The limited DNA sequence data of the polychaetes species are available from the Eastern Arabian Sea. We have sequenced 18S rDNA gene from 54 polychaetes species and 37 species identified up to the species level. The DNA bar-coding data provides for molecular identification of benthic polychaetes that will provide imminent into drivers of species diversity in the Eastern Arabian Sea. The 18S rDNA sequence data set is made publicly available to enable critical or extended analyzes of DNA bar-coding.

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Value of the data

- These data are the first generated using 18S rRNA genes of polychaetes in west coast of India.
- This project presents the diversity of benthic polychaetes communities by using 18S rRNA gene sequencing.
- This data provides other researchers to extend the molecular identification (DNA barcoding).

1. Data

The molecular taxonomy is refreshing traditional taxonomy and helps to increase the taxonomic crisis, alternative and complementary approaches, particularly successful in the identification and delimitation of new species from various groups [1]. Recently, the increased identification of abundance and importance of cryptic species, those are morphologically identical but genetically different [2]. Moreover, the molecular identification has been reformed the exploration of biodiversity for which traditional taxonomy is difficult [3]. There has been increased numbers of unidentified specimens in our collection which limits their use in future studies involving the biogeography. The most commonly occurring polychaete species are shown in the Fig. 1. A total 54 polychaete species were newly sequenced based on the 18S rDNA gene together with 88 sequences submitted to NCBI GenBank (Table 1) including Paraprionospio cristata Zhou, Yokoyama and Li, 2008, and Paraprionospio patiens Yokoyama, 2007. They are most dominant and opportunistic species along the study area.

Fig. 1. Commonly occurring polychaete species-A: Lysidice sp., B: Eteone heteropoda, C: Haplosyllis sp., D: Thornera sp., E: Sternapsis suchtta, F: G: Perinereis cultrifera, H: Lumbrineris funchalensis, I: Pareurythoe borealis, J: Ceratonereis japonica, K-L: Scolelepis sp., M: Pomatoceros triqueter, N: Parasabella saxicola, O: Magelona cincta, P: Pomatostegus actinoceros, Q: Euclymene sp., R: Terebella sp., S: Paraprionospio cordifolia, T: Spiochaetopterus sp.
### Table 1
NCBI Accession number for benthic polychaetes species along the west coast of India.

| Specimen voucher | Morphological ID | NCBI Accession number |
|------------------|------------------|------------------------|
| GP0161–GP0163    | Eurythoe complanata | KT900265–KT900267     |
| GP0164           | Notopygogcaribea   | KT900268               |
| GP0165           | Eurythoe complanata | KT900269               |
| GP0166           | Pareurythoe borealis | KT900270            |
| GP0167–GP0168    | Thomora sp.        | KT900271–KT900272     |
| GP0169–GP0170    | Chloiaviridis       | KT900273–KT900274     |
| GP0171–GP0173    | Eurythoe complanata | KT900275–KT900277     |
| GP0174           | Hermina verruculosa | KT900278               |
| GP0175           | Chloea viridis     | KT900279               |
| GP0176–GP0177    | Notopygog ornate   | KT900280–KT900281     |
| GP0178           | Haplosylis sp.     | KT900282               |
| GP0179           | Pseudonereis sp.   | KT900283               |
| GP0180           | Perinereis cultifera | KT900284            |
| GP0181–GP0182    | Platynereis dumerlii | KT900285–KT900286    |
| GP0183           | Namalycastis abiuma | KT900287              |
| GP0184           | Dendronereis aestuaria | KT900288            |
| GP0185           | Namalycastis abiuma | KT900289              |
| GP0186           | Platynereis australis | KT900290          |
| GP0187           | Nereis sandersi    | KT900291               |
| GP0188           | Glycera capitata   | KT900292               |
| GP0189           | Glycera alba       | KT900293               |
| GP0190           | Eunicice miurai    | KT900294               |
| GP0191–GP0192    | Lysidice sp.       | KT900295–KT900296     |
| GP0193           | Lumbrineris funchalensis | KT900297        |
| GP0194           | Marphysa viridis   | KT900298               |
| GP0195           | Ninoe nigripes     | KT900299               |
| GP0196–GP0197    | Marphysa sp.       | KT900300–KT900301     |
| GP0198           | Diopatra sp.       | KT900302               |
| GP0199           | Eunicice miurai    | KT900303               |
| GP0200–GP0202    | Paraprinoposio cordifolia | KT900304–KT900306|
| GP0203–GP0204    | Paraprinoposio patians | KT900307–KT900308   |
| GP0205           | Paraprinoposio cordifolia | KT900309       |
| GP0206–GP0207    | Scolelepis sp.     | KT900310–KT900311     |
| GP0208           | Magelona cincta    | KT900312               |
| GP0209–GP0212    | Neosabelaria indica | KT900313–KT900316     |
| GP0212–GP0214    | Sabellaria chandrae | KT900317–KT900318    |
| GP0215           | Sabellaria intoshi | KT900319               |
| GP0216–GP0217    | Terebella sp.      | KT900320–KT900321     |
| GP0218           | Paraempolymniaaspiana | KT900322           |
| GP0219–GP0220    | Parasabella saxicola | KT900323–KT900324   |
| GP0221           | Hydroides sanctaeccrus | KT900325     |
| GP0222           | Chitinopomaserrula | KT900326               |
| GP0223           | Pomatoceros triquetra | KT900327            |
| GP0224           | Spirobranchuslatiscapus | KT900328        |
| GP0225           | Thomora sp.        | KX290696               |
| GP0226–GP0227    | Bhawaniacryptopocephala | KX290697–KX290698 |
| GP0228–GP0229    | Perinereis sp.     | KX290699–KX290700     |
| GP0230           | Nectoneanthes oxyoda | KX290701           |
| GP0231–GP0232    | Hermeniave ruculosa | KX290702–KX290703   |
| GP0233           | Hedisteatoka       | KX290704               |
| GP0234–GP0235    | Terebellides sp.   | KX290705–KX290706     |
| GP0236–GP0237    | Paralacydonia paradoxa | KX290707–KX290708   |
| GP0238           | Hesione sp.        | KX290709               |
| GP0239–GP0240    | Spirochaetopterus sp. | KX290710–KX290711   |
| GP0241           | Euclymene sp.      | KX290712               |
2. Experimental design, materials and methods

The sediment samples were collected at the following localities. Sediment samples were collected using 0.04 m² van Veen grabs. Samples were sieved on a 500 μm mesh. In the laboratory, the sediment samples were washed again, sorted, and stored in 95% ethanol. Some of middle segments of polychaete species were removed from these specimens and kept in vials containing absolute ethanol until further use for DNA isolation. Identification of polychaete species was done by observing diagnostic characters parapodia-bearing chitinous chaetae under stereo zoom microscope using keys [4,5].

2.1. DNA extraction, PCR amplification, purification, and sequencing

Genomic DNA was extracted from the specimens using the Qiagen DNeasy Tissue Kit according to manufacturer’s instructions. The 18S rRNA gene amplifications were carried out using primer pair 18F/18R1843 [6]. PCR amplification of the 18S rDNA gene changed into done in overlapping fragments of ~1800 bp length each with modified primer pairs with standard cycle sequencing protocols. Amplifications had been carried out using an Eppendorf Master Cycler Gradient. The following PCR temperature file was used: 95°C for 3 min; 35 cycles at 95°C for 45 s, 60°C for 1 min, and 72°C for 2 min; final extension at 72°C for 5 min. After detection by gel electrophoresis, the products had been purified using the Qiagien PCR Purification Kit (Qiagen). Sequences were produced using the same primers and determined on an Applied Biosystems (ABI) 3730xl. All sequences were submitted to NCBI GenBank (Table 1).

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.09.015.

References

[1] F. Valentini, P. Pompanon, Taberlet, DNA barcoding for ecologists, Trends Ecol. Evol. 24 (2009) 110–117.
[2] M.J. Brasier, H. Wiklund, L. Neal, R. Jeffreys, K. Linse, H. Ruhl, A.G. Glover, DNA barcoding uncovers cryptic diversity in 50% of deep-sea Antarctic polychaetes, R. Soc. Open Sci. 3 (11) (2016) 160432.
[3] C.Q. Tang, F. Leasi, U. Obertegger, A. Kieneke, T.G. Barraclough, D. Fontaneto, The widely used small subunit 18S rDNA molecule greatly underestimates true diversity in biodiversity surveys of the meiofauna, Proc. Natl. Acad. Sci. 109 (40) (2012) 16208–16212.
[4] P. Fauvel, The Fauna of India Including Pakistan, Ceyalon, Burma and Malaya, The Indian Press, Allahabad (1953) 408.
[5] J.H. Day, A Monograph on the Polychaete of Southern Africa, Part I and II. (Trustees of British Museum, Natural History, London (1967) 842.
[6] D.M. Hillis, M.T. Dixon, Ribosomal DNA: molecular evolution and phylogenetic inference, Q. Rev. Biol. 66 (4) (1991) 411–453.