenin is a multifunctional protein involved in both cell adhesion and transcriptional activation | protein LZIC [*Exaiptasia diaphana*] (72.49%) |
| *RE03608* | A disintegrin and metalloproteinase with thrombospondin motifs 9-like | VWA | uncharacterized protein LOC110235415 isoform X3 [*Exaiptasia diaphana*] (40.39%) |
| *RE03607* | probable fructokinase-5 | SIS super family | uncharacterized protein LOC114539494 [*Dendronephthya gigantea*] (58.85%) |
| *RE03606* | DNA fragmentation factor subunit beta-like | DFF40 super family; CIDE\_N domain  cell death-inducing DFF45-like effector | PREDICTED: DNA fragmentation factor subunit beta-like [*Hydra vulgaris*] (46.73%) |