Polar Biology (2026) 49:85
https://doi.org/10.1007/s00300-026-03526-6

RESEARCH

Rare observation of blowflies on a remote island research station: the risk of intra-island human-assisted dispersal

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Received: 9 January 2026 / Revised: 17 June 2026 / Accepted: 24 June 2026

Abstract
Globally, biodiversity loss is accelerating, with biological invasions representing one of the greatest threats to biodiversity and ecosystem functioning. Increasingly, research visits to isolated locations, such as the sub-Antarctic islands, involve stringent biosecurity measures to limit the inadvertent import and establishment of non-native species in these regions. Notwithstanding, human activity remains the predominant source of non-native species on these islands. One such species found on sub-Antarctic Marion Island, assumed to have been introduced during logistical operations several decades ago supporting this South African-administered island, is the blowfly, *Calliphora vicina*. To date, this conspicuous fly has only been observed in a limited area in the south-eastern quadrant of the island near Funk Bay and Kildalkey Bay. Here we report an incident of two living flies observed and captured at the island's meteorological research station in the island's north-east quadrant, which we speculate is likely associated with inadvertent human-mediated dispersal by a field assistant who surveyed seal populations at Funk Bay earlier the same day. Morphological examination and molecular analyses – the latter being the first for this species on Marion Island – confirmed that these specimens represent *C. vicina*. Further molecular analyses suggest the Marion population possibly originated from South Africa. Our observations emphasise the importance not only of strictly applying biosecurity protocols before disembarking onto the island, but also the need for increased vigilance to detect the unintentional movement of established non-native species between sites across Marion Island.

Keywords Southern Ocean · Sub-Antarctic islands · Marion Island · *Calliphora vicina* · Biosecurity

Introduction

Biodiversity loss is happening at unprecedented rates, with the effects of this decline unevenly spread across different geographic regions (Blowes et al. 2019). Multiple factors underlie biodiversity loss (see Leclerc et al. 2018 for expanded discussion), including climate change, human disturbance, biological invasions and the presence of transport corridors. As the number of non-native species that establish increases, driven in part by climate change and the increasing globalisation of human trade and movement (Vantarová et al. 2023; Seebens et al. 2025), biological invasions are considered amongst the most significant disruptors of biodiversity, ecosystem functioning, economies and even human well-being (Bellard et al. 2017; Vantarová et al. 2023; Seebens et al. 2025). While most continental landmasses, as well as tropical and temperate oceanic islands, host a notable number of alien taxa (Seebens et al. 2025),

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Published online: 10 July 2026

Antarctica (including its associated remote sub- and maritime-Antarctic islands) has been relatively unaffected, most likely owing to its isolation, limited human presence, and inhospitable environment (Frenot et al. 2005; Hughes et al. 2025; Leihy et al. 2025). However, contemporary climate change, when combined with increased human activity in the region through tourism and research, has heightened the risk of new introduction and establishment events (Duffy and Lee 2019; Hughes et al. 2020; Bokhorst et al. 2021; Dawson et al. 2022; Seebens et al. 2025).

Oceanic islands, in general, are considered particularly vulnerable to the effects of biological invasions due to their isolation and unique biodiversity (Bellard et al. 2017). Leihy et al. (2023) recently collated data for the maritime Antarctic, sub-Antarctic and more temperate oceanic islands in the Southern Hemisphere. Including terrestrial and freshwater habitats, their study suggests that there are approaching 400 species across this entire region which are classified as invasive, almost 1450 species classified as non-invasive (including transient, synanthropic, or those with restricted distributions), and approximately 1230 species reported as single records and/or without confirmation of establishment. Frenot et al. (2005), in a study restricted to Antarctica and the colder core sub-Antarctic islands, reported lower numbers of established and invasive species, although, as with Hughes et al. (2025) for the maritime Antarctic, used different and stricter criteria to identify these from the literature.

Antarctica itself currently hosts 20 non-native taxa established in the continent's natural environment, along with at least two species present synanthropically within research facilities (Hughes et al. 2025). Those in the natural environment all occur in the maritime Antarctic (i.e., the Antarctic Peninsula and Scotia Arc Archipelagos). Factors contributing to the establishment of non-native taxa in the maritime Antarctic include its relatively close proximity to South America, milder climatic conditions and high levels of human activity (Hughes et al. 2020, 2025). In contrast, the core sub-Antarctic islands currently host ~ 300 established non-native species (Frenot et al. 2005), with the introduction of many of these dating back to the onshore sealing and whaling industries of the Nineteenth and first half of the Twentieth Centuries, although new establishment events continue to be reported (e.g. Tichit et al. 2023).

The Prince Edward Island Archipelago (PEIA) comprises the larger Marion Island (MI) and smaller Prince Edward Island (PEI). These islands were first mentioned by sailors in the mid-1600s and again in the late 1700s. They experienced little human visitation until the early 1800s, when seals were first exploited for commercial gain, with regular visits that continued over the next century. During this time, several non-native plant taxa (le Roux et al. 2013) as well as the invasive house mouse, *Mus musculus*, are thought to have been introduced (Hänel and Chown 1998; Jansen van Vuuren and Chown 2007; Cooper 2008). In December 1947 and early 1948, South Africa annexed the PEIA from the United Kingdom, with its first scientific mission deployed to MI in 1965. Since annexation, a continuous, year-round, presence has been maintained on MI, including the operation of a meteorological station. In comparison, PEI has seen significantly less human activity and harbours far fewer non-native species (Greve et al. 2017, 2020).

Stringent biosecurity measures are now implemented for visitors to many Southern Ocean islands, including the core sub-Antarctic islands. The PEIA are no exception. For example, strict measures when packing and loading cargo are implemented whilst the ship is in the harbour (see Lee and Chown 2009). The standard 4.6 m^3 shipping containers used to transport and offload cargo to the island are fumigated before they are loaded on the ship. In addition, to prevent animal infestations on the ship, a so-called "boot-washing ceremony" is performed at sea before landing, which includes washing of all footwear and the manual inspection of gear and clothing (Lee and Chown 2009; Greve et al. 2017). Offloaded shipping containers are also sprayed with insecticide upon opening. However, the small size and cryptic form of many organisms and propagules can make them extremely difficult to detect, rendering even careful manual inspections unlikely to be fully effective. MI currently hosts a total of 45 known established non-native taxa, with 25 of these considered invasive (Fernández Winzer et al. 2025), while the more pristine PEI hosts only eight non-native taxa, with seven of these considered to be invasive (Greve et al. 2020).

Although awareness is today high of the importance of preventing introductions to the Southern Ocean islands generally and the PEIA specifically, less attention has been given to preventing their spread across islands once established (whether through natural means or further human-mediated assistance). Here, we document the observation on 8 May 2024 of two calliphorid blowfly individuals within the new meteorological research station on MI, and consider their possible source and means of movement to the station. The first records of calliphorid flies on MI are from April 1987, from the upper air observatory of the original meteorological station (Chown and Language 1994). In January 1988, a single specimen was collected at Ship's Cove, approximately 2.5 km north of the station (Chown and Language 1994), the most recent record of the fly anywhere in the vicinity of the station. Three to five years later, field scientists reported seeing numerous blowflies on seal carcases around Kildalkey Bay (in the south-eastern quadrant of the island), roughly 9.7 km south of the station (Chown and Language 1994). These specimens were initially identified as *Calliphora croceipalpis*, the Highveld blowfly, but this

was later changed to *C. vicina* (Hänel et al. 1998). Notably, there is no evidence that the flies became established near or at the meteorological station, nor at Ship's Cove, and they have not been observed at the new station building installed in 2010. The only extant population is therefore south of the station at Kildalkey Bay and Funk Bay.

We identified the specimens recently collected from within the new meteorological station using both morphological and molecular methods. We also generated new sequence data for blowfly specimens collected in South Africa and compared the MI specimens with those from South Africa and other available sequence data. Lastly, we discuss the presence of these flies at the meteorological station within the context of human movement around the island, and discuss the importance of preventing the intra-island transfer of non-native species.

Materials and methods

Sample collection

Two blowfly specimens were observed within the MI meteorological station (S46.87584°; E37.85857°) (Fig. 1) in May 2024. Both specimens were captured and immediately stored in absolute ethanol to enable taxonomic and molecular classification. In Johannesburg, South Africa, two additional blowfly specimens were collected using meat-baited traps to enable, in combination with publicly available global sequence data, an initial analysis of their geographic origin.

Morphological and molecular identification

Morphological examination of the specimens followed the keys of Akbarzadeh et al. (2015) and Lutz et al. (2018). Key morphological characteristics included the stem vein of the wing, the greater ampulla, the lower calypter, the

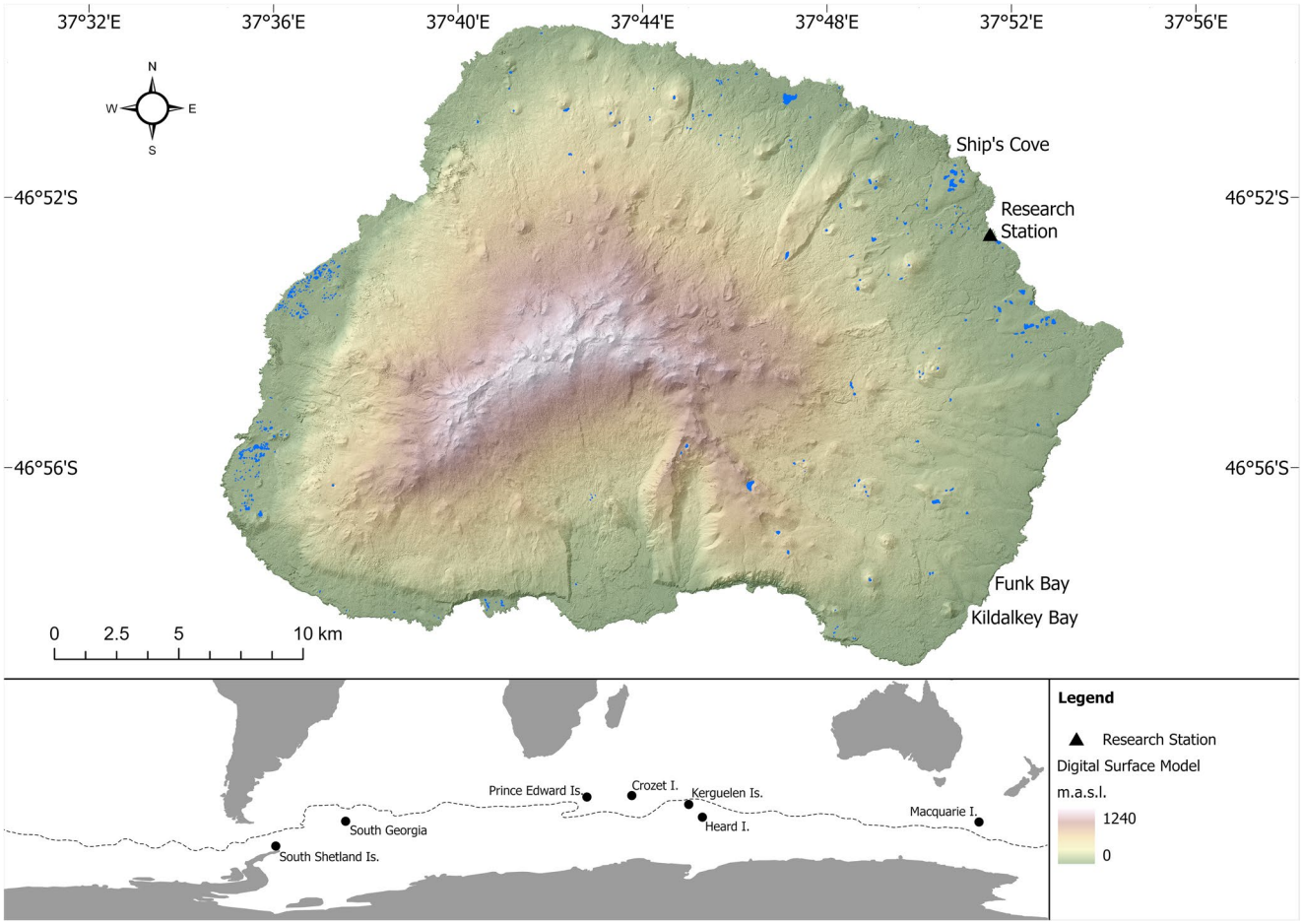

Fig. 1 Digital surface model map of Marion Island and its position (represented as Prince Edward Is. on the inset map) relative to other Antarctic and sub-Antarctic islands within the Southern Ocean near the Antarctic Polar Front (dashed line). Labels displayed on the eastern sector of the island correspond to the locations mentioned in the literature where blowfly specimens have been observed relative to the meteorological research station where the two blowfly specimens for the current study were captured

coxopleural streak, the colouration of the thorax, abdomen, genal dilation, postgena, basicosta and the anterior spiracle (Fig. S1).

Molecular identification involved the extraction of genomic DNA from a leg of each specimen using the E.Z.N.A. Tissue Kit (Omega Bio-tek, Inc., USA), following the manufacturer's recommendations, with the exception of a final elution of 80 µl. Two polymerase chain reactions (PCR) were carried out for two fragments of the mitochondrial cytochrome c oxidase subunit I gene (COI) using the primers described by Folmer et al. (1994) (LCO: GGT CAA CAA ATC ATA AAG ATA TTG; HCO: TAA ACT TCA GGG TGA CCA AAA AAT CA) and Teske et al. (2006) (CrustCOIF: TCA ACA AAT CAY AAA GAY ATT GG; PeracCOIR: TAT WCC TAC WGT RAA TAT ATG ATG). Standard reactions were carried out for each fragment containing 3 µl of a reaction buffer comprising 20 mM TRIS-HCl (pH 8.0), 100 mM NaCl, 0.1 mM EDTA, 1 mM DTT, stabilisers and 50% glycerol, 3 µl 25 mM $MgCl_2$, 3 µl 1 mM of each dNTP, 3 µl 10 µM of both the forward and reverse primers, 0.3 µl 5 units ml^{-1} Taq polymerase and 14.7 µl ddH_2O were used, giving a final reaction volume of 30 µl. DNA concentrations were assessed using a NanoDrop 2000 spectrophotometer (Thermo Scientific, USA) and approximately 20–60 ng of DNA was added for each PCR reaction. For the amplification of the LCO/HCO fragment, each PCR tube was placed into a Labnet MultiGene OptiMax thermal cycler (Labnet International Inc., USA) with the following conditions: initial denaturation for 5 min at 96 °C, 40 cycles of 30 s at 96 °C for denaturation, 30 s at 48 °C for annealing and 50 s at 72 °C for extension, followed by a final extension step at 72 °C for 10 min. For the CrustCOI/PeracCOI reaction, the conditions included an initial denaturation for 3 min at 94 °C, 35 cycles of 30 s at 94 °C for denaturation, 45 s at 47 °C for annealing and 75 s at 72 °C for extension, followed by a final extension step at 72 °C for 5 min. Amplifications were visualised using 2% agarose gel electrophoresis with 0.5X TBE buffer and the GelRed Nucleic Acid Gel Stain (Biotium, USA), and sequenced with both the forward and reverse primers on a 3730XL DNA Analyzer (Applied Biosystems, USA).

Comparison with global sequence data

The Barcode of Life Data Systems (BOLD) Identification Engine (https://id.boldsystems.org/) was used to compare the query sequences to the publicly available animal reference library. Species trees were constructed from this search using the Kimura 2-Parameter distance model, and COI sequences from representative taxa with a good geographic spread were selected and independently downloaded from GenBank (https://www.ncbi.nlm.nih.gov/genbank/). Additional specimens deposited online from publications were manually searched for in Google Scholar using the search engine keywords "*Calliphora vicina*", "barcode", "COI" and each continent name. Three outgroup taxa were downloaded from GenBank: one belonging to the same genus (*C. croceipalpis*; accession number PP595701) and two from a closely related subfamily of Calliphoridae, Luciliinae (*Lucilia richardsi*; accession number OQ611143 and *L. silvarum*; accession number OQ611440), based on the phylogeny described by Nasser et al. (2021). The electropherograms of the target sequences were visualised and checked for ambiguous bases using SnapGene Viewer (SnapGene® software (from Dotmatics; available at https://www.snapgene.com/). All sequences from the target indiv iduals were independently aligned with the ClustalW algorithm in MEGA7 (Kumar et al. 2016) and a concatenated sequence for each specimen was obtained. The complete dataset comprising the four target specimens and 44 downloaded sequences (Table S1) was then aligned using the ClustalW algorithm in MEGA7 and trimmed to achieve a dataset with sequence lengths of 858 bp, matching the partial coding gene that was sequenced for the target individuals. Phylogenetic reconstruction was done using a Bayesian Inference approach implemented in BEAST v2.7.8 (Bouckaert et al. 2014). The phylogeny construction in BEAST was carried out in two stages: first, by including all taxa displayed in Table S1 and, second, by removing the taxa that originated from Australia, USA, Colombia and one China sequence (denoted by (*) in Table S1), since these taxa formed an independent clade in the first stage. Analyses involved identifying the best-fit nucleotide substitution model using ModelFinder (Kalyaanamoorthy et al. 2017), which, based on the Bayesian Information Criterion (BIC), was TN+F+I+R2 for the complete dataset and HKY+F+I for the dataset that excluded the taxa that formed the independent clade. Using the above best-fit substitution models, three independent chains with different starting seeds for a chain length of 100 million generations, a thinning interval of 10000, and 10% burn-in to ensure that stationarity was reached was run for each dataset. Convergence was confirmed using Tracer v1.7 (Rambaut et al. 2018), trees were summarised with TreeAnnotator v2.7.8 (Bouckaert et al. 2014) with a 25% burn-in, and the resulting topologies were visualised in FigTree v1.4.4 (Rambaut 2018).

Results and discussion

Morphologically, the two MI specimens were identified as *Calliphora vicina* Robineau-Desvoidy (Diptera, Calliphoridae). Key morphological characteristics included an orange to yellow genal dilation, the black hairs on the genal dilation

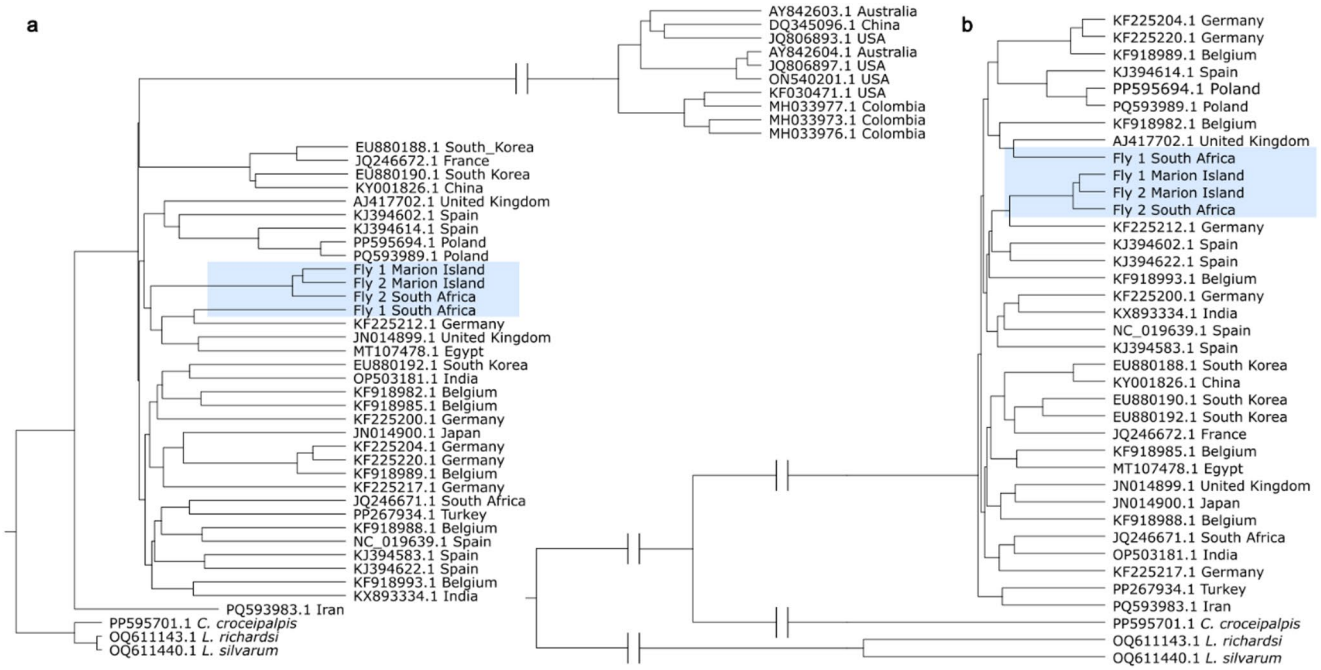

Fig. 2 Bayesian phylogenetic tree identifying the possible origin of the blowflies observed at the research station on Marion Island using (**a**) the complete dataset with sequences from a good geographic spread comprising 48 sequences, and (**b**) a phylogenetic tree which does not include the distinct clade (Australia, China, Colombia, and USA) visible in a. The shaded boxes represent the target individuals. Graphic created in Inkscape

and postgena, the greater ampulla without stiff and erect hairs, a dark lower calypter with hairs on its dorsal surface, a dark yellow basicosta, a yellow anterior spiracle, the stem vein of the wing lacking a row of hairs on the dorsal surface, the absence of the coxopleural streak, and a non-metallic thorax and dark metallic blue abdomen (Fig. S1). An 858-bp fragment of the COI gene of both MI specimens was used for phylogenetic reconstruction and, again, both the BLAST search and the BOLD Identification Engine identified these specimens as *C. vicina*.

Our sequence dataset, comprising 44 sequences freely available for download from GenBank and BOLD (see Table S1), represented much of the global distribution of *C. vicina*. After the initial phylogenetic analysis of this dataset, we removed taxa that formed an independent clade (marked with (*) in Table S1), which allowed for increased resolution of the relationships between the two MI individuals and other taxa in the dataset. The MI individuals clustered with one South African individual, with the next closest taxa originating from Germany, well-nested within a larger European clade (Fig. 2). This pattern should be interpreted with caution, as geographic inferences based on a single mitochondrial marker may be limited by low intraspecific variation, incomplete lineage sorting and the inability of a single locus to fully capture population-level structure (Maddison 1997; Funk and Omland 2003; Zink and Barrowclough 2008). In addition, the small number of MI and South African individuals included in the analysis limits our ability to draw robust conclusions regarding the source population and introduction history. Nevertheless, this assumption is consistent with the suggestion of Chown and Language (1994) that the mode of transport of the individuals that were first observed in 1987 was most likely the South African logistic support vessel.

On MI, *C. vicina* is generally associated with carcasses and other decaying matter, and is currently restricted to the area surrounding Kildalkey Bay. Here, the fly shows a preference for sheltered, nutrient-rich habitats, and is often found basking on warm rocks amongst *Poa cookii* and *Leptinella plumosa* vegetation near penguin colonies, seal aggregations and carrion, with most activity occurring during the warmest parts of the day (Chown and Language 1994). On other sub-Antarctic islands (notably South Georgia and the Kerguelen archipelago), where this species has also been introduced, it is similarly associated with carrion, generally in coastal habitats (Chevrier et al. 1997; Hänel et al. 1998; Convey et al. 2010; Laparie et al. 2016; Daly et al. 2023). On South Georgia, the species was first noted within the abandoned and now preserved Grytviken whaling station in early 2006, spreading within three years to occupy most of the coastline between Fortuna Bay and Ocean Harbour along the north-east coast of the island (no more recent distributional data are available) (Convey et al.

2010). Distributional studies on Kerguelen have confirmed its presence across a large proportion of the warmer eastern parts of the archipelago, but with a westward spread into cooler parts in recent years, putatively associated with climate warming (Chevrier et al. 1997; Lebouvier et al. 2011; Daly et al. 2023). The Kerguelen and the PEIA have comparable and relatively warm sub-Antarctic climates (Convey 2007), suggesting there is likely potential for distributional expansion on Marion Island. South Georgia, by contrast, is the coldest sub-Antarctic island, although showing considerable variation across the island, and experienced intensive industrial activity associated with multiple shore-based whaling stations in the warmer bays along the north-east coast of the Island, which are now the focus of the island's increasing tourism industry. Thus, the fly likely persists on South Georgia supported by the island's very large bird and seal populations.

Non-native species are often good dispersers (Travis and Dytham 2002; Nahrung and Swain 2015). Adult *C. vicina* are capable of strong flight, although they often remain in sheltered microhabitats during strong and frequent winds. An evolutionary trend in insects on remote islands is that of the development of brachyptery (reduced or non-functional wings) (Laparie et al. 2016; Leihy and Chown 2020), specifically in response to strong (often gale-force) winds making flight near-impossible. For instance, 19 of the 23 insect species on the Kerguelen Islands have evolved flightlessness (Laparie et al. 2016), as is also the case with the moth, *Pringleophaga marioni*, endemic to Marion Island. The fly's current spatial restriction to the south-eastern part of Marion Island is consistent with this being the primary site of establishment, on the basis of the simple wind model described by Chown and Avenant (1992), and may suggest it has experienced strong dispersal limitation away from these two coastal bays due to the strength of the prevailing wind from the north-west.

Despite the high levels of biosecurity awareness now required of station personnel and the presence of environmental inspectors with a specific responsibility for monitoring for the presence of non-native species on the island, these flies have not recently been observed in the new station or its surroundings. Researchers in multiple disciplines also regularly travel around much of the island, similarly with no reports of this fly beyond the seal and penguin breeding colonies at Kildalkey and Funk bays. While this absence of reports does not provide categorial proof of a lack of establishment, we suggest that this incident is plausibly associated with human-mediated dispersal by a field assistant who surveyed seal colonies at Funk Bay (Fig. 1) earlier the same day. Observations such as those described here underscore how routine human activities have potential to facilitate the unintentional movement of species across a remote and isolated oceanic island. Furthermore, not only is vigilance necessary for the human-facilitated dispersal of non-native taxa, but also for native species in the context of disturbing the spatial genetic structure that has been documented across the landscape (e.g. Mortimer et al. 2012; Chau et al. 2019; Monsanto et al. 2024). Similar instances, likely linked to human-assisted movement of established non-native insects to new but commonly used research or logistics sites, have been documented on South Georgia (Convey et al. 2011) and Kerguelen (Chevrier et al. 1997), both involving aggressively predatory flightless carabid beetles. Although the blowfly population on MI has been categorised as reproducing and self-sustaining (category C3 of Blackburn et al. 2011), their current threat of serious impact on the island has been considered minor (Greve et al. 2017); this may well change should the species spread across the island.

Conclusions

This study emphasises the importance of robust application of biosecurity measures, not only before disembarking onto Marion Island (see Lee and Chown 2009), but also to control the risks associated with inadvertent human-mediated intra-island dispersal. Together, observations of this type highlight important lessons for protecting other remote sub- and maritime-Antarctic islands, research facilities and conservation areas.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s00300-026-03526-6.

Acknowledgements The authors thank the National Research Foundation (NRF) South African National Antarctic Programme (SANAP) grants awarded to BJvV (NRF SANAP grant number: SANAP230501100411) and DWH (NRF SANAP grant number: SANAP230529111074). PC is supported by NERC core funding to the British Antarctic Survey's 'Biodiversity, Evolution and Adaptation' Team and travel support from the University of Johannesburg. The authors thank the Centre for High Performance Computing (CHPC) in Cape Town, South Africa, which provided an analysis platform and bioinformatics support.

Author contributions DWH and SD collected the samples, DMM conducted the laboratory and data analyses, and DWH generated the map. DMM, DWH, SD, PC, and BJvV provided substantial input in writing the manuscript, and read and approved the final manuscript.

Funding Open access funding provided by University of Johannesburg. Funding support was provided by the National Research Foundation (NRF) South African National Antarctic Programme (SANAP) grants awarded to BJvV (NRF SANAP grant number: SANAP230501100411) and DWH (NRF SANAP grant number: SANAP230529111074). PC is supported by NERC core funding to the British Antarctic Survey's 'Biodiversity, Evolution and Adapta-

tion' Team and travel support from the University of Johannesburg.

Data availability All data used in this study are publicly available through GenBank and are also provided in the Supplementary Information. Data generated specifically for the target individuals can be made available from the corresponding author upon request.

Declarations

Ethical approval Not applicable. No approval of research ethics committees was required because the study was conducted on an unregulated invertebrate species.

Competing interests The authors declare no competing interests.

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