MEMBER COUNTRY: POLAND						
National Report to SCAR for year 2021						
Activity	**Contact Name**	**Address**	**Telephone**	**Fax**	**Email**	**web site**
National SCAR Committee						
President	Piotr Głowacki	Institute of Geophysics, Polish Academy of Sciences, Księcia Janusza 64, 01-452 Warszawa, Poland	(48 22) 691 56 87	(48 22) 691 59 15	glowacki@igf.edu.pl	www.kbp.pan.pl
SCAR Delegates						
Delegate	Wojciech Majewski	Institute of Paleobiology, Polish Academy of Sciences, 51/55 Twarda st., 00-818 Warszawa, Poland	(48 22) 697 88 53	(48 22) 620 62 25	wmaj@twarda.pan.pl	www.paleo.pan.pl
Alternate Delegate	Robert Bialik	Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Department of Antarctic Biology, Pawinskiego 5a, 02-106 Warszawa, Poland	(48 22) 659 57 93	(48 22) 592 21 90	rbialik@ibb.waw.pl	www.arctowski.aq
Standing Scientific Groups						
Life Sciences						
	Katarzyna Chwedorzewska	Warsaw University of Life Sciences, Faculty of Agriculture and Biology, Nowoursynowska 166, 02-787 Warszawa, Poland	(48) 785 600 553		kchwedorzewska@go2.pl	
	Piotr Kukliński	Institute of Oceanology, Polish Academy of Sciences, Powstańców Warszawy 55, 81-967 Sopot, Poland	(48 58) 731 17 96	(48 58) 551 21 30	kuki@iopan.pl	www.iopan.gda.pl

	Maria Olech	Jagiellonian University, Department of Polar Studies and Documentation, Institute of Botany, Kopernika 27, 31-501 Kraków, Poland	(48 12) 421 02 77 ext. 26	(48 12) 423 09 49	olech@ib.uj.edu.pl	www.ib.uj.edu.pl
	Jacek Siciński	University of Łódź, Department of Invertebrate Zoology & Hydrobiology, Banacha 12/16, 90-237 Łódź, Poland	(48 42) 635 42 92	(48 42) 635 44 40	jacek.sicinski@biol.uni.lodz.pl	www.invertebrates.uni.lodz.pl/en/
Geosciences						
	Marek Lewandowski	Institute of Geophysics, Polish Academy of Sciences, Księcia Janusza 64, 01-452 Warszawa, Poland	(48 22) 691 57 64	(48 22) 691 59 15	lemar@igf.edu.pl	www.igf.edu.pl
	Monika A. Kusiak	Institute of Geophysics, Polish Academy of Sciences, Księcia Janusza 64, 01-452 Warszawa, Poland	(48 22) 691 57 49	(48 22) 691 59 15	monika.kusiak@igf.edu.pl	www.igf.edu.pl
	Wojciech Majewski	Institute of Paleobiology, Polish Academy of Sciences, Twarda 51/55, 00-818 Warszawa, Poland	(48 22) 697 88 53	(48 22) 620 62 25	wmaj@twarda.pan.pl	www.paleo.pan.pl
Physical Sciences						
	Robert Bialik	Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Department of Antarctic Biology, Pawinskiego 5a, 02-106 Warszawa, Poland	(48 22) 659 57 93	(48 22) 592 21 90	rbialik@ibb.waw.pl	www.arctowski.aq
	Adam Nawrot	Institute of Geophysics, Polish Academy of Sciences, Księcia Janusza 64, 01-452 Warszawa, Poland	(48 22) 691 58 43	(48 22) 691 59 15	anawrot@igf.edu.pl	www.igf.edu.pl

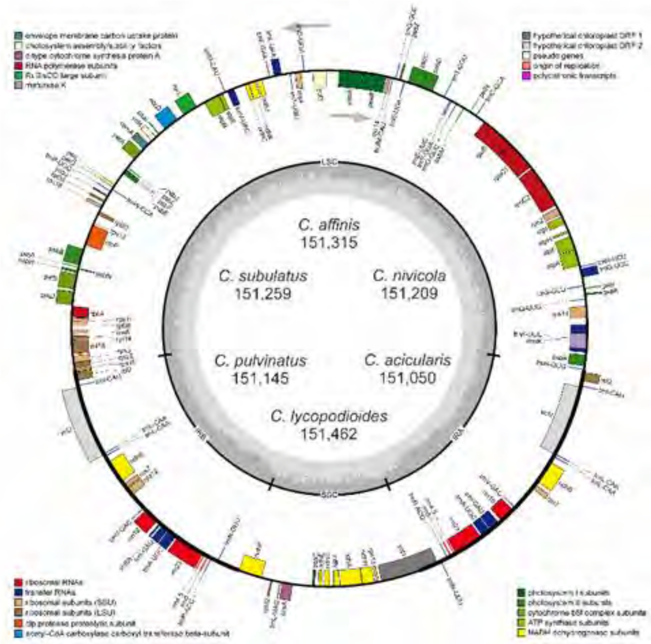
	Grzegorz Rachlewicz	Adam Mickiewicz University in Poznań, Institute of Geoecology and Geoinformation, Krygowskiego 10, 61-680 Poznań, Poland	(48 61) 829 61 83	(48 61) 829 62 71	grzera@amu.edu.pl	polar.amu.edu.pl
Activity	**Contact Name**	**Address**	**Telephone**	**Fax**	**Email**	**web site**
Scientific Research Program						
Ant-ICON						
	Małgorzata Korczak-Abshire	Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Department of Antarctic Biology, Pawinskiego 5a, 02-106 Warszawa, Poland	(48 22) 659 57 94	(48 22) 592 21 90	mka@ibb.waw.pl	www.arctowski.aq
	Adam Nawrot	Institute of Geophysics, Polish Academy of Sciences, Księcia Janusza 64, 01-452 Warszawa, Poland	(48 22) 691 58 43	(48 22) 691 59 15	anawrot@igf.edu.pl	www.igf.edu.pl
	Piotr Androsiuk	Faculty of Biology and Biotechnology, University of Warmia and Mazury, ul. Michała Oczapowskiego 1A, 10-719 Olsztyn, Poland			piotr.androsiuk@uwm.edu.pl	wbib.uwm.edu.pl
INSTANT						
	Grzegorz Rachlewicz	Adam Mickiewicz University in Poznań, Institute of Geoecology and Geoinformation, Krygowskiego 10, 61-680 Poznań, Poland	(48 61) 829 61 83	(48 61) 829 62 71	grzera@amu.edu.pl	polar.amu.edu.pl
	Wojciech Majewski	Institute of Paleobiology, Polish Academy of Sciences, Twarda 51/55, 00-818 Warszawa, Poland	(48 22) 697 88 53	(48 22) 620 62 25	wmaj@twarda.pan.pl	www.paleo.pan.pl
AntClimNow						

EXPERT GROUPS						
Geological heritage and Geoconservation	Robert Bialik	Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Department of Antarctic Biology, Pawinskiego 5a, 02-106 Warszawa, Poland	(48 22) 659 57 93	(48 22) 592 21 90	rbialik@ibb.waw.pl	www.ibb.waw.pl
Remote Sensing Group	Małgorzata Korczak-Abshire	Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Department of Antarctic Biology, Pawinskiego 5a, 02-106 Warszawa, Poland	(48 22) 659 57 94	(48 22) 592 21 90	mka@ibb.waw.pl	www.arctowski.aq
SOOS	Piotr Kukliński	Institute of Oceanology, Polish Academy of Sciences, Powstańców Warszawy 55, 81-967 Sopot, Poland	(48 58) 731 17 96	(48 58) 551 21 30	kuki@iopan.pl	www.iopan.gda.pl
SCADM						
	Katarzyna Chwedorzewska	Warsaw University of Life Sciences, Faculty of Agriculture and Biology, Nowoursynowska 166, 02-787 Warszawa, Poland	(48) 785 600 553		kchwedorzewska@go2.pl	
NATIONAL ANTARCTIC DATA CENTRE						
Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Department of Antarctic Biology, Pawinskiego 5a, 02-106 Warszawa, Poland			(48 22) 846 33 83	(48 42) 846 19 12	secretariate@ibb.waw.pl	www. ibb.waw.pl
Department of Polar Studies and Documentation, Institute of Botany, Jagiellonian University, Kopernika 27, 31-501 Kraków, Poland			(48 12) 421 02 77 ext. 26	(48 12) 423 09 49	olech@ib.uj.edu.pl	www.ib.uj.edu.pl
SCAR-MarBIN (RAMS editors)						
	Jacek Siciński	University of Łódź, Department of Invertebrate Zoology & Hydrobiology, Banacha 12/16, 90-237 Łódź, Poland	(48 42) 635 42 92	(48 42) 635 44 40	jacek.sicinski@biol.uni.lodz.pl	www.invertebrates.uni.lodz.pl/en/

	Magdalena Błażewicz	University of Łódź, Department of Invertebrate Zoology & Hydrobiology, Banacha 12/16, 90-237 Łódź, Poland	(48 42) 635 42 97	(48 42) 635 44 40	magdalena.blazewicz@biol.uni.lodz.pl	www.invertebrates.uni.lodz.pl/en/
	Katarzyna Błachowiak-Samołyk	Institute of Oceanology, Polish Academy of Sciences, Powstańców Warszawy 55, 81-967 Sopot, Poland	(48 58) 731 17 77	(48 58) 551 21 30	kasiab@iopan.gda.pl	www.iopan.gda.pl
	Piotr Kukliński	Institute of Oceanology, Polish Academy of Sciences, Powstańców Warszawy 55, 81-967 Sopot, Poland	(48 58) 731 17 96	(48 58) 551 21 30	kuki@iopan.pl	www.iopan.gda.pl
	Anna Rocka	Institute of Parasitology, Polish Academy of Sciences, Twarda 51/55, 00-818 Warszawa, Poland	(48 22) 751 17 14	(48 22) 620 62 27	abroccy@poczta.onet.pl	www.ipar.pan.pl
A BRIEF SUMMARY OF SCIENTIFIC HIGHLIGHTS:						
See the following pages						

Androsiuk P., Jastrzębski J., Paukszto Ł., Makowczenko K., Okorski A., Pszczółkowska A., Chwedorzewska K., Górecki R. & Giełwanowska I. 2020. Evolutionary dynamics of the chloroplast genome sequences of six *Colobanthus* species. *Scientific Reports* 10: 11522

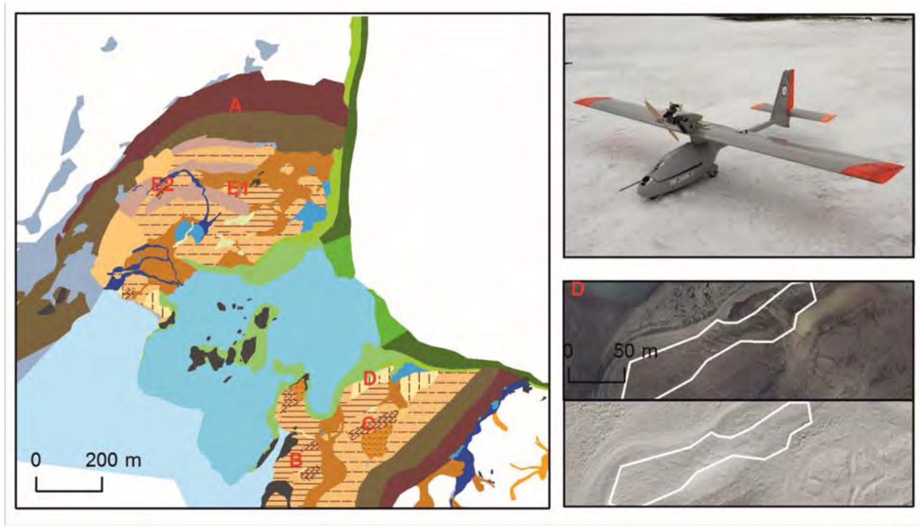
Colobanthus (Caryophyllaceae) contains about 26 species that are mainly distributed in the Southern Hemisphere. *Colobanthus quitensis*, the only representative of Dicotyledoneae in the maritime Antarctic, is the best known representative of that genus. To better understand the evolutionary relationships and mutation patterns in the chloroplast genome of *Colobanthus*, the complete plastome sequences of six species were sequenced. The chloroplast genome sequences of *C. acicularis*, *C. affinis*, *C lycopodioides*, *C. nivicola*, *C. pulvinatus* and *C. subulatus* ranged from 151 050 bp to 151 462 bp. Their typical quadripartite circular structure shares the same overall organization and gene content, with 73 protein-coding genes, 30 tRNA genes, four rRNA genes and five conserved chloroplast open reading frames (ORFs). A total of 153 repeat sequences were revealed in the plastomes of six *Colobanthus* species. The forward repeats dominated over palindromic and reverse repeats. The complementary repeats were found only in cp genome of *C. pulvinatus*. The distribution and type of SSRs were also studied. The mononucleotide SSRs were the most common, whereas hexanucleotide SSRs were detected only in *C. nivicola* and *C. pulvinatus*. Eleven highly variable regions were identified within *Colobanthus* cp genomes that could be utilized as potential markers for phylogeny reconstruction, species identification, or phylogeography of this plant group. Reconstructed phylogeny of all sequenced so far representatives of Caryophyllaceae, including eight *Colobanthus* species, is consistent with the systematic position of studied species, with the representatives of the same genus gathered in one clad. All studied *Colobanthus* species form one group with *C. lycopodioides* sharing the less similarity. The results of this study will be helpful for elucidating *Colobanthus* phylogenetic relationships.



Gene map of the six *Colobanthus* chloroplast genomes. Gene s drawn inside the circle are transcribed clockwise, and those outside are transcribed counterclockwise (indicated by arrows). Differential functional gene groups are color-coded. GC content variations is shown in the middle circle.

Dąbski M., Zmarz A., Rodzewicz M., Korczak-Abshire M., Karsznia I., Lach K.M., Rachlewicz G. & Chwedorzewska K.J. 2020. Mapping glacier forelands based on UAV BVLOS operation in Antarctica. *Remote Sensing* 12: 630.

In recent decades, hundreds of glaciers draining the Antarctic Peninsula and adjacent islands have undergone general retreat. Marginal zones of the glaciers are considered an important indicator of global climate change due to the sensitivity of polar terrestrial ecosystems and rapid proglacial modification of landscapes. We aimed to determine the area and spatial distribution of glacial and fluvioglacial landforms developed on forelands of Ecology (EGF), Sphinx (SGF) and Baranowski (BGF) glaciers, using aerial photographic images taken by a fixed-wing unmanned aerial vehicle (UAV) during the Beyond Visual Line of Sight (BVLOS) flights, followed by Geographic Information System data processing to detect and quantify the landform assemblages. We determined areas occupied by ground moraine and glacial lagoons and found out that the most profound features of EGF are the large latero-frontal moraine ridges from Little Ice Age and the first half of the 20th century. Large areas of ground moraine, frequently fluted and marked with large recessional moraine ridges, dominate on SGF. A significant percentage of bedrock outcrops and end moraine complexes characterize BGF. The landform assemblages are typical for discontinuous fast ice flow of tidewater glaciers over a deformable bed. It was inferred that ice flow velocity decreased as a result of recession from the sea coast, resulting in a significant decrease in the length of ice cliffs and decrease in calving rate. Image acquisition during the fixed-wing UAV BVLOS operation proved to be a very robust technique in harsh polar conditions of King George Island.



Geomorphological map of the Ecology Glacier foreland (left); PW-ZOOM unmanned aerial vehicle (designed, manufactured and tested at the Warsaw University of Technology in Poland) used for photogrammetric flights (upper right); ground moraine with annual push/stagnation moraines visible on orthophoto and digital elevation model (lower right)

Grzesiak J., Kaczyńska A., Gawor J., Żuchniewicz K., Aleksandrzak-Piekarczyk T., Gromadka R., & Zdanowski M.K. 2020. A smelly business: Microbiology of Adélie penguin guano (Point Thomas rookery, Antarctica). ***Science of the Total Environment*** **714: 136714.**

Adélie penguins (*Pygoscelis adeliae*) are the most numerous flightless bird group breeding in coastal areas of maritime and continental Antarctica. Their activity leaves a mark on the land in the form of large guano deposits. This guano is an important nutrient source for terrestrial habitats of ice-free Antarctic areas, most notably by being the source of ammonia vapors which feed the surrounding grass, lichen and algae communities. Although investigated by researchers, the fate of the guano-associated microbial community and its role in decomposition processes remain vague. Therefore, by employing several direct community assessment methods combined with a broad culture-based approach, we provide data on bacterial numbers, their activity and taxonomic affiliation in recently deposited and decayed Adélie penguin guano sampled at the Point Thomas rookery in maritime Antarctica (King George Island). Our research indicates that recently deposited guano harbored mostly bacteria of penguin gut origin, presumably inactive in cold rookery settings. This material was rich in mesophilic enzymes active also at low temperatures, likely mediating early stage decomposition. Fresh guano colonization by environmental bacteria was minor, accomplished mostly by ammonia scavenging *Jeotgalibaca* sp. cells. Decayed guano contained 10-fold higher bacterial numbers with cold-active enzymes dominating the samples. Guano was colonized by uric-acid degrading and lipolytic *Psychrobacter* spp. and proteolytic *Chryseobacterium* sp. among others. Several spore-forming bacteria of penguin gut origin persisted in highly decomposed material, most notably uric-acid fermenting members of the Gottschalkiaceae family.

Point Thomas penguin rookery (left); Bacteria in penguin guano stained with a fluorescent dye (top); Bacterial phyla detected in penguin guano (bottom); *Jeotgalibaca* sp. (red) growing on the metabolites secreted by *Psychrobacter* sp. (cream) growing on uric acid (right).

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