INVESTIGANDO LAS ADAPTACIONES FUNCIONALES DE ORGANISMOS A AMBIENTES EXTREMOS

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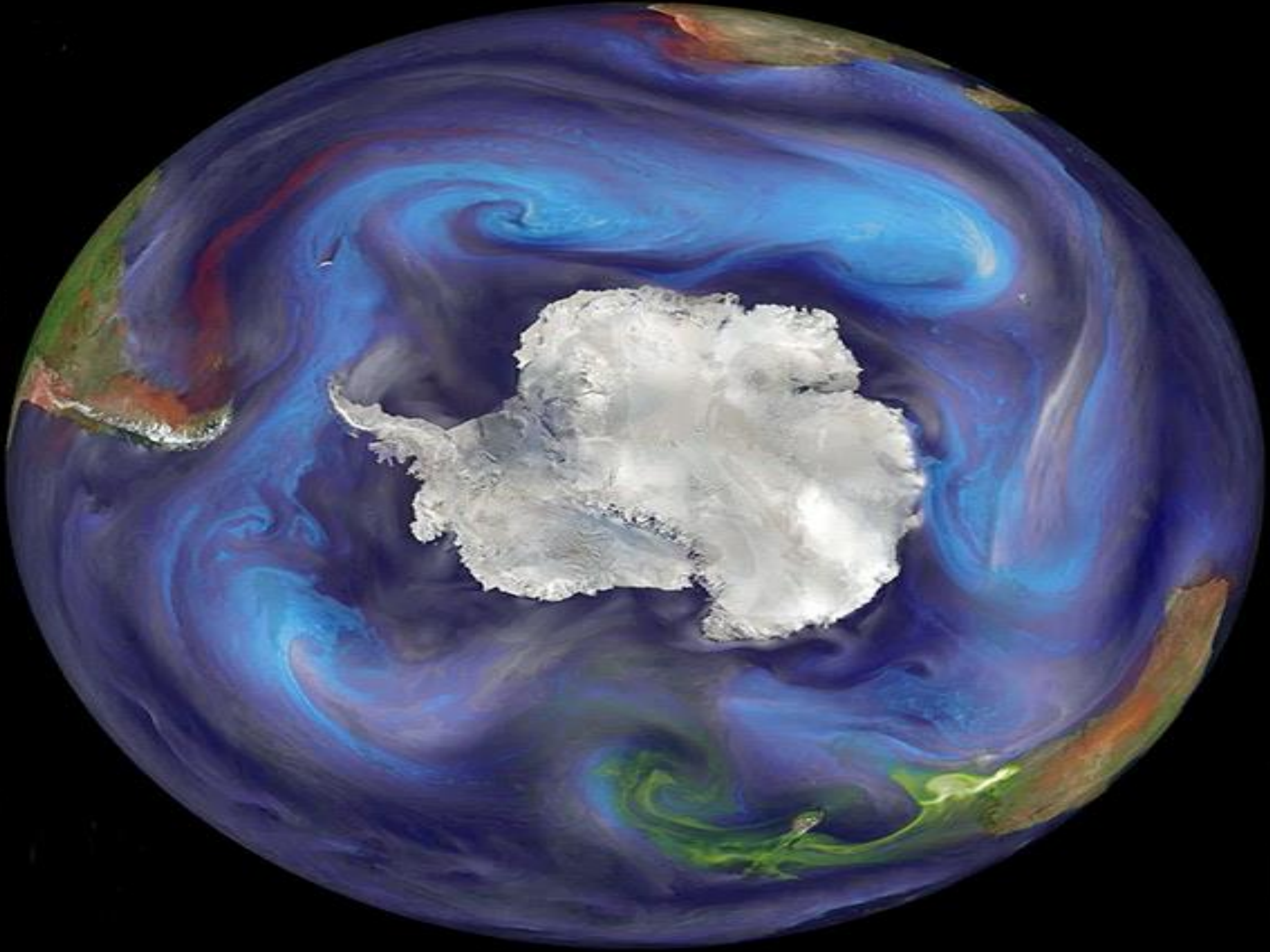
Instituto Antártico Chileno



En los océanos polares la investigación científica a revelado la existencia de mecanismos únicos en la adaptación biológica en ambientes fríos.

Algunos ejemplos:

Moléculas anticongelantes presentes desde bacterias a peces.

Adaptación al frío del proceso de polimerización de microtúbulos.

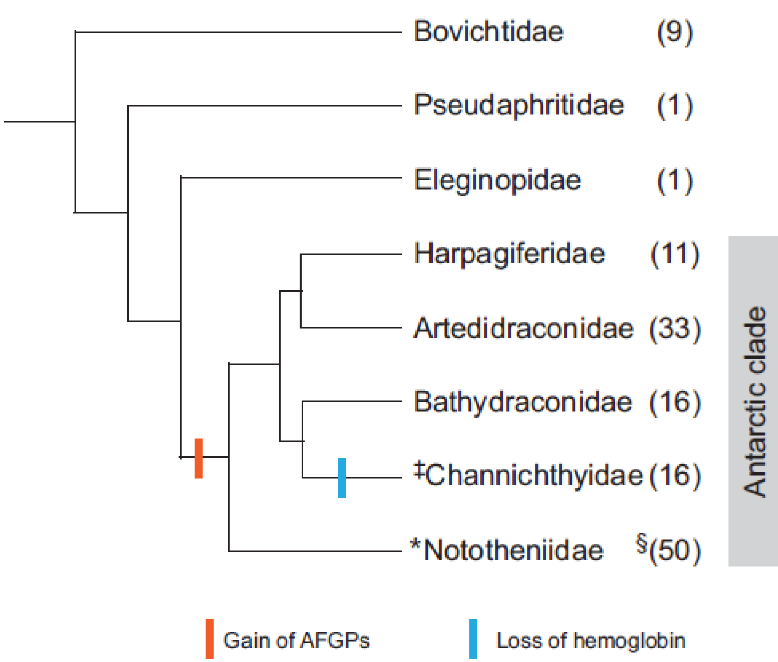
Baja actividad específica enzimática de bombas iónicas.

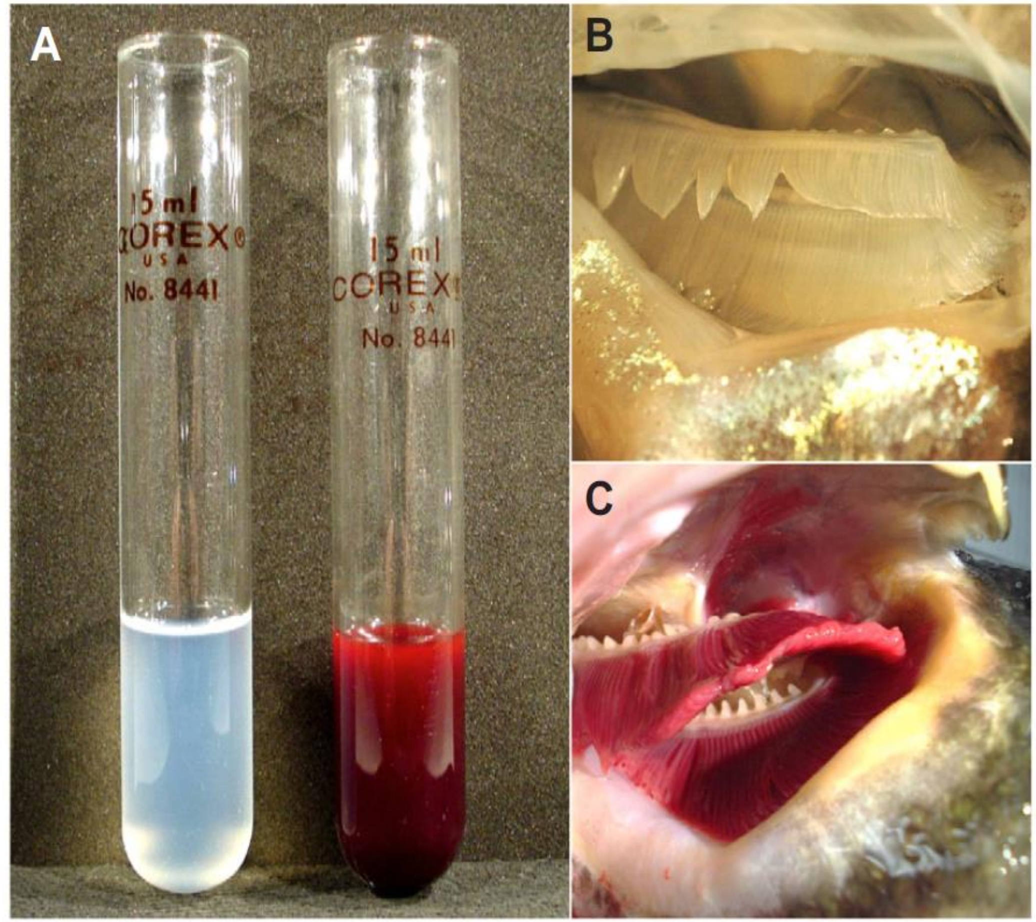
Pérdida de pigmentos respiratorios.

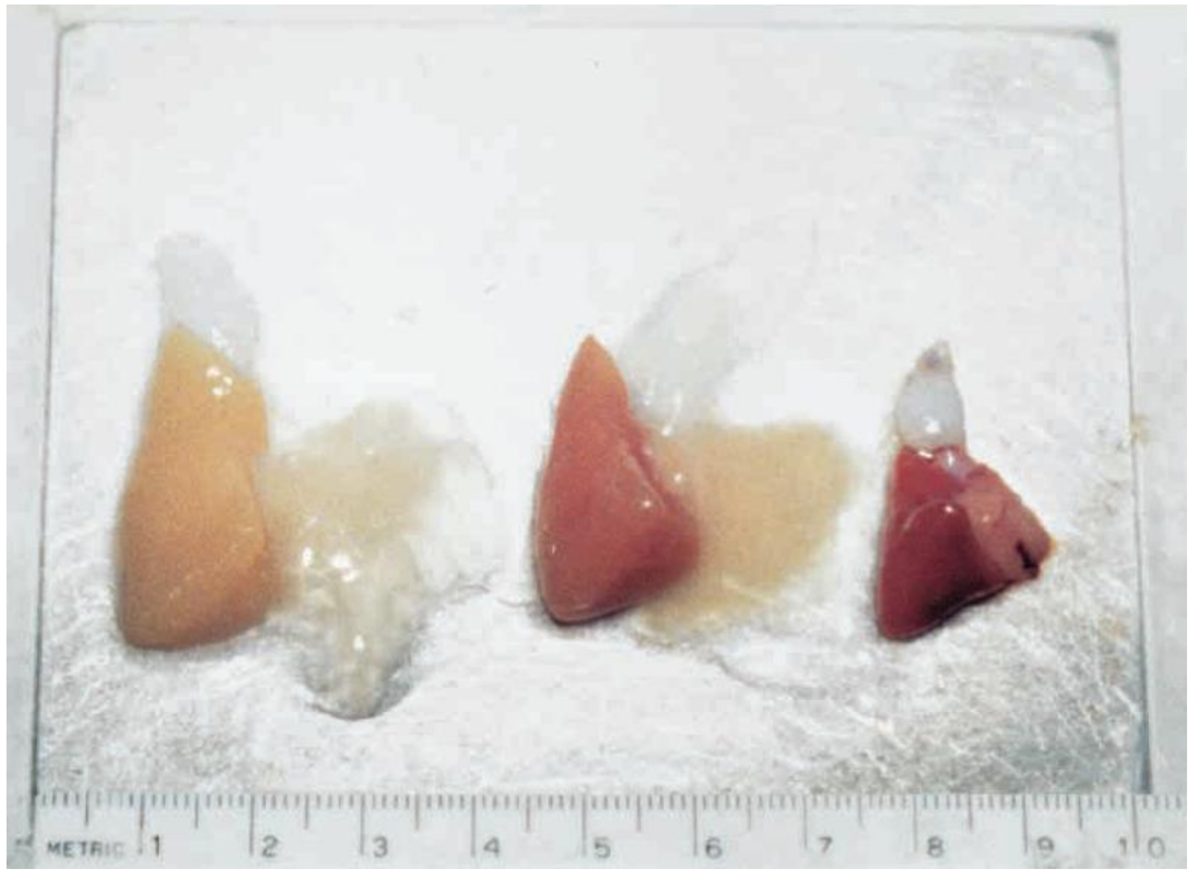
Pérdida de proteínas inducibles de estrés térmico (Heat Shock Protein).

PECES ANTÁRTICOS SIN HEMOBLOGINA

Chaenocephalus aceratus







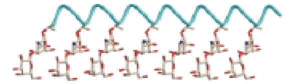
T. J. MOYLAN AND B. D. SIDELL, The Journal of Experimental Biology 203, 1277–1286 (2000).

PROTEINAS ANTICONGELANTES (AFP)

Diversidad de las AFPs

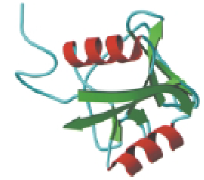
- Proteínas anticongelantes[1,2] secuencia y estructura
  - Peces
    - AFGP
    - AFP
      - Tipo I
      - Tipo II
      - Tipo III
      - Tipo IV
  - Insectos
    - Tm y Dc
    - Cf

CfAFP



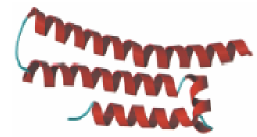
AFGP

AFP tipo I

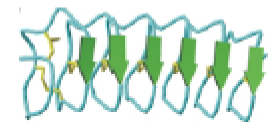


AFP tipo II

AFP tipo III



AFP tipo IV



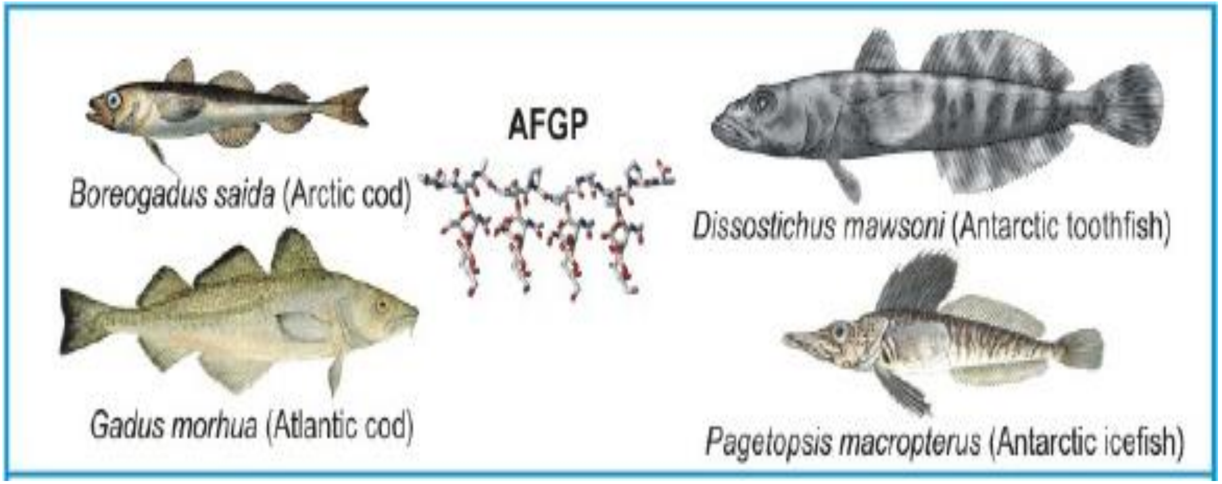
TmAFP

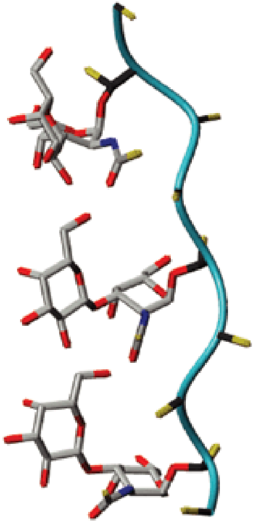
Propiedades de las AFPs en insectos[1]

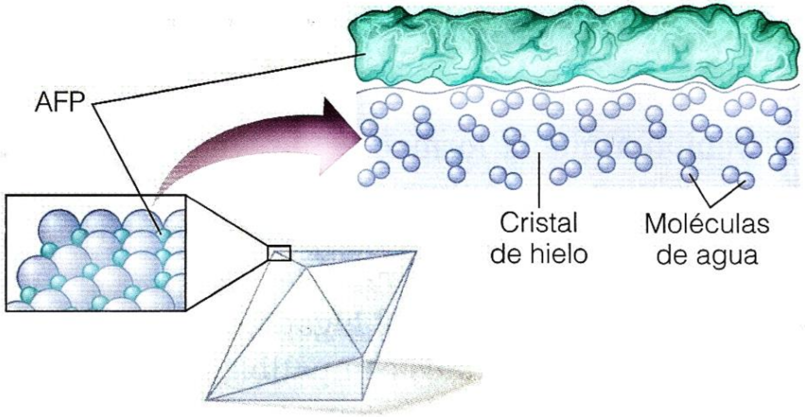
	Escarabajo de fuego	**Gusano de la harina**	**Gusano de brotes de abeto**
Masa Mol. (kDa)	8.7	8.4	9.0
Estruc. Prim.	T+C 12/13 residuos	T+C 12 residuos	S+T
Estruc. Secund.	β-Hojas	β-Hojas	β-Hojas
Estruc. Terciar.	β-Hélices	β-Hélices	β-Hélices
Biosintesis	Pre-proteína	Pre-proteína	Pre-proteína
Heterogeneidad	Isoformas **13**	Isoformas **9**	Isoformas **4**
Genes homolog.	Inhibidor tripsina	Inhibidor tripsina	Inhibidor tripsina

1.Jia, Z.; Davies, P.L.. Trends Biochem Sci. 2002, 27,101.
2.Barrett, J. Int J Biochem Cell Biol. 2001, 33, 105.

Glico-proteínas anticongelantes AFGP

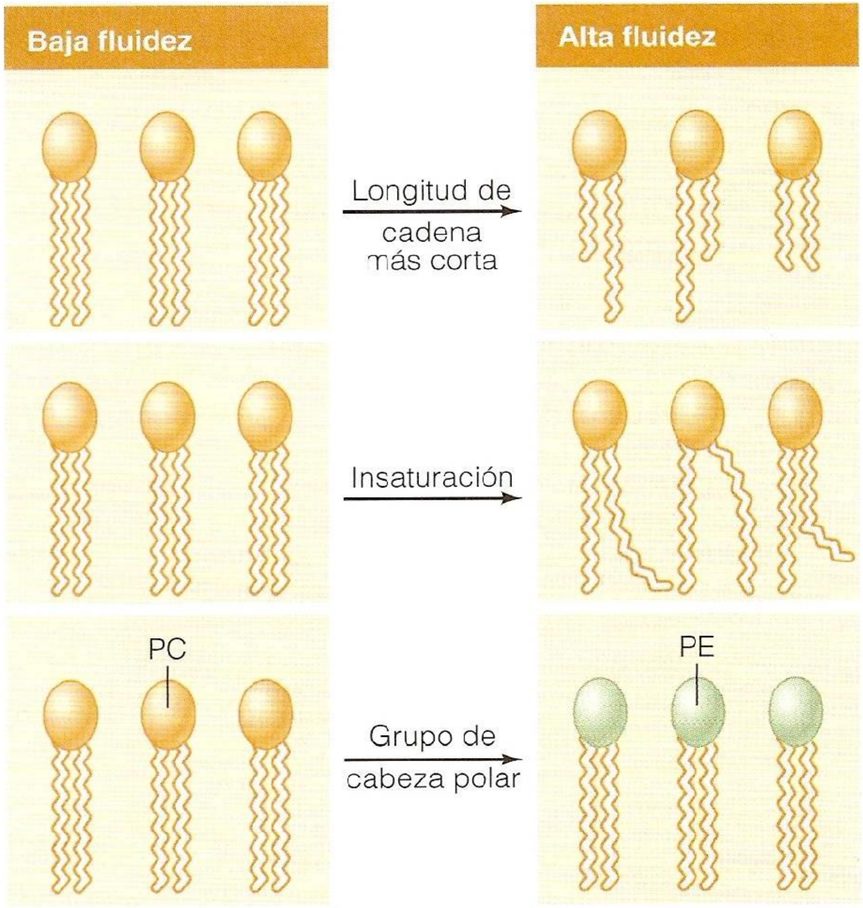






Bacalao ártico
Bacalao atlántico
Pez diente antártico
Pez hielo antártico

PROPIEDADES DE LOS FOSFOLIPIDOS Y LA FLUIDEZ DE LA MEMBRANA



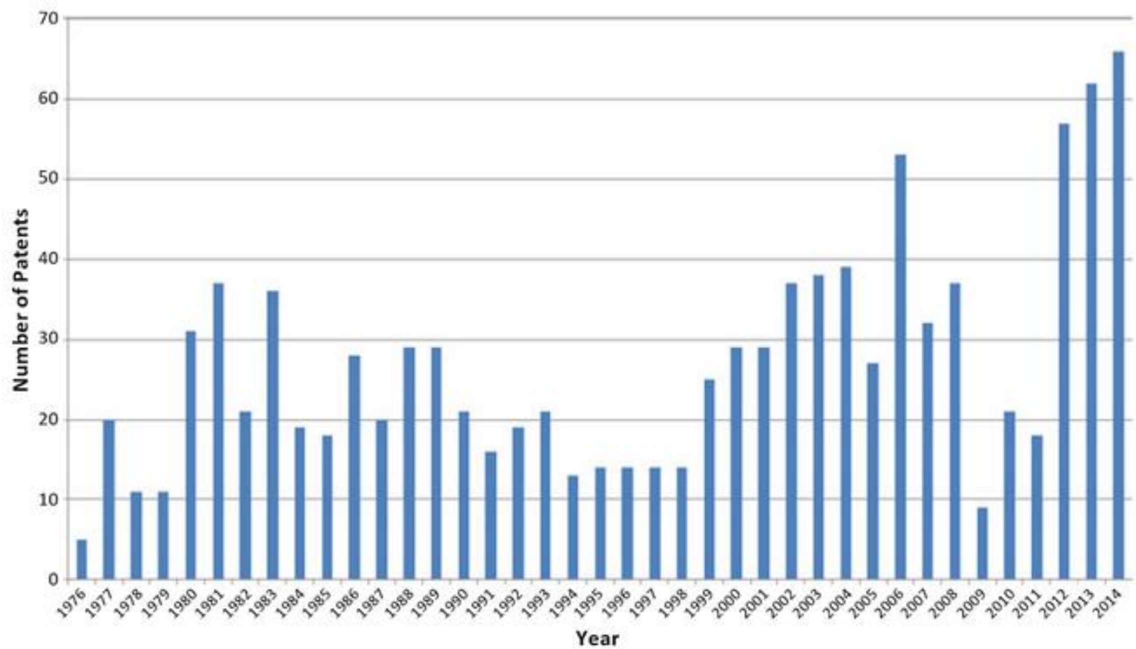


Fig. 11.6 Number of krill-related patents lodged from 1976 to 2014 (Data from the krill patent database presented in Foster et al. (2011) updated in March 2014)

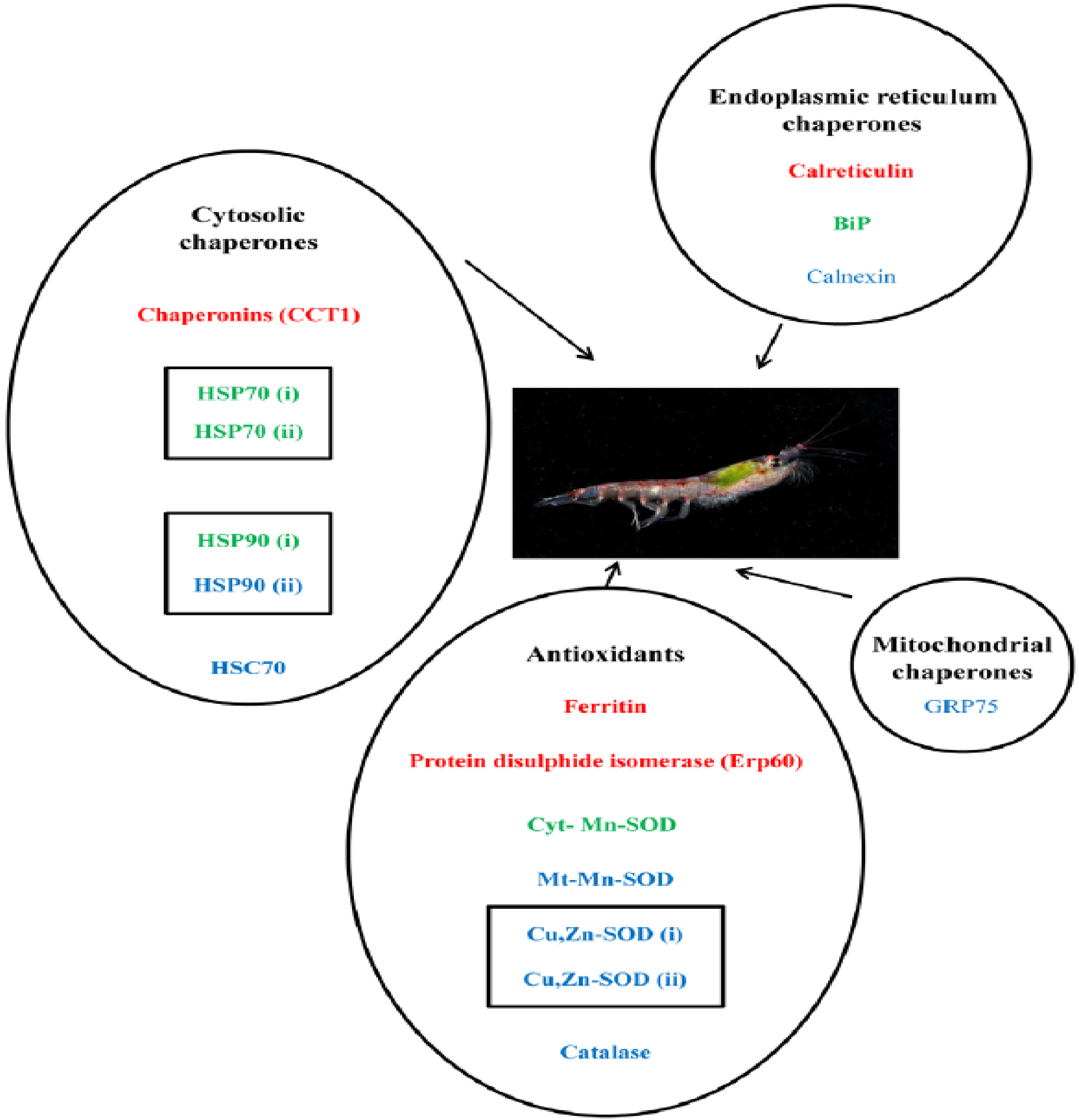


Figure 5. Summary of most highly expressed chaperone and ''stress'' transcripts in *E. superba*. Picture of *E. superba* from the Bellingshausen Sea continental shelf, taken onboard RRS James Clark Ross cruise JR230 (benthic pelagic coupling cruise) by Pete Bucktrout (British Antarctic Survey). Gene names in red = 400+ copies in the transcriptome data, Green = 200–400 gene copies and blue = less than 200 gene copies. Genes labelled (i) and (ii) plus boxed in the diagram are duplicated genes and their analysis fully described in the main text.
doi:10.1371/journal.pone.0015919.g005

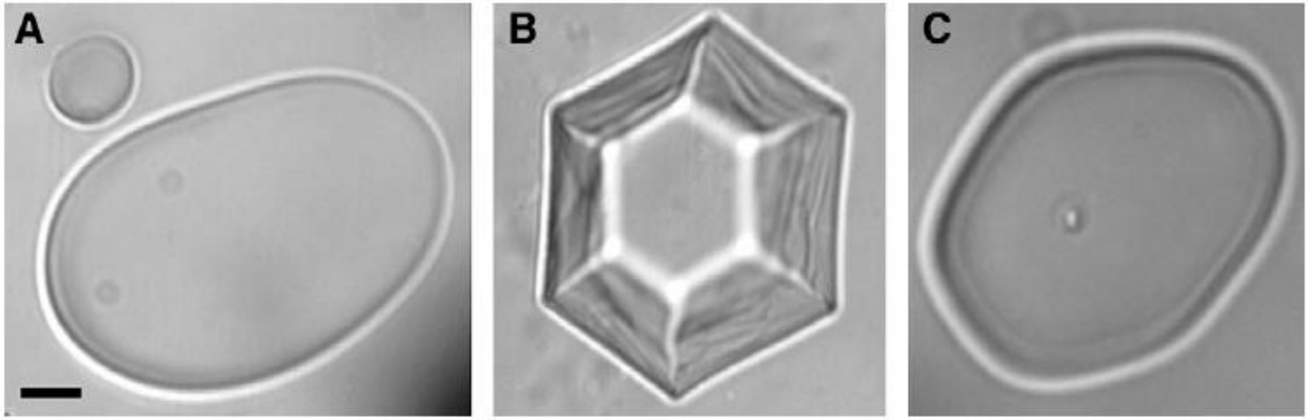
Clark et al., 2011. PlosOne

LA PLANTA QUE MUEVE A LA CIENCIA EN CHILE:
Deschampsia antartica.

Moléculas anticongelantes

Compuestos fotoprotectores

Enzimas: lipasas y proteasas



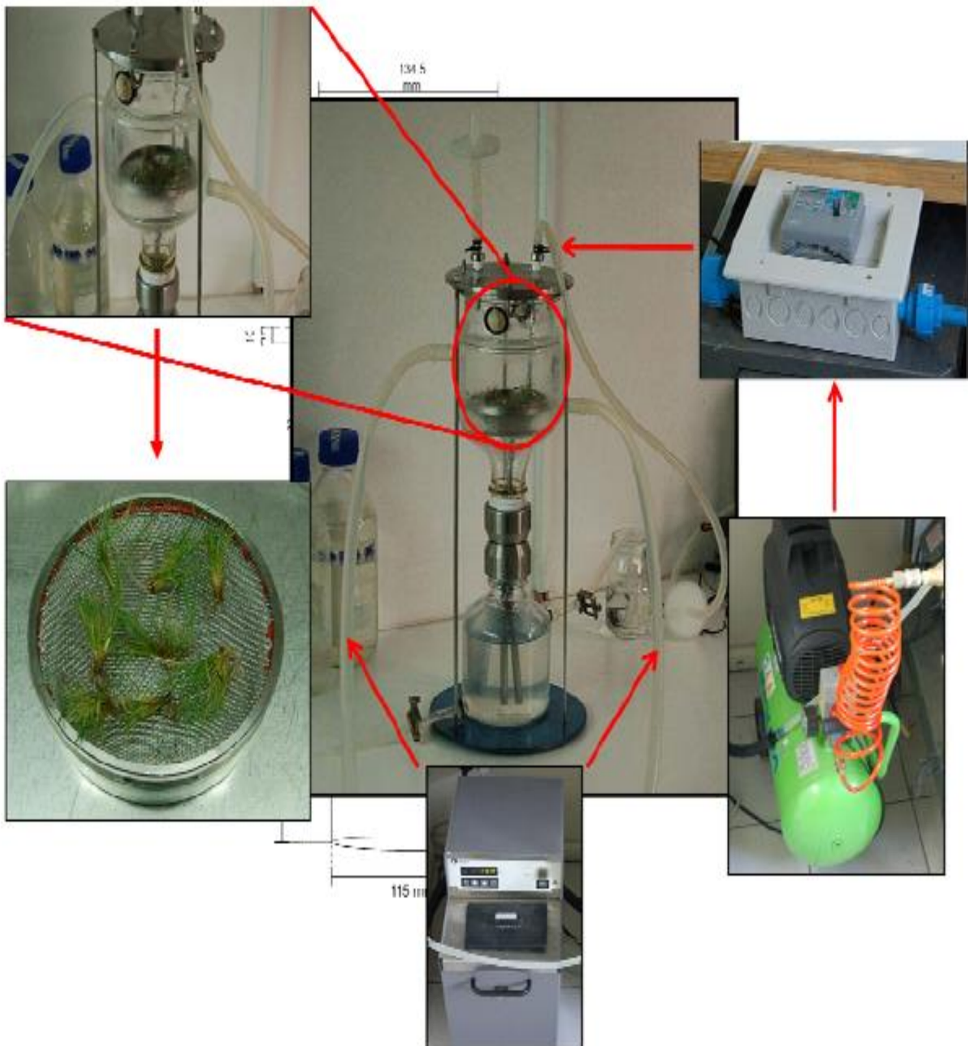
Deschampsia antarctica, desarrollo de un sistema de propagación in vitro.

Material vegetal

Fotos tomadas por Hans Kohler. En A *D. antarctica* en la ECA XLIX, año 2013 en la Peninsúla de Fildes. En B *D. antarctica* en cultivo in vitro de acuerdo a Zamora y col, 2010. En C la micropropagación de *D. antarctica* en el laboratorio de Fisiología y Biotecnología Vegetal en Usach.

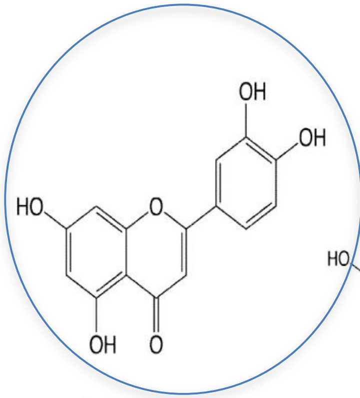
Zamora P. Rasmussen S, Pardo A, Prieto H and Zúñiga, G.E. (2010) Antioxidant responses of in vitro shoots of Deschampsia antarctica to Polyethylene glycol treatment. Antarct Sci 22:163-169

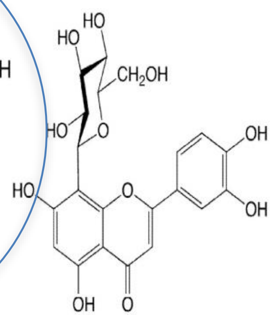
Desarrollo de un bioreactor que permite aplicar radiación UV-B a las plantas

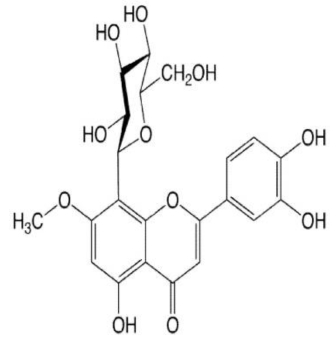


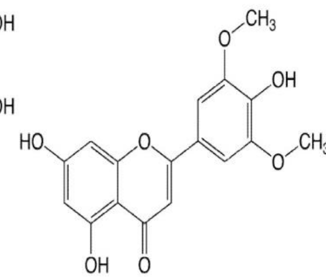
United States Patent Application 20130344528

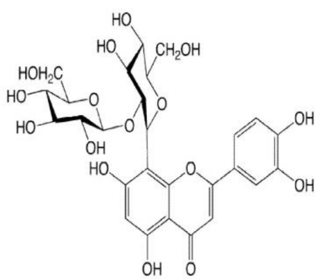
Ejemplos de moléculas identificadas en *Deschampsia antarctica*

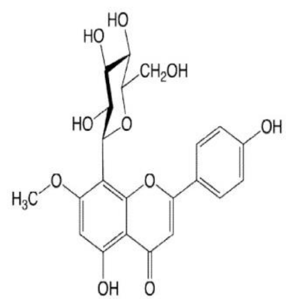

Luteolina

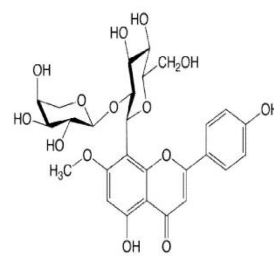

Orientina

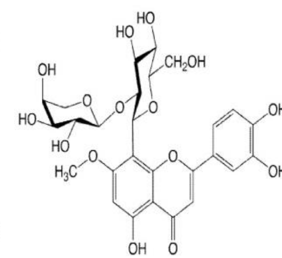

Isoswertiajaponina

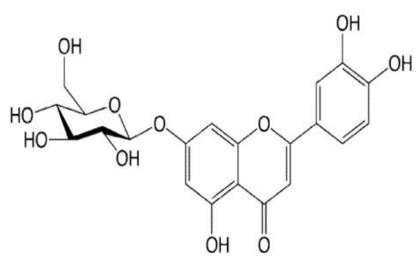

Tricina


Orientina 2′′-O-glucopiranosido


Isoswertisina


Isoswertisina 2′′-O-arabinopiranosido


Isoswertiajaponina 2′′-O-arabinopiranosido


Luteolina-7-*O*-glucósido

Colobanthus quitensis

Colobanthus quitensis cultivado in vitro. En b se observa que esta planta florece.

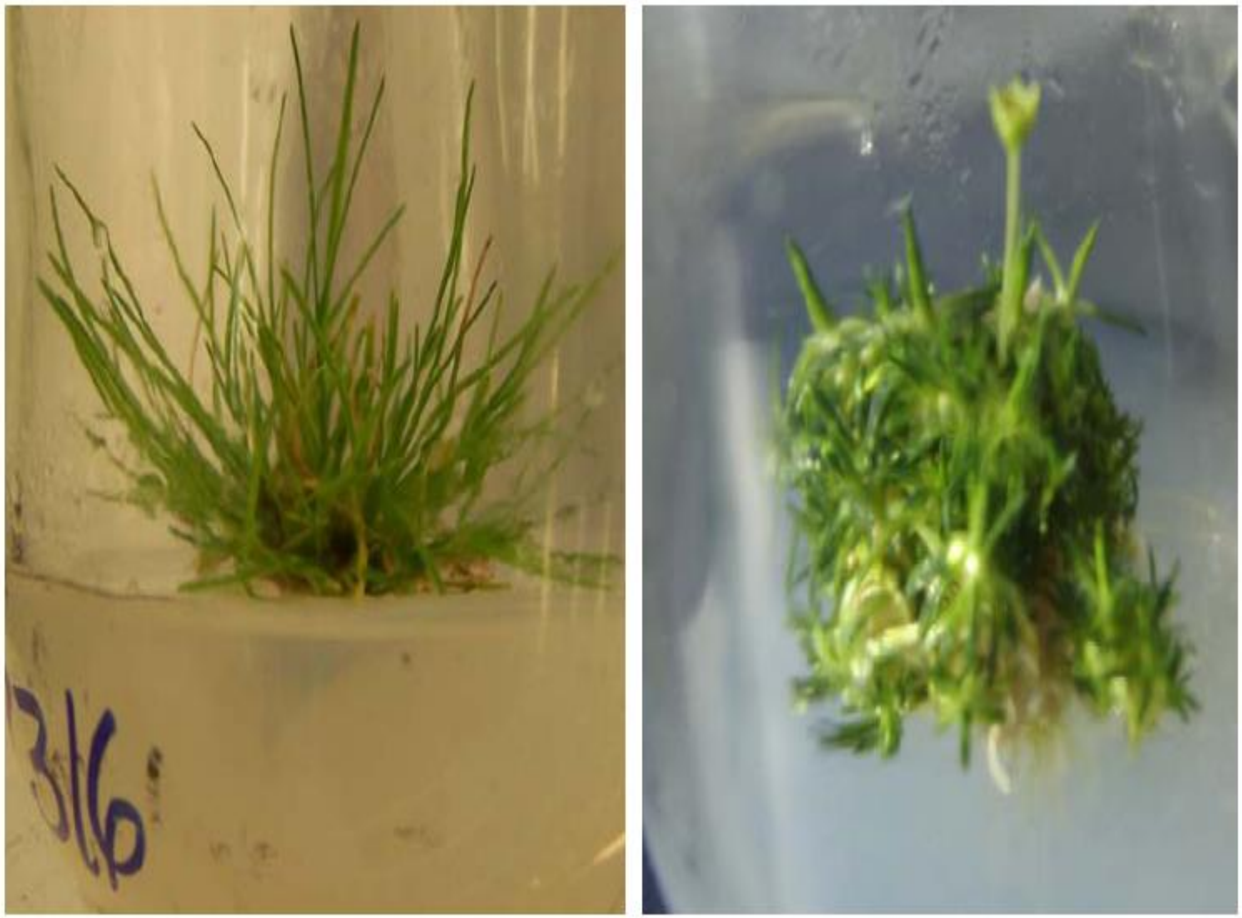
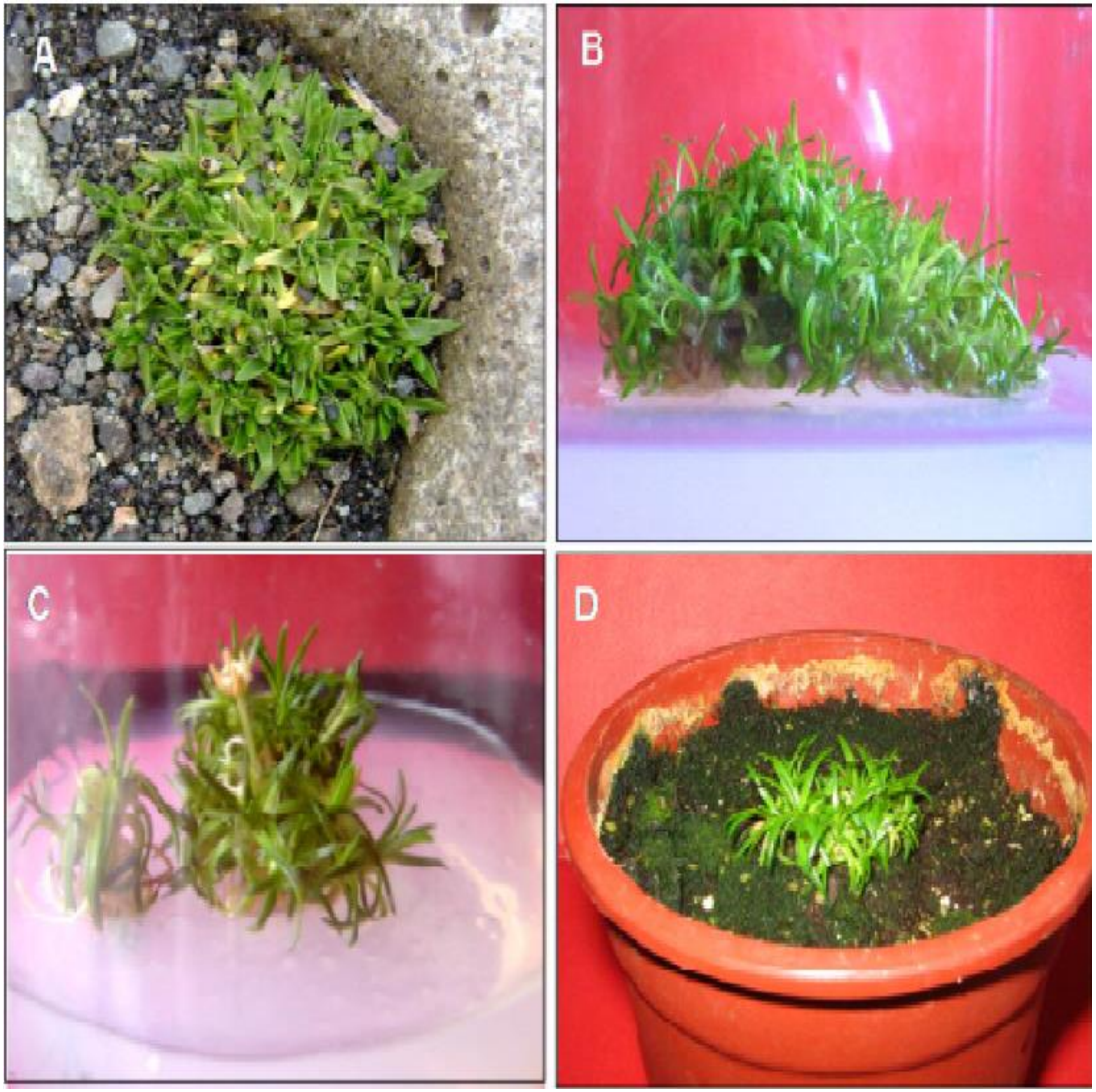
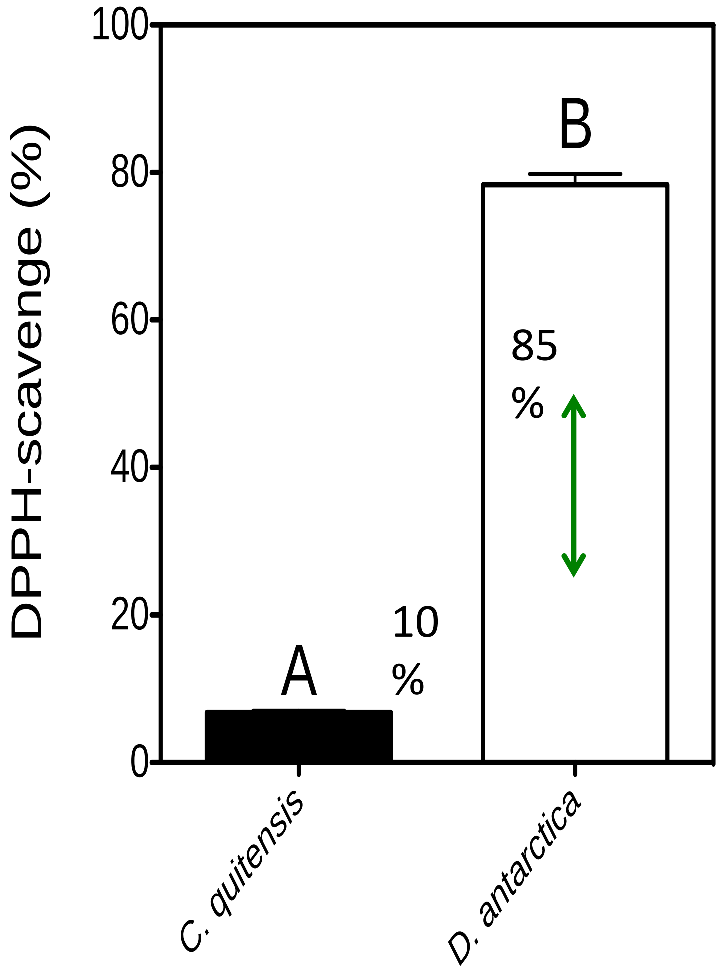
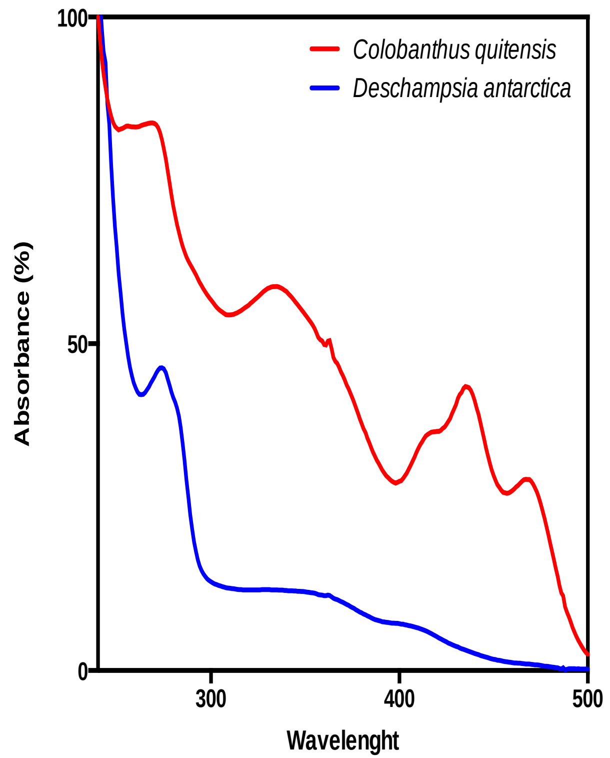


Figura 5. Cultivos *in vitro* de *D. antarctica y C. quitensis*

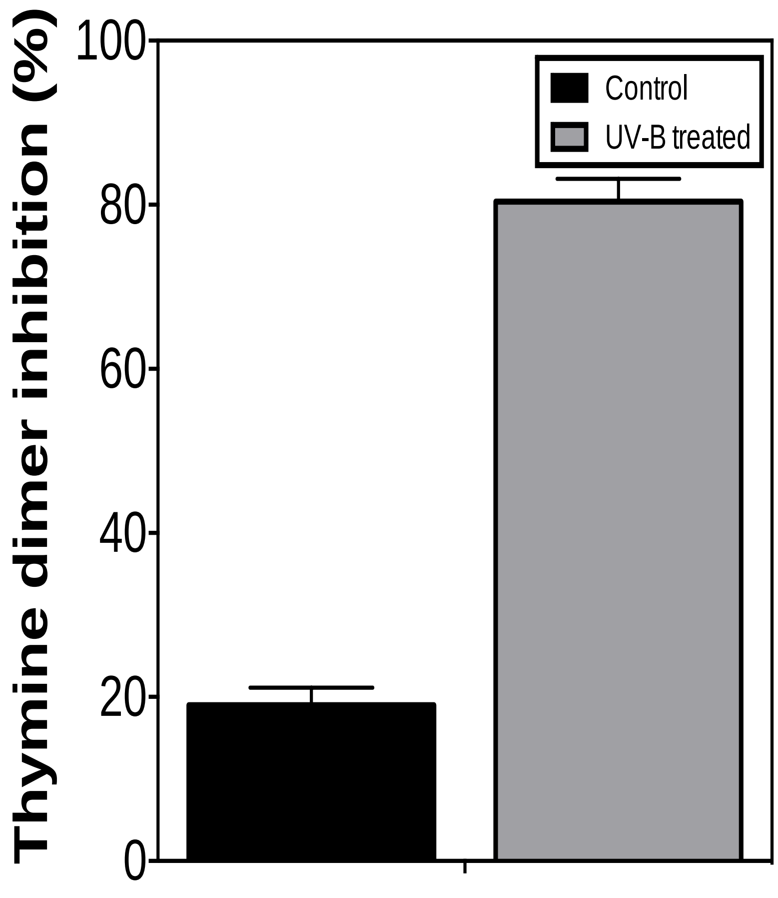
Ciclo completo de *C. quitensis* en condiciones de Laboratorio



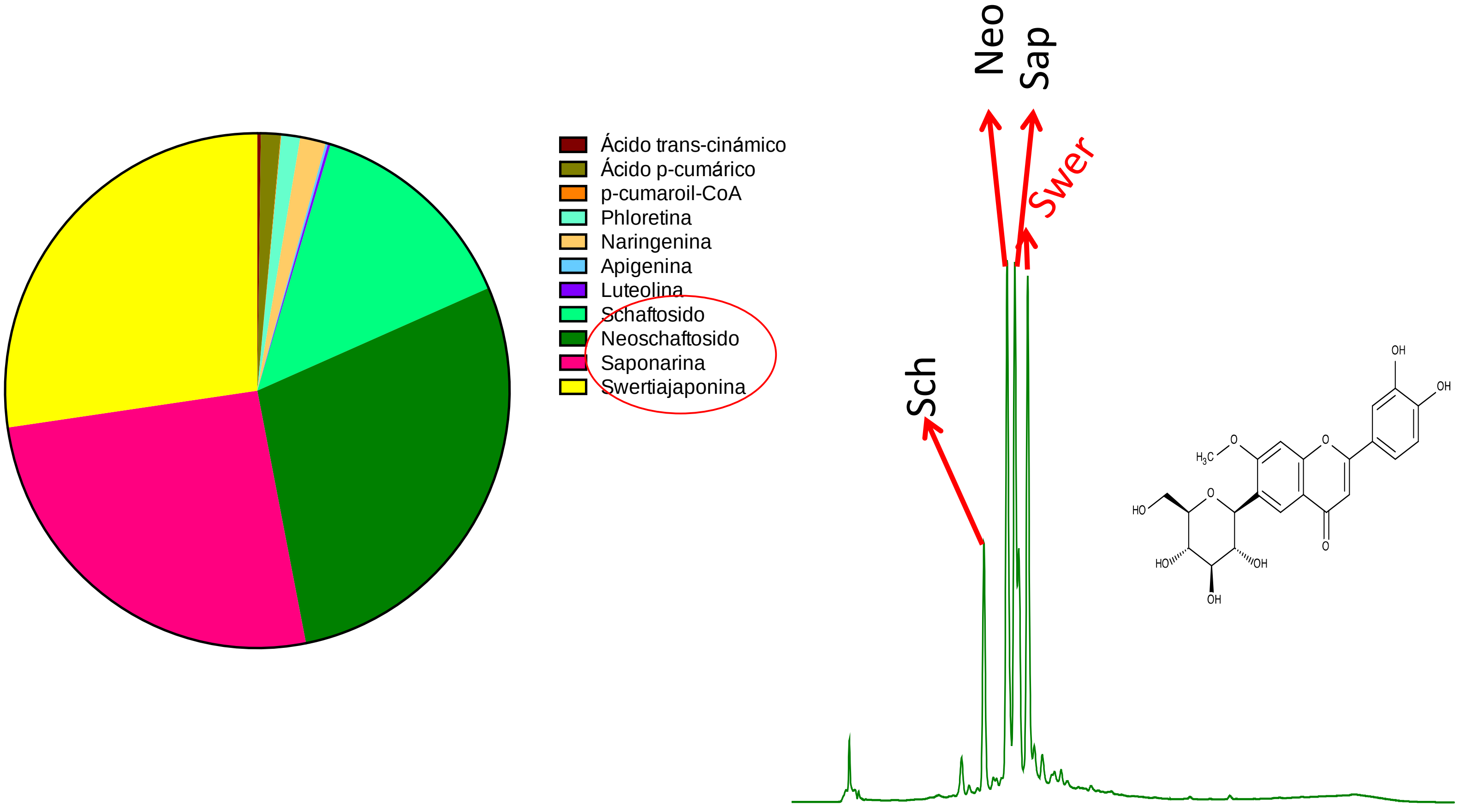

DPPH-scavenge (%)
100
80
60
40
20
0
A
B
10
%
85
%
C. quitensis
D. antarctica


Colobanthus quitensis
Deschampsia antarctica
Absorbance (%)
100
50
0
300
400
500
Wavelenght

Plantas de *C.quitensis* sometidas a radiación UV-B generan moléculas que protegen al DNA celular, al inhibir la formación de dímeros de timina.

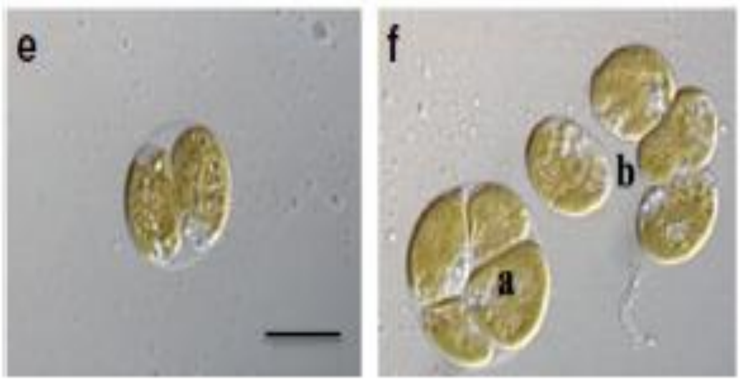


Moléculas identificadas en *C. quitensis*




Facultad
Química y Biología

Ecophysiology of Antarctic snow algae: adaptation mechanisms to a changing polar environment. Ivan Gomez. UACH. Fondecyt Regular. 2016-2019.



Rivas *et al. Revista Chilena de Historia Natural* (2016) 89:7
DOI 10.1186/s40693-016-0050-1

Revista Chilena de Historia Natural

RESEARCH **Open Access**

CrossMark

Photosynthetic UV stress tolerance of the Antarctic snow alga *Chlorella* sp. modified by enhanced temperature?

C. Rivas[1,2*], N. Navarro[1,3], P. Huovinen[1,4] and I. Gómez[1,4]

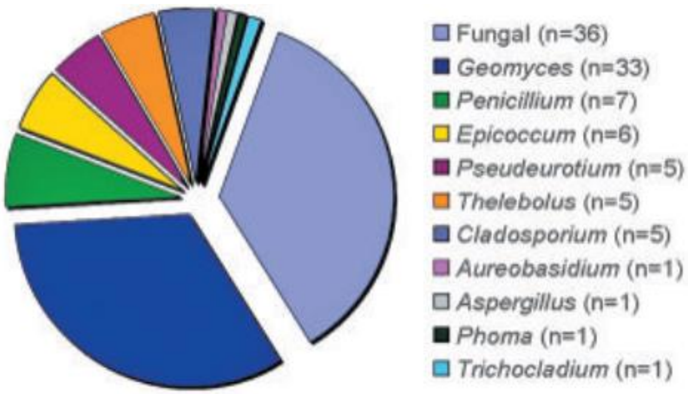
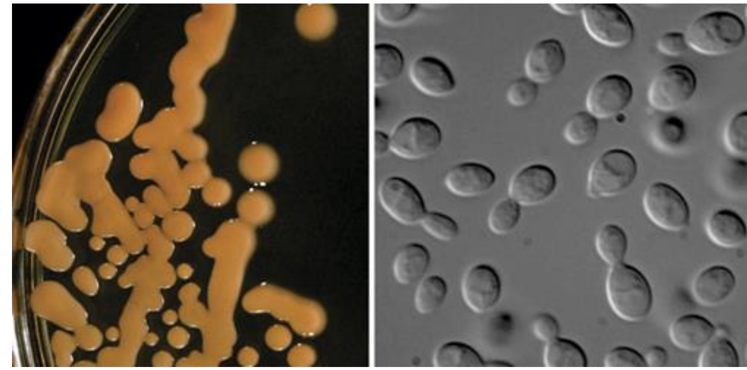


Figura 1. Gráfico de distribución de los géneros fúngicos encontrados en las esponjas marinas antárticas. Se observa que los aislados pertenecientes al género *Geomyces* y sus parientes Fungal sp. son los más abundantes.

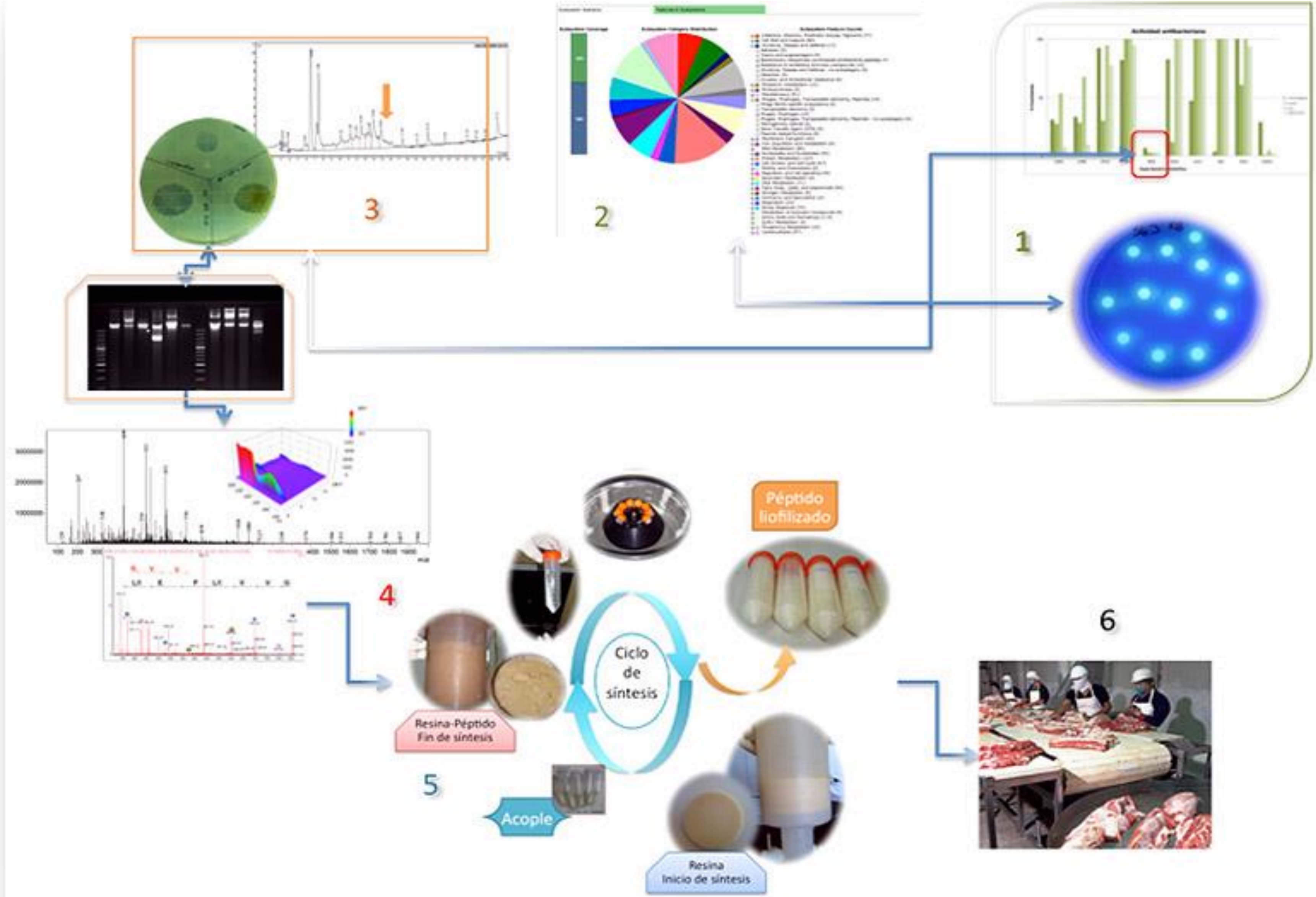


Rhodotorula portillonensis sp. Nov. Laich et al., 2013. Int J Syst Evol Microbiol.

Tedania sp

Dendrilla sp

Cultivable psychrotolerant yeasts associated with Antarctic marine sponges. Vaca et al., 2012. World J Microbiol Biotechnol



1. Selección de bacterias con actividad antibacteriana contra bacterias tipo y bacterias multirresistentes.
2. Secuenciación Genoma: obtención secuencias, rutas de síntesis.
3. Purificación por medio de HPLC y TLC de moléculas activas.
4. Caracterización de masa y huella peptídica.
5. Síntesis péptidos regiones activas y modelamiento bioinformático
6. Ensayos actividad sobre bacterias patógenas y pruebas en plantas frigoríficas

Electronic Journal of Biotechnology 17 (2014) 1–5

Contents lists available at ScienceDirect

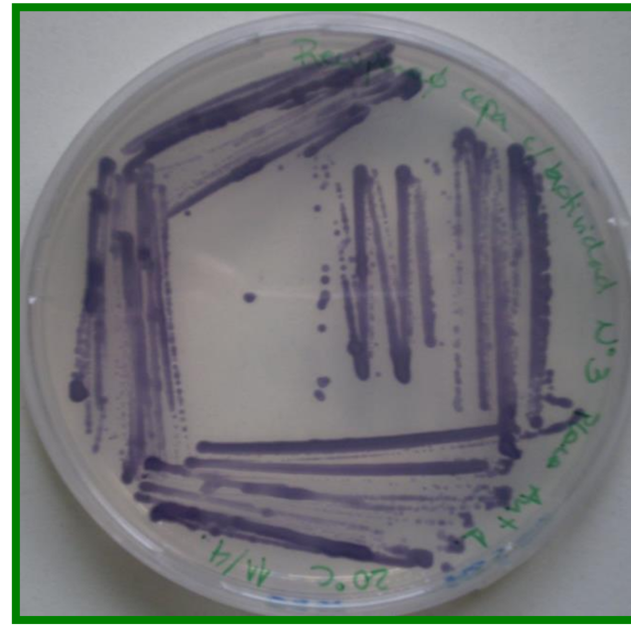
Electronic Journal of Biotechnology

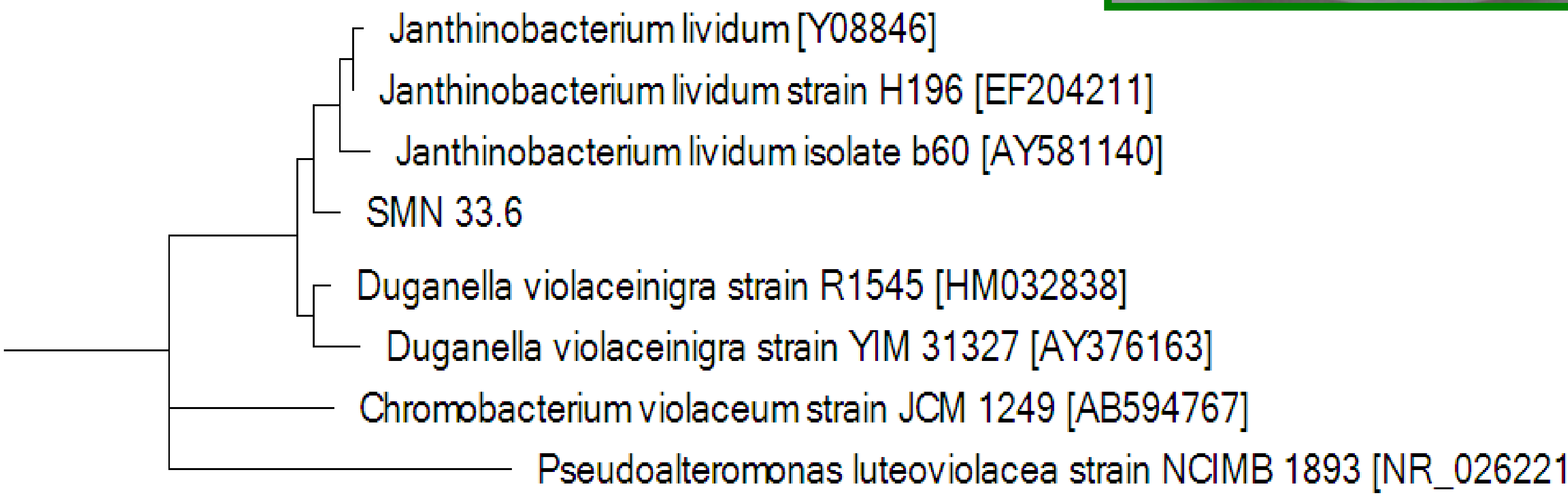
Antibacterial activity of the Antarctic bacterium *Janthinobacterium* sp. SMN 33.6 against multi-resistant Gram-negative bacteria

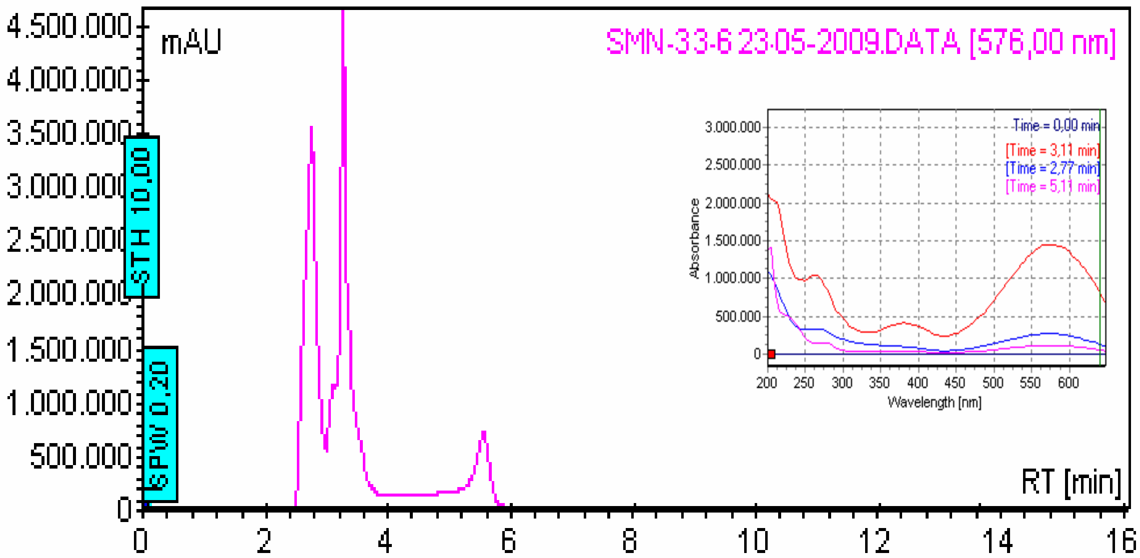
CrossMark

Geraldine Asencio [a], Paris Lavin [a], Karen Alegría [b], Mariana Domínguez [b], Helia Bello [b], Gerardo González-Rocha [b], Marcelo González-Aravena [a,*]

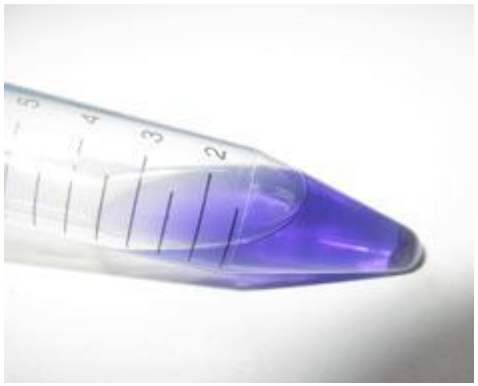
[a] Laboratorio de Biorrecursos Antárticos, Departamento Científico, Instituto Antártico Chileno, Plaza Muñoz Gamero 1055, Punta Arenas, Chile
[b] Laboratorio de Investigación en Agentes Antibacterianos, Departamento de Microbiología, Facultad de Ciencias Biológicas, Universidad de Concepción, Victor Lamas 1290, Concepción, Chile

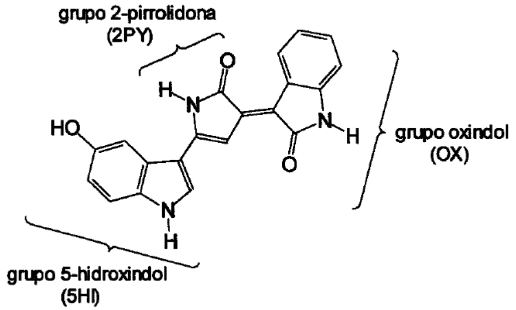






mAU
SMN-33-6 23-05-2009.DATA [576,00 nm]
STH 10,00
SPW 0,20
RT [min]
Time = 0,00 min
[Time = 3,11 min]
[Time = 2,77 min]
[Time = 5,11 min]
Absorbance
Wavelength [nm]



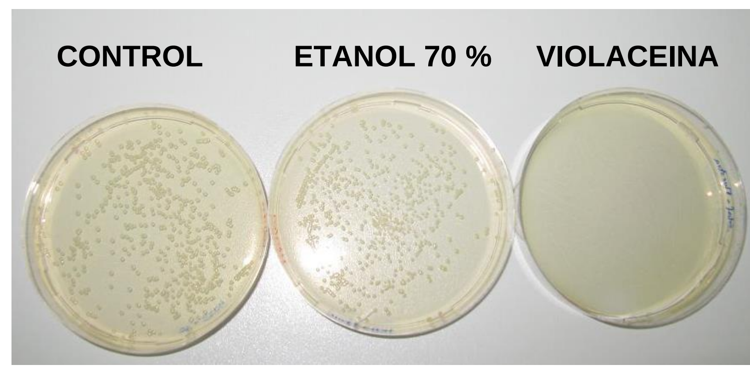


grupo 2-pirrolidona
(2PY)
grupo oxindol
(OX)
grupo 5-hidroxindol
(5HI)

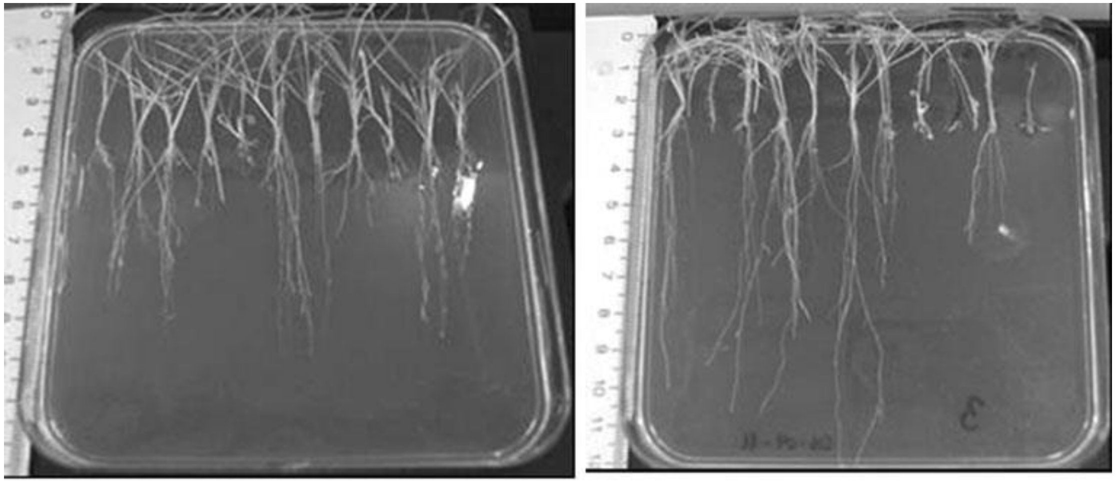
Table 1
In vitro determination of the minimum inhibitory concentration (MIC) and the minimum bactericidal concentration (MBC) of ethanol extract of the strain *Janthinobacterium* sp. SMN 33.6 against multi-resistant nosocomial isolates.

Multi-resistant strains	Strain code	MIC ($\mu g\ ml^{-1}$)	MBC ($\mu g\ ml^{-1}$)
A. baumannii	AB-1 (OXA-58[a])	1	2
E. coli	EC-325 (ESBL)	0.5	2
E. coli	EC-241 (ESBL)	1	16
K. pneumoniae	KB-503 (ESBL)	16	16
K. pneumoniae	KB-495 (ESBL)	16	16
P. aeruginosa	P-145 (VIM-2[a])	1	16
S. marcescens	S-41 (AmpC)	2	2
S. marcescens	S-32 (AmpC)	0.5	2

[a] Carbapenemases; ESBL: extended-spectrum beta-lactamase; AmpC: chromosomal AmpC beta-lactamase.



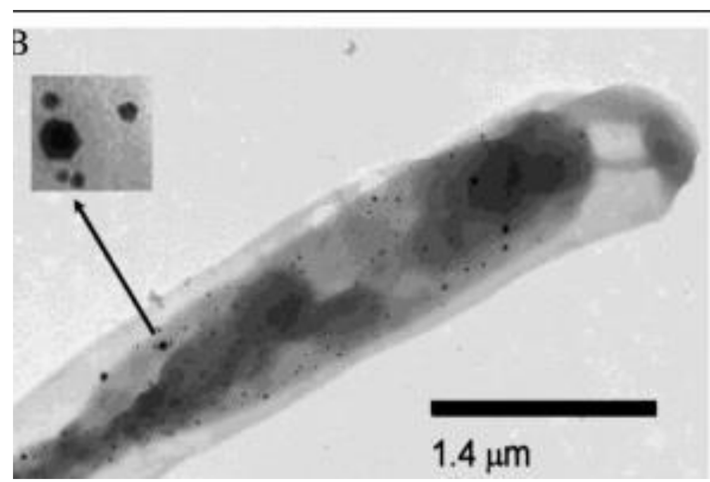
Pseudomonas sp. Da-bac TI-8 es capaz de solubilizar el fosfato y promover el desarrollo de las raices.



(A) Uninoculated Control **(B)** Inoculation with 10^3 CFU/mL

Berrios et al., 2012. Polar Biology

Geobacillus sp , es capaz de sintetizar partículas de oro, las cuales se acumulan intracelularmente.



Correa-Llantén et al., 2013. Microbial Cell Factories

Levaduras antárticas como fuente para la Industria Biotecnológica Nacional

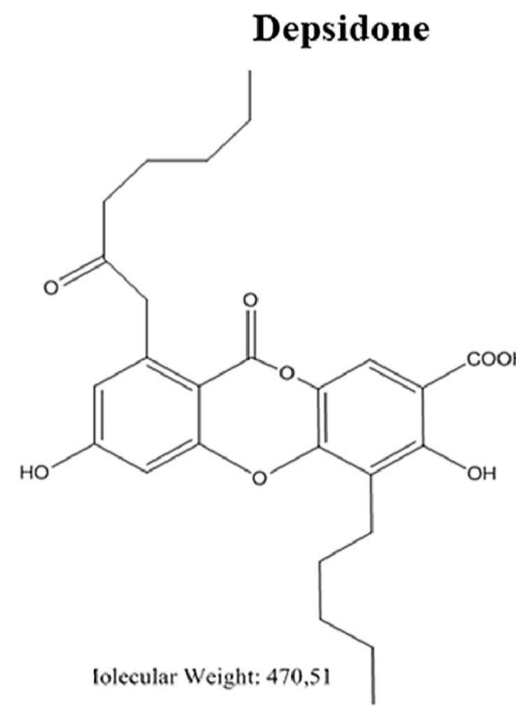
La levadura *Candida sake* H14Cs aislada desde la isla Rey Jorge puede ser utilizada para mejorar las fermentaciones a baja temperatura, teniendo el potencial además de producir menos etanol produciendo atributos particulares al vino.

Ballester-Tomás, L., Prieto, J.A., Gil, J.V., Baeza, M., Randez-Gil, F. 2016. The Antarctic yeast Candida sake: Understanding cold metabolism impact on wine. INTERNATIONAL JOURNAL OF FOOD MICROBIOLOGY, 245: 59-65.

Líquenes Antárticos con potencial para combatir el cáncer y el Alzheimer

La Depsidona producida por *Hypogymnia lugubris* inhibe la proliferación de células de melanoma humano

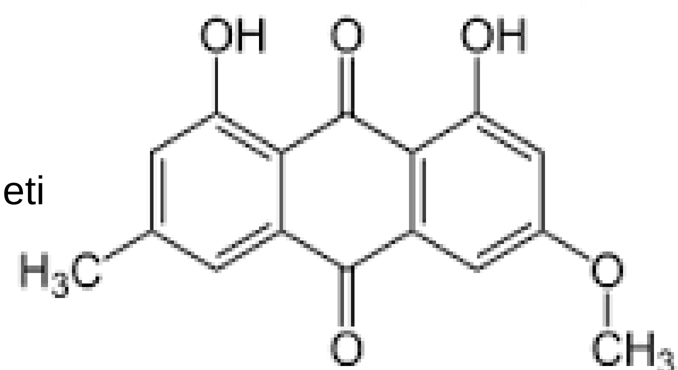
Cardile, V., Graziano, A.C.E., Avola, R, Piovano, M, Russo, A. 2016.Potential anticancer activity of lichen secondary metabolite physodic acid.Chemico-Biological Interactions, 263: 36-45



Physodic acid (**3**)

La Parietina producida por *Ramalina terebrata* inhibe la agregación de la proteína Tau implicada en la enfermedad de Alzheimer

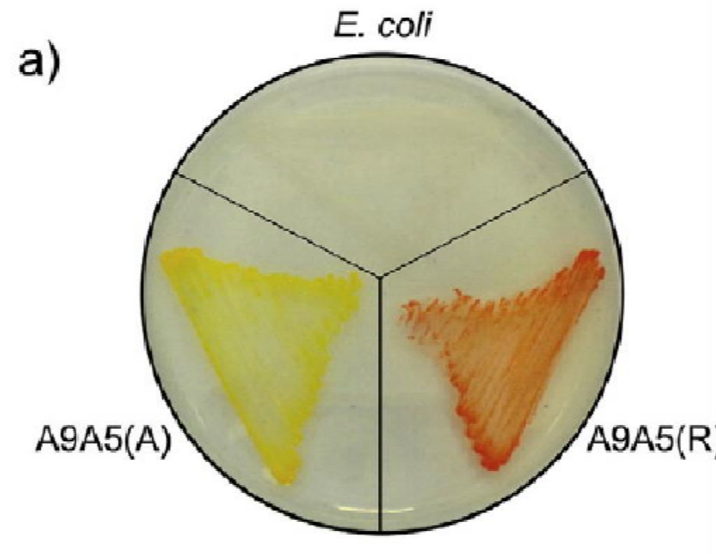
Parieti
n



Cornejo, A., Salgado, F., Caballero, J., Vargas, R., Simirgiotis, M., Areche, C. 2016. Secondary Metabolites in *Ramalina terebrata* Detected by UHPLC/ESI/MS/MS and Identification of Parietin as Tau Protein Inhibitor. International Journal of Molecular Sciences.

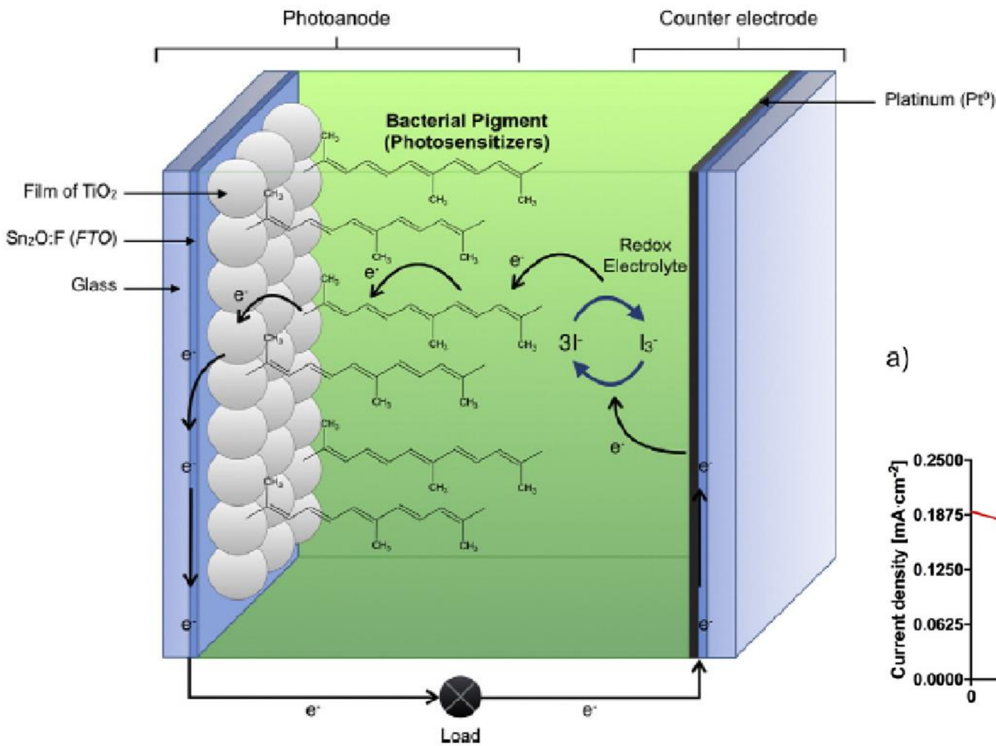
Desarrollo de celdas solares verdes a partir de bacterias antárticas

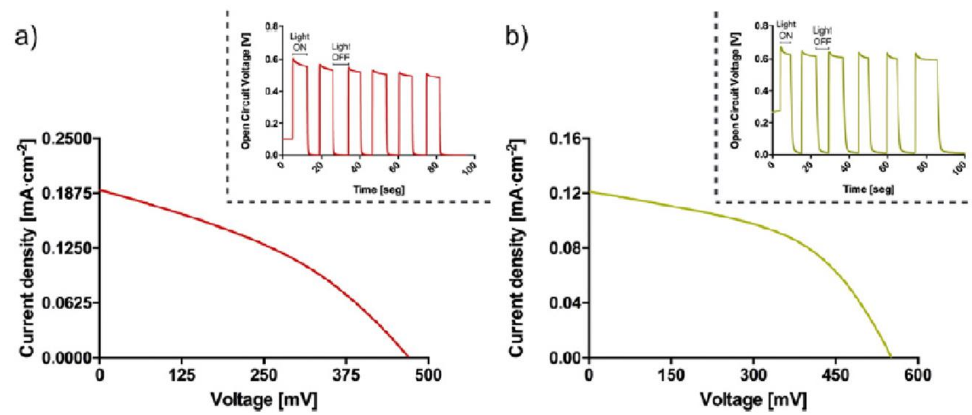
Chryseobacterium sp



Hymenobacter sp

Esquema de la célula solar sensibilizada por colorante





Órdenes-Aenishanslins, N., Anziani-Ostuni, G., Vargas-Reyes, M., Alarcón, J., Tello, A. and Pérez-Donoso, J.M. 2016. Pigments from UV-resistant Antarctic bacteria as photosensitizers in Dye Sensitized Solar Cells. Journal of Photochemistry & Photobiology, B: Biology 162: 707-714.

Therapeutic molecules & deviates for CRC (Antartina). United States Patent Application 20170049839. 2016. Tricin 7-O-beta-D-glucopyranoside, native to the plant *Deschampsia antarctica* and present in aqueous extracts of the plant *Deschampsia Antarctica* said compound having the ability to inhibit tumor growth in mammals with colorectal carcinoma.

Aqueous extracts of Deschampsia antarctica. United States Patent Application 20140193531. 2014.

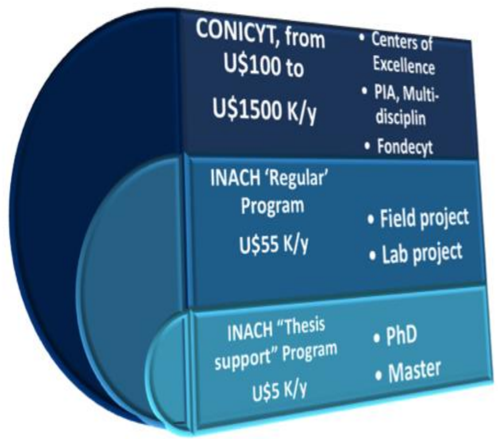
Extracts of D. antarctica, with antineoplastic activity. United States Patent Application 20100310686.2010

Biofertilizer formulation United States Patent 8415271.2013

Novel plant gene (lipase) .United States Patent Application 20090107914. 2009

Low temperature responsive nucleotide sequences and uses thereof . United States Patent Application 20050262586. 2005

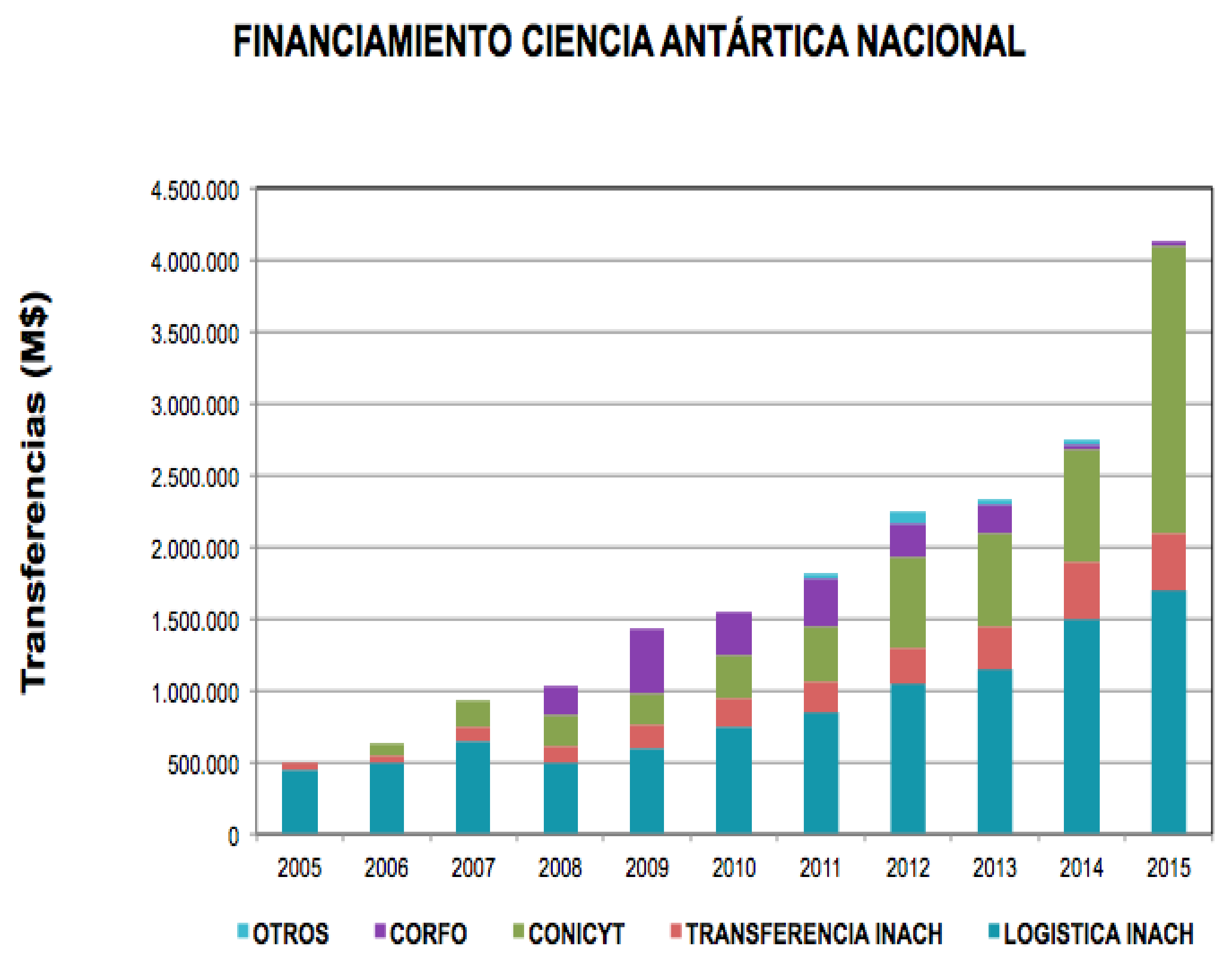
CHILEAN ANTARCTIC FUNDING "LADDER"



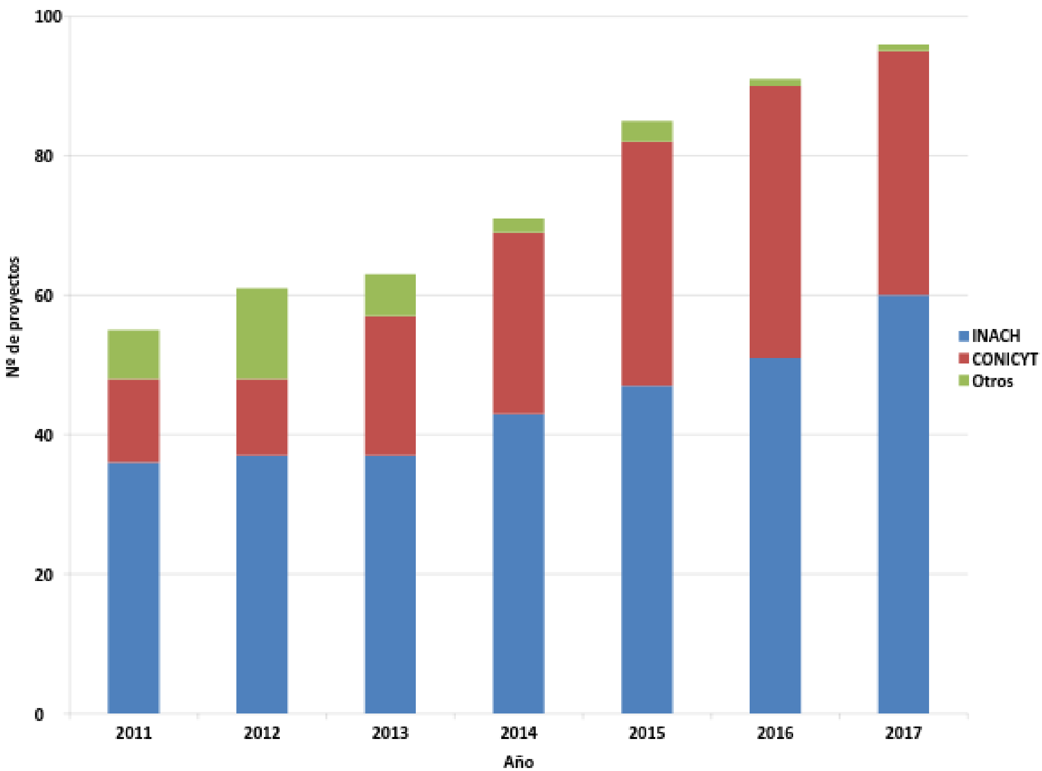
+ INACH LOGISTICS

FINANCING SOURCES

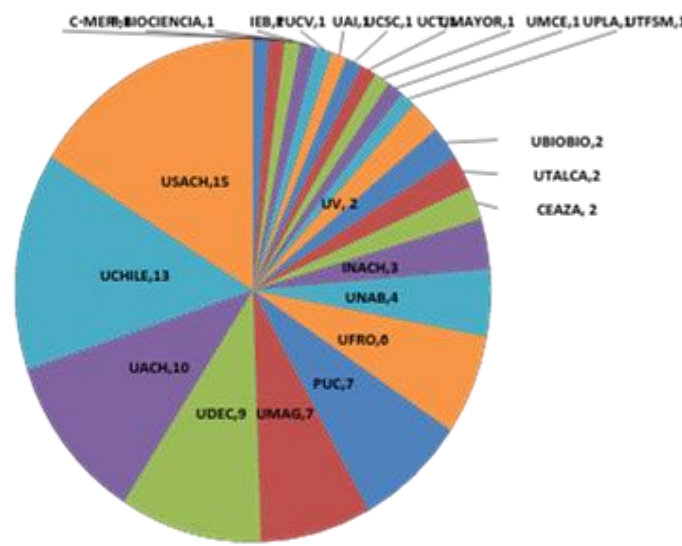
- INACH FIELD PROJECTS
- INACH LAB PROJECTS
- INACH THESIS SUPPORT
- INACH SPECIAL PROJECTS
- PIA INACH
- CORFO-INNOVACHILE
- FONDECYT-INACH
- FONDEF-INACH
- INTERNATIONAL COLLABORATION
- FONDAP
- PAI-CONICYT


FINANCIAMIENTO CIENCIA ANTÁRTICA NACIONAL
Transferencias (M$)
4.500.000
4.000.000
3.500.000
3.000.000
2.500.000
2.000.000
1.500.000
1.000.000
500.000
0
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
OTROS
CORFO
CONICYT
TRANSFERENCIA INACH
LOGISTICA INACH

Number of Projects and composition depending on funding source



IPs from 24 Universities/Research Centres



Line I. The State of the Antarctic Ecosystem

- I.8 Parasite fauna in Antarctic fishes
- I.9 Microevolution of penguins
- I.10 Evolutionary history of the Antarctic pearlwort
- I.11 Viral and bacterial diversity in seawater and Antarctic fish species
- I.12 A biophysical study of ichthyoplankton
- I.13 DNA barcoding of Antarctic parasites
- I.14 Photobionts of genus *Caloplaca*
- I.15 Eukaryote microbial communities
- I.16 New fungal species from Antarctic marine sponges
- I.17 Foraging ecology in extreme environments
- I.1 Phylogeography of Antarctic parasites
- I.2 Diversification of the spiny plunderfish *Harpagifer*
- I.3 Paleogeographic patterns v/s climate change
- I.4 Macroalgal adaptive radiation
- I.5 Biogeographic patterns and processes in mollusks
- I.6 Metagenomics of microbial communities
- I.7 Phylogeography and evolutionary history of *Neobuccinum eatoni*

Line II. Antarctic Thresholds: Ecosystem Resilience and Adaptation

- II.15 Climate adaptation in marine species
- II.16 *Campylobacter* in Antarctica
- II.17 Historic and recent colonizers
- II.18 Active layer of frozen soils
- II.2 Ecophysiology of snow algae
- II.3 Freezing tolerance of Antarctic vascular plants
- II.4 Responses of the Antarctic mosses to global warming
- II.5 Response of soil enzymatic and microbial activity
- II.6 Invertebrates responses to thermal stress conditions
- II.10 Sponges and climate change
- II.11 Photosynthetic responses to warming
- II.12 Addressing global warming scenarios in freshwater ecosystems
- II.13 Biological hot spots along the Antarctic Peninsula continental shelf
- II.14 Endophytic fungi in *Deschampsia antarctica*
- II.1 Antarctic plant ecophysiology
- II.7 Impact of iceloss on coastal benthic ecosystems
- II.8 Evolutionary history of *Colobanthus*
- II.9 Antarctic microbial community in response to deglaciation

Line III. Antarctic Climate Change

- III.1 High latitude marine ecosystems dynamic
- III.2 Influence of the solar activity on the polar environment
- III.3 Iron and light on phytoplankton production
- III.4 Glacier response to climate change in Chile
- III.5 Climate reconstruction at the northern Antarctic Peninsula
- III.6 Ozone and atmosphere-ocean system

Line IV. Physical and Earth Sciences

- IV.8 Radiance distribution in the Antarctic Peninsula
- IV.9 Thermal evolution of the Antarctic Peninsula
- IV.10 Palaeoenvironment in Fildes Peninsula
- IV.7 George VI Ice Shelf tributary glacier types
- IV.1 Space plasmas
- IV.2 Low clouds over the Antarctic Peninsula
- IV.3 Reflectivity of Antarctica
- IV.4 Ozone and solar radiation
- IV.5 Seismic facies variability and sedimentation
- IV.6 Warming, CO2 and leaf respiration of plants

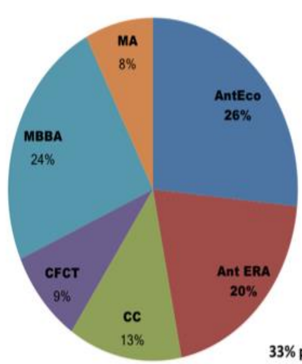
Line V. Antarctic Microbiology and Molecular Biology

- V.4 Gram-positive bacteria associated with marine macroalgae
- V.5 Yeasts in terrestrial habitats
- V.6 Polyphenols isolated from lichens
- V.7 Antifreeze proteins purified from microorganisms
- V.8 Resistance genes from waste waters
- V.9 Microbial consortiums with high acidogenic and methanogenic activity
- V.10 Potential of actinobacteria
- V.11 Microorganisms and nanoparticles
- V.1 Enzyme with beta-galactosidase activity
- V.2 Role of Antarctic root-endophytes in lettuce crops
- V.3 Rhizosphere's bacteria and performance of *Colobanthus*
- V.12 Bacterial diversity in soils
- V.13 Study of cold-active enzymes
- V.14 Nitrous oxide-reducing bacteria
- V.15 Biosurfactants produced by bacteria
- V.16 Nutraceutical metabolites in snow microalgae
- V.17 Antimicrobial activity of Antarctic *Pseudomonas*
- V.18 Psychrophilic bacteria isolated from Antarctic grass
- V.19 Mercury resistance mechanisms in bacteria
- V.20 Biochemical mechanisms of desiccation tolerance in moss
- V.21 Reduction of tellurite and copper in bacteria
- V.22 Tellurite resistance in bacteria
- V.23 Depsides and depsidones from lichens
- V.24 Laccase isolated from *Geobacillus*
- V.25 Antibacterial effect of lichens
- V.26 Cytotoxic activity of actinobacteria
- V.27 Lichens and biofilm formation
- V.28 *Rhodobacter* response to radiation

Line VI. Antarctic Environment

- VI.3 Persistent Organic Pollutants (POPs) in the aquatic food web
- VI.4 Vitamin D and biomarkers
- VI.5 Impacts of Antarctic bases on the aquatic ecosystems
- VI.6 Methane cycling in lakes
- VI.7 Xenobiotics in the South Shetlands
- VI.9 Heavy metals and persistent organic pollutants on Antarctic fauna
- VI.10 Drug residue in Southern Ocean
- VI.11 HAPs in snow
- VI.12 Environmental Antarctic Monitoring Center
- VI.8 Melting Claims
- VI.1 Paint schemes to protect structural steel constructions
- VI.2 Soil communities and pollution

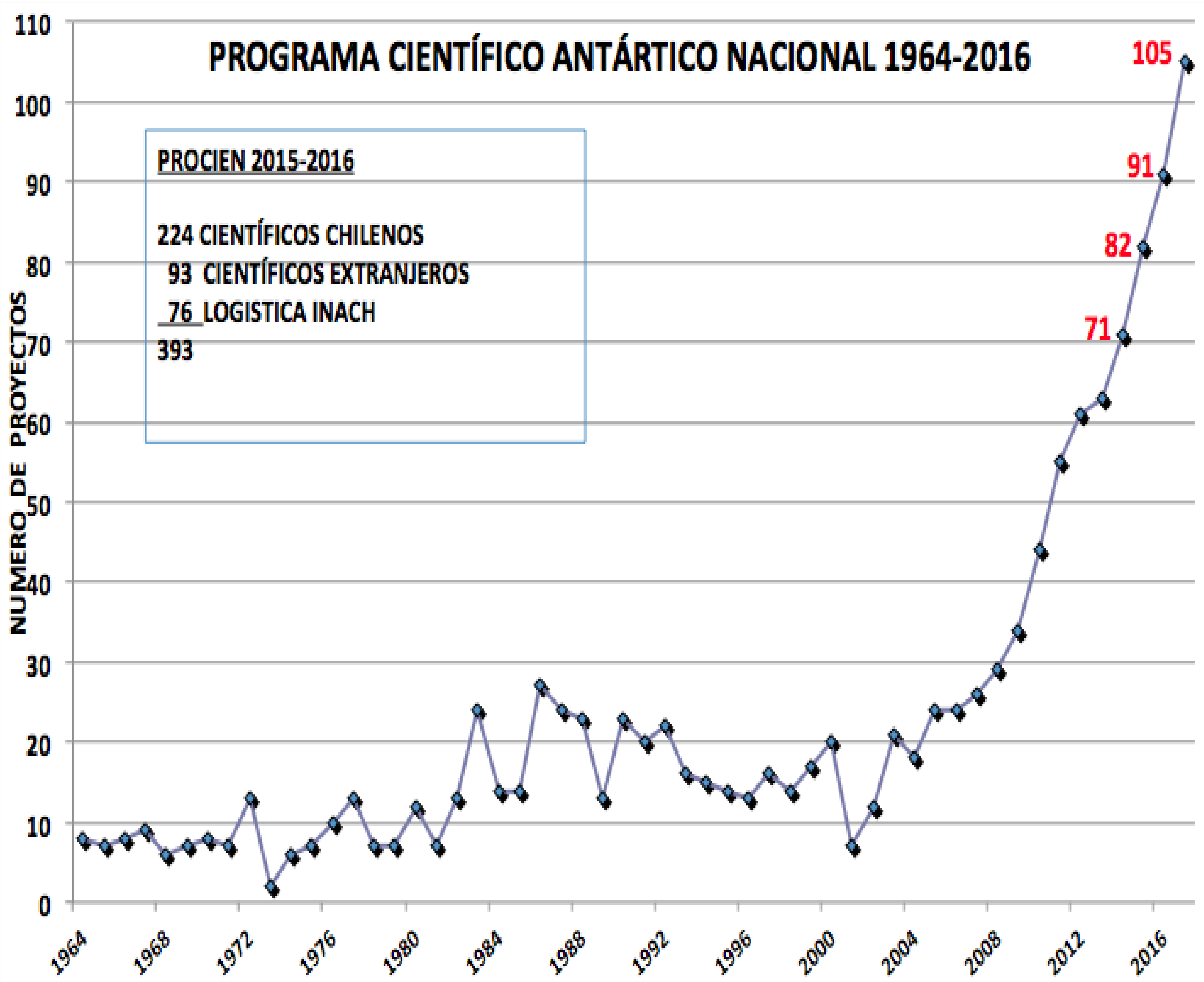
PROCIEN projects by reseach lines



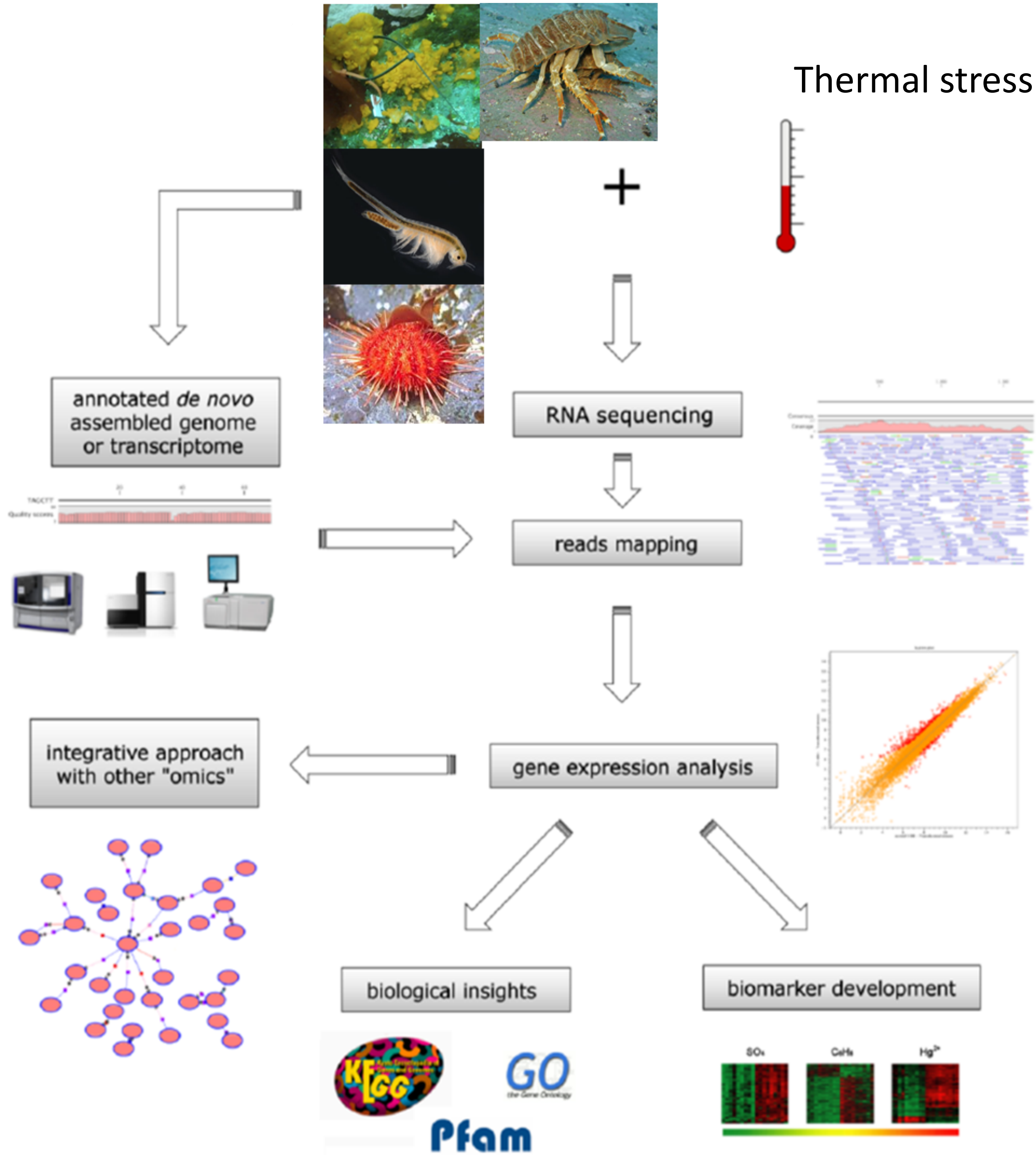
33% projects related to Climate Change

FINANCING SOURCES

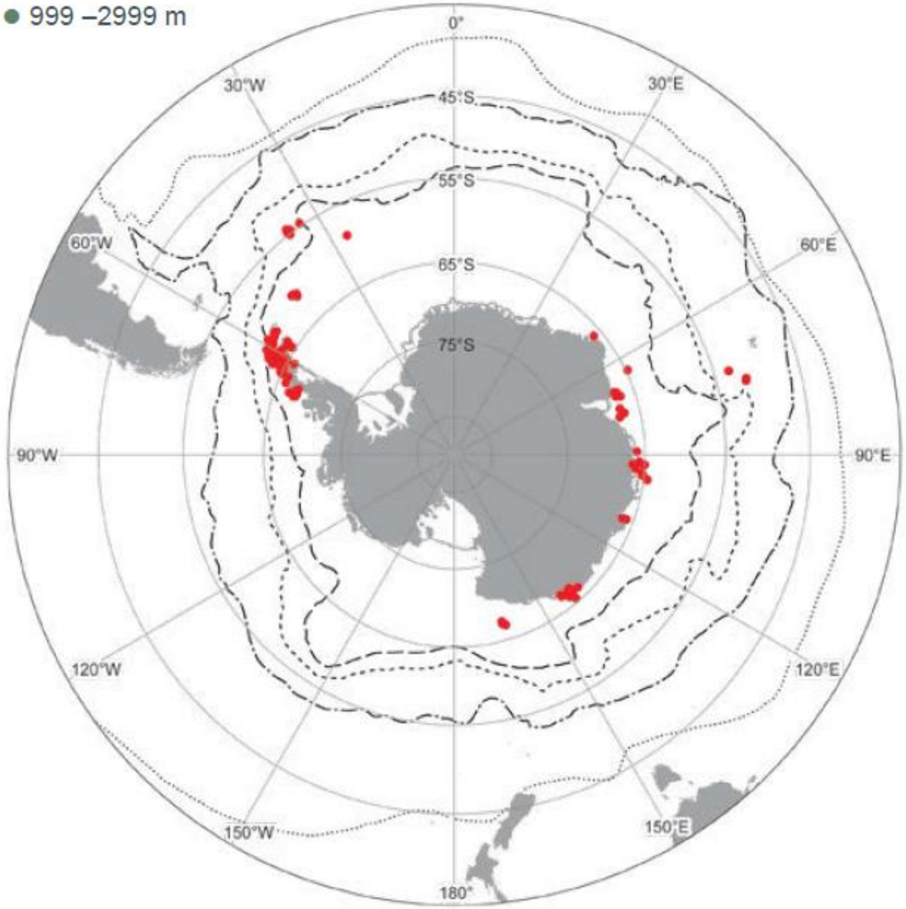
- INACH FIELD PROJECTS
- INACH LAB PROJECTS
- INACH THESIS SUPPORT
- INACH SPECIAL PROJECTS
- PIA INACH
- CORFO-INNOVACHILE
- FONDECYT-INACH
- FONDEF-INACH
- INTERNATIONAL COLLABORATION
- FONDAP
- PAI-CONICYT



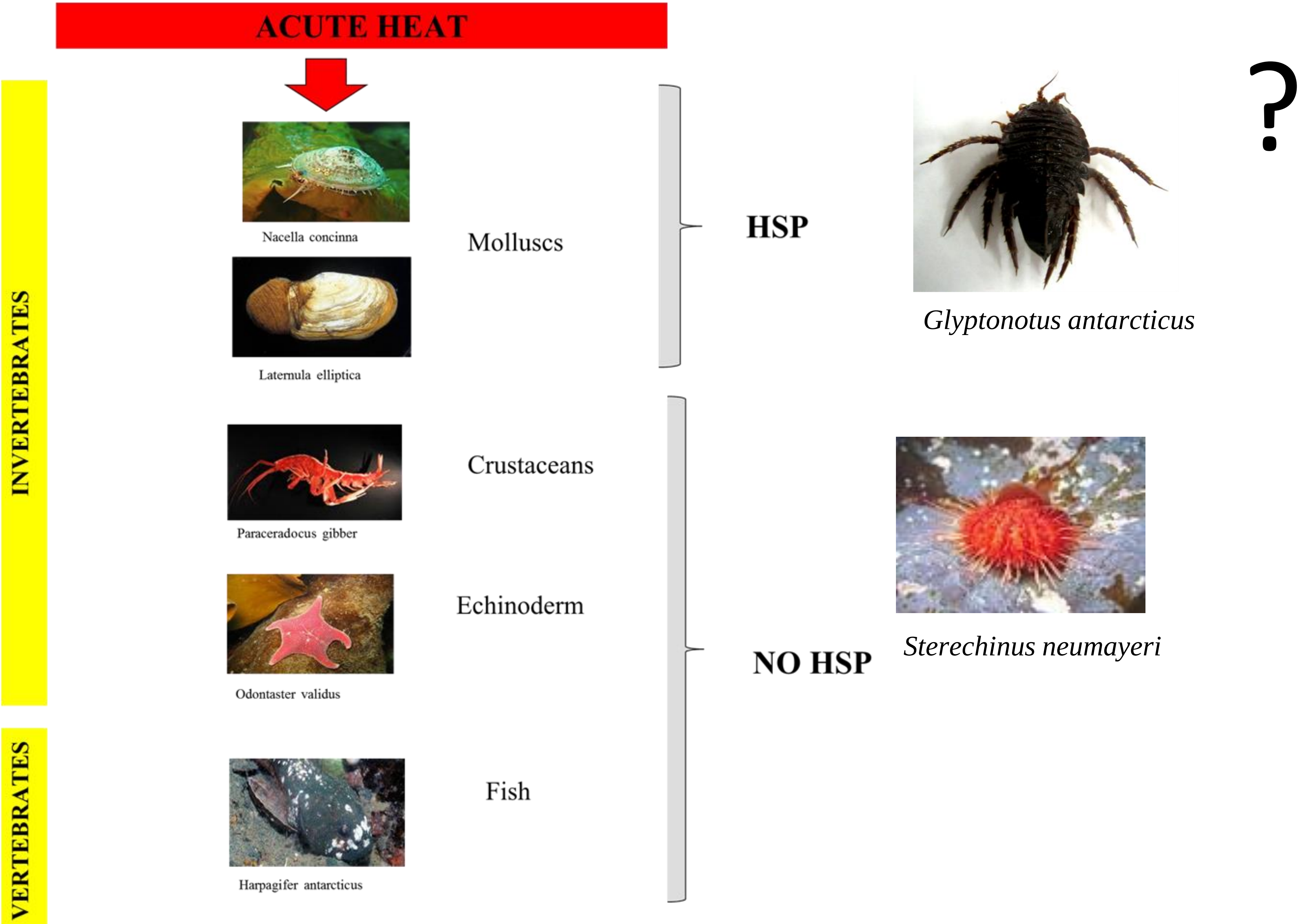
PROGRAMA CIENTÍFICO ANTÁRTICO NACIONAL 1964-2016
PROCIEN 2015-2016
224 CIENTÍFICOS CHILENOS
93 CIENTÍFICOS EXTRANJEROS
76 LOGISTICA INACH
393
NUMERO DE PROYECTOS
105
91
82
71
0
10
20
30
40
50
60
70
80
90
100
110
1964
1968
1972
1976
1980
1984
1988
1992
1996
2000
2004
2008
2012
2016


Thermal stress
+
annotated de novo assembled genome or transcriptome
RNA sequencing
reads mapping
gene expression analysis
integrative approach with other "omics"
biological insights
biomarker development
GO
Pfam

0–999 m
999 –2999 m

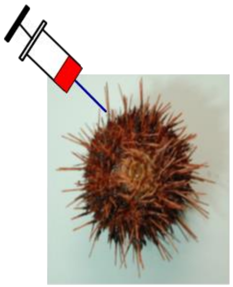


Map 8a ***Sterechinus neumayeri***
0–999 m



Modificado de Clark & Peck, 2009. Marine Genomics

Secuenciación masiva: Next Generation Sequencing by Illumina



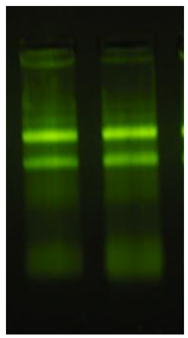
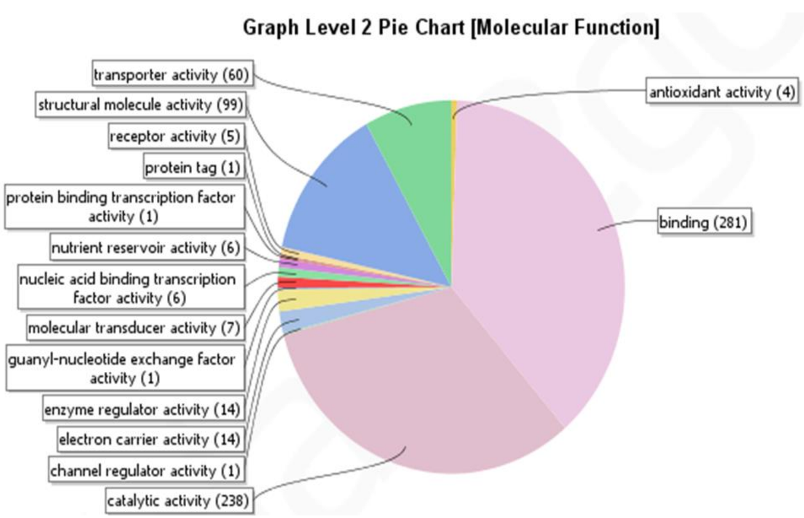
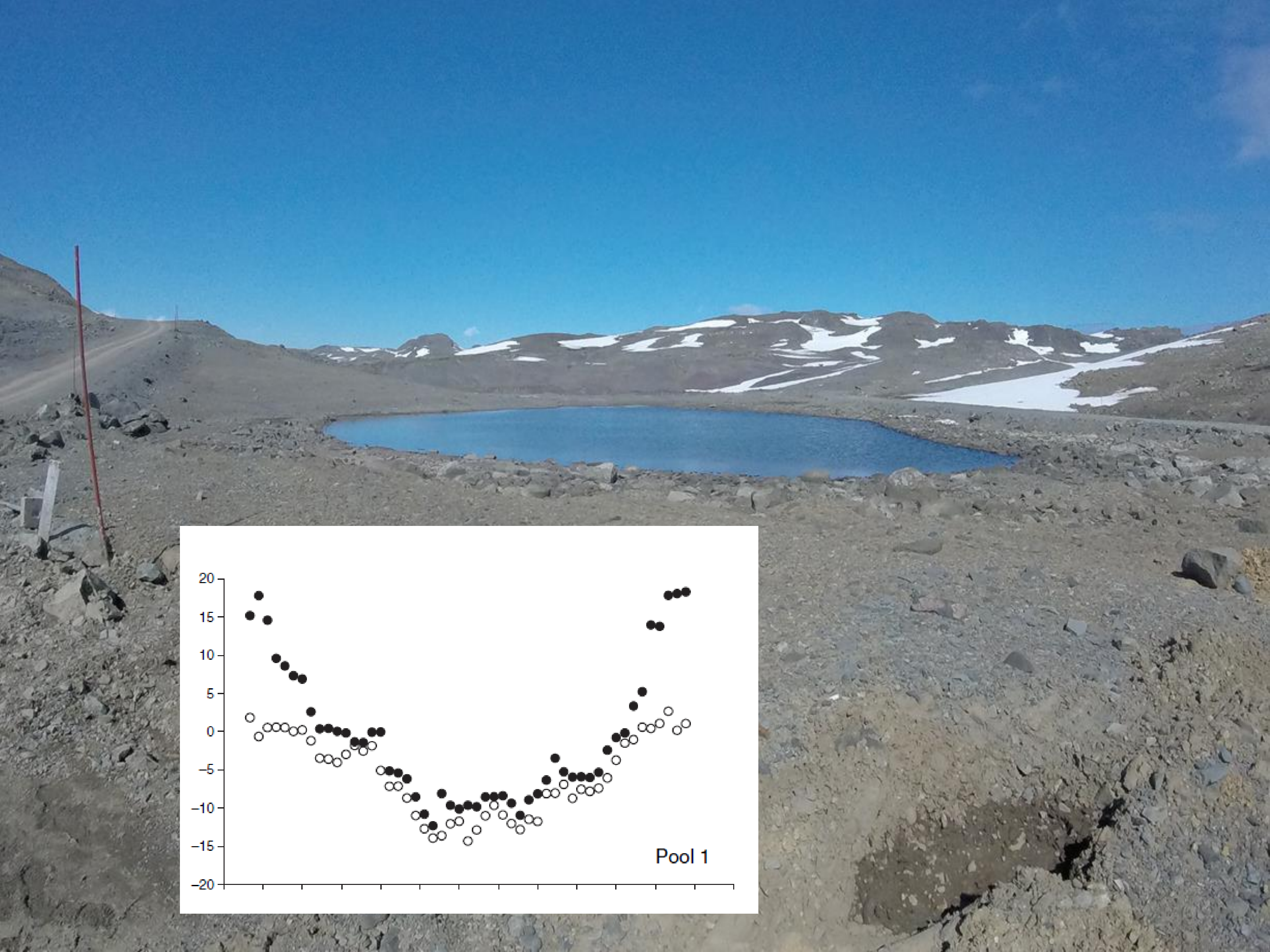


Table 1. Statistic for the transcriptome sequencing from digestive tissue of *Sterechinus neumayeri* and *Glyptonotus antarcticus*.

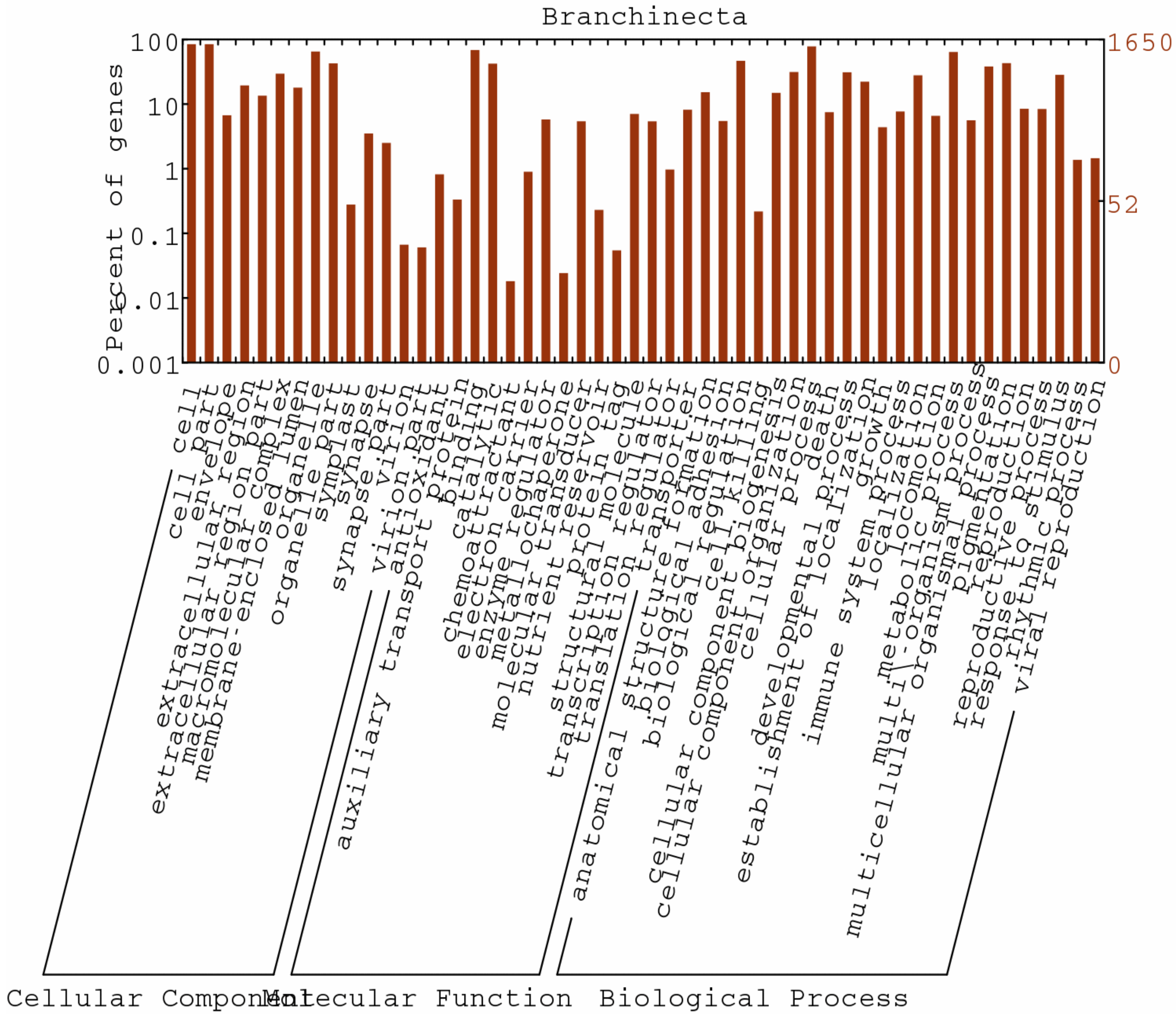
	S. neumayeri	*G. antarcticus*
Number of total reads	213,437,284	168,476,414
Number of assembled contigs	274,048	58,953
Average contig length (bp)	490	520
Median length (bp)	310	326
Maximun contig length (bp)	17,169	14,591
Min length (bp)	202	202
N50 (pb)	684	659

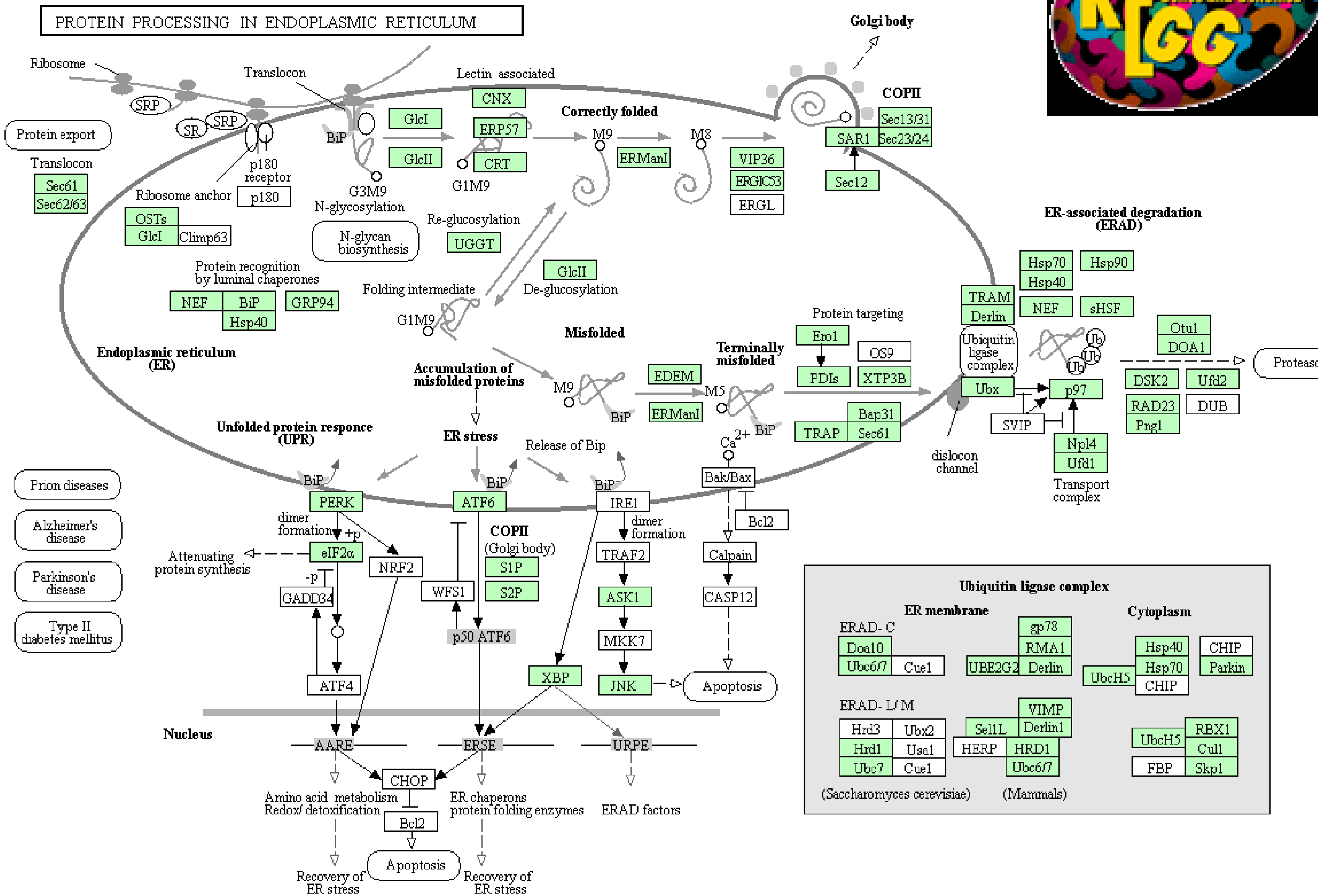


Heat schock proteins (hsp70, 60, 90, 40)
Superoxide dismutase
Catalase
Peroxiredoxin

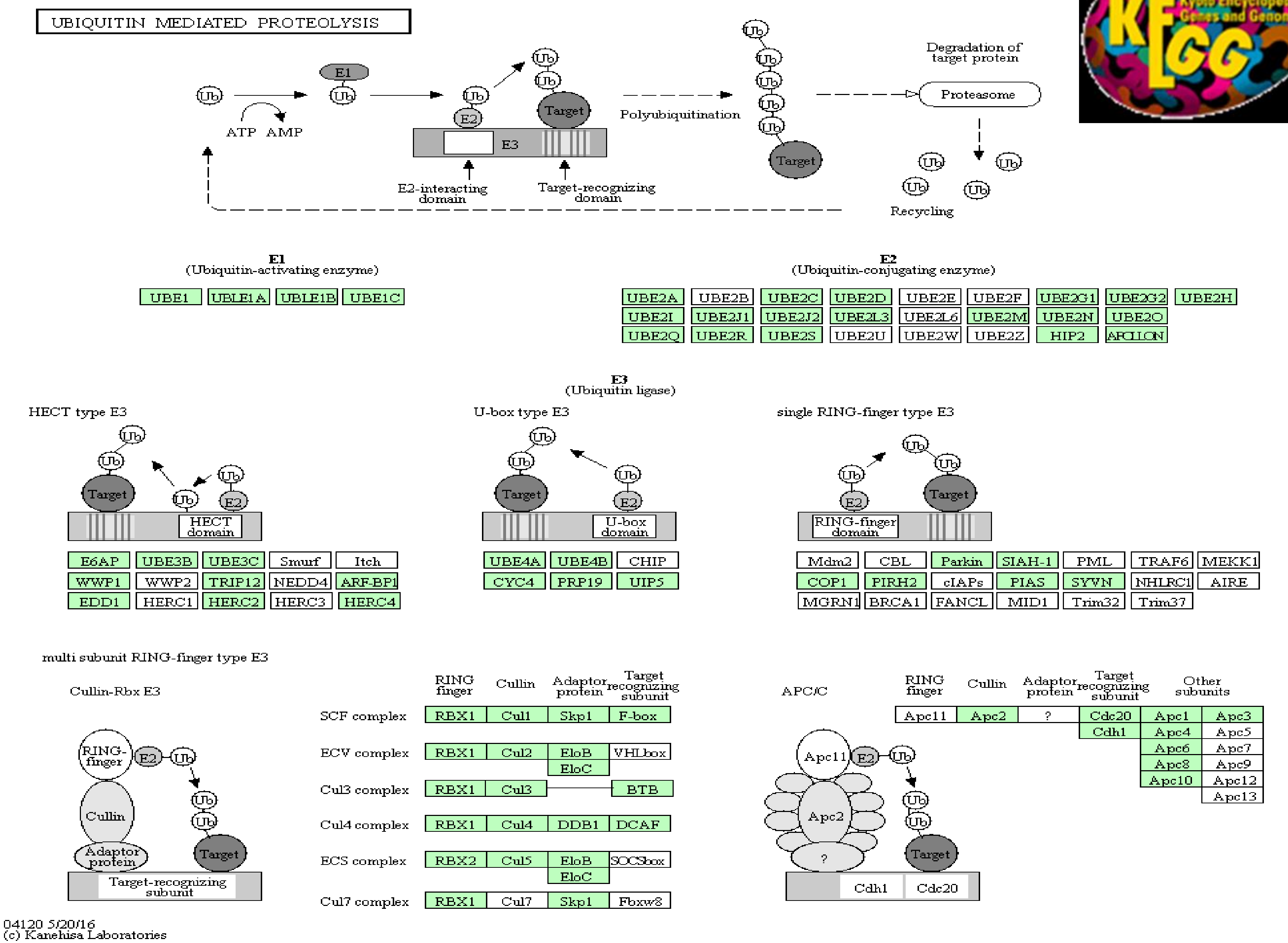


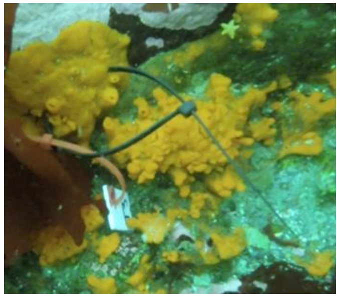
20
15
10
5
0
−5
−10
−15
−20
Pool 1


Branchinecta
Percent of genes
Number of genes
100
10
1
0.1
0.01
0.001
16503
52
0
cell
cell part
envelope
extracellular region
extracellular region part
macromolecular complex
membrane-enclosed lumen
organelle
organelle part
symplast
synapse
synapse part
virion
virion part
antioxidant
auxiliary transport protein
binding
catalytic
chemoattractant
electron carrier
enzyme regulator
metallochaperone
molecular transducer
nutrient reservoir
protein tag
structural molecule
transcription regulator
translation regulator
transporter
anatomical structure formation
biological adhesion
biological regulation
cell killing
cellular component biogenesis
cellular component organization
cellular process
death
developmental process
establishment of localization
growth
immune system process
localization
locomotion
metabolic process
multi-organism process
multicellular organismal process
pigmentation
reproduction
reproductive process
response to stimulus
rhythmic process
viral reproduction
Cellular Component
Molecular Function
Biological Process


PROTEIN PROCESSING IN ENDOPLASMIC RETICULUM
Ribosome
SRP
SR
SRP
Translocon
Protein export
Translocon
Sec61
Sec62/63
p180
receptor
Ribosome anchor
p180
OSTs
GlcI
Climp63
BiP
G3M9
N-glycosylation
N-glycan
biosynthesis
Lectin associated
CNX
GlcI
ERP57
GlcII
CRT
G1M9
Re-glucosylation
UGGT
Correctly folded
M9
M8
ERManI
VIP36
ERGIC53
ERGL
Golgi body
COPII
Sec13/31
SAR1
Sec23/24
Sec12
GlcII
De-glucosylation
Folding intermediate
G1M9
Protein recognition
by luminal chaperones
NEF
BiP
GRP94
Hsp40
Endoplasmic reticulum
(ER)
Misfolded
Accumulation of
misfolded proteins
M9
EDEM
BiP
ERManI
M5
Terminally
misfolded
Protein targeting
Ero1
OS9
PDIs
XTP3B
Bap31
TRAP
Sec61
Ca^{2+}
BiP
ER-associated degradation
(ERAD)
Hsp70
Hsp90
Hsp40
TRAM
Derlin
NEF
sHSF
Ubiquitin
ligase
complex
Ub
Ub
Ub
Otu1
DOA1
Proteasome
Ubx
p97
DSK2
Ufd2
SVIP
RAD23
DUB
Png1
Npl4
Ufd1
dislocon
channel
Transport
complex
Unfolded protein responce
(UPR)
ER stress
Release of Bip
BiP
BiP
BiP
PERK
ATF6
IRE1
Bak/Bax
Bcl2
dimer
formation
+p
eIF2α
Attenuating
protein synthesis
NRF2
-p
GADD34
ATF4
WFS1
COPII
(Golgi body)
S1P
S2P
p50 ATF6
dimer
formation
TRAF2
ASK1
MKK7
JNK
XBP
Calpain
CASP12
Apoptosis
Nucleus
AARE
ERSE
URPE
CHOP
Amino acid metabolism
Redox/ detoxification
Bcl2
Apoptosis
Recovery of
ER stress
ER chaperons
protein folding enzymes
Recovery of
ER stress
ERAD factors
Prion diseases
Alzheimer's
disease
Parkinson's
disease
Type II
diabetes mellitus
Ubiquitin ligase complex
ER membrane
Cytoplasm
ERAD- C
Doa10
Ubc6/7
Cue1
gp78
RMA1
UBE2G2
Derlin
Hsp40
Hsp70
UbcH5
CHIP
CHIP
Parkin
ERAD- L/ M
Hrd3
Ubx2
Hrd1
Usa1
Ubc7
Cue1
VIMP
SelIL
Derlin1
HERP
HRD1
Ubc6/7
UbcH5
RBX1
Cul1
FBP
Skp1
(Saccharomyces cerevisiae)
(Mammals)

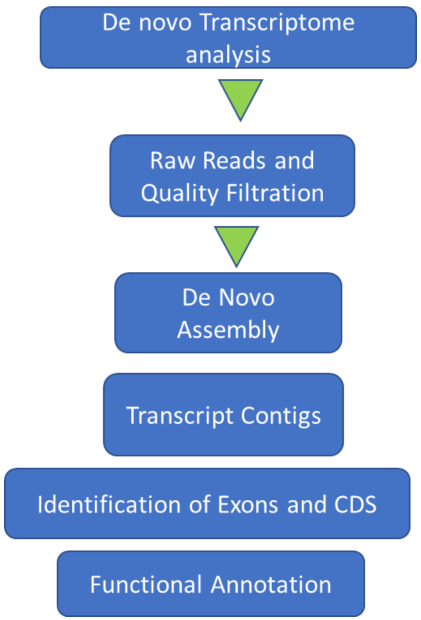
04141 5/14/14


UBIQUITIN MEDIATED PROTEOLYSIS
Ub
ATP AMP
E1
E2
E3
Target
E2-interacting domain
Target-recognizing domain
Polyubiquitination
Degradation of target protein
Proteasome
Recycling
E1
(Ubiquitin-activating enzyme)
UBE1 UBLE1A UBLE1B UBE1C
E2
(Ubiquitin-conjugating enzyme)
UBE2A UBE2B UBE2C UBE2D UBE2E UBE2F UBE2G1 UBE2G2 UBE2H
UBE2I UBE2J1 UBE2J2 UBE2L3 UBE2L6 UBE2M UBE2N UBE2O
UBE2Q UBE2R UBE2S UBE2U UBE2W UBE2Z HIP2 APOLLON
E3
(Ubiquitin ligase)
HECT type E3
HECT domain
E6AP UBE3B UBE3C Smurf Itch
WWP1 WWP2 TRIP12 NEDD4 ARF-BP1
EDD1 HERC1 HERC2 HERC3 HERC4
U-box type E3
U-box domain
UBE4A UBE4B CHIP
CYC4 PRP19 UIP5
single RING-finger type E3
RING-finger domain
Mdm2 CBL Parkin SIAH-1 PML TRAF6 MEKK1
COP1 PIRH2 cIAPs PIAS SYVN NHLRC1 AIRE
MGRN1 BRCA1 FANCL MID1 Trim32 Trim37
multi subunit RING-finger type E3
Cullin-Rbx E3
RING-finger
Cullin
Adaptor protein
Target-recognizing subunit
RING finger | Cullin | Adaptor protein | Target recognizing subunit
SCF complex RBX1 Cul1 Skp1 F-box
ECV complex RBX1 Cul2 EloB EloC VHLbox
Cul3 complex RBX1 Cul3 BTB
Cul4 complex RBX1 Cul4 DDB1 DCAF
ECS complex RBX2 Cul5 EloB EloC SOCSbox
Cul7 complex RBX1 Cul7 Skp1 Fbxw8
APC/C
Apc11
Apc2
?
Cdh1 Cdc20
RING finger | Cullin | Adaptor protein | Target recognizing subunit | Other subunits
Apc11 Apc2 ? Cdc20 Apc1 Apc3
Cdh1 Apc4 Apc5
Apc6 Apc7
Apc8 Apc9
Apc10 Apc12
Apc13
04120 5/20/16
(c) Kanehisa Laboratories



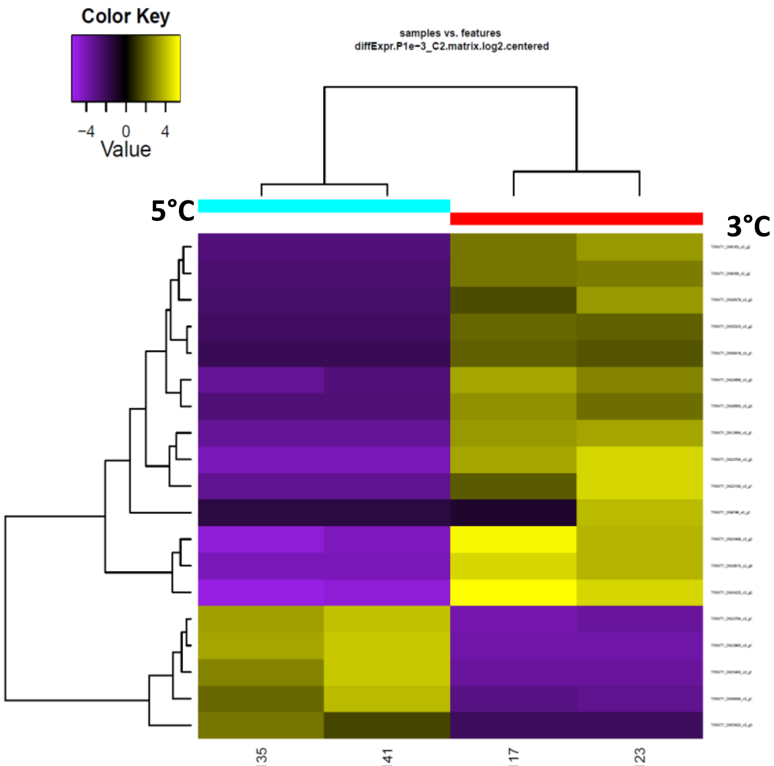
Sample ID	Temperature experiment	Total read base (bp)	Total reads	GC (%)	AT (%)	Q20 (%)	Q30 (%)
Hali_209	0.78°C	5,249,690,938	51,977,138	45.5	54.5	95.46	91.42
Hali_117	3°C	5,759,699,528	57,026,728	46.53	53.47	95.46	91.39
Hali_123	3°C	5,445,979,792	53,920,592	45.29	54.71	95.48	91.49
Hali_135	5°C	5,210,301,140	51,587,140	46.48	53.52	94.93	90.56
Hali_141	5°C	5,310,459,002	52,578,802	45.18	54.82	95.32	91.14

Sample ID : Sample name; Total read bases : Total number of bases sequenced; Total reads : Total number of reads. In illumina paired-end sequencing, read1 and read2 are added; GC(%) : GC content; AT(%) : AT content; Q20(%) : Ratio of reads that have phred quality score of over 20; Q30(%) : Ratio of reads that have phred quality score of over 30.



1. Identification and characterization of Heat Shock Proteins (HSPs).
2. Differential expression in Haliclona during thermal stress response.

Heat map of contigs differentially expressed between the two different thermal stress condition



5°C UP											
id	logFC	logCPM	PValue	FDR	117	123	135	141	Sequence similarity		
TRINITY_DN33462_c0_g1	11,3431557	5,61708894	4,11E-11	5,96E-07	0	0,09	77,632	212,084	bacterial		
TRINITY_DN53922_c0_g3	12,7323051	4,6594475	3,63E-10	2,63E-06	0	0	20,257	9,678	peptidyl-prolyl cis-trans isomerase FKBP6-like [Amphimedon queenslandica]		
TRINITY_DN23764_c0_g1	10,1211206	8,50613471	4,22E-09	2,22E-05	0	0,36	145,992	260,51	Ribosomal protein P		
TRINITY_DN58083_c0_g1	8,44465615	6,00246623	5,36E-09	2,59E-05	0,47	0,158	48,335	172,409	(no hits)		
TRINITY_DN23863_c0_g1	11,7507498	3,68432675	1,48E-08	6,12E-05	0	0	154,615	260,173	(no hits)		
3°C UP											
id	logFC	logCPM	PValue	FDR	117	123	135	141			
TRINITY_DN23764_c0_g2	-16,989541	8,91041013	2,20E-19	1,28E-14	174,698	375,454	0	0	Ribosomal protein P		
TRINITY_DN24223_c2_g2	-11,372908	7,90170213	2,46E-15	7,12E-11	2048,826	1040,513	0,407	0,703	cell number regulator 10-like [Amphimedon queenslandica]		
TRINITY_DN12683_c0_g1	-13,628338	5,55236112	1,48E-12	2,86E-08	98,186	120,418	0	0	allograft inflammatory factor 1 [Suberites domuncula]	****	
TRINITY_DN6163_c0_g2	-13,037593	4,96338023	5,74E-11	6,65E-07	37,374	61,605	0	0	Ubiquitin		
TRINITY_DN23190_c0_g1	-14,046198	5,96933962	7,07E-11	6,83E-07	30,577	198,655	0	0	bacterial		
TRINITY_DN24468_c0_g2	-11,037669	5,2497213	2,63E-10	2,18E-06	961,628	373,844	0	0,534	no hits		
TRINITY_DN30615_c2_g9	-12,409149	4,33780175	1,10E-09	7,06E-06	371,697	222,764	0	0	no hits		
TRINITY_DN8356_c0_g2	-12,074117	4,00488432	2,93E-09	1,70E-05	28,618	33,297	0	0	ubiquitin-conjugating enzyme E2 K-like [Amphimedon queenslandica]		
TRINITY_DN26078_c0_g2	-12,158147	4,08832862	1,04E-08	4,64E-05	13,79	42,812	0	0	COMM domain-containing protein 8-like [Amphimedon queenslandica]		
TRINITY_DN58418_c0_g1	-11,620172	3,55471009	1,86E-08	7,19E-05	15,318	12,015	0	0	uncharacterized protein LOC109582405 [Amphimedon queenslandica]		
TRINITY_DN35203_c0_g2	-11,545808	3,48108228	2,31E-08	8,38E-05	18,315	16,632	0	0	mitogen-activated protein kinase kinase kinase 3-like [Solanum pennellii]		
TRINITY_DN26850_c0_g3	-11,439694	3,37609616	6,15E-08	0,00020948	49,921	29,862	0	0	hypothetical protein [Nitrosospira multiformis]		
TRINITY_DN8786_c0_g1	-14,571158	6,49349459	1,09E-07	0,00035095	0,402	40,841	0	0	oxysterol-binding protein 1-like [Amphimedon queenslandica]		*
TRINITY_DN24856_c0_g2	-8,1751753	5,23614288	2,62E-07	0,00079942	113,974	66,988	0	0,581	nuclease-sensitive element-binding protein 1-like isoform X2 [Amphimedon queenslandica]		

NATURAL
HISTORY
MUSEUM

Proyecto Fondecyt
11150129

1872
CNRS UPMC
Station Biologique
Roscoff

SGBC
SLU Global Bioinformatics Centre

SLU
Swedish University of
Agricultural Sciences

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MARIE CURIE ACTIONS


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