

# Environmental characteristics of Agulhas rings affect interocean plankton transport

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Agulhas rings provide the principal route for ocean waters to circulate from the Indo-Pacific to the Atlantic basin. Their influence on global ocean circulation is well known, but their role in plankton transport is largely unexplored. We show that, although the coarse taxonomic structure of plankton communities is continuous across the Agulhas choke point, South Atlantic plankton diversity is altered compared with Indian Ocean source populations. Modeling and in situ sampling of a young Agulhas ring indicate that strong vertical mixing drives complex nitrogen cycling, shaping community metabolism and biogeochemical signatures as the ring and associated plankton transit westward. The peculiar local environment inside Agulhas rings may provide a selective mechanism contributing to the limited dispersal of Indian Ocean plankton populations into the Atlantic.

The Agulhas Current, which flows down the east coast of Africa, leaks from the Indo-Pacific Ocean into the Atlantic Ocean (1). This leakage, a choke point to heat and salt distribution across the world's oceans, has been increasing over the last decades (2). The influence of the Agulhas leakage on global oceanic circulation makes this area a sensitive lever in climate change scenarios (3). Agulhas leakage has been a gateway for planetary-scale water transport since the early Pleistocene (4), but diatom fossil records suggest that it is not a barrier to plankton dispersal (5). Most of the Agulhas leakage occurs through huge anticyclonic eddies known as Agulhas rings. These 100- to 400-km-diameter rings bud from Indian Ocean subtropical waters at the Agulhas Retroflection (1). Each year, up to half a dozen Agulhas rings escape the Indian Ocean, enter Cape Basin, and drift northwesterly across the South Atlantic, reaching the South American continent over the course of several years (1, 6). During the transit of Agulhas rings, strong westerly "roaring forties" winds prevalent in the southern 40s and 50s latitudes cause intense internal cooling and mixing (7).

We studied the effect of Agulhas rings and the environmental changes they sustain on plankton dispersal. Plankton such as microalgae, which produce half of the atmospheric oxygen derived from photosynthesis each year, are at the base of open-

ocean ecosystem food chains, thus playing an essential role in the functioning of the biosphere. Their dispersal is critical for marine ecosystem resilience in the face of environmental change (8). As part of the Tara Oceans expedition (9), we describe taxonomic and functional plankton assemblages inside Agulhas rings and across the three oceanic systems that converge at the Agulhas choke point: the western Indian Ocean subtropical gyre, the South Atlantic Ocean gyre, and the Southern Ocean below the Antarctic Circumpolar Current (Fig. 1).

## Physical and biological oceanography of the sampling sites

The Indian, South Atlantic, and Southern Oceans were each represented by three sites sampled between May 2010 and January 2011 (Fig. 1 and table S1). A wide range of environmental conditions were encountered (10). We first sampled the two large contiguous Indian and South Atlantic subtropical gyres and the Agulhas ring structures that maintain the physical connection between them. On the western side of the Indian Ocean, station TARA\_052 was characterized by tropical, oligotrophic conditions. Station TARA\_064 was located within an anticyclonic eddy representing the Agulhas Current recirculation. Station TARA\_065 was located at the inner edge of the Agulhas Current on the South African slope

that feeds the Agulhas retroflection and Agulhas ring formation (3). In the South Atlantic Ocean, station TARA\_070, sampled in late winter, was located in the eastern subtropical Atlantic basin. Station TARA\_072 was located within the tropical circulation of the South Atlantic Ocean, and Station TARA\_076 was at the northwest extreme of the South Atlantic subtropical gyre. Two stations (TARA\_068 and TARA\_078) from the west and east South Atlantic Ocean sampled Agulhas rings. Three stations (TARA\_082, TARA\_084, and TARA\_085) in the Southern Ocean were selected to sample the Antarctic Circumpolar Current frontal system. Station TARA\_082 sampled sub-Antarctic waters flowing northward along the Argentinian slope, waters that flow along the Antarctic Circumpolar Current (11) with characteristics typical

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of summer sub-Antarctic surface waters and are stratified by seasonal heating. Station TARA\_084 was located on the southern part of the Antarctic Circumpolar Current, in the Drake Passage between the Polar Front and the South Antarctic Circumpolar Current front (11). Station TARA\_085 was located on the southern edge of the South Antarctic Circumpolar Current front with waters typical of polar regions.

We compared overall plankton community structures between the three oceans using imaging and genetic surveys of samples from the epipelagic zone of each station (12). Prokaryote, phyto-, and zooplankton assemblages were similar across Indian and South Atlantic Ocean samples but different from Southern Ocean samples (Fig. 2A). In the Indian and South Atlantic Oceans, zooplankton communities were dominated by Calanoida, Cyclopoida (Oithonidae), and Poecilostomatoida copepods (12); phytoplankton communities were mainly composed of chlorophytes, pelagophytes, and haptophytes (12). In contrast, Southern Ocean zooplankton communities were distinguished by an abundance of *Limacina* spp. gastropods and Poecilostomatoida copepods. Southern Ocean phytoplankton were primarily diatoms and haptophytes. The divergence was even more conspicuous with respect to prokaryotes, in that picocyanobacteria, dominant in the Indian and South Atlantic Oceans, were absent in the Southern Ocean. The Southern Ocean had a high proportion of Flavobacteria and Rhodobacterales (12). Virus concentrations in the <0.2- $\mu\text{m}$  size fractions were significantly lower in the southernmost Southern Ocean station (13). Viral particles were significantly smaller in two of the three Southern Ocean sampling sites, and two Southern Ocean viromes had significantly lower richness compared with the South Atlantic and Indian Oceans (13). Although nucleocytoplasmic large DNA viruses were similarly distributed in the South Atlantic and Indian Oceans (12), two Southern Ocean sites contained coccolithoviruses also found in the TARA\_068 Agulhas ring but not in the other Indian and South Atlantic stations.

### Biological connection across the Agulhas choke point

Genetic material as represented by ribosomal RNA gene (rDNA) sequences showed exchange patterns across the oceans (shared barcode richness) (14). Despite a smaller interface between the Indian and South Atlantic Oceans than either have with the Southern Ocean, more than three times as much genetic material was in common between the Indian and South Atlantic Oceans than either had with the Southern Ocean (Fig. 2B) (15). Indeed, the Indian–South Atlantic interocean shared barcode richness ( $32 \pm 5\%$ ) was not significantly different from typical intraocean values ( $37 \pm 7\%$ , Tukey post hoc, 0.95 confidence). Shared barcode richness involving the Southern Ocean was significantly lower ( $9 \pm 3\%$ ) (Fig. 2C). We found that the proportion of whole shotgun metagenomic reads shared between samples, both intraoceanic and Indian–South Atlantic interocean similarities, were in the 18 to 30% range, whereas interocean

similarities with Southern Ocean samples were only 5 to 6% (16). The statistically indistinguishable Indo-Atlantic intra- and interocean genetic similarities revealed a high Indo-Atlantic biological connection despite the physical basin discontinuity.

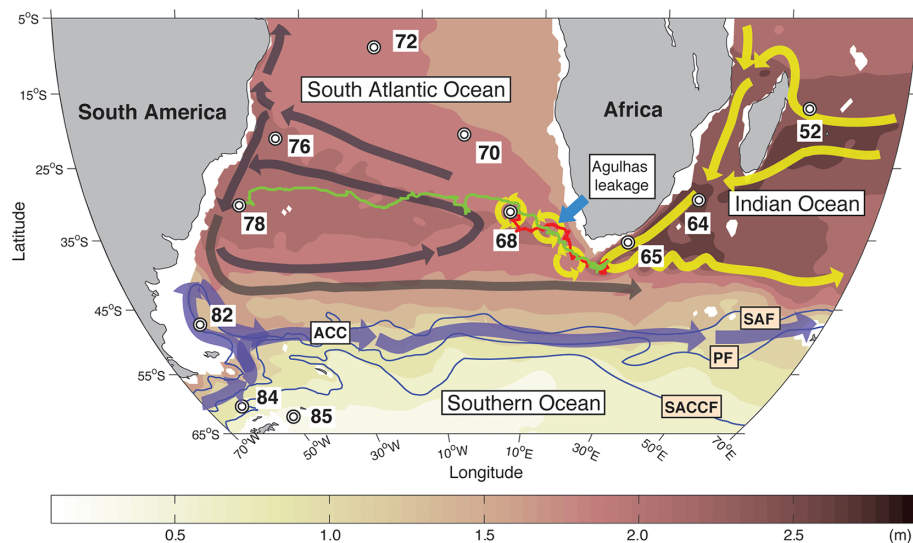
Nonetheless, differences on either side of the Agulhas choke point were evident. We found that prokaryote barcode richness was greater in the South Atlantic than in the Indian Ocean (Fig. 3A) (0.2- to 3- $\mu\text{m}$  size fraction). The opposite trend characterized eukaryotes larger than 20  $\mu\text{m}$  in size. We cannot rule out the possibility that the higher prokaryote diversity observed in the South Atlantic Ocean might be due to a protocol artifact resulting from a difference in prefiltration pore size from 1.6  $\mu\text{m}$  (Indian Ocean) to 3  $\mu\text{m}$  (South Atlantic and Southern Oceans). As also evident from the pan-oceanic Tara Oceans data set (17), smaller size fractions showed greater eukaryote diversity across the Agulhas system. In all size fractions that we analyzed, samples from the Southern Ocean were less diverse than samples from the South Atlantic Ocean and Indian Ocean (Fig. 3A).

When rDNA barcodes were clustered by sequence similarity and considered at operational taxonomic unit (OTU) level (14), more than half (57%) of the OTUs contained higher sub-OTU barcode richness in the Indian Ocean than in the South Atlantic Ocean, whereas less than a third (32%) of OTUs were richer in the South Atlantic Ocean, leaving only 11% as strictly cosmopolitan (Fig. 3B). Taken together, these 1307 OTUs represented 98% of the barcode abundance, indicating that the observed higher barcode richness within

OTUs in the Indian Ocean was not conferred by the rare biosphere. Certain taxa displayed unusual sub-OTU richness profiles across the choke point. Consistent with their relatively large size, Opisthokonta (mostly copepods), Rhizaria (such as radiolarians), and Stramenopiles (in particular diatoms) had much higher sub-OTU barcode richness in the Indian Ocean, whereas only small-sized Hacrobia (mostly haptophytes) showed modest increased sub-OTU barcode richness in the South Atlantic Ocean. The plankton filtering that we observed in fractions above 20  $\mu\text{m}$  through the Agulhas choke point might explain the reduction of marine nekton diversity from the Indian Ocean to the South Atlantic Ocean (18) by propagating up the food web (19).

### In situ sampling of two Agulhas rings

To understand whether the environment of Agulhas rings, the main transporters of water across the choke point, might act as a biological filter between the Indian Ocean and the South Atlantic Ocean, we analyzed data collected in both a young and an old Agulhas ring. The young ring sampled at station TARA\_068 was located in the Cape Basin, west of South Africa, where rings are often observed after their formation at the Agulhas Retroflexion (7, 20). It was a large Agulhas ring that detached from the retroflexion about 9 to 10 months before sampling. This ring first moved northward and then westward in the Cape Basin while interacting with other structures (red track in Fig. 1) (21). Ocean color data collected by satellite showed that surface chlorophyll concentrations were higher in the Cape Basin than at the retroflexion, suggesting that vigorous vertical



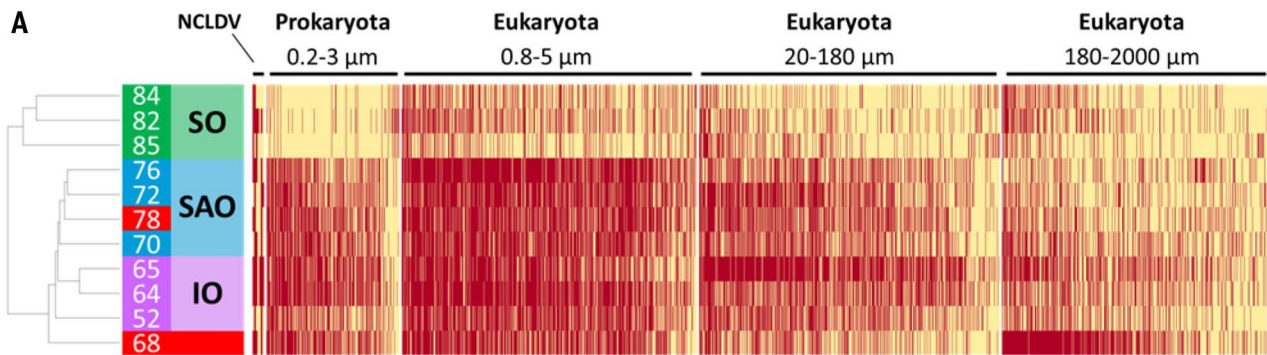
**Fig. 1. The oceanic circulation around the Agulhas choke point and location of Tara Oceans stations.** The map shows the location of sampling stations, together with trajectories of the young and old Agulhas rings (TARA\_068 and TARA\_078, red and green tracks, respectively). The stations here considered as representative of the main basins are (i) TARA\_052, TARA\_064, and TARA\_065 for Indian Ocean; (ii) TARA\_070, TARA\_072, and TARA\_076 for the South Atlantic Ocean; and (iii) TARA\_082, TARA\_084, and TARA\_085 for the Southern Ocean. The mean ocean circulation is schematized by arrows (currents) and background colors [surface climatological dynamic height (0/2000 dbar from CARS2009; [www.cmar.csiro.au/cars](http://www.cmar.csiro.au/cars)) (70)]. Agulhas rings are depicted as circles. The Antarctic Circumpolar Current front positions are from (13).

mixing might have occurred in the Cape Basin (22). At the time of sampling, the anticyclonic Agulhas ring was 130 to 150 km in diameter, was about 30 cm higher than average sea surface height, and was flanked by a 130- to 150-km cyclonic eddy to the north and a larger (>200 km) one to the east (Fig. 4A) (23). Thermosalinograph data showed that filaments of colder, fresher water surrounded the young ring core (Fig. 4A) (23). To position the biological sampling station close to the ring core, a series of conductivity-temperature-depth (CTD) casts was performed (23, 24). The young Agulhas ring had a surface temperature and salinity of 16.8°C and 35.7 practical salinity units (PSU), respectively, and the isopycnal sloping could be traced down to CTD maximal depth (900 to 1000 m). The core of the ring water was 5°C cooler than Indian Ocean subtropical source waters at similar latitudes

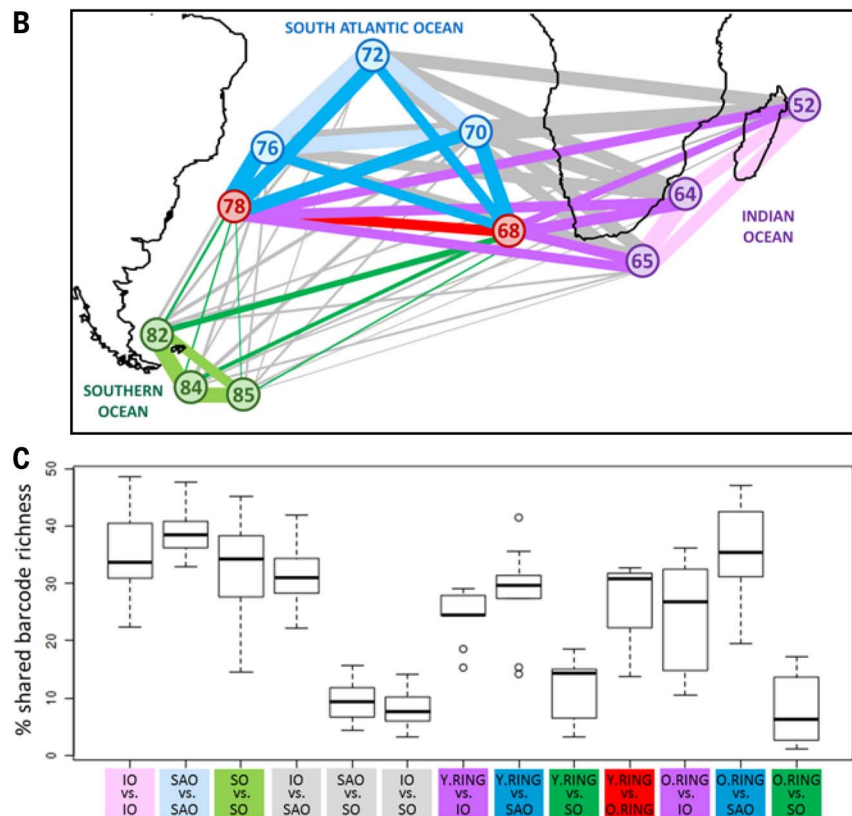
(TARA\_065) (table S1), typical for the subtropical waters south of Africa (17.8°C, 35.56 PSU, respectively) (25). The mixed layer of the young ring was deep (>250 m) compared with seasonal cycles of the mixed layer depths in the region (50 to 100 m) (Fig. 4C), typical of Agulhas rings (26). At larger scales (Fig. 4B) (24), steep spatial gradients were observed, with fresher and colder water in the Cape Basin than in the Agulhas Current because of both lateral mixing with waters from the south and surface fluxes. This confirms that the low temperature of the young Agulhas ring is a general feature of this Indian to South Atlantic Ocean transitional basin. Air-sea exchanges of heat and momentum promoted convection in the ring core, which was not compensated by lateral mixing and advection. The core of the Agulhas ring thus behaved as a subpolar environment traveling across a subtropical region.

At station TARA\_078, we sampled a second structure whose origins were in the Agulhas Retro-reflection, likely a 3-year-old Agulhas ring. This old ring, having crossed the South Atlantic Ocean, was being absorbed by the western boundary current of the South Atlantic subtropical gyre. The structure sampled at station TARA\_078 was characterized by a warm salty core (27). As for the young Agulhas ring sampled, the old ring also had a 100-m-deeper pycnocline than surrounding waters, typical of large anticyclonic structures.

The plankton assemblage of both Agulhas rings most closely resembled the assemblages found in Indian and South Atlantic samples (Fig. 2A). At higher resolution, barcodes (Fig. 2, B and C) and metagenomic reads (16) shared between the Agulhas rings and the Indian or South Atlantic samples showed that the young ring was genetically distinct from both Indian and South Atlantic samples,



**Fig. 2. Agulhas system plankton community structure.** (A) Plankton community structure of the Indian Ocean (IO), South Atlantic Ocean (SAO), Southern Ocean (SO), and Agulhas rings (stations 68 and 78, in red). Bacterial 0.2- to 3- $\mu$ m assemblage structure was determined by counting clade-specific marker genes from bacterial metagenomes. Size fractionated (0.8 to 5, 20 to 180, and 180 to 2000  $\mu$ m) eukaryotic assemblage structure was determined using V9 rDNA barcodes. Nucleocytoplasmic large DNA viruses (NCLDV) 0.2- to 3- $\mu$ m assemblage structure was determined by phylogenetic mapping using 16 NCLDV marker genes. OTU abundances were converted to presence/absence to hierarchically cluster samples using Jaccard distance. (B) Network of pairwise comparisons of shared V9 rDNA barcode richness (shared barcode richness) between the 11 sampling stations of the study. The width of each edge is proportional to the number of shared barcodes between corresponding sampling stations. (C) Box plot of shared barcode richness between stations for 0.8- to 5-, 20- to 180-, and 180- to 2000- $\mu$ m size fractions. The shared barcode richness analysis considers that two V9 rDNA barcodes are shared between two samples if they are 100% identical over their whole length. Shared barcode richness between two samples, s1 and s2, is expressed as the proportion of shared barcode richness relative to the average internal barcode richness of samples s1 and s2. IO, Indian Ocean; SAO, South Atlantic Ocean; SO, Southern Ocean; Y.RING, young ring; O.RING, old ring.





whereas the old ring was similar to its surrounding South Atlantic samples (Tukey post hoc, 0.95 confidence). Light microscopy analyses revealed some plankton groups specific to the young Agulhas ring, such as *Pseudo-nitzschia* spp., which represented 20% of the phytoplankton counts but less than 10% in all other stations (12). Other potentially circumstantial plankton characteristic of the young Agulhas ring included the tintinnid *Dictyocysta pacifica* (12), the diatom *Corethron pennatum* (12), and the dinoflagellate *Tripos limulus* (12). A tiny (less than 15  $\mu\text{m}$  long) pennate diatom from the genus *Nanoneis*, which we saw only in the young Agulhas ring and Indian Ocean stations around the African coasts (28), was an example of the Indo-Atlantic plankton diversity filtering observed at rDNA barcode level and corroborated by microscopy. OTU clustered barcodes revealed a variety of young Agulhas ring sub-OTU richness patterns compared with source and destination oceans (Fig. 5A). Among Copepoda, *Gaetanus variabilis* and *Corycaeus speciosus* were the more cosmopolitan species (Fig. 5B), whereas *Bradya* species found in the young ring were mainly similar to those from the Indian Ocean. *Acartia negligens* and *Neocalanus robustior* displayed high levels of barcode richness specific to each side of the Agulhas choke point. Bacillariophyceae were heavily filtered from Indian to South At-

lantic Oceans (Fig. 5C), and most OTUs (17 out of 20) were absent in the young ring, suggesting that diversity filtering could take place earlier in the ring's 9-month history. Consistent with the observed particularities of the plankton in the young ring, continuous underway optical measurements showed that the ring core photosynthetic community differed from surrounding waters (29–31). Intermediate size cells, and relatively low content of photoprotective pigments, reflected low growth irradiance and suggested a transitional physiological state. Thus, the plankton community in the young Agulhas ring had diverged from plankton communities typical of its original Indian waters but, even 9 months after formation, had not converged with its surrounding South Atlantic waters.

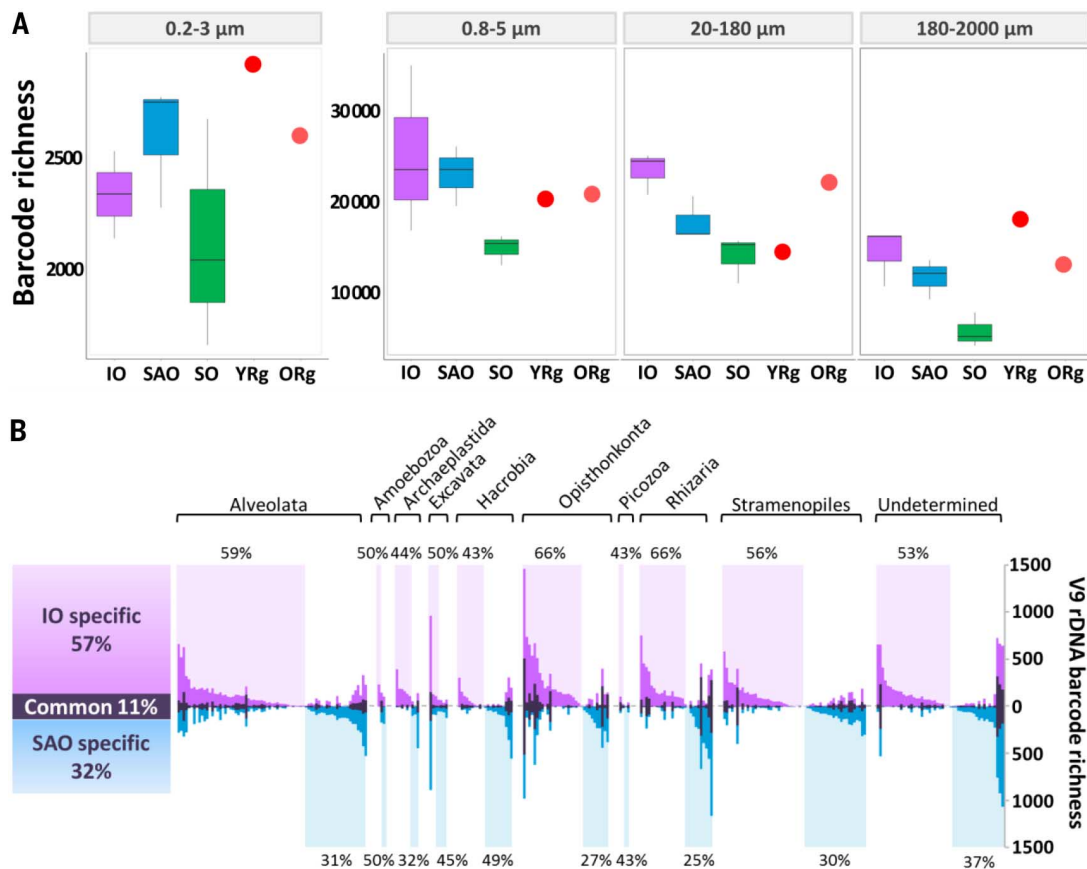
### Deep mixing in Agulhas rings promotes plankton bloom

The upper water column of the young ring showed a high nitrite concentration ( $>0.5 \text{ mmol m}^{-3}$ ) (Fig. 4D) (32). This observation, along with its particularly deep mixed layer ( $>250 \text{ m}$ ), suggested that as Agulhas rings proceed westward in the Cape Basin, vigorous deep mixing of their weakly stratified waters may have entrained nitrate and stimulated phytoplankton blooms. Typically, fresh organic material would then either be exported

as sinking particles or locally recycled, sustaining heterotrophic production of ammonium that would, in turn, be consumed by photoautotrophs in the euphotic layer but nitrified below. The resulting nitrite, eventually oxidized to nitrate, might remain evident at subsurface as observed in the nitrite anomaly of the young ring detected here. This hypothesis was supported by numerical simulations of the Massachusetts Institute of Technology General Circulation Model (33), which resolved Agulhas rings, their phytoplankton populations, and associated nutrient cycling (Fig. 6A). We tracked 12 Agulhas rings in the ocean model and characterized their near-surface biogeochemical cycles (Fig. 6B) (34). As the rings moved westward, storms enhanced surface heat loss, stimulating convection and the entrainment of nitrate. In the model simulations, proliferation of phytoplankton generated subsurface nitrite, which persisted because phytoplankton were light-limited at depth and because nitrification was suppressed by light at the surface (35). The associated blooms were dominated by large opportunistic phytoplankton and nitrate-metabolizing *Synechococcus* spp. analogs, whereas populations of *Prochlorococcus* spp. analogs dominated the quiescent periods (34). Each of the 12 simulated Agulhas rings exhibited this pattern in response to surface forcing by weather systems, and all rings maintained a persistent

### Fig. 3. Diversity of plankton populations specific to Indian and Atlantic Oceans.

(A) Box plot of 16S (0.2 to 3  $\mu\text{m}$ ) and V9 rDNA barcodes richness (0.8- to 5-, 20- to 180-, and 180- to 2000- $\mu\text{m}$  size fractions). Each box represents three sampling stations combined into Indian, South Atlantic, and Southern Ocean. Single Agulhas ring stations are represented as red (young ring) and orange (old ring) crosses. (B) Plankton sub-OTU richness filtering across the Agulhas choke point. Each vertical bar represents a single eukaryotic plankton OTU, each of which contains  $>10$  distinct V9 rDNA barcodes (14). For each OTU are represented the number of distinct barcodes (sub-OTU richness) found exclusively in the South Atlantic Ocean (blue), exclusively in the Indian Ocean (pink), and in both South Atlantic Ocean and Indian Ocean (gray). OTUs are grouped by taxonomic annotation (indicated above the bar plot). For each taxonomic group, the percentage of OTUs with higher sub-OTU richness in the Indian Ocean (shaded in pink) or in the South Atlantic Ocean (shaded in blue) is indicated, respectively, at the top and bottom of the bar plot. A total of 1307 OTUs are presented, representing 98% of total V9 rDNA barcode abundance.

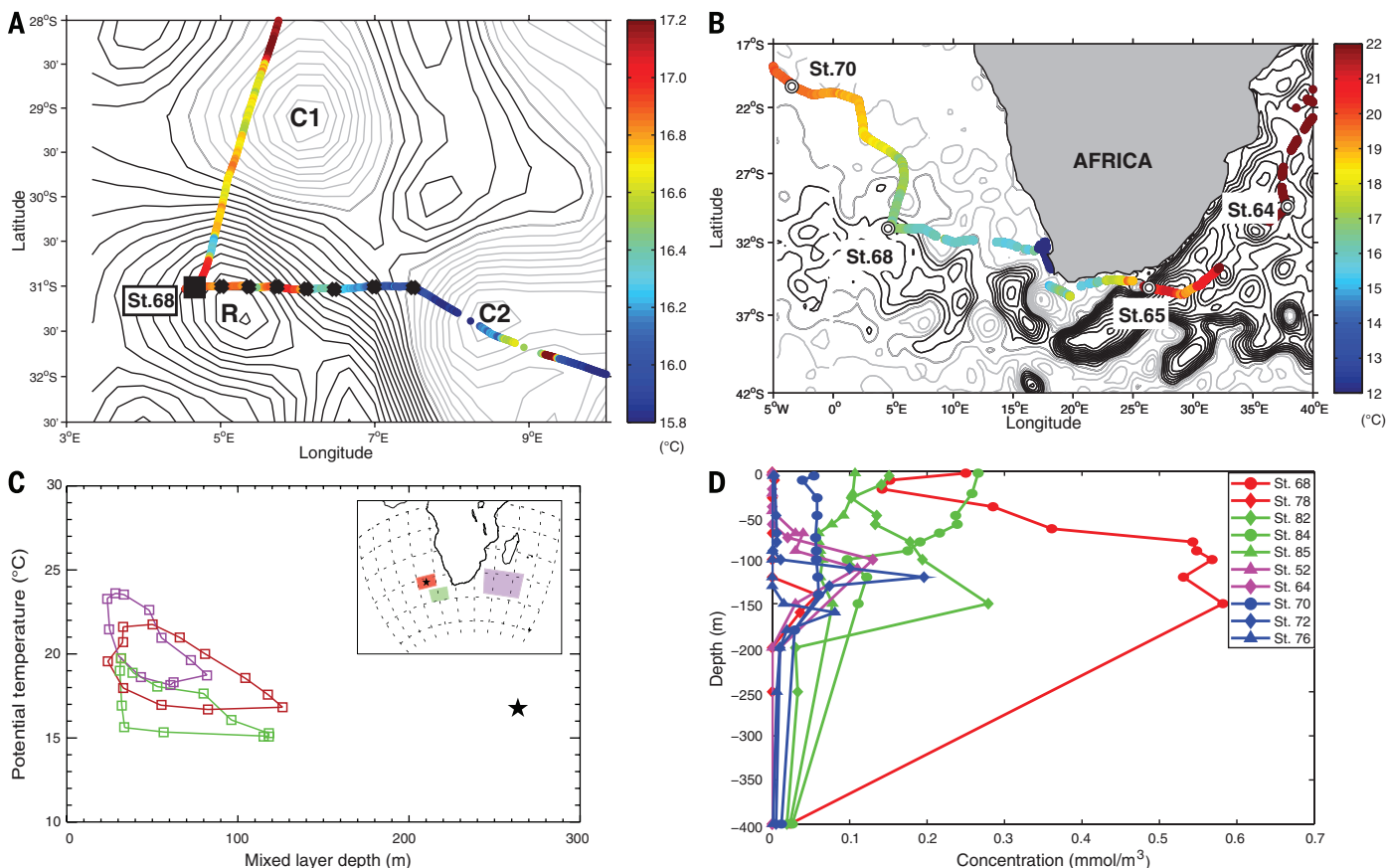


subsurface nitrite maximum in the region, as observed in TARA\_068 and in other biogeochemical surveys (36).

The nitrite peak observed at TARA\_068 in the young Agulhas ring was associated with a differential representation of nitrogen metabolism genes between the ring and the surrounding South Atlantic and Indian Oceans metagenomes derived from 0.2- to 3- $\mu\text{m}$  size fractions (Fig. 7) (37). Agulhas ring overrepresented KEGG (Kyoto Encyclopedia of Genes and Genomes) orthologs (KOs) were involved in both nitrification and denitrification, likely representing the overlap between plankton assemblages involved in the conversion of nitrate to nitrite on the one hand and in denitrification of the accumulating nitrite on the other. Distinct KOs involved in successive denitrification steps were found to be encoded by similar plankton taxa. For instance, KO10945 and KO10946 (involved in ammonium nitrification) and KO00368 (subsequently

involved in nitrite to nitrous oxide denitrification) appeared mostly encoded by Nitrosopumilaceae archaea. KO00264 and KO01674 (involved in ammonium assimilation) were mostly assigned to eukaryotic Mamiellales, whereas the opposite KO00367 and KO00366 (involved in dissimilatory nitrite reduction to ammonium), followed by KO01725 (involved in ammonium assimilation), were encoded by picocyanobacteria. In the specific case of the picocyanobacteria, metagenomic reads corresponding to *nirA* genes showed that the observed young Agulhas ring KO00366 (dissimilatory nitrite reduction) enrichment was mainly due to the overrepresentation of genes from *Prochlorococcus* (Fig. 8B). This enrichment was found to be associated with a concomitant shift in population structure from *Prochlorococcus* high-light II ecotypes (HLII, mostly lacking *nirA* genes) to codominance of high-light I (HLI) and low-light I (LLI) ecotypes. Indeed, among the several

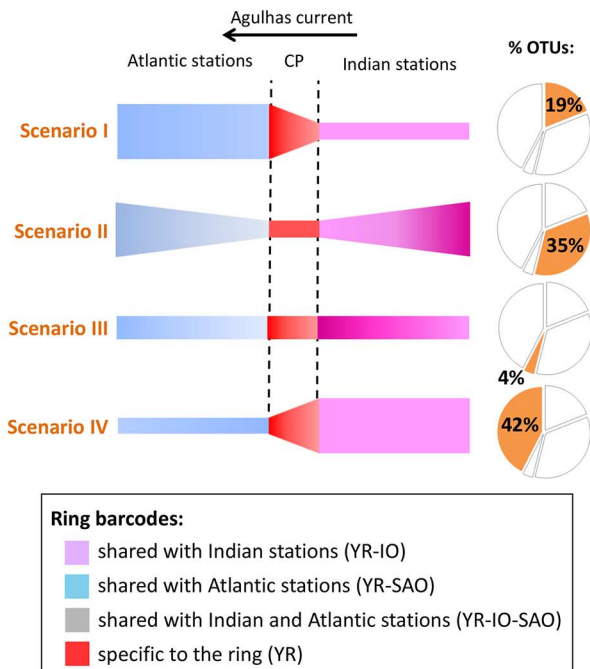
*Prochlorococcus* and *Synechococcus* ecotypes identified based on their genetic diversity and physiology (38, 39), neutral marker (*petB*) (Fig. 8A) recruitments showed that dominant clades in the Indian Ocean upper mixed layer were *Prochlorococcus* HLII and *Synechococcus* clade II, as expected given the known (sub)tropical preference of these groups (40). Both clades nearly completely disappeared (less than 5%) in the mixed cold waters of the young ring and only began to increase again when the surface water warmed up along the South Atlantic Ocean transect. Conversely, young ring water was characterized by a large proportion of *Prochlorococcus* HLI and LLI and *Synechococcus* clade IV, two clades typical of temperate waters. Besides temperature, the *Prochlorococcus* community shift from HLII to HLI + LLI observed in the young ring was likely also driven by the nitrite anomaly. Indeed, whereas most *Synechococcus* strains isolated so far are able to



**Fig. 4. Properties of the young Agulhas ring (TARA\_068).** (A) Daily sea surface height around young Agulhas ring station TARA\_068 [absolute dynamic topography (ADT) from [www.avisio.altimetry.fr](http://www.avisio.altimetry.fr)]. R, C1, and C2, respectively, denote the centers of the Agulhas ring and two cyclonic eddies. The contour interval is 0.02 dyn/m. The ADT values are for 13 September 2010. Light gray isolines, ADT < 0.46 dyn/m. The crosses indicate the CTD stations, and the square symbol indicates the position of the biological station TARA\_068. The biological station coincides with the westernmost CTD station. ADT is affected by interpolation errors, which is why CTD casts were performed at sea so as to have a fine-scale description of the feature before defining the position of the biological station (23). Superimposed are the continuous underway temperatures ( $^{\circ}\text{C}$ ) from the on-board thermosalinograph. (B) Same as (A) but at the regional scale.

Round symbols correspond to biological sampling stations. The contour interval is 0.1 dyn/m. (C) Seasonal distribution of the median values of the mixed layer depths and temperatures at 10 m (from ARGO) provided by the IFREMER/LOS Mixed Layer Depth Climatology L2 database ([www.ifremer.fr/cerweb/deboyer/mld](http://www.ifremer.fr/cerweb/deboyer/mld)) updated to 27 July 2011. The mixed layer is defined using a temperature criterion. The star symbol represents the young ring station TARA\_068. (Inset) Geographic position of the areas used to select the mixed layer and temperature data. The mixed layer depth measured at TARA\_068 is outside the 90th percentile of the distribution of mixed layer depths for the same month for both the subtropical (red and magenta) regions. The temperature matches the median for the same month and region of sampling. (D) Nitrite ( $\text{NO}_2$ ) concentrations from CTD casts at different sampling sites (expressed in  $\text{mmol/m}^3$ ).

## A Diversity scenarios



**Fig. 5. Plankton diversity patterns.** (A) Schematic representation of four scenarios of diversity patterns between the Indian and South Atlantic basins (I to IV): Plankton is transported from the Indian Ocean (pink, right) to the South Atlantic Ocean (blue, left) through the choke point (red, CP). The thickness of each colored section represents the level of diversity specific to each region. The observed percentage of V9 rDNA OTUs corresponding to each scenario is indicated in the pie charts to the left (out of 1063 OTUs of the full V9 rDNA barcode data set). (B) V9 rDNA OTU diversity patterns for copepods and Bacillariophyta. Each circle on the charts represents a V9 rDNA OTU plotted with coordinates proportional to ribotypes specific to the Indian Ocean (x axis) and the South Atlantic Ocean (y axis). For instance, the copepod *Acartia negligens* in the top right corner of sector II corresponds to the “bow tie” scenario II of (A) (i.e., a copepod with representative V9 rDNA barcodes in both Indian and South Atlantic Oceans, the vast majority of which are specific to their respective ocean basin). In contrast, the majority of barcodes for *Sinocalanus sinensis* in sector III are found in both Indian and South Atlantic Oceans [cosmopolitan OTU corresponding to the “Everything is everywhere” flat diversity diagram of (A), scenario III]. If more than 10 barcodes were found in the young Agulhas ring (TARA\_068), their distribution is indicated in a pie chart (colors are coded in the legend inset); otherwise, the OTU is represented by an empty circle. Circle sizes are proportional to the number of considered barcodes for each OTU. The Bacillariophyta OTU defined as *Raphid pennate* sp. likely corresponds to the *Pseudo-nitzschia* cells observed by light microscopy.

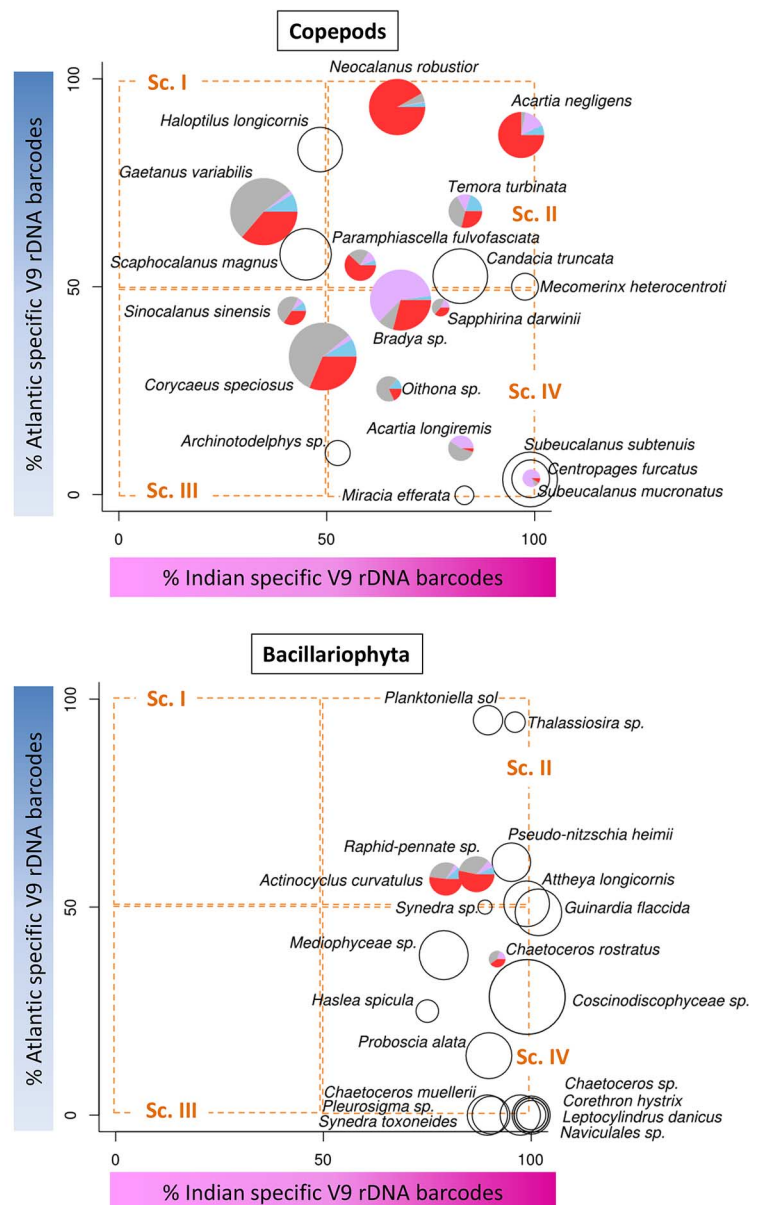
use nitrate, nitrite, and ammonium, only the *Prochlorococcus* LLI and IV and some populations of HL clades, having acquired the *nirA* gene by lateral gene transfer, are able to assimilate nitrite. In the young ring, overrepresentation of cyanobacterial orthologs involved in nitrite reduction could thus have resulted from environmental pressure selecting LLI (87% of the *nirA* recruitments) and HL populations (13%) that possessed this ability. Because the capacity to assimilate nitrite in this latter ecotype reflects the availability of this nutrient in the environment (41), these in situ observations of picocyanobacteria indicated that the nitrogen cycle disturbance occurring in the

young ring exerts community-wide selective pressure on Agulhas ring plankton.

## Discussion

We found that whether or not the Agulhas choke point is considered a barrier to plankton dispersal depends on the taxonomic resolution at which the analysis is performed. At coarse taxonomic resolution, our observations of Indo-Atlantic continuous plankton structure—from viruses to fish larvae—suggested unlimited dispersal, consistent with previous reports (5, 42). However, at finer resolution, our genetic data revealed that the Agulhas choke point strongly affects patterns

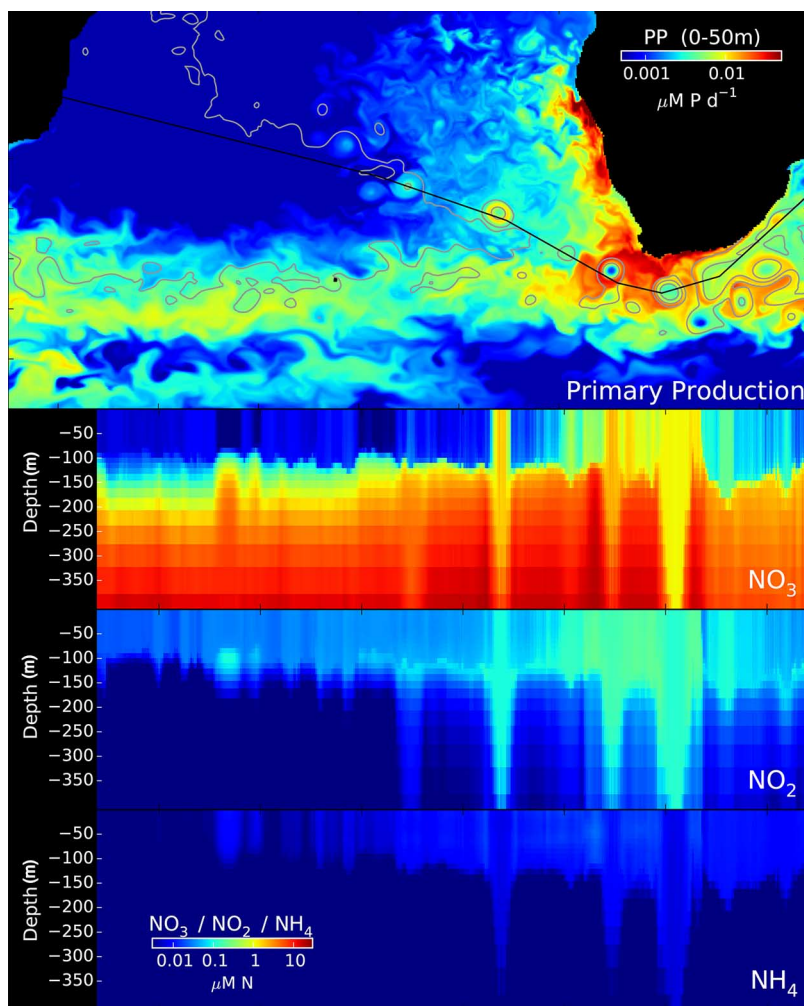
## B Diversity patterns



of plankton genetic diversity. As anticipated in (5), the diversity filtering by Agulhas rings likely escaped detection using fossil records because of the limited taxonomic resolution afforded by fossil diatom morphology (42). The community-wide evidence presented here confirms observations on individual living species (43, 44), suggesting that dispersal filters mitigate the panmictic ocean hypothesis for plankton above 20  $\mu\text{m}$ .

The lower diversity we observed in the South Atlantic Ocean for micro- and mesoplankton (>20  $\mu\text{m}$ ) may be due to local abiotic/biotic pressure or to limitations in dispersal (33, 45). Biogeography emerging from a model with only neutral drift (46) predicts





**Fig. 6. Modeled nitrogen stocks along Agulhas ring track. (Top)** Simulated primary production (PP) in the Agulhas system using the MIT-GCM model. The solid black line shows the average northwesterly path of 12 distinct virtual Agulhas rings tracked over the course of the simulation. Color scale for PP is given in the top right inset, with warmer colors indicating higher PP. **(Bottom)** Modeled profiles of  $\text{NO}_3$ ,  $\text{NO}_2$ , and  $\text{NH}_4$  along the Agulhas ring average track (x axis) presented in (A). The y axis is the depth (in meters) in the water column. The color scale is given in the bottom left inset, with warmer colors indicating higher concentrations of nitrogen compounds.

basin-to-basin genetic differences that are qualitatively consistent with our data. However, the increased proportion of *Prochlorococcus* HL populations carrying the *nirA* gene in the young Agulhas ring indicates that selection is at work in Agulhas rings. Based on our analysis of two Agulhas rings, we propose that environmental disturbances in Agulhas rings reshape their plankton diversity as they travel from the Indian Ocean to the South Atlantic Ocean. Such selective pressure may contribute to the South Atlantic Ocean plankton diversity shift relative to its upstream Indo-Pacific basin. Thus, environmental selection applied at a choke point in ocean circulation may constitute a barrier to dispersal (47, 48). Furthermore, we show that taxonomic groups were not equally affected by the ring transport, both within and between phyla, with a noticeable effect of organism size. The differential effects due to organism size highlight the difficulty in generalizing ecological and evolutionary rules from limited sampling of species or functional types.

Considering the sensitivity of Agulhas leakage to climate change (1, 49), better understanding of the plankton dynamics in Agulhas rings will be required if we are to understand and predict ecosystem resilience at the planetary scale. Considering the breadth of changes already observed in the 9-month-old Agulhas ring, it would be interesting to acquire samples from specific Agulhas rings tracked from early formation to dissipation. Finally, our data suggest that the abundance of Indian Ocean species in South Atlantic Ocean sedimentary records, used as proxies of Agulhas leakage intensity (4), may actually also depend on the physical and biological characteristics of the Agulhas rings.

## Materials and methods

### Sampling

The *Tara* Oceans sampling protocols schematized in Karsenti *et al.* (9) are described in Pesant *et al.* (50); specific methods for 0.8- to 5-, 20- to 180-, and

180- to 2000- $\mu\text{m}$  size fractions in de Vargas *et al.* (17); for 0.2- to 3- $\mu\text{m}$  size fractions in Sunagawa *et al.* (51); and for <0.2- $\mu\text{m}$  size fraction in Brum *et al.* (52). Due to their fragility, 1.6- $\mu\text{m}$  glass fiber filters initially used for prokaryote sampling were replaced by more resistant 3- $\mu\text{m}$  polycarbonate filters from station TARA\_066 onward. In the present text, both 0.2- to 1.6- $\mu\text{m}$  and 0.2- to 3- $\mu\text{m}$  prokaryote size fractions are simply referred to as 0.2 to 3  $\mu\text{m}$ .

### Data acquisition

A range of analytical methods covering different levels of taxonomic resolution (pigments, flow cytometry, optical microscopy, marker gene barcodes, and metagenomics) were used to describe the planktonic composition at each sampled station. Viruses from the <0.2  $\mu\text{m}$  size fraction were studied by epifluorescence microscopy, by quantitative transmission electron microscopy, and by sequencing DNA as described in Brum *et al.* (52). Flow cytometry was used to discriminate high-DNA-content bacteria (HNA), low-DNA-content bacteria (LNA), *Prochlorococcus* and *Synechococcus* picocyanobacteria, and two different groups (based on their size) of photosynthetic picoeukaryotes, as described previously (53). Pigment concentrations measured by high-performance liquid chromatography (HPLC) were used to estimate the dominant classes of phytoplankton using the CHEMTAX procedure (54). Tintinnids, diatoms, and dinoflagellates were identified and counted by light microscopy from the 20- to 180- $\mu\text{m}$  lugol or formaldehyde fixed-size fraction. Zooplankton enumeration was performed on formal fixed samples using the ZOOSCAN semi-automated classification of digital images (55). Sequencing, clustering, and annotation of 18S-V9 rDNA barcodes are described in de Vargas *et al.* (17). Metagenome sequencing, assembly, and annotation are described in Sunagawa *et al.* (51). NCLDV taxonomic assignments in the 0.2- to 3- $\mu\text{m}$  samples were carried out using 18 lineage-specific markers as described in Hingamp *et al.* (56). Virome sequencing and annotation are described in Brum *et al.* (52). Samples and their associated contextual data are described at PANGAEA (57–59).

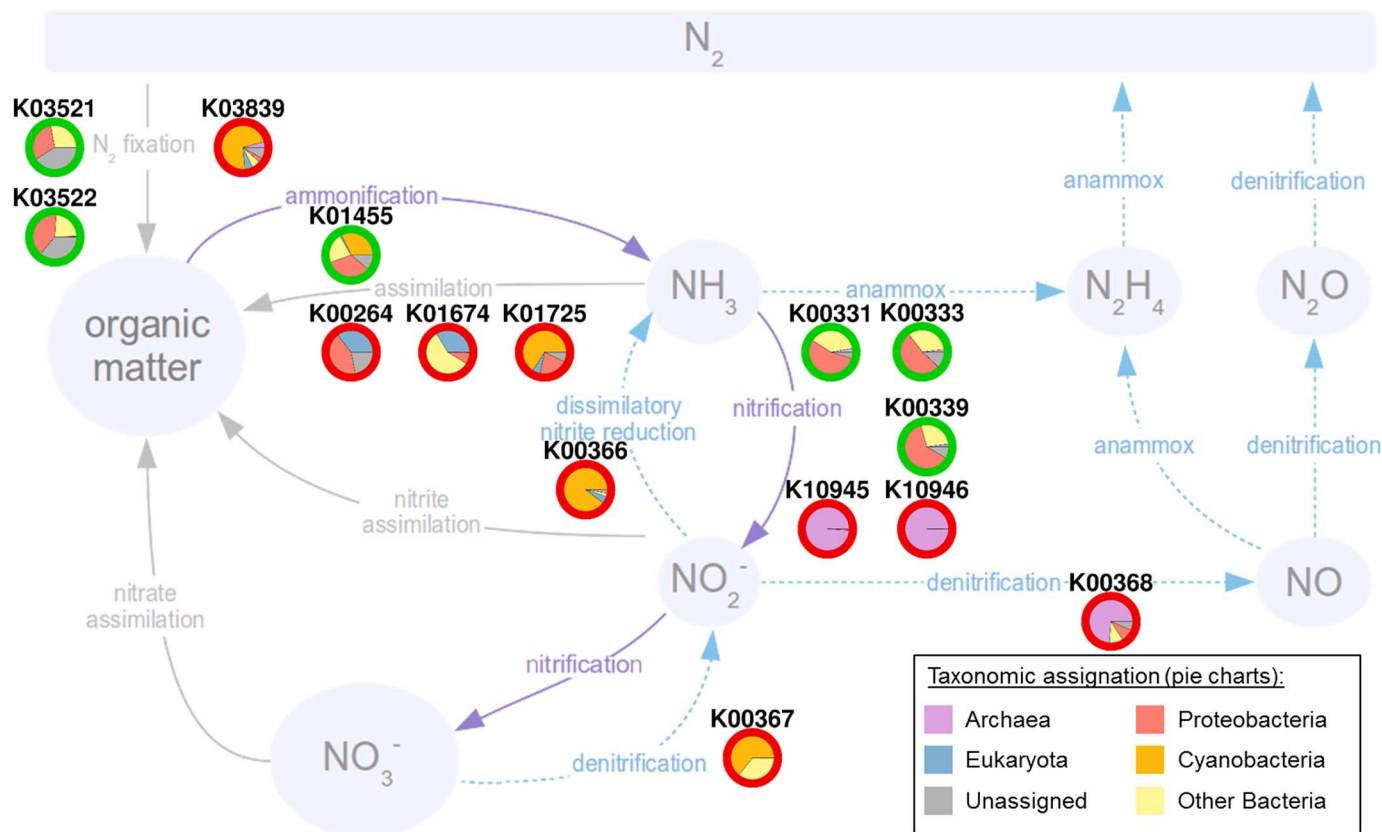
### Data analysis

#### Origin of sampled Agulhas rings

Using visual and automated approaches, the origins of the TARA\_068 and TARA\_078 stations were traced back from the daily altimetric data (Fig. 1) (21). The automated approach used either the Lagrangian tracing of numerical particles initialized in the center of a given structure and transported by the geostrophic velocity field calculated from sea surface height gradients, or the connection in space and time of adjacent extreme values in sea level anomaly maps.

#### V9 rDNA barcodes

To normalize for differences in sequencing effort, V9 rDNA barcode libraries were resampled 50 times for the number of reads corresponding to the smallest library in each size fraction: 0.8 to 5  $\mu\text{m}$ , 776,358 reads; 20 to 180  $\mu\text{m}$ , 1,170,592 reads; and 180 to 2000  $\mu\text{m}$ , 767,940 reads. V9 rDNA barcode counts were then converted to the average number



**Fig. 7. Nitrite anomaly in the young Agulhas ring is accompanied by shifts in nitrogen pathway–related genes.** Metagenomic over- and underrepresented nitrogen pathway genes in young Agulhas ring. Over- (red circles) and under- (green circles) represented metagenome functional annotations (KEGG Orthologs, KO#) involved in the nitrogen pathway in the young ring compared to Indian and South Atlantic Oceans reference stations, at surface and deep chlorophyll maximum depth. Pie charts inside circles represent the taxonomic distribution for each ortholog.

of times seen in the 50 resampling events, and barcodes with less than 10 reads were removed as potential sequencing artifacts. We used down-sampled barcode richness (number of distinct V9 rDNA barcodes) as a diversity descriptor because using V9 rDNA barcode abundances to compare plankton assemblages would likely be biased due to (i) technical limitations described in de Vargas *et al.* (17) and (ii) seasonality effects induced by the timing of samplings (table S1). Barcode richness was well correlated with Shannon and Simpson indexes (0.94 and 0.78, respectively). The shared barcode richness between each pair of samples (14) was estimated by counting, for the three larger size fractions (0.8 to 5, 20 to 180, and 180 to 2000  $\mu\text{m}$ ), the proportion of V9 rDNA barcodes 100% identical over their whole length. V9 rDNA barcodes were clustered into OTUs by swarm clustering as described by de Vargas *et al.* (17). The sub-OTU richness comparison between two samples s1 and s2 (14) produces three values: the number of V9 rDNA barcodes in common, the number of V9 rDNA barcodes unique to s1, and the number of V9 rDNA barcodes unique to s2. These numbers can be represented directly as bar graphs (Fig. 3B) or as dot plots of specific V9 rDNA barcode richness (Fig. 5).

#### Metagenomic analysis

Similarity was estimated using whole shotgun metagenomes for all four available size fractions

(0.2 to 3, 0.8 to 5, 20 to 180, and 180 to 2000  $\mu\text{m}$ ). Because pairwise comparisons of all raw metagenome reads are intractable given the present data volume, we used a heuristic in which two metagenomic 100–base pair (bp) reads were considered similar if at least two nonoverlapping 33-bp subsequences were strictly identical (Compareads method) (60). For prokaryotic fractions (0.2 to 3  $\mu\text{m}$ ), taxonomic abundance was estimated using the number of 16S  $m_i$  tags (51). The functional annotation, taxonomic assignment, and gene abundance estimation of the pan-oceanic Ocean Microbial Reference Gene Catalog (OM-RGC) (243 samples, including all those analyzed here) generated from Tara Oceans 0.2- to 3- $\mu\text{m}$  metagenomic reads are described in Sunagawa *et al.* (51). Gene abundances were computed for the set of genes annotated to the nitrogen metabolism KO (61) group by counting the number of reads from each sample that mapped to each KO-associated gene. Abundances were normalized as reads per kilobase per million mapped reads (RPKM). Gene abundances were then aggregated (summed) for each KO group. To compare abundances between the young ring (TARA\_068) and other stations, a *t* test was used. KOs with a *P* value <0.05 and a total abundance (over all stations) >10 were considered as significant (37). *Prochlorococcus* and *Synechococcus* community composition was analyzed in the 0.2- to 3- $\mu\text{m}$  size fraction at the clade

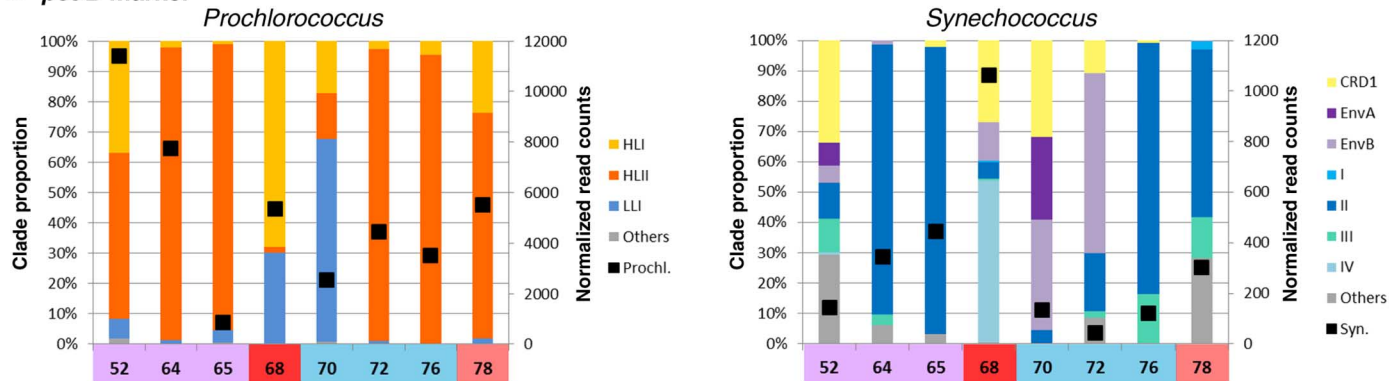
level by recruiting reads targeting the high-resolution marker gene *petB*, coding for cytochrome  $b_6$  (62). The *petB* reads were first extracted from metagenomes using Basic Local Alignment Search Tool (BLASTx+) against the *petB* sequences of *Synechococcus* sp. WH8102 and *Prochlorococcus marinus* MED4. These reads were subsequently aligned against a reference data set of 270 *petB* sequences using BLASTn (with parameters set at -G 8 -E 6 -r 5 -q -4 -W 8 -e 1 -F "m L" -U T). *petB* reads exhibiting >80% identity over >90% of sequence length were then taxonomically assigned to the clade of the best BLAST hit. Read counts per clade were normalized based on the sequencing effort for each metagenomic sample. A similar approach was used with *nirA* (KO 00366) and *narB* genes (KO 00367), which were highlighted in the nitrogen-related KO analysis (Fig. 7). Phylogenetic assignment was realized at the highest possible taxonomic level using a reference data set constituted of sequences retrieved from Cyanorak v2 ([www.sb-roscoff.fr/cyanorak/](http://www.sb-roscoff.fr/cyanorak/)) and Global Ocean Sampling (41, 63) databases.

#### Nitrogen cycle modeling

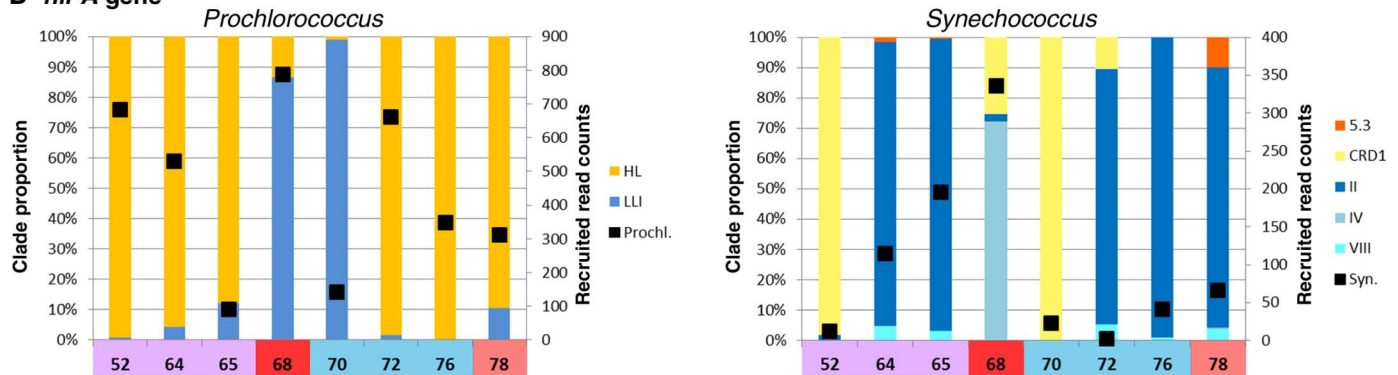
Numerical simulations of global ocean circulation were based on the Massachusetts Institute of Technology General Circulation Model (MIT-GCM) (64), incorporating biogeochemical and ecological components (65, 66). It resolved mesoscale



## A *pet B* marker



## B *nir A* gene



**Fig. 8. Picocyanobacterial clade shift in the young Agulhas ring. (A)** Relative abundance of *Prochlorococcus* and *Synechococcus* clades, estimated by *petB* read recruitments from 0.2- to 3- $\mu$ m metagenomes. Solid squares correspond to read counts normalized based on the sequencing effort (right axis). **(B)** Relative abundance of *nirA* gene from *Prochlorococcus* and *Synechococcus* clades estimated

by number of reads recruited from 0.2- to 3- $\mu$ m metagenomes. The bar colors correspond to cyanobacterial clades indicated in the inset legends for each panel. Solid squares correspond to the number of reads recruited (right axis). Data are shown for stations TARA\_052 to TARA\_078 only, because too few cyanobacteria were found in Southern Ocean stations TARA\_082, TARA\_084, and TARA\_085.

features in the tropics and was eddy-permitting in subpolar regions. The physical configurations were integrated from 1992 to 1999 and constrained to be consistent with observed hydrography and altimetry (67). Three inorganic fixed nitrogen pools were resolved—nitrate, nitrite, and ammonium—as well as particulate and dissolved detrital organic nitrogen. Phytoplankton types were able to use some or all of the fixed nitrogen pools. Aerobic respiration and remineralization by heterotrophic microbes was parameterized as a simple sequence of transformations from detrital organic nitrogen, to ammonium, then nitrification to nitrite and nitrate. In accordance with empirical evidence (35), nitrification was assumed to be inhibited by light. Nitrification is described in the model by simple first-order kinetics, with rates tuned to qualitatively capture the patterns of nitrogen species in the Atlantic (66).

### Continuous spectral analysis

A continuous flow-through system equipped with a high-spectral-resolution spectrophotometer (ACS, WET Labs, Inc.) was used for data collection during the *Tara* Oceans expedition, as described previously (68). Phytoplankton pigment concentrations, estimates of phytoplankton size  $\gamma$ , total chlorophyll *a* concentration, and particulate organic carbon

(POC) are derived from the absorption and attenuation spectra (69) for the 1-km<sup>2</sup>-binned *Tara* Oceans data set available at PANGAEA (<http://doi.pangaea.de/10.1594/PANGAEA.836318>).

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#### SUPPLEMENTARY MATERIALS

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