

Report of the Workshop on the Review of the Status of the Franciscana

Virtual Meeting, 7–9 April 2021

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1. INTRODUCTORY ITEMS

The workshop was held from 7–9 April 2021. The workshop convener, Miguel Iñíguez welcomed meeting participants (Annex 1) and noted that the workshop, which had originally been planned as an in-person meeting to advance the review of the status of the franciscana by the IWC Scientific Committee (SC), could not be convened due to the coronavirus pandemic. Instead, a three-day virtual meeting with a reduced agenda was organized to address two specific topics as part of the review: population structure and abundance estimates. He also noted that an in-person meeting to advance with the review of the status of the franciscana should occur later this year or early next year, prior to the conclusion of the review of the franciscana by the IWC SC in 2022. Iñíguez thanked Aimée Lang, Paulo Ott, and Alex Zerbini for coordinating the intersessional work on stock structure and abundance estimation, which would be discussed during the workshop.

1.1 Election of the Chair

Iñíguez was elected chair. Lang and Zerbini co-chaired the discussions on stock structure and abundance estimation, respectively.

1.2 Appointment of Rapporteurs

Frank Cipriano was nominated rapporteur.

1.3 Adoption of the Agenda

The workshop Agenda is given in Annex 2.

1.4 Documents Available

The list of available documents is provided in Annex 3.

2. STOCK STRUCTURE

2.1 Overview of past advice

The first comprehensive review of franciscana population structure by the IWC SC took place in 2004 (IWC, 2005). The SC considered the available genetic evidence (Lázaro *et al.*, 2004; Mendez *et al.*, 2004; Ott, 2002; Secchi *et al.*, 1998; Valsecchi and Zanelatto, 2003) and the summary presented in Secchi *et al.* (2003). The Secchi *et al.* (2003) summary reviewed biological, ecological, morphological, and genetic information and suggested that four stocks (corresponding to FMA I, II, III, and IV) should be recognized for the purposes of assessment. While noting that the support for the separation of FMA III and IV was less than that for the delineation of the other units, the SC concluded that the delineations of the four FMAs identified by Secchi *et al.* (2003) were useful in evaluating the status of the franciscana.

In 2014 (IWC, 2015) the SC reviewed Cunha *et al.* (2014), in which mtDNA control region sequence data from additional samples collected within FMA I and II were combined with previously analyzed mtDNA sequence data (Lázaro *et al.*, 2004; Secchi *et al.*, 1998). Based on their results, the authors suggested that FMA I should be recognized as a separate ESU from the three southern areas based on strong quantitative mtDNA differentiation in AMOVA analysis ($\Phi_{CT} = 0.42\text{--}0.44$) and reciprocal monophyly of the mtDNA lineages (after removing one sequence that grouped with the other FMAs but could not be verified). Cunha *et al.* (2014) also proposed that FMA I be split into two subareas (FMA Ia and Ib) based on the presence of a single shared haplotype in FMA Ia and a high level of mtDNA genetic differentiation ($\Phi_{CT} = 0.72$) between the two subareas. Additional review of the available data occurred during a subsequent workshop (Franciscana Consortium, 2016), where it was agreed that the split of FMA I into two management areas (FMA Ia and FMA Ib) should be recognized. The report of this workshop was subsequently endorsed by the SC (IWC, 2017).

2.2 Newly proposed subdivisions

At SC68b, the SDDNA Working Group reviewed several papers related to franciscana population structure (see 10.4.2, IWC 2020). Two of these papers (Cunha *et al.*, 2020a; Cunha *et al.*, 2020b) presented new evidence for population structure within FMAII, while Cunha *et al.* (2020c) reviewed the available evidence relating to stock structure across the range of the franciscana. These papers proposed that 11 management units should be recognized (including subdivisions within FMA I, II, and IV; see Figure 1). While Cunha *et al.* (2020c) provided a valuable summary of the data supporting the proposed subdivisions, the SDDNA Working Group noted that evaluating the level of confidence in each subdivision would require an in-depth review of the individual papers and agreed to form an intersessional correspondence group (ICG) to further evaluate the level of support for each of the proposed subdivisions based on genetic and other (e.g., morphology, contaminants) lines of evidence. ICG membership and terms of reference are provided in Annex 5.

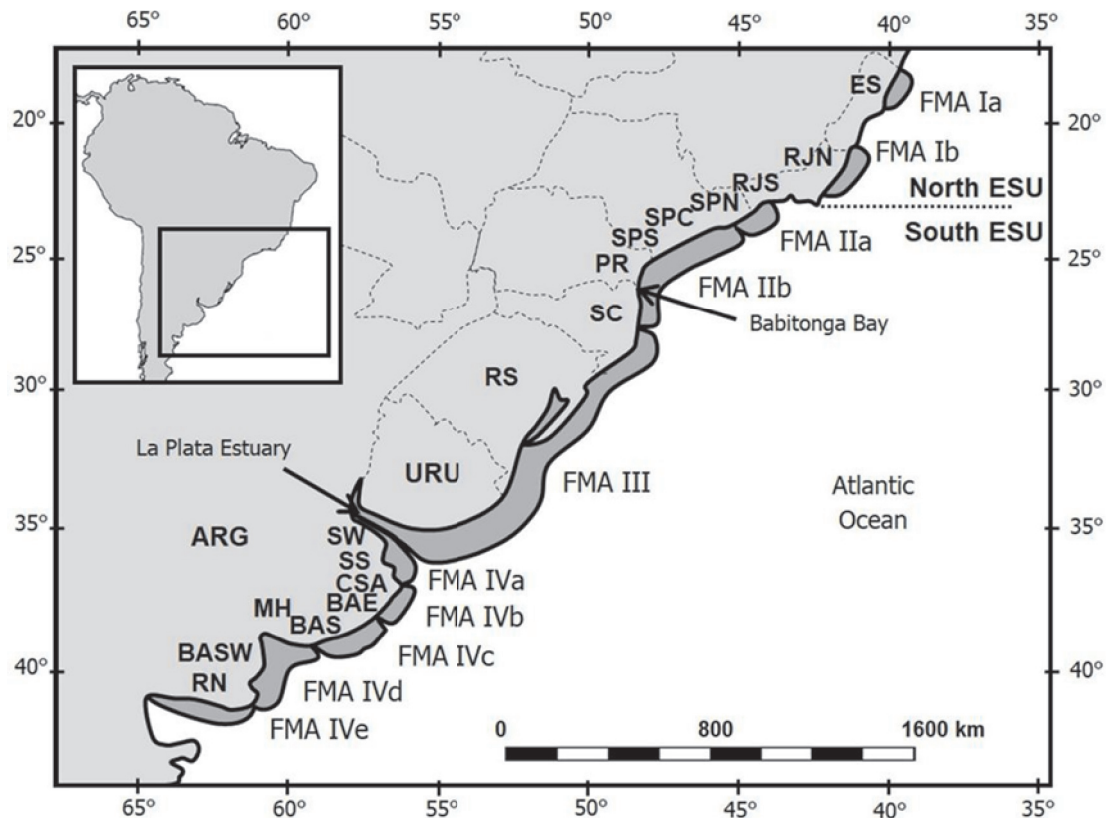


Fig. 1. Map showing the 11 proposed management units for franciscanas, including the ten labelled FMA subdivisions and Babitonga Bay (Cunha *et al.*, 2020b; Cunha *et al.*, 2020c).

Although the ICG made progress on summarizing the available data from genetic and non-genetic sources during the intersessional period following SC68b, it was not able to complete this task. In order to further this intersessional work, it was agreed that one of the objectives of the pre-meeting on franciscana assessment would be to review and discuss the genetic evidence pertaining to each of the proposed FMA subdivisions.

2.3 Genetic support for proposed subdivisions

FMA I – Subsequent to the review of the proposed FMA I subdivisions in 2015 and 2016, de Oliveira *et al.* (2020) used an expanded sample set ($n = 68$ stranded individuals) to explore mtDNA and nuclear ($n = 12$ loci) diversity within FMA I. Three haplotypes were identified within FMA Ia, with most individuals (48 of 50 sequenced) carrying the one haplotype previously identified within this area (Cunha *et al.*, 2014). Of the remaining two individuals, one carried a haplotype previously found within FMA Ib and a second carried a previously unidentified haplotype that was more closely related to the haplotypes from southern Rio de Janeiro (FMA IIa), leading the authors to suspect that it came from an animal that had been entangled elsewhere and then discarded near FMA Ia. Of the five individuals from FMA Ib that were also sequenced in this study, one had the common haplotype previously found only in FMA Ia individuals. MtDNA haplotype diversity within FMA Ia ($h = 0.041$) was markedly lower than that reported for other areas ($h = 0.476–1.00$). The effective population size (N_e) based on genotyped individuals ($n = 43$) was estimated to be 117.9 individuals (95% CI: 27.8 – Infinity) for FMA Ia. No substructure within FMA Ia was identified in AMOVA analyses using samples collected in the northern ($n = 21$, mtDNA; $n = 16$, microsatellites) versus central portion ($n = 28$, mtDNA; $n = 27$ for microsatellites) of FMA Ia. A STRUCTURE analysis using the microsatellite datasets also failed to detect multiple genetic clusters within the data.

Four of the microsatellite loci in the de Oliveira *et al.* (2020) study showed evidence of possible null alleles, and thus the nuclear analyses of population structure were run using three different subsets of loci ($n = 10$, 8 and 6 loci, the latter of which did not include any loci with evidence of null alleles). The results of the analyses were generally similar across the three subsets, and none of the comparisons revealed statistically significant differences. In discussion, it was noted that while the rationale underlying the removal of loci with potentially null alleles was valid, analyses using the smaller subsets of loci (< 10) may have had limited power to detect subtle structure within FMA Ia. It was also suggested that using an exact test to compare haplotype and genotype frequencies between areas, rather than an AMOVA, might have more power to detect differences. In summary, while the available evidence did not suggest strong genetic structure between the two compared regions of FMA Ia, subtle structure, if it exists, may not have been detected.

FMAII – Cunha *et al.* (2014) conducted an AMOVA analysis of mtDNA control region sequences collected from regions within the South ESU and found that the most likely scenario included a split between FMA IIa, FMA IIb, and the combined FMA III and FMA IV. Based on these results, as well as the comparison of contaminant loads across regions (Lailson-Brito *et al.*, 2011), Cunha *et al.* (2014) suggested that FMAII be provisionally split into two subareas, FMA IIa and FMA IIb. To further investigate this proposed subdivision, Cunha *et al.* (2020a) generated mtDNA control region sequence data from additional samples within FMA IIa ($n_{\text{Total}} = 18$) and then compared that data with 150 previously generated mtDNA sequences from throughout the range of the franciscana. Pairwise comparisons between areas found relatively strong differentiation between FMA IIa and sampled regions within FMAIII and FMAIV, and differences were also identified between the most southern sampled region within FMA IIa (RJS) and two of the three sampled regions within FMA IIb. AMOVA analysis found stronger support for splitting FMA IIa from the rest of the south ESU ($F_{\text{CT}} = 0.34$) but a scenario where FMA IIa, FMA IIb, and the combined FMAIII–IV was also supported ($F_{\text{CT}} = 0.267$).

In discussion, it was noted that even with the additional samples, the sample size representing FMA IIa remains small, raising the possibility that sampling effects bias estimates of genetic structure. In particular, non-random sampling of related individuals, which could occur if related animals are entangled together as has been seen in some areas (e.g., Costa-Urrutia *et al.*, 2012), could lead to the spurious inference of population structure. The generation of microsatellite data, which is underway for FMA IIa and FMA IIb but has been delayed due to the pandemic, would allow potentially related individuals to be identified and provide further insight into whether genetic structure exists between these two subareas.

Cunha *et al.* (2020b) investigated population structure within FMA IIb by comparing samples collected from a small group of franciscanas that inhabit Babitonga Bay (BB) in southern Brazil with those collected from franciscanas in nearby coastal areas. Within the BB samples ($n = 28$), only two mtDNA haplotypes were identified; the haplotypes were not closely related and both were found in moderate frequencies. These two haplotypes were also found in the coastal samples, which carried a total of six haplotypes. Based on analysis of seven microsatellite loci, the effective size (N_e) of the BB group was 12.3 (95% CI: 2.5–31.2). Significant nuclear and mitochondrial genetic differences were identified. STRUCTURE analysis that incorporated admixture and a location prior identified two clusters within the dataset, with all except one of the coastal individuals being assigned (at $Q > 0.5$) to the coastal cluster and all except two of the BB individuals being assigned to a BB cluster.

In discussion, it was noted that the pattern of mtDNA diversity found among the BB individuals is consistent with what would be expected if a small number of franciscanas had colonized BB from coastal waters and had been isolated over recent time scales, such that they could warrant separate management.

Three of the seven microsatellite loci used in the BB analysis showed evidence of departure from Hardy Weinberg equilibrium (HWE), potentially indicating the presence of null alleles that would result in biased estimates of genetic differentiation (Waples, 2018). Pre-meeting participants suggested that the nuclear analyses be repeated after excluding the loci that deviated from HWE. As noted above, reducing the number of loci analysed will decrease the power to detect genetic differences; however, greater confidence could be placed on the findings if the nuclear genetic differences between the groups remained apparent after removal of the potentially problematic loci. Further, it would be informative to rerun the STRUCTURE analyses without the *a priori* incorporation of information on the location of sampling (“location prior”).

The number of individuals using BB is small (50 individuals, $CV = 0.30$; Cremer and Simões-Lopes, 2008) and thus a relatively high proportion of the animals using the area have been sampled. While the BB sample set contained multiple pairs of individuals that were estimated to be related based on microsatellite analysis, the presence of some related individuals in the sample set would be expected and does not necessarily indicate preferential sampling of relatives that would lead to biased parameter estimates. The pre-meeting participants advised that future efforts should focus on genotyping a greater number of microsatellite loci rather than on collecting and analyzing additional samples.

Although the focus of the pre-meeting was to evaluate the available genetic data, it was noted that both photo-identification data and tagging data have been collected from BB individuals. Both lines of evidence are consistent with animals showing a high degree of residency to the bay and will be valuable to integrate with the genetic data in future discussions.

FMA III – FMA III is the longest management area (~1150 km) and includes the northern portion of a large estuarine system, the La Plata Estuary (LPE). Initial comparisons of mtDNA control region haplotype frequencies between franciscanas sampled in the southern region of Rio Grande do Sul state (RS, $n = 15$) and samples collected from the La Plata Estuary region ($n = 38$, all except one of which were collected in Uruguay) did not find significant differences ($F_{\text{ST}} = 0.032$, $p = 0.112$; Lázaro *et al.*, 2004). A subsequent study by Costa-Urrutia *et al.* (2012) compared samples from the LPE ($n = 21$) with samples from the surrounding coastal waters ($n = 23$) using microsatellites ($n = 12$ loci). Small but significant differences between areas were identified ($F_{\text{ST}} = 0.02$, $p < 0.01$). Bayesian clustering analysis indicated the presence of two clusters within the dataset. All of the coastal samples assigned to a single cluster. Some of the LPE samples had high assignment probabilities ($> = 0.95$) to a second cluster comprised only of LPE samples while others, potentially representing animals that had died and then drifted into the estuarine waters, assigned to the coastal cluster (> 0.90). Two had equivocal assignments. Comparison of the two clusters identified by STRUCTURE revealed significant differences in microsatellite allele frequencies

($F_{ST} = 0.06$, $p = 0.002$). The mtDNA control region haplotypes were sequenced for a subset of the LPE samples, and mtDNA comparisons were made between LPE individuals that assigned to the coastal cluster and those that assigned to the cluster comprised only of LPE individuals. No significant differences were identified ($F_{ST} = 0.06$, $p = 0.06$; $F_{ST} = 0.02$, $p = 0.12$).

Costa-Urrutia *et al.* (2012) noted that their evidence supports considering franciscanas in the LPE to be a separate management unit. The initial comparison of the coastal samples with the full set of LPE samples revealed small but significant differences, providing some support for this conclusion. However, in discussion it was noted that using the microsatellite data to assign LPE individuals to two clusters (one which largely comprised the Atlantic Coastal samples and the other which included only LPE individuals) and then subsequently to estimate genetic differentiation between those clusters was problematic. While the mtDNA comparison between LPE individuals assigned to the two different clusters could be considered an independent analysis, that comparison did not yield significant results and thus did not provide support for considering the LPE dolphins as a separate unit.

Ott (2002) examined population structure within FMA III using both mtDNA and microsatellite loci ($n = 12$ loci). Comparison of samples collected in the northern RS ($n = 34$) with those collected in the southern RS ($n = 31$) and Uruguay ($n = 38$) revealed significant differences in mtDNA haplotype frequencies ($F_{ST} = 0.066$, $p < 0.05$; $F_{ST} = 0.098$, $p < 0.05$, respectively). Differences in haplotype frequencies between samples collected in southern Santa Catarina state (SC) and northern RS were also significant ($F_{ST} = 0.251$, $p < 0.01$), as were all comparisons of southern SC and the other areas when genetic distance measures were incorporated (v. northern RS, $F_{ST} = 0.244$, $p < 0.001$; v. southern RS $F_{ST} = 0.138$, $p < 0.01$; v. Uruguay $F_{ST} = 0.098$, $p < 0.05$). However, the sample size from southern SC was small ($n = 7$) and may not have been representative. When these same sample sets were compared using microsatellites, none of the pairwise comparisons were significant. Based on the nuclear results, the boundary between FMA II and FMA III was shifted northward approximately 225km to Florianópolis, Brazil, to incorporate southern SC into FMA III.

In summary, while the lack of significant nuclear differentiation between coastal areas in southern SC, RS and Uruguay suggested that gene flow is occurring between these areas, the small but significant differences observed by Costa-Urrutia *et al.* (2012) between coastal areas and the LPE region suggest that further investigations into population structure between these regions are needed. However, given the lack of clear evidence for population structure within FMA III, no subdivisions of this FMA are currently proposed.

Although not reviewed prior to the pre-meeting, Santos (2011) also analyzed samples from SC, RS, Uruguay and northern Argentina and did not find evidence of substructure in a genetic clustering analysis based on 12 microsatellite loci. This paper will be made available for future intersessional discussions.

FMA IV – Genetic data (mtDNA haplotype sequences and microsatellite genotypes) exist for samples collected from nine sites within FMA IV (Gariboldi *et al.*, 2015; Gariboldi *et al.*, 2016; Mendez *et al.*, 2008; Mendez *et al.*, 2010; Negri *et al.*, 2016), but overlap in geographic coverage between studies is low. Mendez *et al.* (2010), which expanded on the mtDNA analyses of Mendez *et al.* (2008), compared mtDNA haplotype sequences, microsatellite genotypes ($n = 12$ loci) and environmental data (chlorophyll concentration, water turbidity and surface temperature) between six sites within FMA IV. Buenos Aires Southwest (BASW) had the lowest mtDNA diversity ($h = 0.615$, $n = 13$ samples), followed by Samborombón South (SS) ($h = 0.770$, $n = 118$ samples). Pairwise genetic comparisons revealed differences between most contiguous sites in one or both genetic markers, and mean values for environmental parameters differed significantly between contiguous areas. STRUCTURE analysis identified three clusters. In combination, the data suggested the existence of at least three biologically meaningful stocks in Argentinean waters, corresponding to Samborombón West (SW)/Samborombón South (SS); Cabo San Antonio (CSA)/Buenos Aires East (BAE); and Buenos Aires South (BAS)/Buenos Aires Southwest (BASW). The authors noted, however, that additional fine-scale structure, particularly in Northern Buenos Aires, needed to be investigated with larger sample sizes. While patterns in the mtDNA corresponded with isolation by geographical distance, patterns in the microsatellite data corresponded with isolation by environmental distance (Mendez *et al.*, 2010).

Negri *et al.* (2016) analyzed mtDNA data generated from franciscanas in four regions (from north to south: NC, Necochea; CL, Claromecó; MH, Monte Hermoso; and BBI, Bahía Blanca) but did not find differences between four sites. Gariboldi *et al.* (2015, 2016), which included samples analyzed in Negri *et al.* (2016), compared mtDNA control region sequence data and microsatellite genotypes ($n = 10$ loci) between four sites within FMAIV: NC, CL (which is in the same region as BAS in the Mendez *et al.* studies), MH, and Río Negro (RN). For the mtDNA analysis, all comparisons with MH resulted in significant differences; comparisons between other areas did not, even though these areas were located north and south of MH. Monte Hermoso also had lower haplotype diversity ($h = 0.641$) than did the other sites ($h = 0.764$ – 0.895). For the microsatellite analysis, MH remained different from all other areas, and RN (the southernmost site) also differed significantly from the northern sites, which did not differ from each other. Bayesian clustering analysis identified three genetic clusters within the dataset, with one cluster consisting primarily of MH individuals, another of RN individuals, and a third cluster comprising NC + CL animals.

Taken together, the results of the two sets of studies suggested that up to five stocks exist within FMA IV: FMA IVa, including SW and SS; FMA IVb, including CSA and BAE; FMA IVc, including NC and BAS/CL; FMA IVd, including MH and BASW; and FMA IVe, including RN. It has been noted, however, that an analysis of all available samples could provide additional resolution on the patterns of structuring within FMA IV.

MH is located slightly northeast of an area where the coastline indents to encompass the estuarine waters of Bahía Blanca. Few samples are available from BBL, limiting understanding of the relationship of franciscanas in this area with those in MH. However, the differentiation of MH from the other sampled sites was notable given the lack of significant mtDNA differences found between sampling locations to the north and south of MH, suggesting that some individuals disperse between coastal waters to the north and south of MH but don't pass through this area. Gariboldi *et al.* (2015, 2016) proposed that the differentiation of MH dolphins from nearby regions may have originated from and been maintained by resource specialization, which is consistent with findings of different dietary preferences between individuals from CL and those from MH (Paso Viola *et al.*, 2014). A similar pattern was found by Mendez *et al.* (2008, 2010), in which San Clemente showed relatively strong differentiation from Uruguay to the north and from CSA to the south, while Uruguay and CSA did not differ significantly from each other.

Summary – In discussion, the pre-meeting participants noted that assessing isolation by environmental distance using the approach that Mendez *et al.* (2010) used in the Buenos Aires region could be useful for delineating structure and/or identifying environmental boundaries in other areas.

While noting the value of reviewing the available genetic evidence pertaining to the proposed FMA subdivisions, the pre-meeting participants **agreed** that review of the other (non-genetic) lines of evidence was needed before drawing any conclusions about the newly proposed subareas. Although the participants recognized the need to provide advice based on the currently available data, the additional analyses proposed to better resolve whether the Babbitonga Bay (BB) subarea should be recognized as a separate FMA require rerunning analyses with slightly modified datasets, a task which may be feasible to finish over the next intersessional period. As such, the participants **encouraged** the authors to complete these suggested analyses intersessionally and to report on the results prior to or at the in-person workshop that is planned for later in 2021 or early 2022.

For the purposes of this pre-meeting, the participants agreed that the discussion of abundance estimates should continue to focus on the previously agreed FMA subdivisions (FMA Ia, FMA Ib, FMA II, FMA III, and FMA IV). Although additional discussion of the support for BB being recognized as a separate unit will continue intersessionally, the participants **agreed** that on a precautionary basis the abundance of this group would be evaluated separately given that an area-specific abundance estimate exists for this area. Abundance estimates for the subdivided areas within FMA IV are not currently available; generating such estimates may be recommended in the future depending on the outcome of the continued discussion of stock structure within this region.

2.4 Other (non-genetic) support for proposed subdivisions

Due to time limitations, pre-meeting participants were not able to review other lines of evidence pertaining to the proposed FMA subdivisions. However, in discussion of both the proposed BB management unit and the proposed FMA IV subdivisions, it was noted that satellite telemetry data will soon be published and will be useful for informing future discussions. The pre-meeting participants look forward to reviewing that work intersessionally.

2.5 Future work

Following review of the pre-meeting report at SC68c, the workshop agreed the ICG will continue their intersessional review of both genetic and non-genetic data pertaining to the proposed subdivisions. A final report summarizing the ICG's advice will be presented at the in-person workshop on franciscana assessment that is planned for 2021/2022 and will also be reviewed at next year's meeting.

3. ABUNDANCE ESTIMATES

The review of estimates of abundance of franciscanas will inform the ongoing assessment of the status of the species by the IWC SC. At last year's annual meeting (SC/68b), a number of documents related to estimation of abundance were received by the Committee but there was insufficient time to review them. Therefore, an intersessional correspondence group (ICG) was established to review estimates of franciscana abundance and correction factors for this species. The ICG included reviewers and data analysts. Each document received was examined by at least two reviewers, who were instructed to evaluate abundance estimates following the guidelines developed by the Committee (IWC, 2020, p. 276) and, whenever necessary, to liaise with analysts if clarification was needed. The reviews were presented and discussed during the Workshop. Workshop participants also categorized the estimates of abundance according to the criteria developed by the SC (IWC, 2018) and made recommendations for further analysis that could be completed before the review of the status of the franciscana is concluded next year. Abundance estimates reviewed by the workshop are listed in Annex 4 and they are all proposed to be considered "level 1" with respect to their extent of review by the SC. A summary of the discussions, the rationale for categorization of the abundance estimates and recommendations for additional work are provided below.

The Workshop thanked the reviewers (Ana Cañadas, Thomas Doniol-Valcroze, Megan Ferguson, Geof Givens, Helena Herr, David Miller, Debi Palka and Alex Zerbini) as well as the analysts (Artur Andriolo, Mariano Coscarella, Marta Cremer, Enrique Crespo, Daniel Danilewicz, Camila Domit, Federico Sucunza and Alex Zerbini) for their contributions.

3.1 Correction factors for visibility and group size bias

A number of correction factors for perception and availability bias have been developed to correct estimates of franciscana abundance. Surface intervals and dive durations of franciscanas were estimated from shore-based stations (2m above sea level) and vessels in Bahía Anegada, Argentina (Bordino *et al.*, 1999). These values were used to correct for availability bias in aerial surveys in FMA III (Secchi *et al.* 2001, Danilewicz *et al.*, 2010) and FMA IV (Crespo *et al.* 2010). Computing availability bias correction factors from surface and dive intervals obtained by surface platforms (i.e. shore stations or boats) may result in overestimated bias because of the field of view and perspective differ from those of observers in an aircraft (e.g., animals near but below the surface can be seen from an airplane, but usually not from a surface platform). Therefore, additional factors to correct for animals missed on the trackline and for underestimation of group size during aerial surveys were developed by Zerbini *et al.* (2011) and Sucunza *et al.* (2018). Sucunza *et al.* (2020a) re-examined data in those two papers and added information on surface and dive intervals to refine the correction factors. Two experiments were conducted. Experiment 1 consisted of simultaneous aerial and small boat surveys to compute the density of franciscanas in Babitonga Bay, southern Brazil. Estimates of density and group size from boat observations were assumed to represent true density (i.e., $g(0) = 1$ was assumed, because surveys were conducted in good weather conditions [Beaufort 0–2] in a relatively protected environment where ocean swell is not present and no responsive movement was documented). A correction factor (CF = 4.42, CV = 0.04) for visibility and group size bias for aerial surveys was developed as the ratio of the density estimated from boats ($D = 2.99$ individuals/km², CV = 0.23) to the density estimated from aircraft ($D = 0.68$ individuals/km², CV = 0.28) (Sucunza *et al.*, 2020a). In addition, generalized linear models (GLMs) were used to assess differences in group size estimated from the boats and the airplane and indicated that boat group size estimates are ~30–35% greater than those computed from an airplane. Experiment 2 consisted of helicopter surveys to assess surface and dive times of franciscanas and estimate availability bias in two areas, Babitonga Bay, a region with relatively shallow and turbid waters, and Ubatuba, an area with deeper and clearer waters. Surface and dive times across the two areas were significantly different, but the proportion of time a franciscana group spent at the surface were similar (Babitonga Bay = 0.36 [SE = 0.23], Ubatuba = 0.34 [SE = 0.09]). The proportion of time at surface for both areas combined (0.35 [SE = 0.19]) was used to compute availability at 0.39 (SE = 0.009), assuming the period of time a franciscana group is available on the trackline to an observer in an aircraft was 6 seconds.

The Workshop reviewed the information provided in Sucunza *et al.* (2020). In discussion, it was noted that Experiment 1 used standard line transect survey methods. It was also noted that derivation of the CV of the correction factor for visibility and group size bias combined (CV = 0.04) was unclear and appeared too small given the CVs of the individual density estimates. In addition, the assumption that $g(0) = 1$ could lead to negative bias in the estimate of density for the boat surveys and, consequently, a positively biased estimate of the correction factor. Regarding Experiment 2, it was noted that the CV = 0.02 (SE = 0.009) for the adjusted availability correction was substantially smaller than the one for the instantaneous correction (CV = 0.54), which could be related to an error in the implementation of the bootstrap procedures. It was also noted that although an average value of 6 seconds available (at the surface) was used in the calculation of availability, actual times were recorded during surveys and these could also be used. Although no significant effect of water clarity/turbidity on availability bias was observed in these experiments, this variable should still be considered in future studies (e.g., as a covariate in fitting detection functions to perpendicular distance data), especially in areas with higher turbidity. Finally, it was noted that uncertainty in the estimation of group size bias was not computed, but that would be required if abundance estimates were to be corrected for this source of bias.

Authors of Sucunza *et al.* (2020) agreed to review the CVs of the estimates of the overall correction factor and of availability, to compute a CV for the group size bias correction factor, and to provide this information prior to the conclusion of the review of the status of the franciscana by the SC in 2022.

The Workshop **concluded** that use of the overall correction factor (CF = 4.42) would be valid for other franciscana aerial surveys once the CV of this estimate is revised if these other surveys were conducted in conditions similar to those observed during Experiment 1 (e.g. similar aircraft, observers with comparable experience, and similar distribution of franciscana group sizes) and if estimates of correction factors specific to each survey could not be computed. The Workshop also **concluded** that correction of rangewide abundance estimates for availability and group size bias would be appropriate once uncertainty for the estimates provided in Sucunza *et al.* (2020a) is properly computed. The Workshop **recommended** that computation of survey-specific correction factors should be attempted whenever feasible and that potential regional or seasonal differences in group sizes and surface and dive intervals should be considered in future surveys.

3.2 FMA Ia

Aerial surveys to estimate abundance were conducted in 2011 and again in 2018 (Danilewicz *et al.*, 2012; Sucunza *et al.*, 2020b). These surveys suggested that, at least during the summer, franciscanas in FMA Ia occupy a relatively small area (along 173 km of coastline off Espírito Santo state, Brazil), between Conceição da Barra (18°35'S) and Santa Cruz (19°56'S). An estimate of abundance could not be computed for the 2011 survey because no franciscana groups were detected on-effort that year (Danilewicz *et al.*, 2012). An estimate was computed for the 2018 survey using standard line transect methods (Sucunza *et al.* 2020b). This study divided the survey area into two regions: north and south. Effort consisted of a

set of parallel tracklines allocated perpendicular to the coastline as far as 16.5km from shore. A total of 2,986 km was surveyed and 17 franciscana groups (41 individuals in total, mean group size = 2.41, CV = 0.14) were seen within 8 km from shore. Abundance corrected for visibility and group size biases using the correction factor of 4.42 (CV = 0.04) described above was estimated at 200 (CV = 0.61) and 395 (CV = 0.58) dolphins for the northern and southern areas, respectively. Population size in the whole of FMA Ia was estimated at 595 individuals (CV = 0.44).

In discussion, it was noted that surveys in FMA Ia were well designed and executed. It was also noted that the detection function was estimated using a half normal model, but it would also be useful to assess whether a better fit is obtained with a hazard rate function. The authors pointed out that this study was an example where the correction factor for visibility and group size bias discussed in the previous section was applied because surveys in FMA Ia used the same aircraft and observers used in computing the correction factor. The Workshop **agreed** to classify the abundance estimate for FMA Ia in 2018 as Category P for the present, but noted that it could be elevated to Category 1 when the CV for the correction factor has been revised as discussed in section 3.1 above.

3.3 FMA Ib

Aerial surveys to assess distribution and abundance of franciscanas in FMA Ib were carried out in December 2011, March 2017 and August 2019 and abundance was computed for 2011 and 2017 using line transect methods (Danilewicz *et al.*, 2012; Danilewicz *et al.*, 2020). Similar to FMA Ia, franciscanas in FMA Ib had a restricted distribution, within only 125km of linear coastline between Sao Joao da Barra (21°56'S) and Carapebus (22°16'S). Sightings were made as far as 15.1 n. miles from shore, but the majority of the sightings (70%) were within 4 n. miles from shore (Danilewicz *et al.*, 2020). In 2011, a total of 1,010 km was surveyed and 15 franciscana groups were detected on effort. Average group size was estimated at 2.54 individuals (CV = 0.18). Density and abundance corrected for visibility and group size bias using the correction factor described above (4.4., CV = 0.04, Sucunza *et al.*, 2020) were estimated, respectively, at 0.3 individuals/km² and 1,692 individuals (CV = 0.47). In 2017, survey effort totaled 2,150 km and 29 sightings were recorded on-effort. Average group size was estimated at 2.5 individuals (CV = 0.46). Density and abundance, corrected for visibility and group size bias, were computed as 0.316 ind./km² and 1,280 individuals (CV = 0.44). Density estimates were similar between the two years, but the two abundance estimates are not directly comparable because the area surveyed was slightly different across years.

The Workshop noted that the design and methods in Danilewicz *et al.* (2020) were appropriate but that it was unclear which of the various detection probability models considered was used for inference and to better assess model fit. Authors agreed to provide a more detailed description of model selection and model fit in a revised document prior to next year's SC meeting. It was noted that this study also used the correction factor for visibility and group size bias discussed in section 3.1 because the aircraft and observers used in the survey were the same as those in the surveys used to compute the correction factor. The Workshop **agreed** to classify the estimates provided in Danilewicz *et al.* (2020) as Category P, but they could be elevated to Category 1 once model selection and model fit are further investigated and the CV for the correction factor is revised.

3.4 FMA II

Abundance estimates in FMA II were computed for the entire management area (Zerbini *et al.*, 2010; Sucunza *et al.*, 2020c) and also for a small estuarine region known as the Paranaguá Estuarine Complex (Weyn, 2016). The first range-wide abundance estimate was computed from aerial surveys conducted during austral summer 2008/09 by Zerbini *et al.* (2010), but this estimate is now outdated because of changes in the southern boundary of FMA II (Anonymous, 2016; see also item above) and because new factors to correct for visibility and group size bias have become available since then.

A revised range-wide estimate of abundance for franciscanas in FMA II was computed by Sucunza *et al.*, (2020a) using mark-recapture distance sampling methods (Laake and Borchers, 2004) to estimate perception bias, and was corrected for availability bias using correction factors developed by Sucunza *et al.* (2018). Estimates were provided for the whole stock (N = 6,827, CV = 0.26, Table 3, Annex 4) and for two putative sub-populations designated FMA IIa (N = 1,915, CV = 0.32) and FMA IIb (4,353, CV = 0.24).

In discussion of Sucunza *et al.* (2020c), it was noted that this estimate used independent estimates of perception and availability bias, differently from estimates for FMA Ia and Ib. It was also noted that the strip transect analysis for 0–80m was corrected with a p(0) value for combined observers, but only one observer was involved so the correction applied should be based on the p(0) for one observer. The estimate provided by Sucunza *et al.* (2020c) was not corrected for group size bias and the Workshop agreed such correction was appropriate. The Workshop **concluded** that the estimate of abundance for FMA II (N = 6,827, CV = 0.26) in this paper could be accepted as Category 2 but once correction for group size bias is applied, it could be elevated to Category 1. This categorization would also apply for sub-areas FMA IIa and IIb if these are found to represent two separate units once ongoing discussion on franciscana stock structure by the SD/DNA working group are concluded.

A boat-based line transect estimate of 198 franciscanas (CV = 0.31) was computed for the Paranaguá Estuarine Complex, in Paraná State, during 2012–2013 (Weyn, 2016). Coastal waters off Paraná State comprise a portion of the range of franciscanas in FMA II and it is still unclear whether franciscanas in this estuarine complex correspond to a separate

population (such as the one in Babitonga Bay, see item 3.7 below) or they represent animals that seasonally occur in the estuarine area but are part of the larger FMA II.

In discussion, the Workshop recognized that data in Weyn (2016) can be used to compute estimates of abundance of franciscanas within the study area, but that the current analysis requires refinement. In particular, it was noted that the $g(0) = 1$ assumption is likely violated and that partial overlap in the survey strata may lead to incorrect estimates of abundance. The Workshop **agreed** that this estimate should not be accepted at this stage, and encouraged a reanalysis of the data and submission of new estimates for further consideration.

3.5 FMA III

Multiple estimates of franciscana abundance were computed within the range of FMA III, one in each of the years 1996, 2004 and 2015 (Secchi *et al.*, 2001; Danilewicz *et al.*, 2010; Sucunza *et al.*, 2020d). For all these estimates, sampling occurred in the Brazilian portion of the range of the stock. Surveys to assess franciscana abundance have never been conducted in Uruguay.

The first abundance estimate for FMA III was computed from aerial surveys conducted in 1996 (Secchi *et al.*, 2001) In this study, 1,428 km were surveyed in a small coastal area (435 km²) between the coastline and 9.3km from shore in a region located approximately in the center of the range of the stock (close to the mouth of Patos Lagoon, Rio Grande do Sul State [RS], Brazil). A total of 29 sightings (35 individuals, average group size = 1.16, CV = 0.07) were made on-effort and density within the survey area, corrected for availability (but not perception or group size) bias, was estimated at 0.657 ind./km² (CV = 0.34). This density estimate was extrapolated to the (non-surveyed) range of the stock (both in southern Brazil and Uruguay, total area of approximately 64,000 km²) to compute an estimate of abundance of nearly 42,000 individuals (CV = 0.34).

The abundance estimate in Secchi *et al.* (2001) was reviewed by the IWC SC in 2004 (IWC, 2005). The Committee concluded that the estimate of abundance presented in this paper could be either positively or negatively biased. Potential sources of positive bias include the extrapolation of density from high-use areas close to shore to other areas of potentially lower density. Potential sources of negative bias include: under-estimation of mean group size during aerial surveys; poor sightability under the aircraft; and perception bias. The Committee noted that most of these potential biases would lead to an under-estimate of density in surveyed areas, but that the extrapolation of observed density to unsurveyed areas could lead to a positive bias in the abundance estimate. The Committee concluded, therefore, “that it was not appropriate to consider the results of these surveys as providing minimum estimates of abundance” (IWC, 2005). The Workshop **agreed** with the conclusions by the Committee in 2004 and classified this estimate as Category P.

A second aerial survey to estimate franciscana abundance in Rio Grande do Sul (RS) in 2004 expanded the sampling area of Secchi *et al.* (2001) and used a different survey design (Danilewicz *et al.*, 2010). A total of 1,256 km was surveyed along the coast of RS with tracklines going as far offshore as 13 n. miles and covering an area of 13,341 km². Thirty-one franciscanas were seen in 25 groups (average group size = 1.36 [CV not available] for groups seen on-effort and 2.0 [CV not available] for groups seen off-effort). Density within the survey area was corrected for availability bias and estimated at 0.51 franciscanas/km² (CV = 0.32). Total estimated abundance within the survey area was 6,839 franciscanas (CV = 0.32). The sensitivity of abundance estimates to different values of expected group size, and correction factors for availability bias and for perception bias (Laake *et al.*, 1997) were examined. This sensitivity analysis led to estimates of density ranging from 0.205 to 3.17 ind./km² (Danilewicz *et al.*, 2010).

In discussion, it was noted that methods were generally well implemented and that training of observers and removal of segments of effort where glare were greater than 80% were good practice. The use of a correction factor for availability bias computed from boat surveys could lead to overestimation of abundance but given the range of estimates of availability in section 3.1, positive bias in the estimated abundance would be small. The Workshop noted that the estimate in Danilewicz *et al.* (2010) corresponds to a portion (~20%) of the range of franciscanas in FMA III and therefore is not representative of the total range of the franciscana in this management area. In conclusion, it was **agreed** that considering the sources of negative bias and that the estimate does not apply to all of FMA III (only 20%), the estimate provided in this paper was classified as Category 3.

In the mid-2010s, the boundary between FMA II and FMA III was shifted northwards and the latter now includes the southern portion of Santa Catarina state (Anonymous, 2016). A new aerial survey conducted in 2014 expanded the sampling region defined in Danilewicz *et al.* (2010) to accommodate the new boundary and also expanded sampling to more offshore habitats in some areas (Sucunza *et al.*, 2020d). Parallel tracklines were allocated perpendicular to the shore from the coastline up to the 50m isobath, resulting in a comprehensive sampling of the franciscana habitat in southern Brazil. A total of 3,853 km was surveyed on effort and 84 franciscana groups were recorded (167 individuals, mean group size = 1.99, SE = 0.91, median = 2, range = 1–5). Density corrected for visibility bias and group size bias using the correction factor described above (4.42, CV = 0.04, Sucunza *et al.*, 2020a) was estimated at 0.31 individuals/km² (CV = 0.24, 95% CI = 0.19–0.50). Density extrapolated to the survey region yielded an estimate of 9,651 individuals (CV = 0.24, 95% CI = 6,013–15,490).

In review, it was noted that the survey design and implementation in Sucunza *et al.* (2020d) was appropriate and methods are standard, but that it also applies for a portion (35%) of the range of the franciscana in FMA III. It was unclear why only

half normal models were used to fit perpendicular distance data and what the rationale for binning the data was. It was also noted that this study used the correction factor for visibility and group size bias developed by Sucunza *et al.* (2020a) and discussed under item 3.1 above. Authors agreed to update this analysis including proposing additional models (e.g. hazard rate) for estimation of detection probability, considering pooling group sizes for use as a covariate in these models, providing additional information on model fit, and updating the estimates of abundance when the CV of the correction factor in Sucunza *et al.* (2020a) is revised. A revised paper is expected to be provided before the review of the franciscana's status by the SC is completed. The Workshop **agreed** to list the estimate for FMA III provided in Sucunza *et al.* (2020d, N = 9,651, CV = 0.24) as Category 2 because of greater spatial coverage when compared to Danilewicz *et al.* (2010) and also because Brazil may want to use the estimate for conservative (precautionary) management within their own waters.

None of the estimates of abundance presented above is comparable because of differences in survey areas. A major difficulty in estimating the abundance of franciscanas within FMA III as a whole lie in the fact that waters off Uruguay have never been surveyed. At last year's meeting the SC approved a project to conduct aerial surveys in Uruguay and estimate franciscana abundance within the entire FMA III range; however, due to pandemic travelling restrictions the aerial surveys in Uruguay were postponed to 2022.

3.6 FMA IV

Bordino *et al.* (2004) conducted boat surveys in winter and spring off the coast of Buenos Aires Province, Argentina, to assess franciscana abundance and trends between 1996–1998 and 2000–2003. Surveys were conducted in good visibility conditions (Beaufort 0–2) and extended offshore to a distance of 9.3km from shore. Density was estimated using conventional distance sampling methods in four coastal habitats which, together, encompassed an area of 540km². A total of 87 sightings were recorded with a mean group size of 2.3 dolphins. Density and abundance within the study area were estimated at, respectively 0.38 ind./km² (95%CI = 0.21–0.68) and 206 individuals (95%CI = 103–315), assuming $g(0) = 1$. Density was extrapolated to the whole range of the species within Buenos Aires Province (an area of 82,500km²) to estimate a population within the Province of 31,350 (95%CI = 15,262–47,850) dolphins (Bordino *et al.*, 2004).

The estimates of density and abundance provided in Bordino *et al.* (2004) were reviewed by the IWC SC in 2004 (IWC, 2005). The Committee concluded that the estimate of abundance presented in this paper could be either positively or negatively biased. The main source of positive bias corresponded to the extrapolation of density from areas of high use closer to shore to other areas of potentially lower density offshore. Negative bias would have resulted from the $g(0) = 1$ assumption and from responsive movement away from the boat during the surveys. The Committee concluded that it was not appropriate to consider the results of these surveys as minimum estimates of abundance (IWC, 2005). The Workshop **agreed** with these conclusions and classified this estimate as Category P.

Aerial surveys between Buenos Aires Province and the northern coast of Golfo San Matías, Rio Negro Province were conducted in 2003 and 2004 (Crespo *et al.*, 2004; 2010). Preliminary analyses of these surveys were presented to the SC during the 2004 franciscana review (Crespo *et al.*, 2004) and final analyses were provided in Crespo *et al.* (2010). The survey area was divided into four strata, two in the north (a coastal stratum – 0–30 m isobath – and an offshore stratum – 30–50 m isobath) and two in the south (also coastal and offshore). Four sets of zigzag tracklines were allocated across these regions, and the area where these tracklines were allocated represented just a fraction of the total area of each stratum. Surveys were conducted in three periods, two in the summer (February 2003 and 2004) and one in the fall (April/May 2003). Overall, 6,634 km were flown and a total of 101 franciscanas were observed in 71 sightings (average group size = 1.43). Density and abundance were computed using standard line transect sampling methods and corrected for availability bias. Because there were no seasonal differences in estimates of density, data from autumn surveys were used because of better survey conditions in that season. In the northern regions (off the northern Buenos Aires Province) corrected density was higher in the coastal stratum (0.377 ind./km², CV = 0.21), but declined further offshore (0.178 ind./km², CV = 0.37). Due to the small sample size, density was computed for both coastal and offshore strata in the south (0.197 ind./km², CV = 0.61). Abundance was computed for the northern coastal stratum by extrapolating density computed in the surveyed area (about 1/3 of the total area) to the whole stratum. For the northern offshore stratum, abundance was calculated only for the area covered by the survey (that is, no extrapolation to unsurveyed areas) because the sampling region in this stratum represented a much smaller proportion of the total stratum area. In the south, abundance was estimated only for the coastal stratum by extrapolating density computed in the covered portion to the whole area of the stratum.

A new series of aerial surveys to estimate franciscana abundance in Argentina started in 2019. These surveys were designed to sample areas similar to those described in Crespo *et al.* (2010). However, the surveys were interrupted because of the coronavirus pandemic and therefore, only a portion of the survey area was covered (Crespo *et al.*, 2020). The new survey was able to cover the northern coastal stratum (as defined in Crespo *et al.* 2010), but at a different time period (spring in the new survey, autumn in Crespo *et al.*, 2010). Estimates of density and abundance were presented for comparison with the 2003/4 surveys (Crespo *et al.* 2020). A total of 1,532 km of trackline were covered and 41 franciscana groups were seen on effort (mean group size = 1.34, CV = 0.11). Density and abundance corrected for availability bias were estimated at, respectively, 0.608 ind./km² and 13,356 individuals (CV = 0.28) in N one piecethe northern coastal stratum. While the 2003/4

and 2019 surveys are not entirely comparable, the new study suggests that density of franciscanas in the study area is higher than previously thought (Crespo *et al.*, 2020).

Crespo *et al.* (2010) and (2020) were discussed jointly. A number of potential sources of negative bias (e.g., lack of correction for perception bias, underestimation of group size, responsive movement [avoidance] of franciscana groups due to the noise of the plane, procedures adopted to perform left truncation of perpendicular distance data prior to estimation of detection probability) or positive bias (e.g., extrapolation of abundance to unsurveyed areas) were identified. Authors explained that survey design was primarily influenced by logistical limitations of the aircraft (e.g., location of airfields for refueling). The Workshop noted that the 2003 and 2004 surveys in Crespo *et al.* (2010) had been reviewed by the SC in 2004 and that the Committee had concluded that it was not appropriate to consider the results as minimum estimates of abundance (IWC, 2005). The Workshop also **agreed** that estimates of density in the covered area could be used to compute minimum abundance estimates and requested the authors to provide this information in the future. For the time being, the estimates provided in Crespo *et al.* (2010) will be considered Category P. The Workshop **concluded** that the 2019 abundance estimate provided in Crespo *et al.* (2020) should also be Category P because the survey has not yet been completed due to the coronavirus pandemic. The Workshop **encouraged** the authors to finalize the survey and provide new estimates in the future.

3.7 Babitonga Bay

Two estimates of abundance were computed for Babitonga Bay, an area of approximately 160km² off the coast of Santa Catarina State, Brazil. There is evidence that this population is isolated from franciscanas in coastal areas outside the bay (see discussion in section 2 above) and may represent a separate management unit.

Boat-based surveys were conducted with line transect methods between 2000 and 2003 by Cremer and Simões-Lopes (2008). Surveys were carried out in good visibility conditions (Beaufort 0–1). Data collected over 92 sampling days were pooled and density and abundance were computed using conventional distance sampling methods. A total of 38 sightings were made in 1,294km of survey effort and mean group size was estimated at 4.2 dolphins (CV = 0.12). Density and abundance were computed for two regions, the whole survey area (A1 in Cremer and Simões-Lopes, 2008) and sub-areas where franciscanas were detected (A2). Density and abundance were estimated at, respectively, 0.318 individuals/km² and 50 individuals (CV = 0.30) in A1 and 0.459 individuals/km² and 47 individuals (CV = 0.30) in A2.

In discussion, the Workshop considered that the survey design was appropriate, was properly implemented and followed standard methods. It was noted that estimates of group size were relatively high compared to other boat surveys (e.g., Weyn 2016 and Sucunza *et al.*, 2020b) but the estimates would not be biased if differences were due solely to different definitions of what constitutes a group (e.g., the observers in Cremer and Simões-Lopes [2008] tended to lump smaller groups into a single sighting). The workshop noted that the effective search width (ESW) in this study was nearly twice the ESW in Sucunza *et al.* (2020a), which was conducted in 2011 in the same region, with similar methods, and some of the same observers. Calibration experiments in the 2011 study showed that observers tended to overestimate distance by as much as 40%. The use of overestimated distances to compute detection probability in Cremer and Simoes-Lopes (2008) would result in positive bias in the estimation of ESW and negative bias in the estimate of abundance. For this reason, the Workshop **agreed** to classify this estimate as Category 2.

Boat-based line transect surveys were conducted in Babitonga Bay in 2011 as part of experiments designed to estimate correction factors to correct for bias in aerial surveys of franciscanas (Sucunza *et al.*, 2020a). Tracklines were allocated in an area of high density of franciscanas within the Bay and surveys were conducted in relatively good conditions (Beaufort 0–2). During this study, calibration experiments were carried out to assess and correct for potential biases in visual estimation of distance by the observers. A total of 114 franciscana groups were detected in 447 km of survey effort. Average group size was estimated at 2.91 individuals (CV = 0.23). One out of five observers underestimated distance by 9%, while the remaining four observers overestimated distance by 8–40% on average. Density and abundance were estimated at, respectively, 2.99 ind/km² and 49 dolphins (CV = 0.23). Estimates from these surveys are not directly comparable (e.g. to assess trends in abundance) to those from Cremer and Simões-Lopes (2008) because the areas surveyed are different.

In discussion, the Workshop noted that the area covered by the boat surveys corresponded to a fraction of the range of the franciscana within Babitonga Bay and that this would result in a negatively biased estimate of abundance. Negative bias would also result from the assumption that $g(0) = 1$, particularly when the survey was conducted in Beaufort 2. The Workshop **concluded** that these sources of negative bias justified classifying the estimate in Sucunza *et al.* (2020a) as Category 2.

3.8 Future work

The Workshop **agreed** the following tasks would be performed before completion of the review of the status of the franciscana by the SC at the 2022 SC meeting (analysts identified in parentheses):

- (1) The CV of the correction factor for visibility and group size bias presented in Sucunza *et al.* (2020a) will be revised and the estimates computed with this correction factor will be updated (Sucunza, Danilewicz, Zerbini).
- (2) An estimate of uncertainty for group size bias correction computed by Sucunza *et al.* (2020a) will be calculated and applied to the estimate of abundance in FMA II (Sucunza *et al.* 2020c) (Sucunza, Zerbini).

- (3) The estimate of abundance for the 2010 FMA III survey (Sucunza *et al.*, 2020d) will be revised following the discussion provided in item 3.5 above (Sucunza, Danilewicz).
- (4) If the situation with the coronavirus pandemic improves, surveys in FMA IV will be completed and new estimates of abundance will be computed (Crespo and Coscarella).

4. CONCLUDING REMARKS

Workshop participants acknowledged the progress made on discussions about population structure and abundance during the meeting and hoped that further progress can be made through an in-person meeting planned to be held prior to the 2022 meeting of the Scientific Committee if the restrictions imposed by the coronavirus pandemic are relaxed.

Participants also acknowledged the hard work conducted by the intersessional correspondence groups and by all reviewers who contributed their time to reviewing estimates of abundance. The Workshop organizers thanked the IWC Secretariat for its support and help to ensure the successful completion of the Workshop.

Finally, participants thanked Cipriano for the excellent work as rapporteur and Iñíguez, Lang and Zerbini for leading the discussions during the Workshop.

The meeting was adjourned on 9 April 2021 at 17:38 UK time.

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Annex 1

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Annex 2

Agenda

1. INTRODUCTORY ITEMS
 2. POPULATION STRUCTURE
 - a. Overview of past advice
 - b. Review of newly proposed subdivisions
 - c. Genetic support for proposed subdivisions
 - i. FMAII
 - ii. FMAIII
 - iii. FMAIV
 - iv. Summary
 - d. Other (non-genetic) support for proposed subdivisions
 - e. Next steps
 3. ABUNDANCE ESTIMATES
 - a. Correction factors for visibility and group size bias
 - b. FMA Ia
 - d. FMA Ib
 - e. FMA II
 - e. FMA III
 - f. FMA IV
 - g. Babitonga Bay
 - h. Future work
 4. OTHER
 5. CONCLUDING REMARKS
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Annex 3

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Stock structure

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Annex 4

List of Franciscana Abundance Estimates Reviewed During the Workshop

Stock	Region	Cat.	Date stamp	Range of years	Method	Corr.	Estimate	CV	Approx. 95% CI	Reference	Comments
FMA Ia	Range wide	P	2017	2017-2018	LT	A, P, GS	595	0.44		Sucunza et al. (2020b), SC/68b/ASI/5	Can be elevated to Cat. 1 when CV of correction factor is updated
FMA Ib	Range wide	P	2010		LT	A, P, GS	1,692	0.47		Danilewicz et al. (2020), SC/68b/ASI/07_rev1	Can be elevated to Cat. 1 when CV of correction factor is updated
FMA Ib	Range wide	P	2017		LT	A, P, GS	1,280	0.43		Danilewicz et al. (2020), SC/68b/ASI/07_rev1	Can be elevated to Cat. 1 when CV of correction factor is updated
FMA II	Range wide	2	2009	2008-2009	LT, MR	A, P	6,827	0.26		Sucunza et al. (2020c), SC/68b/ASI/05	Can be elevated to Cat. 1 when corrected for group size bias
FMA II	Paranaguá Bay			2012-2013	LT		198	0.31		Weyn (2016)	unclear whether population in the bay corresponds to a fraction of dolphins in FMA II
FMA III	Range wide	P	1996		LT	A	42,078	0.34		Secchi et al. (2001)	survey covered ~2% of the range of FMA III
FMA III	Rio Grande do Sul, Brazil	3	2004		LT	A	6,839	0.32		Danilewicz et al. (2010)	survey covered 20% of the range of FMA III
FMA III	Rio Grande do Sul, Brazil	2	2010		LT	A, P, GS	9,651	0.24		Sucunza et al. (2020d), SC/68b/ASI/06	survey covered 35% of the area of FMA III
FMA IV	Buenos Aires Province	P		1996-1998, 2003-2004	LT		31,350		15,262-47,850	Bordino et al. 2004, SC/56/SM13	survey covered a portion of FMA IV
FMA IV	Northern area (0-30m)	P		2003-2004	LT	A	8,279		4,904-13,960	Crespo et al. 2010	survey covered a portion of FMA IV
FMA IV	Southern area	P		2003-2004	LT	A	5,896		5,896-17,999	Crespo et al. 2010	survey covered a portion of FMA IV
FMA IV	North offshore stratum (30-50m)	P		2003-2004	LT	A	470			Crespo et al. 2010	survey covered a portion of FMA IV
FMA IV	Buenos Aires Province	P	2019		LT	A	13,356	0.28		Crespo et al. 2020, SC/68b/ASI/03	survey covered a portion of FMA IV
Babitonga Bay		2		2001-2003	LT		47	0.3		Cremer and Simões-Lopes, 2008	part of FMA II, but treating as a separate management unit as suggested by SD/DNA group
Babitonga Bay		2	2011		LT		49	0.23		Sucunza et al. (2020a), SC/68b/ASI/04_rev1	part of FMA II, but treating as a separate management unit as suggested by SD/DNA group

LT – Line transect, MR – mark-recapture, A – availability, T – perception, GS – Group size.

Annex 5

Intersessional Correspondence Group on Franciscana Population Structure

Membership: Lang (Co-Convenor), Ott (Co-Convenor), Andriolo, Archer, Cipriano, Cunha, de Oliveira, Farro, Gariboldi, Hoelzel, Mendez, Pampoulie, Passadore, Secchi, Tiedemann, Torres Florez, and Zerbini.

The terms of reference for the group are to (1) summarise the data available from genetic and other (i.e., non-genetic) lines of evidence that could be used to infer population structure; (2) evaluate the level of support for each of the proposed subdivisions based on this combined data; and (3) provide advice on future work (additional analyses, sample collection efforts) to address remaining questions.
