

DRAFT DOCUMENT

September 2011

A1 Title: State of the Antarctic Ecosystem (AntECO)

A2 Name of SSG Submitting the proposal Life Sciences

A3 Expected duration of program 8 years

A4 Estimated SCAR funding required over the total program lifetime (\$128, 000 = \$16, 000 per year)

A5 Program Summary

Biological diversity is the sum of all those organisms that determine how ecosystems function, and underpins the life-support system of our planet. This programme has been designed to focus on past and present patterns of biodiversity across terrestrial, limnological, glacial and marine environments within the Antarctic, sub-Antarctic and Southern Ocean regions, to provide the scientific knowledge on biodiversity, including genetic diversity, species diversity and ecosystem diversity that, coupled with increased knowledge of species biology, can be used for the conservation and management of Antarctic ecosystems.

Under the framework of EBA, initiatives such as CAML, SCAR-MarBIN and ANTABIF have demonstrated how internationally coordinated research and standardized techniques can rapidly advance knowledge of the state of Antarctic ecosystems. These have improved our understanding of key elements of Antarctic biodiversity, its linkage with global biodiversity and aspects of its phylogenetic and biogeographic history, highlighting the importance of cross-disciplinary links with the oceanographic, glaciological and climate communities in particular.

The new challenges are to further the knowledge on current biodiversity and patterns therein, to distinguish the impact of present processes from historical signals, and use this knowledge to develop scenarios of its future state through interdisciplinary approaches. To do so we will promote the use of both established and innovative technologies, on scales from the latest molecular analyses to remote sensing, that will provide the means for synthesis and integration across the entire region over physical and temporal scales and at resolutions that until now have not been possible.

Authors: see Appendix 1.

37 **B1 Program Objectives**

38 The AntECO program aims to promote, stimulate and coordinate international interdisciplinary
39 research relevant to Antarctic ecosystems. The over-arching theme is to promote the use
40 bioinformatics and ecoinformatics approaches to understand spatial patterns in Antarctic
41 biodiversity from genes to ecosystems, to determine how these patterns have evolved through
42 time, and to identify the implications for conservation management, including mitigation of
43 forecast threats, in a time of rapid environmental change. The objectives are succinctly
44 encompassed by the phrase: ‘surveys, sequences, systematics and synthesis’.

45 Key scientific questions:

- 46 ➤ How has Antarctic biodiversity evolved in response to past environmental change and
47 what does this tell us about its capacity to respond to future change?
- 48 ➤ What are the systematic and environmental geographic features of Antarctic biodiversity,
49 and what mechanisms underpin the current distribution and abundance of biodiversity?
- 50 ➤ Given the evolved geographic distribution of diversity and forecasts threats, what
51 conservation actions are required for mitigation of, and adaptation to, change?

52 The programme is divided into three interlinked themes: a) Evolved patterns, b) Spatial patterns,
53 and c) Governance, mitigation and adaptation. A high priority will be placed on providing
54 biological information for, and increasing linkages across, the SCAR standing scientific groups,
55 in particular with relevant areas of oceanography, glaciology, soil science, permafrost,
56 geochemistry, geosciences, and climatology, particularly through links with programme
57 ANTARCTIC 21. It will also involve important synergies with the physiological limits and
58 tipping points identified by the ‘AntETR’ programme (Appendix 2 – *Venn diagram of linkages*).
59 The integrated information will be made available through SC-ATS to the Antarctic Treaty
60 System.

61
62 **B2 Scientific background**

63 In the face of global climate change, one of the biggest questions facing humanity is what will
64 happen to global biodiversity in the near future. Gaining an improved understanding of the
65 effect of past climate change and tectonic events on speciation, extinction and rates of evolution
66 will help us to predict the effect that future changes will have on Antarctic biodiversity.
67 Antarctica’s unique marine and terrestrial biota, together with its thermal isolation and
68 reasonably well-defined climatic, tectonic and glacial history make it an ideal test case in which
69 to study the origins, evolution and maintenance of biodiversity.

70 Major climatic and geological events in Antarctica’s history are likely to have precipitated
71 extinctions in Antarctic taxa, giving rise to vacant niches and providing opportunities for
72 speciation. Such events may have also facilitated the colonisation of other areas (e.g. the deep
73 sea) from a suggested centre of origin in Antarctica. Relatively minor climatic and geological
74 events in Antarctica’s recent history have also resulted in shifts in species distribution, species
75 succession and establishment that will continue to have an impact on biodiversity.

76 Understanding recent past events (since the Late Pleistocene) is key to our ability to produce
77 models and projections of near-future possible scenarios. Linking climate record with the
78 genetic structure of extant populations is a major challenge which is waiting to be addressed by
79 the scientific community using the innovative technologies which are now available

80 Despite numerous studies on the biogeography of the 'Antarctic' region, there is little consensus
81 on fine scale patterns of biodiversity, particularly in the terrestrial realm (Chown and Convey
82 2007). Obtaining such a view about how the various regions of Antarctica and the surrounding
83 islands relate to each other in terms of their biodiversity has taken on renewed urgency as a
84 consequence of conservation threats and requirements in the region. These are threefold. First,
85 although the continent and oceans south of 60°S are designated as areas for peace and science
86 there is increasing concern about the effects of climate change, invasion, and other forms of
87 disturbance (Ayres et al. 2008; Tin et al. 2009). Thus, there is increasing emphasis on Antarctic
88 Specially Protected Areas and how they are performing to conserve the biodiversity of
89 Antarctica given these threats. Second, the sub-Antarctic islands are subject to similar changes,
90 and understanding which islands are most significant from a conservation perspective is of
91 considerable significance (Shaw et al. 2010). Finally, because the extent of movement of both
92 science and tourism between areas in the Antarctic is increasing, the likelihood of transfer of
93 propagules among islands or between ice-free areas in the Antarctic is also growing (Lee and
94 Chown 2007; Hughes and Convey 2010). Understanding the relationships among areas both
95 from a species and population perspective is therefore important.

96 Genetic techniques are now often used provide more definitive answers regarding the
97 provenance and historical distribution of species (e.g. Rogers 2007). Only a few recent genetic
98 studies have provided further evidence of terrestrial organism dispersal into Antarctica after the
99 last glacial maximum with the majority providing support for vicariant speciation as the most
100 important factor driving the diversity and distribution of Antarctic terrestrial biota (Stevens et al.
101 2006; Convey et al. 2008). While dispersal cannot be discounted completely there does appear to
102 be a growing recognition that many Antarctic species have actually survived in small isolated
103 populations for perhaps millions of years (Convey et al. 2009). In addition to this increasing
104 body of molecular data that suggests that some of the Antarctic species may have survived in
105 'refugia' during glacial cycles, it is also becoming clear that, in general, the extant distribution of
106 shelf species is the result of recent recolonizations. Understanding recent past (since the Late
107 Pleistocene) is key to our ability to produce models and projections of near-future possible
108 scenarios. Linking climate record with the genetic structure of extant populations is a major
109 challenge which is waiting to be addressed by the scientific community using the innovative
110 technologies which are now available.

111 This program aims to integrate patterns and processes resulting from historical climate change
112 and understanding of contemporary ecosystem function in order to form a predictive framework
113 for understanding the impacts of future climate change on the Antarctic and Southern Ocean
114 biota, and to inform best future management practice.

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116

117 **B2.1 Evolved patterns**

118 The Antarctic and Southern Ocean biota provide an ideal test case with which to characterise the
119 effect of climatic and tectonic change on molecular evolutionary processes and biodiversity.
120 The climatic, tectonic and glacial history of Antarctica is reasonably well defined (Clarke &
121 Crame, 2003) and is understood to be integral in shaping Antarctic biota. For example, events
122 such as the opening of the Drake Passage, leading to thermal isolation of the continent, marked
123 and sudden temperature changes (such as the late Paleocene thermal maximum) and orbitally-
124 forced glacial cycles have all been suggested as important in shaping the present day Antarctic
125 marine biota (Clarke & Crame, 1992). Furthermore, the opening of the Drake Passage and the
126 subsequent establishment of deep-water connections between the Southern Ocean and the rest of
127 the major ocean basins of the world, has been suggested to have facilitated recolonisation of
128 deep sea areas after extinction events due to deep ocean oxygen depletion (Rogers 2000; Little &
129 Vrijenhoek, 2003; Strugnell et al., 2008). The resulting influences of these events and processes
130 should leave discernible signatures in the molecular information systems of Antarctic organisms.

131 On land and in lakes, there has been a paradigm shift in the general understanding of the
132 antiquity, endemism and regionalisation of the contemporary biota, many elements of which
133 have survived and evolved on the continent through multiple Miocene, Pliocene and Pleistocene
134 glacial cycles. The requirement for refugia has implications for our understanding of the
135 glaciological and geological evolution of the continent and its ice sheets. Studies of changes in
136 biodiversity across the most recent glacial interglacial cycle have shown that the present day
137 biota contains a mixture of often cryptic species that result from isolation in glacial refugia and
138 post-glacial colonists, and have identified species that are sensitive to quite minor changes in the
139 physical environment.

140 Our knowledge of the diversity of Antarctic marine and terrestrial biota has greatly increased
141 recently with the availability of new databases, (e.g. SCAR-MarBIN, Antabif, RiSCC/EBA),
142 syntheses (e.g. Convey et al. 2008, 2009; Vyverman et al. 2010) and the development and
143 application of molecular sequencing techniques (e.g. Smith et al., 2006; Wilson et al., 2009;
144 González-Wevar et al., 2010). These studies confirm some unexpectedly high levels of
145 taxonomic diversity (e.g., Smith et al., 2006), and previously unsuspected levels of cryptic
146 speciation, and the presence of a number of species rich clades (e.g. peracarid crustaceans,
147 trematomid fish, nudibranchs, pycnogonids, octopus). Other studies have found widespread
148 distributions of a single taxon (e.g. Raupach et al., 2010). Nonetheless, large data gaps still
149 occur, especially for marine invertebrate taxa, and must be considered in study design.

150 Together these findings have focused attention on the timing, nature and potential causes of
151 diversification leading to species-rich clades, reinvigorated debate on whether polar regions
152 should be regarded as evolutionary sources or sinks (Goldberg et al. 2005; Strugnell et al., 2008;
153 Strugnell et al., 2010), and highlighted the environmental factors that are most likely to shape
154 future biodiversity.

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158 **B2.2 Spatial variation**

159 Antarctica and the Southern Ocean contains ecosystems across the full range of complexity,
160 from the most simple ecosystems of the inland frigid deserts and nunataks to some of the most
161 complex marine benthic ecosystems known. This provides an ideal/unique resource with which
162 to explore fundamental rules of ecosystem assembly structure and function.

163 There is also a need to obtain an understanding of the variation in biodiversity in a spatially
164 explicit way. This is achieved, by not only widening exploration 'space, but also by exploring
165 abiotic, environmental and historical proxies for biodiversity. It is also important to recognise
166 the importance of strategic approaches in obtaining this information, and utilise and test tools
167 that have been trialled elsewhere.

168 There remain very large gaps in our knowledge of even some fundamental aspects of Antarctic
169 terrestrial and marine biology. These include such aspects as ecosystem structure and function
170 and the true diversity of biota including microbial species. These gaps inhibit higher levels of
171 understanding, such as the exact inter-relationship between organism and microclimate, the
172 structures and functions of biological assemblages and the true nature of chemical cycling,
173 without which understanding of ecosystem responses to climate change cannot be advanced.

174 Genetic data can provide more definitive answers regarding the diversity and distribution of
175 species (e.g. Rogers 2007). Regional biodiversity surveys such as recently undertaken by the
176 NZTABS program (which include modern molecular phylogenetic analyses) are excellent
177 models for more extensive analyses. Only a few recent genetic studies have provided evidence
178 of organism dispersal into Antarctica after the last glacial maximum with the majority providing
179 support for vicariant speciation as the most important factor driving the diversity and distribution
180 of Antarctic biota.

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182 **B2.3 Governance, mitigation and adaptation**

183 Despite numerous studies on the biogeography of the region, there is little consensus on fine
184 scale patterns of biodiversity, (Chown and Convey 2007). Obtaining a view on how the various
185 terrestrial regions of Antarctica and the surrounding islands relate to each other in terms of their
186 biodiversity has taken on renewed urgency as a consequence of conservation threats and
187 requirements in the region. The Antarctic Treaty System seeks to protect Antarctic biodiversity
188 across the terrestrial and marine biomes. Considerable progress has been made in identifying
189 areas of important and vulnerable marine biodiversity through initiatives like CAML, and with
190 the support of organisations like CCAMLR these are starting to be recognised by the creation of
191 Marine Protected Areas. Ongoing links between AntECO (as a biodiversity information provider
192 and analyst) and CCAMLR are going to be critical in the ongoing management of important
193 marine and terrestrial areas. Data from a range of sources (including bird and seal population and
194 tracking data, information from organisations like ACAP and potentially fishing information
195 from CCAMLR) can be used to assist in the identification of important marine biodiversity areas
196 and potentially feed in the MPA assessment procedures.

197 Although the continent and oceans south of 60°S are designated as areas for peace and science
198 there is increasing concern about the effects of climate change, invasion, and other forms of
199 disturbance (Ayres et al. 2008; Tin et al. 2009). In the terrestrial realm, there is increasing
200 emphasis on Antarctic Specially Protected Areas and how they are performing to conserve the
201 biodiversity of Antarctica given these threats. The sub-Antarctic islands are subject to similar
202 changes, and understanding which islands are most significant from a conservation perspective
203 is of considerable significance (Shaw et al. 2010). Conservation concerns are also exacerbated
204 by an increase in the extent of movement of both scientists and tourists between areas in the
205 Antarctic and therefore the likelihood of propagule transfer among islands or between ice-free
206 areas in the Antarctic is also growing (Lee and Chown 2007; Hughes and Convey 2010; Cowan
207 et al. 2011). Understanding the relationships among areas both from a species and population
208 perspective is therefore important.

209

210 **B3 Program rationale/justification**

211 The Antarctic is experiencing unprecedented (at least in recent geological history) rapid change
212 and it is now critically important to assess the state of the ecosystem so that we can measure
213 current change, predict future trajectories of change and inform best practice in environmental
214 management and stewardship in the Antarctic. By using a combination of surveys, systematics,
215 sequences and synthesis we hope to clarify the evolutionary and ecological drivers of spatial
216 variation in diversity and apply this information to not only identify, but also to mitigate threats.

217 There are two principal factors supporting the timeliness of this proposal.

218 The Antarctic continent is under growing threat from impacts, which could fundamentally
219 change elements of its biology. The dramatic changes in climatic conditions, particularly in
220 Western Antarctica and the Antarctic Peninsula, have the capacity to induce massive long-term
221 changes in biological communities. The consequences of these changes can only be understood
222 by elucidating how historical changes have affected communities in the past, and by obtaining
223 present day baseline data.

224 In addition, the rapid rise in human impact on small but important areas of the continent,
225 resulting from the ever-growing activities of national operators and the ecotourism industry,
226 represents a real threat. Physical impacts, disturbance, chemical contamination and the input of
227 macroscopic and microscopic propagules all represent perturbations of sensitive Antarctic
228 ecosystems and communities. Research programs designed to assess, monitor and quantify such
229 processes are vital as tools for establishing viable management and control strategies.

230 Technical developments in molecular biology over the past few decades have greatly facilitated
231 the investigation (and accurate understanding) of species origins/history/trajectories and
232 diversity. The key to addressing these issues is to use integrated and cross-disciplinary
233 approaches - for example, remote sensing, spatial analyses, computer modelling in conjunction
234 with bio- and eco-informatics.

235 With the very recent expansion of high throughput 3rd generation DNA sequence analysis, the
236 opportunities to comprehensively assess species diversity and community structure are

237 unparalleled. These technical opportunities also coincide with analytical advances and a
238 perception of genetic diversity as a resource, not only for the expansion of biotechnology, but
239 also for understanding fundamental aspects of species interactions and organismal adaptation.

240 In the marine realm there has been significant increase in biodiversity knowledge through
241 initiatives like CAML, although for most of the Southern Ocean and its benthic environments
242 the scale at which data are available is far from satisfactory and continues to limit analyses.
243 Consequently, databases like SCAR-MarBIN are becoming useful tools in assessing biodiversity
244 and identifying areas that are vulnerable or unique. However, nothing similar has been
245 undertaken for the terrestrial realm except at small, localised scales. Preliminary analyses
246 undertaken by SCAR have shown that there are no biodiversity records for a significant
247 proportion of ice-free Antarctica (Terauds and Chown 2010). Such gaps could be addressed in a
248 number of ways including concerted and targeted field surveys (in a similar manner to CAML)
249 and the incorporation of existing data into the terrestrial equivalent of SCAR-MarBIN – the
250 SCAR Antarctic Biodiversity Database. The refinement and development of appropriate spatial
251 frameworks with which to categorise and assess biodiversity on the Antarctic continent is a key
252 element of any ongoing conservation management of the region. Given the recent completion of
253 the preliminary SCAR analyses of the Environmental Domains, (Keyes ref) it is timely for
254 AntECO to facilitate and co-ordinate the progression of this research. These frameworks can
255 then be used with Antarctic biodiversity data and also with characteristics of Antarctic
256 biodiversity (i.e. dispersal mechanisms, genetic variability, rarity, vulnerability etc.) to assess the
257 current set of protected areas and inform the choice any new protected areas that are required.

258

259 **B4 Methodology and preliminary implementation plan**

260 The essence of this program is informatics (and the technologies which generate the data on
261 which informatics is based). Utilising existing and emerging technologies in molecular research,
262 spatial analyses and meta-analyses will allow us to better understand biodiversity patterns and
263 processes in Antarctica. The threats to biodiversity now and in the future will also be a major
264 product of these analyses and by linking these data with outputs from AntEATR and
265 ANTARCTIC 21 a comprehensive model of Antarctic biodiversity protection can be created.

266 This programme will be addressed by:

- 267 ➤ Elucidating the molecular evolutionary history of Antarctic and Southern Ocean biota using
268 the latest multigene phylogenetic reconstruction methods (e.g. Heled and Drummond 2010).
269 Synthesis across taxa will enable broadscale patterns to be detected and shed light on
270 potential past refugia during glacial maxima. Taking advantage of the latest developments
271 in Bayesian comparative methods (e.g. Knowles, 2009; Huang et al. 2011) will allow
272 integration of paleontological and molecular data to produce bounded estimates of genetic
273 divergence times, species diversification rates, and patterns of concerted responses by
274 multiple taxa (communities) to shared geophysical drivers of environmental change. These
275 will be linked to improved models of physical histories to infer the environmental drivers of
276 past evolutionary change.

- 277 ➤ Determining late Quaternary and Holocene changes in biodiversity of the marine, lacustrine
 278 and terrestrial biota using established methods (see Hodgson et al. 2009 and references
 279 therein) and identifying which environmental factors are significantly related to these
 280 changes.
- 281 ➤ Establishing and developing new cross-disciplinary links (through international workshops)
 282 between members of the molecular evolution, glaciological, oceanographic, climatological
 283 and climate modelling communities, to facilitate these ambitious integrated approaches to
 284 reconstructing the evolutionary and biodiversity history of Antarctica.
- 285 ➤ Implementing cutting edge historical seascape and landscape genetics techniques (e.g.
 286 Galindo et al. 2010) in conjunction with simulation studies, to quantify the past connectivity
 287 of the Southern Ocean and Antarctic biodiversity to the global biosphere.
- 288 ➤ Analyzing past changes in biodiversity in groups that leave morphological or
 289 biogeochemical remains in sediments and taking advantage of these historical specimens for
 290 use in ancient DNA and biomolecular archeological studies to elucidate past genetic
 291 diversity and palaeoenvironments.
- 292 ➤ Organising interdisciplinary workshops to identify emerging evolutionary patterns and to
 293 facilitate interpretation of extant taxon distributions (held within these databases) in the light
 294 of the historical evolutionary patterns and also to identify current and future threats to
 295 biodiversity.
- 296 ➤ Using state of the art software (e.g. GIS, multivariate statistical approaches) to analyse and
 297 synthesise large and complex data sets, taking advantage of SCARs georeferenced
 298 community datasets (e.g. SCAR-MarBin, ANTABIF). Continued engagement of these
 299 initiatives will be promoted to store, collate and make this data accessible to the broader
 300 Antarctic community. Develop the successful approach of CAML and initiate co-ordinated
 301 holistic sampling approaches involving standardised gears for biodiversity census which
 302 include recording of environmental parameters, and populate existing georeferenced
 303 databases (e.g., SCAR- MarBIN, ANTABIF, SCAR Antarctic Biodiversity Database,
 304 Barcode of Life Database) with these data to make them internationally available.
 305 Encourage the submission of existing data to these databases (particularly the terrestrial one)
 306 to assist in biodiversity assessments.
- 307 ➤ Apply cutting edge remote sensing and other technological innovations (such as the use of
 308 digital elevation models) to detect biotic changes (both spatially and temporally) and also
 309 provide additional parameters to increase environmental model resolution. Use these
 310 techniques to build up a model of environmental proxies for biodiversity.
- 311 ➤ Employ mathematical modelling and simulation techniques utilising the improved census
 312 (direct and remotely sensed) and molecular data and higher resolution environmental data to
 313 investigate potential impacts under a range of environmental scenarios to facilitate our
 314 understanding of the threats to biodiversity.
- 315 ➤ Implement established and 3rd generation sequencing techniques for exploring
 316 microevolutionary processes in order to better understand species and population structure
 317 and diversity, population history, molecular adaptation and to provide a baseline for
 318 monitoring of future population change.

- 319 ➤ Develop autecological studies which enhance our understanding of individual species’
320 functional roles within community and ecosystem structure.
- 321 ➤ Establish protocols for a genetic monitoring program to detect the range shifts, demographic
322 expansions and contractions, and changes in genetic structure and diversity that may result
323 from environmental changes. This will provide guidance in establishing protocols for
324 environmental protection.
- 325 ➤ Populate appropriate spatial frameworks with up to date and comprehensive biodiversity
326 data to identify patterns in biodiversity with particularly attention to biodiversity hotspots
327 and areas of unique biodiversity.
- 328 ➤ Undertake modelling and prediction of biodiversity-environment interactions, pattern
329 analyses and bioregionalisation.

330 This research follows on seamlessly from the recent biodiversity analyses undertaken by SCAR
331 and will feed directly into the process of testing the distribution, extent and representative nature
332 of existing ASPAs. A new assessment of current biodiversity will also allow the us to test how
333 well the existing portfolio of ASPAs satisfy the principles and intent of the Madrid Protocol.
334 Additionally these analyses will facilitate the development and testing of physical/environmental
335 surrogates for sites of high biodiversity and geodiversity values, which has been identified as
336 another important aspect of protected area assessment, particularly in data sparse environments.
337 However, it is explicitly noted that there is a real need for improved co-ordination of activities
338 and standardization of methodologies within the relevant international scientific communities
339 (Wall et al., 2011).

340
341 Figure 1. Program Timeline

342 **To be inserted**

343

344 **B5 Program management and governance**

345 The program AntECO is composed of field analyses, laboratory experimental programs and
346 modelling approaches. The implementation and the adaptation of single components depend on
347 the cooperation between specialists since the AntECO remit incorporates numerous
348 subdisciplines, habitats and groups of organisms.

349 The most effective approach to coordinate and enhance the objectives and outcomes of AntECO
350 is communication between dispersed research groups. The management of this program will
351 thus be most effectively achieved through a coordinated series of workshops and conferences.
352 The principal vehicle for these meetings will be the existing SCAR conference structure (SCAR
353 Open Science Conferences and SCAR Biology Symposia), but such meetings should be
354 supplemented with more focussed workshops as necessary.

355 Program managers will actively encourage post-graduate student opportunities, (e.g., Antarctic
356 Science Bursaries , Gateway Antarctic funding, etc). Importance will be placed on building

357 multidisciplinary links and ensuring capacity building so that all parties (including those less
 358 resourced) can utilise the resources available most effectively.

359
 360

361 **B6 Deliverable outcomes from the program including public awareness**

362 The following are quantifiable (and appropriate) deliverables from the program.

- 363 ➤ Potential cross linkages between SRPs (ANTARCTIC 21, AntECO, AntETR) – papers
- 364 authored by scientists across SRPs/disciplines/nationalities/etc...
- 365 ➤ Publications in peer-reviewed journals (research publications and reviews)
- 366 ➤ Preparation of relevant strategy and advisory documents
- 367 ➤ Population of relevant databases with spatially significant population datasets
- 368 ➤ Presentations at appropriate scholarly meetings, workshops and conferences
- 369 ➤ Training and graduation of post graduate students (MSc and PhD)
- 370 ➤ Presentations at public (non-scientific) forums
- 371 ➤ Establishment of new public interaction sites (web pages etc.)
- 372 ➤ Relevant media activities

373 Coordinators of the AntECO program will be expected to assemble relevant output data as part
 374 of the requisite reporting structure.

375

376 **B7 Biennial milestones against which progress can be evaluated**

377 Using the criteria identified in B8 below, the following general biennial milestones for the 10-
 378 year duration of the project can be identified:

379

Activity	Period of program (yrs)				
	1-2	3-4	5-6	7-8	9-10
AntECO-related symposia	✓	✓	✓	✓	✓
Participation of multiple international laboratories	✓	✓✓	✓✓✓	✓✓✓	✓✓✓
Evidence of cross-disciplinary activities	✓	✓✓	✓✓✓	✓✓✓	✓✓✓
Leveraging of research funding	✓	✓✓	✓✓✓	✓✓✓	✓✓✓

Published research outputs		✓	✓✓	✓✓✓	✓✓✓
Evidence of student training and development		✓	✓✓	✓✓✓	✓✓✓
Synthesis document - Final State of the Antarctic Ecosystem report					✓✓✓

380

381 **B8 Success factors**

382 The following can be considered as performance criteria:

- 383 ➤ Relevant meetings, symposia, workshops etc organised and implemented.
- 384 ○ The coordination role of this program will be largely implemented through
- 385 international meetings; such meetings may be held under the auspices of the
- 386 relevant parent organisations or by more specialised sub-groupings with field-
- 387 specific interests.
- 388 ➤ Number of participating laboratories and organisations.
- 389 ○ The expectations of a successful program would include participation of
- 390 laboratories across many or all of the Antarctic-active nations, covering all
- 391 aspects of the physical and biological fields relevant to the AntECO concept.
- 392 ➤ Aggregated staff and student numbers involved in AntECO-relates programs.
- 393 ○ The performance and productivity of any research program is intimately linked to
- 394 the personnel involved. Quantification of research staff numbers and level
- 395 provides and effective measure of performance and success in achieving AntECO
- 396 objectives.
- 397 ➤ Funding related to AntECO objectives leveraged from national and international grant
- 398 bodies.
- 399 ➤ As the role of the AntECO program is to motivate and steer research relevant to the
- 400 AntECO objectives, virtually all substantive activities will inevitably be supported by
- 401 national agencies.
- 402 ➤ Evidence of cross-boundary and cross-national collaborations.
- 403 ➤ Relevant outputs (research student graduates, publications; advisory documents etc.).

404

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406 **B9** **References**

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445

446 *Supporting information (2 pages)*

447

448 C1 Names of proposed chief officer and 3 other lead investigators (include 1 para bio, but
449 not publications)

450

451 C2 Why is SCAR support needed for this program (what is the value added)?

452

453 C3 Anticipated degree of national and international involvement

454

455 C4 Indicative budget for the first 4-years (2 SCAR cycles)

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457

458 **Appendix 1. Authors of the AntECO proposal**
459
460 Aleks Terauds, Australian Antarctic Division, AU
461 Angelika Brandt, University of Hamburg, DE
462 David Barnes, British Antarctic Survey, UK
463 Don Cowan, University of the Western Cape, SA (coordinator)
464 Huw Griffiths, British Antarctic Survey, UK
465 Ian Hogg, University of Waikato, NZ
466 Jan Strugnell, La Trobe UNiversity, AU
467 Louise Allcock, National University of Ireland, UK
468 Mark Hindell, University of Tasmania, AU
469 Nerida Wilson
470 Nicoletta Cannone, University of Subria, IT
471 Pete Convey, British Antarctic Survey, UK
472 Piero Luporini, Unicam, IT
473 Stefano Schiaparelli, UNIGE, IT
474 Win Vymerman, University of Ghent, BE
475
476

477 Appendix 2. Venn Diagram of linkages between AntECO and AngtER

478

479 To be inserted