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| --- | --- | --- | --- | --- | --- |
| Title | Region | combination | Others | Primer | calculation |
| Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia | V3  V4  V4 and V5  V4 and V5  V4 and V5  V4 and V5  V4 and V5  V5 and V7  V7  V7  V7 and V8  V7 and V8  V9 | fw- rv 0.324-0.769  Fwd1-Rev3 0.791-0.709  563–1132,0.853-0.873  574–1132, 0.788-0.873  574\*--1132,0.844-0.873  616–1132, 0.793-0.873  616\*--1132,0.804-0.873  897-1423, 0.801-0.825  1132–1423,0.873-0.825  1266–1423,0.865-0.825  1132-1391F,0.873-0.795  1266-1391F,0.865-0.795  1391F-EukB,0.795-0.0001 | as short as pairs of 150 bp paired-end reads or 400 bp single-end reads;  primer pair 563–1132, 574–1132,616–1132,897-1423,  1132–1423,1132–1391F and 1266–1391F,covering variable regions 4, 6, 7 and 8 and amplifying regions between 167 and 569 bp in length.  563-1132, 574\*--1132 and 616\*--1132 | 391f YGGAGARGGAGCHTGAGA  550f GGRCMAGBCTGGTGCCAG  563f GCCAGCAVCYGCGGTAAY  574f CGGTAAYTCCAGCTCYAV  574\*f CGGTAAYTCCAGCTCYV  616f TTAAAAVGYTCGTAGTYG  616\*f TTAAARVGYTCGTAGTYG  897f AGAGGTGRAATTCTHRGA  1132f AYTTRAAGDAATTGACGG  1132r CCGTCAATTHCTTYAART  1182f AATTYGACTCAACDCRGG  1266f RGTGGTGCATGGCCGYTB  1423f AACAGGTCHGWRATGCCC  1423r GGGCATYWCDGACCTGTT  1612r ACAAAKGGCAGGGACDYA  1626r GACRGGMGGTGTGBACAA  1380F CCCTGCCHTTTGTACACAC  1389F TTGTACACACCGCCC  1510R CCTTCYGCAGGTTCACCTAC  1391F GTACACACCGCCCGTC  EukB TGATCCTTCTGCAGGTTCACCTAC  Fwd1 CCAGCASCYGCGGTAATTCC  Rev3 ACTTTCGTTCTTGATYRA  fw ATTAGGGTTCGATTCCGGAGAGG  rv CTGGAATTACCGCGGSTGCTG | 391f 0.727234666108436  550f 0.834345125950736  563f 0.85360407508199  574f 0.788954015770009  574\_f 0.844986393133766  616f 0.793210522643221  616\_f 0.804514688437653  897f 0.801235084781244  1132f 0.873491033424046  1132r 0.873491033424046  1182f 0.847079757169772  1266f 0.865710697090224  1423f 0.82506454539111  1423r 0.82506454539111  1612r 0.775870490544972  1626r 0.80723606168446  1380F 0.780789896029586  1389F 0.806049822064057  1510R 0.00823389854162306  1391F 0.795548112483427  EukB 0.000104668201800293  Fwd1 0.791570720815016  Rev3 0.709964412811388  fw 0.324785430186309  rv 0.769415951433954 |
| Not all are free-living: high-throughput DNA  metabarcoding reveals a diverse community of protists  parasitizing soil metazoa | V1–V3 | EUK20f- EUK302r+3  0.255-0.694 | target a 500- to 700-bp-long region；This part of the 18S rDNA contains the highly variable  regions V1–V3, enabling high taxonomic discrimination  between taxa; protist | EUK20f TGCCAGTAGTCATATGCTTGT  EUK302r+3 ACCAGACTTGYCCTCCAAT | EUK20f 0.255669527597516  EUK302r\_3 0.694299071941944 |
| Community patterns and temporal variation of picoeukaryotes  in response to changes in the Yellow Sea Warm Current | V4 | 573FWD-951REV  0.713-0.656 | picoeukaryotes | 573FWD CGCGGTAATTCCAGCTCCA  951REV TTGGYRAATGCTTTCGC | 573FWD 0.713313795268997  951REV 0.656932523899239 |
| Multiple identification of most important waterborne protozoa in surface  water used for irrigation purposes by 18S rRNA amplicon-based  metagenomics | V4 hypervariable region | EUKAF- EUKAR  0.746-0.565 |  | EUKAF GCCGCGGTAATTCCAGCTC  EUKAR CYTTCGYYCTTGATTRA | EUKAF 0.746877398646291  EUKAR 0.565243179122183 |
| Characterization of the 18S rRNA Gene for Designing  Universal Eukaryote Specific Primers | V4 or V7/V8  V4 or V7/V8  V4 and V5 | F-574 -R-952,0.669-0.557  F-1183 and R-1631  0.807-0.690  F-566 and R-1200  0.750-0.761 | *Saccharomyces cerevisiae* | F-555 AAGTCTGGTGCCAGCAGCCG  F-565 CCAGCAGCCGCGGTAATTCC  F-566 CAGCAGCCGCGGTAATTCC  F-573 CGCGGTAATTCCAGCTCCA  F-574 GCGGTAATTCCAGCTCCAA  F-1183 AATTTGACTCAACACGGG  F-1422 ATAACAGGTCTGTGATGC  F-1624 CCTTTGTACACACCGCCCGTCG  R-574 CGGCTGCTGGCACCAGACTTGC  R-1196 TGTTGAGTCAAATTAAGC  R-1200 CCCGTGTTGAGTCAAATTAAGC  R-1289 ACTAAGAACGGCCATGCACC  R-1438 CATCACAGACCTGTTATTGC  R-1631 TACAAAGGGCAGGGACG  R-952 TTGGCAAATGCTTTCGC | F-555 0.774056241713767  F-565 0.747610076058893  F-566 0.750471006908101  F-573 0.713313795268997  F-574 0.669108924708674  F-1183 0.807445398088061  F-1422 0.778033633382178  F-1624 0.742132440164678  R-574 0.763868536738539  R-1196 0.789651803782011  R-1200 0.761496057497732  R-1289 0.807515176889261  R-1438 0.741050868746075  R-1631 0.690461237875933  R-952 0.55707905938176 |
| Sample Preservation, DNA or RNA  Extraction and Data Analysis for  High-Throughput Phytoplankton  Community Sequencing | V1 to V3  V8 to V9 | Euk1A--Euk516R  0.278-0.751  V8F-­-1510R  0.759-0.008(0.069) |  | Euk1A CTGGTTGATCCTGCCAG  Euk516R ACCAGACTTGCCCTCC  V8F ATAACAGGTCTGTGATGCCCT  1510R CCTTCYGCAGGTTCACCTAC | Euk1A 0.278347637987579  Euk516R 0.751413020724304  V8F 0.759856255669528  1510R 0.00823389854162306 |
| Revisions to the Classification, Nomenclature, and Diversity of Eukaryotes | V4  V4  V4  V4  V4  V4 | APU-1R& EK-42F, 0.0009&0.449  RibA & S20R, 0.0018& 0.790  RibA & RibB, 0.0018&0  Euk82F&Euk1498R,0.326&0.326  42F & 1510R, 0.449& 0.008  1F & 1528R, 0.0003&0.0001  EukF & EukR 0.627&0.813  EukF0&EukR0, 0.0018&0.0029  TAReuk454FWD1&TAReukREV3 0.7915&0.709  Prym03-3&Hapto1R,0.00219&0.003  528FLong&PRYM01+7,0.669&0.003  Pavlova-V4F&1528R,0.0005&0.0001  1F & Pavlova-V4F2R, 0.0003&0.00059  Pry421F & Pry1572R, 0.002&0.0017  Hap220F&Pav1702R,0.0002&0.00045  Nu-SSU-0024-5’ F & NuSSU-1757-3’ R  0.237&0.2933  AU2-F (& inner AUPH1)& AU4-R  0.0111(&0.527)&0  SAR-V3-SSU F&R,0&0  St1:EuglySSUF & EuglyLSUR, 0.002&0  St2: 0EuglySSUF & EuglySSUR 0&0  Euk 82F & Euk 1498 R, 0.326&0.326  PF1 & R4, 3.4\*10-5&0.0002  TAReuk454FWD1 & TAReukREV3,  0.791&0.7099  346Fmix(with 2) & 785R-mix(with 2),  0.002(0.005)&0(0.1)(0(0.1))  Next. For & Rev,0&0  3NDF & 1256R, 0.798&0.018  25F & 1256R, 0.305&0.018  14F1&s17, 0.0028&0.0035  ITS-F&ITS-R,0&0  Mon-F & Mon-R, 0&0.316  EukA & EukB, 0.278&0.0001  EukA-F&EukB-R,0.278&0(1.9inweb)  Helio1979R, 0.001  PolySSU1 & PolySSU1R, 0.0027 | |  |  | | --- | --- | | Amorphea | Apusomonadida |   Amoebozoa Tubulinea, Discosea, Variosea  Amoebozoa Tubulinea, Discosea, Variosea  Amoebozoa Arcellinida  Opisthokonta Choanoflagellata  Haptista Haptophyta  Haptista Haptophyta  Haptista Haptophyta  Haptista Haptophyta  Haptista Haptophyta  Haptista Haptophyta  Haptista Haptophyta  Haptista Haptophyta  Haptista Haptophyta  Haptista Haptophyta  Cryptista  Fungi  Stramenopiles Sar(no match found in silva page)  Stramenopiles Euglyphid  Stramenopiles Amphitremida  Alveolata Apicomplexa  Alveolata Apicomplexa  Alveolata Apicomplexa  Alveolata Dinoflagellata  Rhizaria Cercozoa  Rhizaria  Rhizaria Foraminifera  Excavates Parabasalia (no match in silva page)  Excavates Preaxostyla: Oxymonadida(Mon-F no match in silva page)  Excavates Preaxostyla: Paratrimastigida, Trimastigida  Protist, general, General Medlin primers  Haptista Centroplasthelida (reverse primer only)  Fungi Chytridiomycota (reverse primer only) | RibB ACCTGGTTGATCCTDCCAGT  APU-1R CTTCCTTTGGTTAAAACAC  S20R GACGGGCGGTGTGTACAA  Euk\_1498R CYGCAGGTTCACCTAC  1510R CCTTCYGCAGGTTCACCTAC  PolySSU1R TGATCCTTCYGCAGGTTCACC  EF1aZ-1R GAACGGCCATGCACCACCACC  1528R TGATCCTTCTGCAGGTTCACCTAC  EukR0 TGATCCTTCYGCAGGTTCAC  EukR CCGTGTTGAGTCAAATT  TAReukREV3 ACTTTCGTTCTTGATYRA  EK-42F CTCAARGAYTAAGCCATGCA  RibA ACCTGGTTGATCCTDCCAGT  Euk82F GAAACTGCGAATGGCTC  42F CTCAARGAYTAAGCCATGCA  AU2-F RTCTCACTAAGCCATTC  inner\_AUPH1 AGAGCTMTCAATCTGTCAATCCT  1F AACCTGGTTGATCCTGCCAGT  EukF0 ACCTGGTTGATCCTGCCAG  EukF GGGTTCGATTCCGGAGAG  TAReuk454FWD1 CCAGCASCYGCGGTAATTCC  Prym03-3 GTAAATTGCCCGAATCCTG  528FLong GCGGTAATTCCAGCTCCAA  Pavlova-V4F GTGAAATTCTTAGACCCACGGA  Pry421F AGCAGGCGCGTAAATTGCCCG  Hap220F ACCGGTCTCCGGTTGCGTGC  Nu-SSU-0024-5\_F CTGGTTGATCCTGCCAGTAGT  EuglySSUF GCGTACAGCTCATTATATCAGCA  0EuglySSUF GCGTACAGCTCATTATATCAGCA  Eucox1F GAYATGGCKTTNCCAAGATTAAA  Euk\_82F GAAACTGCGAATGGCTC  PF1 GCGCTACCTGGTTGATCCTGCC  TAReuk454F\_WD1 ACTTTCGTTCTTGATYR  346Fmix CADCGACGGGTAACGGGGAATTA  346Fmix CAGYGACGGGTAACGGGGAATTA  3NDF GGCAAGTCTGGTGCCAG  25F CATATGCTTGTCTCAAAGATTAAGCCA  14F1 AAGGGCACCACAAGAACGC  EukA CTGGTTGATCCTGCCAG  EukA-F CTGGTTGATCCTGCCAG  Euk34r GCATCGCCAGTTCTGCTTACC  Hapto1R CGAAACCAACAAAATAGCAC  PRYM01\_7 GATCAGTGAAAACATCCCTGG  1528R TGATCCTTCTGCAGGTTCACCTAC  Pavlova-V4F2R GTGAAATTCTTAGACCCACGGA  Pry1572R TCAACGYRCGCTGATGACA  Pav1702R TAGATGATAAGGTTTGGGTG  Helio1979R CACACTTACWAGGAYTTCCTCGTTSAAGACG  NuSSU-1757-3 CAGGTTCACCTACGGAAACCT  R ATGTGTATAAGAGACAGRACTACGAGCTTTTTAACTGC  EuglySSUR GCACCACCACCCATAGAATCWAGAAAGATC  Euk\_1498\_R CYGCAGGTTCACCTAC  998R GATCACCTTCTAATTTACCWACAACTG  R4 GATCCTTCTGCAGGTTCACCTAC  TAReukREV3 ACTTTCGTTCTTGATYR  Rev GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG  1256R GCACCACCACCCAYAGAATCAAGAAAGAWCTTC  s17 CGGTCACGTTCGTTGC  Mon-R TCACCTACGGAAACCTT  EukB TGATCCTTCTGCAGGTTCACCTAC  EuglyLSUR GTTTGGCACCTTAACTCGCG  0EuglySSUF GCGTACAGCTCATTATATCAGCA  EuglySSUR GCACCACCACCCATAGAATCWAGAAAGATC  785Rmix1 TATTCCATGCTGIAGTATTCA  785Rmix2 TATTCCATGCTAAASTATTCA  Next. For TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG[CCAGCASCYGCGGTAATTCC]  Rev GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG[ACTTTCGTTCTTGATYRATGA]  ITS-F TTCAGTTCAGCGGGTCTTCC  ITS-R GTAGGTGAACCTGCCGTTGG  Mon-F GAAGTCATATGCTGTCTCAA  EukB-R TGATCCTTCTGCAGGTTCACCTAC  AU4-R ACTTCTGGRTGICCRAARAAYCA | APU-1R 0.000942013816202638  S20R 0.790244923592213  Euk\_1498R 0.326320563812714  1510R 0.00823389854162306  PolySSU1R 0.00272137324680762  EF1aZ-1R 0.662235712790454  1528R 0.000104668201800293  EukR0 0.00293070965040821  EukR 0.813062591584677  TAReukREV3 0.709964412811388  EK-42F 0.44993371013886  RibA 0.00181424883120508  Euk82F 0.326320563812714  42F 0.44993371013886  AU2-F 0.0111297187914312  inner\_AUPH1 0.527353290070477  1F 0.000314004605400879  EukF0 0.00184913823180518  EukF 0.627171865187356  TAReuk454FWD1 0.791570720815016  Prym03-3 0.00219803223780615  528FLong 0.669108924708674  Pavlova-V4F 0.000593119810201661  Pry421F 0.00216314283720606  Hap220F 0.000209336403600586  Nu-SSU-0024-5\_F 0.237282813481264  EuglySSUF 0.00205847463540576  Euk\_82F 0.326320563812714  PF1 3.48894006000977e-05  TAReuk454F\_WD1 0.723152606238225  346Fmix 0.00202358523480567  346Fmix 0.00526829949061475  3NDF 0.798339264531435  25F 0.305003140046054  14F1 0.00286093084920801  EukA 0.278347637987579  EukA-F 0.278347637987579  Euk34r 6.97788012001954e-05  Hapto1R 0.0030353778522085  PRYM01\_7 0.00324471425580909  1528R 0.000104668201800293  Pavlova-V4F2R0.000593119810201661  Pry1572R 0.00174447003000488  Pav1702R 0.00045356220780127  Helio1979R 0.00101179261740283  NuSSU-1757-3 0.293384969646221  EuglySSUR 0.0154211150652432  Euk\_1498\_R 0.326320563812714  R4 0.000244225804200684  TAReukREV3 0.723152606238225  1256R 0.018212267113251  s17 0.00355871886120996  Mon-R 0.316691089247087  EukB 0.000104668201800293 |