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## Remarkably low genetic diversity and hierarchical population structure in common bottlenose dolphins (*Tursiops truncatus*) from coastal waters of the Southwestern Atlantic Ocean

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Knowledge about the ecology of bottlenose dolphins in the Southwestern Atlantic Ocean is scarce. Increased by-catch rates over the last decade in coastal waters of southern Brazil have raised concerns about the decline in abundance of regional dolphin communities. Lack of relevant data, including information on population structure and connectivity, have hampered an assessment of Brazilian bottlenose dolphin communities conservation status. Here we combined analyses of 16 microsatellite loci and mitochondrial DNA (mtDNA) control region sequences to investigate genetic diversity, structure and connectivity in 124 biopsy samples collected over six communities of photographically known coastal bottlenose dolphins in southern Brazil, Uruguay and central Argentina. Levels of nuclear genetic diversity were the lowest ever reported for bottlenose dolphins (mean values of allelic diversity and heterozygosity across all loci were 3.6 and 0.21, respectively), a result that possibly reflects the small size of local communities. On a broad geographical scale, remarkably strong and significant differentiation was evident between bottlenose dolphins from southern Brazil-Uruguay (SB-U) and Baía San Antonio (BSA), Argentina (AMOVA mtDNA  $\Phi_{ST}$  = 0.43; nuclear  $F_{ST}$  = 0.46), with negligible contemporary gene flow detected between them based on Bayesian estimates. On a finer scale, moderate but also significant differentiation (AMOVA mtDNA  $\Phi_{ST}$  = 0.29; nuclear  $F_{ST}$  = 0.13) and asymmetric gene flow was detected between five neighbouring communities in SB-U. We propose that BSA and SB-U represent two distinct Evolutionarily Significant Units (ESUs), and that communities from SB-U comprise five distinct Management Units (MUs). Under this scenario, conservation efforts should prioritize the areas in Southern Brazil where dolphins from three MUs overlap in their home ranges and where by-catch rates are higher.