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Singapore Declaration
<i>I hereby declare that the information provided in this Annual report is reliable, and that I adhere to the Singapore Declaration, contained in Conicyt Exempt Resolution No. 157 of January 24, 2013, as a global guide for responsible conduct in research.</i>

<i>Institute / Nucleus Director Name</i>	<i>Institute / Nucleus Alternate Director Name</i>
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<i>Director's Signature</i>	<i>Alternate Director's Signature</i>
	

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1. Introduction & Executive Summary

The Millennium Institute of Genome Regulation Center (MI-CGR, 2022-2032) is the continuation of a project that began in 2010 as a pioneering center in Chile dedicated to genomic sciences in a multidisciplinary manner. The primary objective of the IM-CGR is to generate scientific knowledge in the fields of genomics, functional genomics, gene interaction networks, and omics sciences, all applied to biodiversity conservation, strategies to counter climate change, biotechnology, and the sustainable production of food. In its inception, the MI-CGR defined three main research lines: 1) Functional Genomics of Adaptation and Convergent Evolution, 2) Interaction Networks Governing Genome Structure in Communities, and 3) Genomics for Conservation, Ecosystem Health, and Sustainable Food Production.

In 2024, Research Line 1 uncovered key insights into the biochemical strategies of wild plants thriving in the Atacama Desert, adaptation mechanisms of marine viruses to cold environments and of bacteria to salt stress, and the evolutionary history of guanacos, *Orestias* pupfish, and banded penguins based on genomic data. Research Line 2 made significant discoveries in the interactions between the microbiota and diverse organisms like wild seaweed, cultivated grapes, penguins, and farmed salmon. Finally, Research Line 3 obtained notable results on plant and fruit resistance to biotic stress, and a deeper understanding of the mechanisms controlling commercially important traits in crops like avocados, potatoes, and peaches.

In 2024, our scientific team consisted of 9 Associate (Principal) Researchers, 10 Adjunct Researchers, 25 Postdoctoral Researchers, 9 Young Researchers, and 113 students, affiliated with four hosting universities and three adjunct universities. 22 students completed their thesis projects in 2024, of which 16 were undergraduate students, 4 were Master's, and 2 were D.

In terms of productivity, during the reported period we generated 74 publications, of which:

- 72 were research articles in peer-reviewed journals and 2 were books or book chapters
- 42 (58%) research articles were published in Q1 journals and 23 (31%) in Q2 journals
- 47 (64%) were published in Open Access (OA) journals or traditional/hybrid journals
- 30 (41%) were collaborative publications among IM-CRG researchers (compared to 25% in 2023)
- 19 (26%) had students as co-authors (in 2023 it was also 26%)
- 18 (24%) resulted from a formal collaboration network
- The average impact factor of our publications in 2024 was 4.98 (compared to 5.11 in 2023).

In 2024, we expanded our collaboration networks, partly due to the formalization of some of them, and on the other hand, because of the relaunching of one of the Center's flagship initiatives, the Chilean 1000 Genomes Project. This initiative allowed us to establish collaborative partnerships with national Centers of Scientific Excellence and increase interaction with both the public and private sectors.

2024 was a year of intense engagement with the public, which was reflected in 21 outreach activities distributed across 5 of the country's 16 regions, as well as 40 appearances in the media. It is important to highlight that in 2024 we published the two pledged products from the 2023 MSI Projection to the External Environment: a [children's book](#) and a [documentary video](#) (freely available on our website), both based on the experience at the Genomic Biodiversity in Extreme Environments Workshop held in San Pedro de Atacama from September 30 to October 6, 2023. In Annex 8, we provide an overview by the Director on the main achievements reached by the Institute during 2024.

1.1 Resumen Ejecutivo

El Instituto Milenio Centro de Regulación del Genoma (IM-CRG, 2022-2032) es la continuación de un proyecto que comenzó en 2011 como un centro pionero en Chile dedicado a las ciencias genómicas de manera multidisciplinaria. El objetivo principal del IM-CRG es generar conocimiento científico en los campos de la genómica, la genómica funcional, las redes de interacción génica y las ciencias ómicas, todas aplicadas a la conservación de la biodiversidad, a las estrategias para contrarrestar el cambio climático, la biotecnología y a la producción sostenible de alimentos. El IM-CRG definió en su génesis tres principales líneas de investigación: 1) Genómica funcional de la adaptación y evolución convergente, 2) Redes de interacción que rigen la estructura del genoma en comunidades de organismos y 3) Genómica para la conservación, la salud de los ecosistemas y la producción sostenible de alimentos.

En 2024, la línea 1 descubrió información clave sobre las estrategias bioquímicas de las plantas silvestres que prosperan en el Desierto de Atacama, los mecanismos de adaptación de los virus marinos a ambientes fríos y de las bacterias al estrés salino, y la historia evolutiva de los Guanacos, los peces *Orestias* y los pingüinos *Spheniscus* a partir de datos genómicos. La línea 2 hizo importantes descubrimientos sobre las interacciones entre la microbiota y algas marinas silvestres, uvas cultivadas, pingüinos y salmones de cultivo. Finalmente, la línea 3 obtuvo resultados notables sobre la resistencia de las plantas y frutas al estrés biótico, y una comprensión más profunda de los mecanismos que controlan los rasgos comercialmente importantes en cultivos como aguacates, papas y duraznos.

En 2024, nuestro equipo científico se compuso de 9 Investigadores Asociados (Principales), 10 Adjuntos, 25 Postdoctorales, 9 Jóvenes y 113 estudiantes, pertenecientes a cuatro universidades albergantes y tres universidades adjuntas. Nos complace informar que 22 estudiantes finalizaron sus proyectos de tesis en 2024, de los cuales 16 fueron de pregrado, 4 de Magister y 2 de doctorado.

En términos de productividad, en el período reportado producimos 74 publicaciones, de las cuales:

- 72 fueron artículos de investigación en revistas con revisión de pares y 2 fueron libros o capítulos de libros
- 43 (58%) fueron en revistas Q1 y 23 (31%) fueron en Q2
- 47 (64%) fueron publicados en modalidad acceso abierto
- 30 (41%) fueron publicaciones colaborativas entre Investigadores del IM-CRG (en 2023 fue 25%)
- 19 (26%) tuvo estudiantes como co-autores (en 2023 también fue 26%)
- 18 (24%) fue el resultado de una red formal de colaboración
- El promedio de factor de impacto de nuestras publicaciones fue de 4.98 (en 2023 fue 5.11).

En 2024, aumentamos nuestras redes de colaboración, en parte por la formalización de algunas y, por otro lado, debido al relanzamiento de una iniciativa insigne del Centro, 1000 Genomas Chile. Esta permitió establecer alianzas colaborativas con Centros de Excelencia Científica nacionales y aumentar la interacción con el sector público y el privado.

2024 fue un año de intensa interacción con la ciudadanía, lo que se manifestó en 21 actividades de divulgación distribuidas en 5 de las 16 regiones del país, además de 40 apariciones en medios de comunicación. Es importante destacar que en 2024 publicamos los dos productos comprometidos del Fondo de Proyección al Medio Externo 2023: [libro infantil](#) y un [video documental](#) (disponibles de forma gratuita en nuestro sitio web), ambos basados en la experiencia en el Taller de Biodiversidad

Genómica en Ambientes Extremos, realizado en San Pedro de Atacama en 2023. Para más detalle, ver el Anexo 8.

1.2. Outstanding Achievements

There are several outstanding achievements that we would like to highlight:

- Our research team published 72 articles in peer-reviewed journals, with an average impact factor of 4.98. In 2024, Journal Impact Factors saw an average decline across all publishers and categories, making it noteworthy that the average impact factor of our publications remained nearly unchanged from the previous year (the average impact factor of our 2023 publications was 5.11).
- Our researchers organized a wide variety of scientific events in 2024, including the VIII International Conference on Plant Cell Wall Biology with over 120 attendees from 40 research institutions in 25 countries, the COP16 Side Event: New ideas based on omics-sciences, mathematical modeling and remote sensing for ocean conservation tools, held in Cali, Colombia, with nearly 50 attendees that included representatives from the Public Sector, 4 Symposia at the XLVII Annual Meeting of the Chilean Biochemistry and Molecular Biology Society, 2 Symposia at the First Zoology Congress in Chile, the first International School of Science Education, held in Italy with more than 50 attendees, and 5 Interactomics Seminars, one of which was presented in person by an international speaker.
- Our research team shared its work at 45 congresses and scientific meetings in 2024, 34 of which were international. Out of a total of 114 oral presentations and posters, 42 were delivered by students, and 17 by Postdoctoral or Young Researchers.
- 113 students were mentored during 2024 (54 women, 61 men), with 22 completing their theses. The vast majority of those who completed their theses went on to enroll in a Master or D program or began a postdoctoral project, while the others started working in industry.
- Our research team actively participated in establishing and strengthening connections with other sectors, with 25 activities during 2024, including meetings, conferences and panel discussions.
- Our researchers and students took part in 21 outreach activities across 5 of the country's 16 regions, 10 of which were organized by our Center. Through these activities, we engaged with nearly 4,500 individuals, mostly school students. Additionally, in 2024 our Center had 40 appearances in the media.
- We relaunched MI-CGR's signature project with a new leadership and renewed focus: the [Chilean 1000 Genomes Project](#). This initiative aims to characterize the genomic biodiversity of Chile's territory, uncovering the DNA particularities of species that are characteristic and representative of the country. This groundbreaking scientific initiative will provide valuable information on endemic, native, cultural, and commercially important species, potentially paving the way for conservation strategies and the development of biotechnological products applicable to various sectors of the national economy.

2. Scientific and technological research

Scientific research: Research Lines' Development

Our scientific work is strategically arranged in three main lines of research, as well as our research team. **Research line 1 (RL1)** focuses on discovering the molecular and evolutionary basis of animal-plant-microbiome-abiotic interactions in extreme arid (Atacama Desert) and cold (Antarctica) environments. The RL1 team seeks to identify genes and genome features involved in the tolerance to extreme conditions by analyzing existing whole-genome sequence data, as well as to understand convergent evolution in extreme environments.

In 2024, researchers of the RL1 team worked with genomic data from guanacos (*Lama guanicoe*) to study its evolutionary history, its adaptation capacity to extreme environments and its susceptibility to anthropogenic impacts. The guanaco is the largest wild ungulate in South America and is well adapted to a wide range of habitats, including the Sechura Desert, the high Andes Mountains, and the subantarctic Navarino Island. Researchers analyzed differentiation patterns, subspecies divergence, changes in population sizes, and adaptive genomic diversity, almost all linked to environmental variables and colonization events.

Additionally, RL1 team members worked with other two species native to South America, the arboreal marsupial “monito del monte”, and the annual killifish *Garcialebias charrua*. Nocturnal mammal monito del monte (*Dromiciops gliroides*) is recognized as one of the two South American true hibernators and can be found in the Valdivian temperate rainforest, a unique ecosystem that is particularly threatened by climate change. RL1 researchers worked with *G. charrua*, a fish whose embryos go through diapause as an adaptation strategy to extreme environments, to explore the molecular basis of diapause induction using a transcriptomic approach. This project revealed genes, and genome features related to diapause I induction, including several previously unknown proteins. Another team worked with red-tailed tropicbird (*Phaethon rubricauda*) to study its genetic vulnerability to human impact. The study revealed that the Pacific colonies of the species are at genetic risk and vulnerable to future population declines.

Mechanisms mediating global gene expression control in eukaryotic model systems were studied. One of their most relevant models involves the Andean killifish *Orestias ascotanensis*, which inhabits the high-altitude Ascotán Salt Pan, an environment with variable salinity, high UV exposure, low oxygen, and extreme daily temperature fluctuations. These conditions make it an excellent model for studying high-altitude fish biology. Because most of the transcriptomic responses of *O. ascotanensis* to seasonal acclimation remain unexplored, the team has investigated seasonal and tissue-specific transcriptomic profiles. Thus RNA-seq was performed on 42 libraries from gills, skin, and muscle tissues of 14 individuals collected in summer (n=7) and winter (n=7). Each library sequencing exhibited a median of 105 million reads, reflecting an adequate performance that allowed subsequent comparative analyses. Principal component analysis revealed strong tissue-specific expression, and seasonal differential expression analyses identified significant transcriptomic changes within each tissue. Moreover, a bioinformatics pipeline identified 10,365 high-confidence long non-coding RNAs (lncRNAs), predicted by at least three computational tools. Compared to protein-coding genes, lncRNAs exhibited higher tissue specificity, with a predominance of monoexonic structures and

shorter exon lengths. This dataset provides the first comprehensive view of seasonal mRNA and lncRNA expression in *O. ascotanensis* tissues. These results are included in a scientific manuscript that was submitted for publication and that is currently under revision.

The Talabre-Lejía transect (TLT) in the Atacama Desert has been studied for over 14 years by several MI-CGR researchers, as this is an ideal system to study responses of the rhizochemistry to a gradient of extreme abiotic constraints (i.e. elevation, scarcity of water, nutrient deprivation, pH and high solar irradiance). The research addresses whether and how rhizochemicals and associated bacterial communities responded to a linear variation in abiotic constraints across the elevation gradient and investigates the specificity level of this response across plant species. In 2024, starting from a previous study that highlighted convergent responses in multiple chemical families aboveground, hypothesizing that inter-species similarities might also occur belowground at the chemical and bacterial community level. To answer these questions, predictive metabolomics have been combined with soil metagenomics to investigate how rhizochemistry responded to environmental constraints and how it, in turn, shaped soil bacterial communities across stress gradients in the Atacama Desert. The results suggest that rhizochemical adjustments predicted the environment (i.e. elevation, R² between 96% and 74%) of two plant species, identifying rhizochemical markers for plant resilience to harsh edaphic conditions. These metabolites (e.g. glutamic and succinic acid, catechins) were consistent across years and could predict the elevation of two independent plant species, suggesting biochemical convergence. Next, convergent patterns in the dynamics of bacterial communities were also observed across the elevation gradient. Finally, rhizosphere predictors were associated with variation in composition and abundance of bacterial species. Biochemical markers and convergences as well as potential roles of associated predictive bacterial families reflected the requirements for plant life under extreme conditions. Overall, their findings highlighted convergent patterns belowground, which represent exciting insights in the context of evolutionary biology and may indicate unique metabolic sets also relevant for crop engineering and soil quality diagnostics. Besides, these results emphasize the need to integrate ecology with omic approaches to explore plant-soil interactions and to better predict their responses to climate change.

Research line 2 (RL2) aims to unveil the influence of environmental changes on biotic networks and unique ecological niches using mathematical modeling, metagenomics, and systems biology. The RL2 team seeks to find quantitative relationships between the distributions of organisms, their metabolic and gene regulatory functions. In 2024, the RL2 research team worked with unique ecological niches such as the Baiyangdian Lake (China), the Atacama Desert (Chile), Patagonian fjords (Chile), Lake Villarrica (Chile), Antarctic volcanic soils (Antarctica), and Southern African dryland soil (South Africa). RL2 researchers studied bacterial-fungal interactions in compost and bulk soil from a table grape orchard in central Chile, bacterial-protist mutualism interaction between Chilean Patagonian fjords bacteria and toxic *Alexandrium catenella*, bacterial-plant interaction with gram-negative bacteria *Variovorax* and wheat under salt stress conditions, pathogen-environment interactions in the human-impacted and commercially relevant Baiyangdian Lake, and bacteria-archaea-plant interaction in microbial hotspots in dunes colonized by native epiphyte *Tillandsia landbeckii*, as well as the adaptation strategies of giant viruses to low-temperature marine ecosystems, antibiotic resistance of bacteria isolated from Lake Villarrica surface sediments, microbial communities in poly-extreme environmental conditions and in penguin-influenced Antarctic environments.

Associate Researcher Alejandro Maass is the codirector of the CEODOS Chile Mission, a consortium of institutions of scientific excellence such as the Center for Mathematical Modelling, the Center for

Oceanographic Research in the Southwest Pacific, the Center for Climate and Resilience Research, Inria Chile, and our Millenium Institute Center for Genome Regulation, among others. The CEODOS Chile Mission is an associate program to TARA Ocean that aims to provide the country with the first assessment of planktonic diversity with the use of genomics, bioinformatics and groundbreaking data science to quantify ocean's health through the microorganisms responsible for CO₂ absorption and other greenhouse gases.

The role of gene regulation in mediating microbial responses to environmental changes was evaluated. This topic remains largely unexplored even though bacterial communities play crucial roles in global biogeochemical cycles and climate processes. Understanding their responses is essential for predicting the impacts of climate change, particularly on marine ecosystems. Many studies concerning this issue have focused on taxonomic and functional changes, but our project investigated the relationship between shifts in environmental variables and the regulatory potential of transcription factors (TFs) within the oceanic microbiome by analyzing metagenomic data from TARA Oceans expeditions. Specifically, associated 88 classes of TFs with an affinity index to intergenic regions—termed the regulatory profile—which serves as a proxy for TF regulatory potential. The analysis shows that regulatory profiles are sensitive indicators of climate variations, strongly associated with environmental parameters like temperature, salinity, nutrient concentrations, and carbon flux. Focusing on TFs regulating genes in metabolism, carbon cycling, and nutrient stress responses, they link TF activity to key environmental variables. They identified distinct TFs affected by different climate variables; for example, they found that increasing temperatures lead to higher levels of AgaR, highlighting specific regulatory responses to environmental factors. Furthermore, because TFs reduce complexity compared to genes while effectively capturing environmental fluctuations, this approach offers a valuable framework for future ecosystem studies. These insights not only enhance our understanding of microbial adaptation but also contribute to more accurate models of oceanic biogeochemical cycles under climate change. This study is also funded by an additional grant: Exploration Project 13220002, led by two MI-CGR Associate Researchers (Director Alejandro Maass, deputy Director Verónica Cambiazo).

Research line 3 (RL3) aims to generate and test hypotheses related to the impacts of climate change and environmental degradation, and to propose biotechnological solutions to biodiversity conservation and sustainable production in agriculture and aquaculture. For this, the RL3 research team is determined to use genomic tools to provide a more accurate estimation of biodiversity and detect SNPs involved in local adaptation to specific environmental conditions, which can be incorporated into species distribution models under scenarios of climate change. Genomic tools can also help to understand the mechanisms that control commercially important characteristics of fruit crops by integrating omics and phenotyping data. In aquaculture, RL3 aims to understand the physiological and molecular aspects of the bacteria *Piscirickettsia salmonis*, a disease with high impact in the salmonid industry in Chile. With applications in the food, pharmaceutical, and bioenergy industries, RL3 aims to systematically search for pigments, exopolysaccharides, toxins, osmoregulators, antibiotics and antivirals with biotechnological potential, and improve their stability.

In 2024, researchers of the agriculture branch of the RL3 team worked mainly with avocado (*Persea americana*), tara pods (*Caesalpinia spinosa*), Chilean potato (*Solanum crispum*), quinoa (*Chenopodium quinoa*), peach (*Prunus persica*), common bean (*Phaseolus vulgaris*) and inca nut (*Plukenetia volubilis*). The pharmaceutical-health branch of the RL3 team worked in pathogenic bacteria *Salmonella enterica* in surface waters from Latin America, in hydatid disease-causing

Echinococcus granulosus sensu stricto, and the immunostimulant hemocyanin of the Chilean gastropod *Concholepas concholepas*.

Mechanisms underlying different fruit quality traits in a changing environment was recently evaluated integrating omics data (e.g., transcriptomic and metabolomic) and hormonal approach to investigate for example the genomic regulation underlying the blackspot exocarp physiological disorder in Hass avocados. The findings associate this disorder with elevated levels of jasmonates, salicylic acid, cytokinins, and gibberellins in affected black tissues. Additionally, overexpression of genes linked to lignin biosynthesis and long-chain fatty acid pathways was observed, along with the accumulation of fatty acids such as oleic, palmitic, and linoleic acids. These changes suggest that the disorder may result from plant defense mechanisms reinforcing exocarp tissue under postharvest stress. This study highlights the critical role of genomic regulation through specific hormonal and metabolic pathways, providing a foundation for future mitigation strategies via postharvest management and genomic marker selection.

Research has been developed in functional genomics applied to postharvest physiology, with multiple projects focused on improving the production and exportation of Chilean Hass Avocados. According to Fruits from Chile, more than 99% of the avocados that Chile exports are of the Hass variety. Therefore, research on postharvest physiology and sustainable production of Hass avocado are quite relevant for our country. In 2024, projects were dedicated to model the softening behavior of Hass avocado destined to local and distant markets, to study the metabolite profile during ripening of Hass avocados, and to generate a novel omics data integration approach to assess rootstock-scion interactions in Hass avocados. She was also involved in a project to study the effects of delaying the storage of Hass avocados on skin color, bioactive compounds and antioxidant capacity, and another that aimed to uncover phytochemicals quantitative evolution in Hass avocado during ripening. This year a research project was developed on peach (*Prunus persica*) and the gene regulatory network associated with sugar accumulation; additional developed project is related to the formation of contaminants like acrylamide during the production of potato chips from Tara (*Caesalpinia spinosa*) and Chilean potatoes (*Solanum crispum*) and was involved in a publication about proteins from the inca nut (*Plukenetia volubilis*).

On-going research is focused on the molecular mechanisms regulating tomato fruit harvest time during early developmental stages. This involves analyzing the role of a master regulator transcription factor, SINAC072, and its target genes, SIHB12 and SIMYBR1, in modulating fruit development and associated traits. Using innovative genomic tools like CRISPR-Cas9, RNA-seq, and DAP-seq, the group will construct regulatory networks that clarify how these factors influence key phenotypic characteristics.

Also, from the agriculture branch of RL3, additional research developed is on the common bean that opens the possibility to prime plants for modulating the pectin component in order to obtain crops more resistant to diseases; and on peaches that open new avenues for developing novel disease control strategies for stone fruits. Lastly, for the conservation biology perspective, a paper was published on the effects of sustainable agricultural practices on soil microbial diversity, composition, and functions.

For RL3, genomics has been applied to genetic selection in Aquaculture, since the animal production industry relies almost entirely on genetically improved stocks, mostly certain species such as Atlantic salmon, rainbow trout, and tilapia, where a significant proportion of production is derived from

genetically improved individuals. Our project has been using high-density SNP genotyping panels has enabled a more refined dissection of the genetic architecture of quantitative traits and their underlying quantitative trait loci (QTL) through the implementation of genome-wide association studies (GWAS), thereby enhancing our understanding of phenotype-genotype relationships. An example is a paper published in 2024 evaluating the genetic diversity in farmed populations of Nile tilapia (*Oreochromis niloticus*) from Brazil using SNP markers. During 2024, also wild fish species (*Arapaima gigas*) had genome sequenced for a potential use in aquaculture.

For the last decade, *Salmonella enterica* several serovars that are serious human pathogens and can cause the food poisoning disease salmonellosis, have emerged. Salmonellosis is a disease of mandatory notification in Chile and considering the rise of antibiotic resistance worldwide, studies on the genomic characterization of the population structure and antibiotic resistance of *S. enterica* serovar Infantis in Chile 2009–2022, on the genomic landscape of *S. enterica* serotypes Typhimurium, Newport, and Infantis in Latin American surface waters: a comparative analysis, and on the epidemiology, diversity and persistence of *S. enterica* in surface waters of Chile, Brazil and Mexico are extremely important for ecosystemic health.

Scientific research: Chilean 1000 Genomes Project

In 2024, we relaunched MI-CGR's signature project, which aims to generate *de novo* reference genomes of eukaryotic species in Chile and promote scientific knowledge in genomics in the country. From 2018 to date, the Chilean 1000 Genomes Project has explored the genomics of endemic and exotic organisms relevant for the conservation of our genetic heritage, renewable natural resources, agriculture, and aquaculture. Some of them are: *Cistanthe longiscapa*, a plant species from the Atacama Desert, *Vitis vinifera* (sultana grape), *Piscirickettsia salmonis*, a commercially important bacteria as a pathogen of salmon, the genomes of 4 species of *Orestias* fish from the high Andes of Chile, and *Prunus persica*. The latter was a collaborative effort with the International Peach Genome Initiative. Additionally, the genome of *Salmo salar* (Atlantic salmon) was sequenced in a project conducted jointly with centers in Canada and Norway.

For the Chilean 1000 Genomes Project, in 2024 we secured private funding from ORG.one project and Oxford Nanopore Technologies to perform the extraction of high molecular weight DNA and sequencing of reference genomes from endangered species, such as *Lontra provocax*, *Sephanoides fernandensis*, and *Chiasognathus jouscelini*. We also raised funding from national companies for the performance of short-read genome sequencing using MGI technology: from TCL Group for *Hippocamelus bisulcus*, and from AustralOmics for *Pudu puda*. Scientific results from the first year of 1000 Genomes Chile will be showcased in its II Workshop to take place in April 2025.

2.1 Methodological and technical procedures

Research Questions and Hypotheses

At the conception of the MI-CGR, we set some research questions to guide our work. The main ones were:

- What are the fundamental genetic and evolutionary mechanisms used by organisms -and communities of organisms- to adapt and evolve in response to environmental factors and biological interactions?

- How are environmental signals perceived by plants, leading to transcriptional, metabolic, physiological, and ultimately phenotypic changes?
- What mechanisms explain genomic or metabolomic co-occurrence patterns?
- How can regulatory networks be established on a supra-organismal level?
- How can resilience and resistance be a factor in community dynamics in extreme environments or when confronted with local or global perturbations such as climate change?
- How and why are organisms living in the Atacama Desert, Antarctic niches, the ocean and areas near salmon and wine industries? And how are these networks of organisms configured by environmental change?
- How do changing environmental conditions (i.e. drought, climatic events) impact on the production and quality of commercially interesting fruits?

In the past 3 years, new and more specific questions have arisen:

- Is epitranscriptomics a mechanism of adaptation to stress conditions?
- What is the predominant strategy to mobilize genetic elements between organisms in natural extreme environments?
- What are the most frequent defense systems against mobile genetic elements in extreme environments?
- What is the mechanism used by an organism or community of organisms to choose its metabolic phenotype?
- What is the role of facilitation mechanisms for the survival of the species that inhabit the Atacama Desert?
- What are the metabolomic mechanisms associated to the facilitation and structuring processes of plant communities in Atacama?

Methodologies and Techniques

Among the many methodologies and techniques employed by our group in 2024, here we highlight the main ones:

Research line 1 (RL1): Our research explores adaptation and convergent evolution through a multi-omics approach, integrating field experiments under varying environmental conditions with genomic, epigenomic, transcriptomic (mRNA, tRNA), proteomic, and metabolomic analyses.

Our genomic studies include: i) Phylogenomics – phylogenetic reconstruction (e.g., RAxML); ii) Demographic history inference – using methods such as PSMC and Stairway Plot; iii) Population genomics – analyses such as Admixture, PCA, and Fst; iv) Introgression estimation – using tools like D-suite; v) Adaptive evolution – detection of selection signatures (e.g., Fst outliers, RAI_{SD}) and enrichment analysis. Introgressive adaptation is investigated by combining introgression detection methods with selection signature analyses. Convergent evolution is assessed by identifying selection signals on phylogenetic branches of independently evolved clades (e.g., Arctic alcid seabirds vs. Antarctic penguins). Genomic variation under selection and gene expression patterns are analyzed across different environmental conditions (abiotic factors) and in response to biotic interactions, such as with commensal or pathogenic microorganisms.

Research line 2 (RL2): We integrate biochemical (chromatography, spectrophotometry, enzymatic assays, antioxidant capacity), molecular (gene and tRNA sequencing using nanopore technology), and

microbiological techniques (microorganism isolation, culture maintenance of cyanobacteria, bacteria, fungi, and archaea).

We evaluate microbial biomass concentration and diversity in natural and extreme environments (e.g., Atacama Desert soils and hot springs, Antarctic ecosystems, marine environments) through DNA extraction, shotgun sequencing, and Illumina-based metabarcoding. Meta-omics approaches—including metagenomics, metatranscriptomics, and metaviromics—are combined with environmental metadata (soil nutrients, pH, temperature, humidity) to understand microbial dynamics. We employ systems biology, mathematical modeling, and data science approaches. Specifically, we use multi-objective optimization to explore metabolic capacities within microbial communities or specific organisms. Community-level biological characteristics—such as genomic features, metabolic genes, regulatory elements, and taxonomic profiles—are analyzed using machine learning and artificial intelligence tools. Techniques are employed combining systems biology, mathematical modeling, and data science. More specifically, multi-objective optimization techniques to explore the metabolic space determined in bacterial communities or by specific organisms. Abundance of a community's biological characteristics (mostly genomic, such as metabolic genes, regulatory signals, and taxonomy) are evaluated using data learning methods and artificial intelligence.

Research line 3 (RL3): We identify candidate genes associated with aquaculture traits (e.g., growth, immune response) and key agronomic features, particularly those involved in fruit development and ripening. For instance, we study two contrasting *Prunus persica* varieties ('Early Juan' and 'Super August'), which differ in ripening speed, a trait crucial for determining optimal harvest time. Using a multi-omics approach—including methylome and transcriptome profiling (mRNA, lncRNA, sRNA)—we identified candidate genes related to cytokinins and cell wall metabolism, which are likely regulated by DNA methylation. These genes hold promise as targets for gene editing in breeding programs. We are also characterizing a powdery mildew-resistant *Vitis vinifera* variety to identify resistance genes and understand how they reprogram the transcriptome during infection. The genome of this resistant variety is being assembled using HiFi sequencing and Hi-C scaffolding, facilitating high-quality annotation and deeper insight into resistance mechanisms.

In aquaculture research, breeding programs, selection candidates for Atlantic salmon, rainbow trout, and tilapia have been genotyped using high-throughput platforms, such as SNP arrays. Quality control filters are applied to the resulting genotype datasets to ensure reliability and consistency. Tools such as PLINK 1.9 beta and statistical packages in R (e.g., GenABEL) are commonly employed to perform filtering based on parameters such as minor allele frequency (MAF), SNP call rate, and deviation from Hardy-Weinberg equilibrium, among others. The curated SNP data are subsequently used to estimate genomic and genetic breeding values (GEBVs and EBVs, respectively) for selection candidates. These estimations are typically conducted using genomic evaluation methodologies, notably the Genomic Best Linear Unbiased Predictor (GBLUP), implemented via the BLUPF90, software written in Fortran 90/95 designed for mixed model equations in animal breeding. The single-step GBLUP (ssGBLUP) approach integrates both genotypic and phenotypic information in a unified framework, allowing for improved accuracy of selection. Our project also has applies RNA-seq, bacterial whole-proteome mass spectrometry, and confocal microscopy to unravel the regulatory pathways involved in *P. salmonis* infectivity and stress responses during intracellular growth.

Open Science

Our team preferentially uses open access repositories and online research tools. Here we list some of them: IMG/VR v4 (<https://img.jgi.doe.gov/vr/>), GTDB-tk r220 (<https://gtdb.ecogenomic.org/>), Refseq (<https://www.ncbi.nlm.nih.gov/refseq/>), BioArt (<https://bioart.niaid.nih.gov/>), Github (<https://github.com/>), GISAID (<https://gisaid.org/>), and ModENCODE (<http://data.modencode.org/>).

2.2 Associative & collaborative work

Comments to the 2023 Annual Report

We would like to address the evaluation given to our 2023 Annual Report in terms of scientific/technological research, where the only reviewer noted that “*there is little information about how this will extend into the future and produce eventually results that link the three research lines*” and “*the Center should keep up this direction and foster collaboration and interaction between groups*”. We recognize that a Millennium Center like ours is expected to create added value and go beyond funding individual scientific projects. To meet this expectation, we have focused on fostering an environment that encourages synergy and the exchange of diverse perspectives and expertise, as well as providing the necessary resources and support for collaborative research. In 2024, 41% of our publications resulted from collaborative efforts among IM-CRG researchers, marking a significant increase from 25% in 2023. Additionally, 24% of our publications were the outcome of formal collaborative networks, such as the 1000 Genomes Chile Network.

Among the collaborative publications in 2024, we would like to highlight the article titled “Rhizochemistry and soil bacterial community are tailored to natural stress gradients” published in the journal *Soil Biology and Biochemistry* (impact factor 9.8) that involved Associate Researchers Dr. Rodrigo Gutiérrez (RL1) and Dr. Mauricio González (RL2), Adjunct Researcher Dr. Claudio Latorre (RL2), and Young Researchers Francisca Díaz and Constanza Aguado-Norese. This work combined predictive metabolomics with soil metagenomics to investigate how rhizochemistry responds to environmental constraints and how it in turn shaped soil bacterial communities across stress gradients in the Atacama Desert. Authors declared that the results emphasize the need to integrate ecology with omics approaches, including genomics, to explore plant-soil interactions and better predict their responses to climate change.

We would also like to highlight the article titled “Genomes of the *Orestias* pupfish from the Andean Altiplano shed light on their evolutionary history and phylogenetic relationships within Cyprinodontiformes” published in the journal *BMC Genomics* that involved Associate Researchers Dr. Miguel Allende (RL1), Dr. Alejandro Maass (RL2), Dr. Mauricio González (RL2), Dr. Rodrigo Gutiérrez (RL1) and Dr. Ariel Orellana (RL3), Adjunct Researcher Dr. Martín Montecino (RL1), Postdoctoral Researcher Dr. Pamela Morales, and then D students Dr. Camilo Valdivieso and Dr. Felipe Gajardo. This study aimed to clarify the phylogenetic position of *Orestias* within the Cyprinodontiformes order with the use of complete genome sequencing. The team concluded that *Orestias* is not part of the Cyprinodontidae family and submitted that it belongs to the Orestiidae family, as previously suggested, and that it is the sister group of the Fluviphylacidae family. This study was also carried out under the umbrella of the 1000 Genomes Chile formal collaborative network.

Lastly, we would like to highlight the article titled “Life on the edge: Microbial diversity, resistome, and virulome in soils from the union glacier cold desert” published in the journal *Science of The Total Environment* (impact factor 8.2) that involved Associate Researcher Dr. Verónica Cambiazo (RL3), Adjunct Researcher Dr. Jacqueline Acuña (RL2) and Young Researcher Dr. Alexis Gaete. Among other results, this study identified genes as indicators of cold desert soil, that include several putative beta-lactamases and aminoglycoside inactivation enzymes.

Network Projects

In 2023, we set aside special funds for collaborative projects that are led by an Adjunct Researcher and in which multiple Associate Researchers effectively interact with each other and with Adjunct Researchers. These projects -dubbed “Network Projects”- received funding for two years and resulted in students and Postdoctoral Researchers that are co-mentored by more than one MI-CGR Researcher. Here is a summary of the preliminary findings of each Network:

Network 1: We analyzed codon usage bias in transcriptomes of various tissues of *Orestias* fish, collected in winter and summer, and observed little variation between seasons, but a significant bias between different tissues. A parallel study carried out in Atacama Desert cyanobacteria, shows significant variations in the abundance of tRNAs in the *Nodularia* TAL-12 strain, with notable increases in tRNA-Glu, tRNA-Gly, tRNA-Leu, and tRNA-fMet, which are essential for the synthesis of osmoprotectants and stress-related proteins. RNAseq experiments on samples exposed to UV-A irradiation demonstrated that certain tRNA-modifying enzymes, particularly those modifying the anticodon loop, showed altered expression levels, highlighting their role in adaptation to stress in cyanobacterial communities in extreme environments. We have submitted a proposal titled “Abundance of tRNA in Atacama Desert Cyanobacteria by Nanopore Sequencing” to attend the Oxford Nanopore conference, “London is Calling,” scheduled for May 20-23, where we hope to present the results we have obtained so far. This Network is composed of one Associate Researcher, three Adjunct Researchers, one Young Researcher and one student.

Network 2: We performed transcriptomic analysis on sweet cherry (*Prunus avium* cv. *Lapins*) during infection with *Pseudomonas syringae* pv. *syringae* (Pss), which revealed differentially expressed genes. Then, a gene regulatory network (GRN) was built using *Arabidopsis thaliana* as a template, integrating cherry-specific data. Four transcription factors (TFs) —WRKY33, WRKY70, ERF012, and NGA1—and seven target genes (TGs) were evaluated by RT-qPCR after 24-hour elicitation with microbe-associated molecular patterns (MAMPs) Flg22 and xyn11/EIX. All TFs were downregulated by Flg22; NGA1 also responded to xyn11/EIX. Most TGs were repressed, except CASP-like protein, which was upregulated. These results suggest a general repression of TFs and TGs upon MAMP exposure, despite their induction during infection. This Network is composed of one Associate Researcher, one Adjunct Researcher, one Postdoctoral Researcher and one student, Daniela Muñoz; it is also integrated by researchers from formal collaborative networks BioSAV and SYSTEMIX. This work was part of Ms. Muñoz’s Master’s thesis, which earned highest distinction at the University of O’Higgins and was presented at the 6th Argentine Congress of Phytopathology.

Network 3: We conducted a pilot study in six avocado orchards covering Chile's V Region's coastal, intermediate, and interior zones. Amplicon sequencing of 16S rRNA and ITS revealed that microbial

diversity varied significantly between locations and harvest times but not between healthy and disorder-prone avocados in the case of Color Desynchronization with Softening Phenotype. However, specific bacterial and fungal taxa were overrepresented in disorder-prone avocados, as identified through LEfSe analysis and Indicator Species Analysis. Additionally, microbial co-occurrence networks differed significantly between healthy and affected fruits, suggesting that shifts in microbial interactions may influence disorder development. Among the key microbial taxa identified, healthy avocados showed an overrepresentation of bacterial genera such as *Variovorax*, *Sphingomonas*, *Hymenobacter*, and *Curtobacterium*. In contrast, disorder-prone avocados were enriched in fungal taxa, including *Cladosporium*, *Xenosonderhenia*, *Erythrobasidiales*, and *Expbasidium*. These findings suggest that microbial biomarkers can be identified pre-storage, allowing early detection of physiological disorders. Alpha and beta diversity metrics alone did not distinguish healthy from affected fruits, highlighting the need for functional and pathway-level analyses. Additionally, network analysis revealed shifts in microbial interactions, supporting the hypothesis that microbiome changes contribute to disorder onset. These findings emphasize the potential of microbial community profiling in postharvest management strategies and provides evidence for the potential of microbiome-based early prediction of physiological disorders in avocados. Specific microbial taxa and metabolic markers may serve as predictive indicators of fruit quality and disorder susceptibility. Ultimately, this research aims to reduce postharvest losses, enhance fruit quality monitoring, and develop microbiome-based management strategies for sustainable avocado production and export. This Network is composed of three Associate Researchers and four Adjunct Researchers.

This first round of Network Projects are set to finish in 2025, and it will take some time for this collaborative work to translate into collaborative publications, but Researchers and students have already presented their results in scientific events with very positive feedback.

1000 Genomes Chile

Alongside the Network Projects, we engaged in associative work within the relaunched 1000 Genomes Chile initiative, a multidisciplinary and collaborative initiative that brings together leading scientific centers in the country and researchers from top Chilean universities. 1000 Genomes Chile has allowed us to establish collaborative partnerships with national Centers of Scientific Excellence, namely the Advanced Center for Chronic Diseases (ACCDiS), the Center for Mathematical Modeling (CMM), the Institute of Ecology and Biodiversity (IEB), the Millennium Institute for Integrative Biology (iBio), the Millennium Institute of Antarctic and Subantarctic Ecosystems (BASE), and Cape Horn International Center (CHIC). In addition, 1000 Genomes Chile is affiliated to the Earth BioGenome Project (EBP).

2.3 Results and impact

Academic Productivity

During the reported period, we published 72 research articles in peer-reviewed journals and 2 books or book chapters. At the MI-CGR, we recognize the importance of sharing our results and disseminating our findings to the broader research community, extending beyond our immediate academic network, and we are committed to the principle of open knowledge within our possibilities. Despite the rising costs associated with Open Access (OA) publishing, we are proud to report that 65% of our publications were made available in OA journals or in an OA format through traditional or hybrid journals.

As a center with a highly multidisciplinary nature, bringing together fields ranging from mathematics to molecular biology, it is expected that the average impact factor may be influenced by these differences. However, we emphasize that most IM-CRG publications are featured in prestigious journals within the subfields we focus on. But, despite the overall decline in Journal Impact Factors reported in the 2024 Journal Citation Reports, we are proud to share that the average impact factor of our publications has remained essentially unchanged, with only a modest decrease from 5.11 in 2023 to 4.98 in 2024.

We would like to highlight the study of banded penguins that involved Dr. Vianna, two of her students and one postdoctoral researcher, titled “Comparative genomics supports ecologically induced selection as a putative driver of banded penguin diversification”. This study was published in the journal *Molecular Biology and Evolution* (impact factor 11.00) and used comparative genomics to identify the molecular mechanism and genomics adaptive traits that have facilitated the diversification of Galápagos (*Spheniscus mendiculus*), Humboldt (*Spheniscus humboldti*), Magellanic (*Spheniscus magellanicus*), and African (*Spheniscus demersus*) penguins. The study discovered that high temperatures in tropical habitats may have favored selection on loci associated with spermatogenesis, thermoregulation, osmoregulation, hypoxia, and social behavior, leading to reproductive isolation and local adaptation of banded penguins, a key step towards further understanding the genomic basis of adaptation and speciation.

We would also like to highlight the article titled “Adaptation strategies of giant viruses to low-temperature marine ecosystems” published in *The ISME Journal* (impact factor 10.8) and led by Associate Researcher Dr. Beatriz Díez and then D candidate Marianne Buscaglia. This research project analyzed cold adaptations in giant viruses from austral marine environments. The team generated a catalog of giant virus metagenome-assembled genomes (GVMAGs) from austral cold marine environments and combined it with previously published GVMAGs. Their results indicate that giant viruses from the Arctic, Antarctica, and Chilean Patagonia exhibit changes in both the amino acid frequencies of their proteins and the gene content of their genomes compared to temperate giant viruses, changes that potentially enable them to thrive in cold environments. The team proposes that the cold adaptations of giant viruses result from environmental constraints affecting virus-host co-evolutionary processes. Such processes include giant virus-encoded genes that lead to proteins with features enhancing host fitness under adverse environmental conditions, such as low temperatures, and that ensure efficient viral housekeeping such as transcription, genome maintenance, and viral packaging. Dr. Buscaglia went on to do a postdoctoral project with Dr. Alejandro Maass to apply her expertise with data from TARA Oceans expeditions. It is worth mentioning that this project turned out to be very attractive to the media as it was led by a female scientist and the topic is out of the ordinary.

Finally, we would like to make the point that research with the highest impact factors is not always the most engaging or appealing to the general public. A clear example of this is the article titled “Genomes of the Orestias pupfish from the Andean Altiplano shed light on their evolutionary history and phylogenetic relationships within Cyprinodontiformes” published in *BMC Genomics*. This study received widespread media attention, with coverage in both national and international outlets.

Social Impact

In 2024, our researchers and students participated in 21 outreach activities across 5 of the country’s 16 regions, with 10 of them organized by our Center. Through these efforts, we were able to engage with nearly 4,500 people, including both children and adults.

Most of our activities were aimed at school children and vulnerable educational institutions, because our primary outreach goal since the beginning of our Center has been to bring genomic sciences and genome sequencing into classrooms and directly to the public. Thus, in July we visited the Araucanía Region to organize a “Festival of Genes” in the Cultural Center of the town of Nueva Imperial with the support of Adjunct Researcher Dr. Jacqueline Acuña from the University of La Frontera (UFRO), two postdoctoral researchers and two D students. At the Cultural Center we installed a science fair with demonstrations, experiment displays, and a short talk about basic genomics. Dr. Acuña also brought her “Mobile Laboratory”, a fully equipped van for fieldwork, and students were able to go inside. In one day, we received nearly 400 children and their teachers from different local schools. In September, we visited the Antofagasta Region to organize another “Festival of Genes”, this time with the support of Adjunct Researcher Dr. Alexandra Galetovic from the University of Antofagasta and three D candidates. In three days, we visited the cities of Antofagasta, Tocopilla and Taltal, where we installed the festival in three schools and one cultural center, and we also offered a conference for university students. Overall, the scope of this activity was a little over 500 people. In November, we visited the Atacama Region for an activity focused on two schools, one in the city of Copiapó and the other in Vallenar. There we performed the sequencing of the genome of *Cistanthe longiscapa*, a characteristic plant of the Desierto Florido (Flowering Desert), with the support of Associate Researcher Dr. Ariel Orellana’s team from Andrés Bello University, that included one D candidate and one research assistant.

2.4 Summary table

Category of Publication ¹	MSI Center Members	Number of Publications coauthored by students	Total Number of Publications
ISI/WOS Publications or Similar to ISI/WOS Standard	Associate Researchers	15	41
	Others Researchers	3	27
SCOPUS Publications or Similar to SCOPUS Standard	Associate Researchers	1	3
	Others Researchers	0	0
SCIELO Publications or Similar to SCIELO Standard	Associate Researchers	0	0
	Others Researchers	0	2
Books & Chapters of Books	Associate Researchers	0	2
	Others Researchers	0	0
Other Scientific Publications	Associate Researchers	0	0
	Others Researchers	0	0
Total		19	75

¹ We checked the journal's listing on the Web of Science Master Journal List, either by title or ISSN number.

3. Other relevant scientific achievements

Scientific Events

In 2024, our Associate and Adjunct Researchers organized a wide variety of scientific events, including the VIII International Conference on Plant Cell Wall Biology with over 120 attendees from 40 research institutions in 25 countries; this was organized by Dr. Ariel Orellana. Dr. Alejandro Maass

organized the COP16 Side Event: New ideas based on omics-sciences, mathematical modeling and remote sensing for ocean conservation tools, held in Cali, Colombia, with nearly 50 attendees that included decision makers. Dr. Miguel Allende was part of the organization of the first International School of Science Education, held in Italy with more than 50 attendees. Dr. Rodrigo Gutiérrez, Dr. Ariel Orellana, Dr. Martín Montecino, and Dr. Mauricio Latorre organized one Symposia each at the XLVII Annual Meeting of the Chilean Biochemistry and Molecular Biology Society, while Young Researchers and students organized 2 Symposia at the First Zoology Congress in Chile.

We also organized 5 Interactomics Seminars, one of which was presented by an international speaker, and the first 1000 Genomes Chile Workshop, with over 100 attendees. The first 1000 Genomes Chile Workshop had Dr. Camila Mazzoni, founder of the European Reference Genome Atlas, as keynote speaker.

Additionally, our research team shared its work at 45 congresses and scientific meetings in 2024, of which 34 had an international scope. It is worth highlighting that MI-CGR Researchers were Keynote Speakers in 18 of these events. Also, out of a total of 114 oral presentations and posters, 42 were delivered by students, and 17 by Postdoctoral or Young Researchers.

Technological Transference and Industrial Property

A relevant scientific achievement that was pointed out by the reviewer of our 2023 Annual Report was patenting, or the lack of it: *“Given that the Center has interactions with companies and industry and given that the three research lines are something that companies should be interested in, one would expect that this aspect is on the scientists’ mind and actively pursued”*. While it is true that our researchers hold long-standing connections with the productive sector, patenting and technological transference are not included in the 4 main aims of a Millenium Institute (i.e. frontier scientific research, training of young scientists, formal collaborative networks, and scientific communication). Therefore, it is not our priority to patent or transfer the results of our scientific work. Nonetheless, Adjunct Researcher Dr. Mauricio Latorre from the University of O’Higgins, presented two patents in 2024, both regarding a bioleaching method using bacterial strains *Pseudomonas* sp. and *Pseudomonas rustica* isolated from mining tailings. The presented patents also included D candidates and Master students, all tutored by Dr. Latorre.

We also submitted a request to the National Institute of Industrial Property for the registration of the brand “1000 Genomes” to our name. This will allow us the exclusive use of the brand and the legal protection of all its products (e.g. publications and outreach material). This request is being assessed, and we hope to have news in early 2025. In addition, as the MI-CGR is the author of the [children's book](#) produced with the 2023 MSI Projection to the External Environment, we own the copyright to the book. We have no intention of selling this book, rather, it is given out for free at the different outreach instances that we participate in.

Editorial Boards

Seven Associate Researchers and three Adjunct Researchers are part of the Editorial Boards of eleven scientific journals, all of which are ISI/WoS or Similar to ISI/WoS standard. These journals are some of the top in their respective fields in the Scimago Journal Rank.

- Dr. Alejandro Maass has been on the Editorial Board of the journal Discrete and Continuous Dynamical Systems since 2019. This journal publishes peer-reviewed papers of the highest quality on the theory, methods and applications of analysis, differential equations and

dynamical systems and is in the top 10 journals on discrete mathematics and combinatorics in the SJR.

- Dr. Romina Pedreschi has been on the Editorial Board of the journal *Postharvest Biology and Technology* since 2016. This is a top journal in the field of postharvest biology and technology. This journal is in the top 30 journals on agronomy and crop science in the SJR.
- Dr. Rodrigo Gutiérrez has been on the Editorial Board of the *Journal of Experimental Botany* since 2010, *Molecular Plant* since 2017, and *The Plant Cell* since 2018. These are in the top 30 journals on plant science in the SJR.
- Dr. Ariel Orellana has been on the Editorial Board of the journal *Frontiers in Plant Sciences* since 2012. This journal is in the top 60 journals on plant science in the SJR.
- Dr. Beatriz Díez has been on the Editorial Board of the journal *International Microbiology* since 2018. This journal is in the top 100 journals on microbiology in the SJR.
- Dr. Verónica Cambiazo, Dr. Mauricio González and Dr. Martín Montecino are on the Editorial Board of the journal *Biological Research*, published by the Society of Biology of Chile. This is an open access, peer-reviewed journal that encompasses diverse fields of experimental biology, such as biochemistry, bioinformatics, biotechnology, cell biology, cancer, chemical biology, developmental biology, evolutionary biology, genetics, genomics, immunology, marine biology, microbiology, molecular biology, neuroscience, plant biology, physiology, stem cell research, structural biology and systems biology.
- Dr. Claudio Latorre has been on the Editorial Board of the journals *Quaternary Science Reviews* since 2022, and *Climate of the Past* since 2021. *Climate of the Past* is the number one journal on paleontology in the SJR, while *Quaternary Science Reviews* is in the top 20 journals on geology in the SJR.

Awards and Accolades

We are aware that the researchers that constitute our Center are highly distinguished in their respective fields and have made -and continue to make- great impact in the specific topics they research. This was recognized by external entities in different ways:

- In early 2024, Deputy Director Dr. Juliana Vianna was appointed Councilor of the Society for Molecular Biology and Evolution (SMBE). The SMBE Council (2024-2026) is composed of 15 researchers and Dr. Vianna is one of only two Latin American representatives.
- In March of 2024, Dr. Liane Bassini was elected Vice president of the Association of Veterinarians Specialized in Aquaculture, which promotes the development of veterinarians in aquaculture production, driving innovation and knowledge in the field.
- In April of 2024, Dr. Claudio Meneses was elected President of the Chilean Society of Plant Biology, which brings together researchers in plant biology from the country.
- In July of 2024, Dr. Rodrigo Gutiérrez was appointed Associate Member of the European Molecular Biology Organization (EMBO), recognizing his academic career in the life sciences and his significant contribution to the field of biological research at an international level. The same month Dr. Alejandro Maass was appointed Member of the *Conseil d'orientation* of the National Institute for Mathematical Sciences and their Interactions, CNRS-France. Last year, Dr. Maass had been honored as a CNRS Ambassador Fellow, a title awarded for the first time to outstanding researchers.
- Lastly, in August of 2024, Dr. Ariel Orellana was appointed Member of the Science Academy of Latin America, an honor that highlights his outstanding career and work in cell biology, biochemistry, and plant genomics. His appointment underscored the impact his research and teaching have had on the scientific development of the region.

4. Education and Capacity Building

Education, Training and Capacity Building:

MSI RESEARCHER	NUMBER									TOTAL NUMBER PER MSI RESEARCHER
	Undergraduate students			Graduate students						
				Masters			Doctoral			
	F	M	ND	F	M	ND	F	M	ND	TOTAL
Miguel Allende	0	0	0	1	2	0	0	0	0	3
Juliana Vianna	2	3	0	1	1	0	6	2	0	15
Rodrigo Gutiérrez	1	1	0	0	0	0	4	3	0	9
Romina Pedreschi	0	0	0	1	1	0	2	1	0	5
Beatriz Díez	3	4	0	0	2	0	2	3	0	14
Ariel Orellana	0	0	0	0	0	0	0	1	0	1
Alejandro Maass	0	0	0	0	2	0	0	1	0	3
Verónica Cambiazo	0	3	0	0	0	0	2	0	0	5
Mauricio González	0	0	0	0	0	0	1	0	0	1
Alexandra Galetovic	1	2	0	1	0	0	0	0	0	4
Álvaro Glavic	1	2	0	1	2	0	2	0	0	8
Aurora Gaxiola	5	1	0	1	1	0	3	3	0	14
Angélica Reyes	0	0	0	1	0	0	1	0	0	2
Martín Montecino	0	2	0	0	0	0	1	1	0	4
Jacqueline Acuña	0	0	0	0	0	0	1	1	0	2
Liane Bassini	0	2	0	0	0	0	0	0	0	2
Mauricio Latorre	2	1	0	4	1	0	0	2	0	10
Claudio Latorre	3	6	0	0	0	0	1	0	0	10
Claudio Meneses	0	0	0	0	0	0	1	2	0	3
TOTAL	18	27	0	11	12	0	27	20	0	115

Formal Training Programs

MI-CGR Researchers integrate a variety of Academic Councils in their institutions and actively participate in teaching activities:

Director Dr. Miguel Allende together with Associate Researcher Dr. Mauricio González and Adjunct Researcher Dr. Álvaro Glavic from the University of Chile integrate the Academic Council of the D

Program in Cell Biology, Molecular Biology and Neurosciences. Dr. Allende is also an Adjunct Member of the Academic Council of the D Programs in Biotechnology and Microbiology; he too serves as coordinator and lecturer in these programs' courses. In addition, Dr. Allende regularly acts as an external evaluator in postgraduate thesis examinations in different universities across the country. Dr. Glavic also serves as lecturer in the D Program in Biomedical Sciences and undergraduate degrees in Molecular Biotechnology Engineering, Biology, and Chemistry. Dr. González together with Associate Researcher Dr. Verónica Cambiazo from the University of Chile integrate the Academic Council of the D Program in Molecular Biotechnology. Dr. González also integrates the Academic Council of the D programs in Nutrition and Food Technology, and Agricultural and Forestry Sciences. Dr. Verónica Cambiazo also integrates the Academic Council of the D programs in Agricultural and Forestry Sciences.

Deputy Director Dr. Juliana Vianna and Adjunct Researcher Dr. Aurora Gaxiola from the Pontifical Catholic University of Chile integrate the Academic Council of the D Program in Biological Sciences with specialization in Ecology. Dr. Vianna also integrates the Master Program in Natural Resources from her university, and of the D Program in Bioinformatics of the Andrés Bello University.

Associate Researcher Dr. Alejandro Maass from the University of Chile integrates the Academic Council of the undergraduate program of Mathematical Civil Engineer, of the Master programs of Engineering Sciences with a specialization in Applied Mathematics, Data Science, and Medical Informatics, and of the D Program of Engineering Sciences with a specialization in Mathematical Modeling. He is also involved in the development of a new joint D Program in Data Science between the University of Chile and the Pontifical Catholic University of Chile. He also serves as lecturer in these programs' courses and as a member of evaluation committees.

Associate Researcher Dr. Beatriz Díez was the coordinator of the Specialization Course in Molecular Genetics and Microbiology of the D Program in Biological Sciences and coordinator of the undergraduate course in Biology of Microorganisms at Pontifical Catholic University of Chile until her transference to Mayor University, where she will integrate the D Program in Integrative Genomics and other courses.

Associate Researcher Dr. Romina Pedreschi from the Pontifical Catholic University of Valparaíso integrates the Academic Council of the Master Program in Agronomical and Environmental Sciences and the D Program in Agricultural and Food Sciences.

Associate Researcher Dr. Rodrigo Gutiérrez together with Adjunct Researcher Dr. Claudio Meneses from the Pontifical Catholic University of Chile integrate the Academic Council of the D Program in Biological Sciences with specialization in Molecular Genetics and Microbiology. Dr. Meneses is the Director of the D Program in Vegetal Biotechnology and Dr. Gutiérrez integrates its Academic Council.

Associate Researcher Dr. Ariel Orellana from the Andrés Bello University integrates the Academic Council of the D Program in Biotechnology and also the D Program in Bioinformatics and System biology at the UNAB.

Adjunct Researcher Dr. Alexandra Galetovic from the University of Antofagasta coordinates undergraduate courses such as Toxicology, Biochemistry of Extremophile Microorganisms, and Enzymology for the degrees of Biochemistry, Marine Biology, Medicine, and Nutrition.

Adjunct Researcher Dr. Mauricio Latorre from the University of O'Higgins is the Director of the Master Program in Biotechnology and integrates the Academic Council of the D Program in Bioengineering from his university and the Master Program in Nutrition and Food with specialization in Healthy Food from the University of Chile.

Training Present and Future Researchers

In 2024, 113 students received training and mentorship from MI-CGR Researchers. In addition, we had 9 Young Researchers and 25 Postdoctoral Researchers actively working towards the objectives of the MI-CRG. Students and young researchers were co-authors in several publications: 26% of our publications had students as co-authors (in 6 publications, MI-CGR students were first authors), and 35% of our publications had Young or Postdoctoral Researchers as co-authors (in 6 publications they were first authors). Students and young researchers were crucial for the dissemination of our work in congresses and scientific meetings in 2024: out of a total of 114 oral presentations and posters in 44 events, 42 were delivered by students, and 17 by Postdoctoral or Young Researchers. Students and young researchers also took part in 14 of the 21 outreach activities we had in 2024. It is worth mentioning that our students integrate several of our active formal collaborative networks.

During the reported period, 22 students completed their thesis projects, of which 16 were undergraduate students, 4 were Master's, and 2 were D. It is worth noting that students from RL3 who finished their thesis in 2024 went on to secure a position in the industry, while students from RL1 and RL2 started Master or D programs. We mostly rely on the connections of our Researchers for the insertion of graduates into the academic world and that has proven effective since the beginning of the Center.

Out of the 113 students, 53 (47%) were female, 59 (52%) were male and 1 (1%) was non-binary. Last year, the same percentage (47%) of our students were female and, even though these are good percentages, we are outlining a formal plan to incorporate more female students, with an emphasis on regional students. We are also working on maintaining the proportion of co-authorship of students, as last year 26% of our publications had students as co-authors.

In 2024 we hosted two internships: one is a Postdoctoral Researcher from Spain who will finish her internship in late 2025 and the other one was a Design student from the University of Chile who has finished her internship. One of our students did an internship in the Houston Methodist Research Institute, Texas, with tutor Dr. Diana Panesso, who studies the molecular epidemiology of staphylococci and enterococci, and the molecular and genetic basis of antibiotic resistance.

5. Collaborative networks

We increased our Formal Collaboration Networks from 5 (2023) to 23. As mentioned previously, some networks are completely new, while others are the result of the formalization of existing collaborative partnerships. It is worth mentioning that 24% of the research articles we published in 2024 resulted from a Formal Collaboration Network.

In terms of national collaboration, the main source of collaboration with external institutions and researchers has been the 1000 Genomes Chile Project. It has become a scientific network with over 50 people from the main universities and research centers in Chile. We too share researchers and students with some of the centers associated to 1000 Genomes Chile, such is the case of the Millenium Institute of Integrative Biology, the Millenium Institute of Biodiversity in Antarctic and Subantarctic Environments, the Institute of Ecology and Biodiversity and the Cape Horne International Center.

1000 Genomes Chile has allowed us to leverage resources from the private sector. We secured private funding from the ORG.one project and Oxford Nanopore Technologies to perform the extraction of high molecular weight DNA and sequencing of reference genomes from endangered species, such as *Lontra provocax*, *Sephanoides fernandensis*, and *Chiasognathus jousselini*. We also raised funding from national companies for the performance of short-read genome sequencing using MGI technology: from TCL Group for *Hippocamelus bisulcus*, and from AustralOmics for *Pudu puda*.

Adjunct Researcher Dr. Mauricio Latorre is the Director of a collaborative center with public funding (Systems Biology Center for the study of extremophile communities from mining tailings) and codirector of a center for Systems Biology for Plant Health at his university. Researchers and students from both these centers have been intensively working together with the MI-CGR team in 2024, specially in our Network Project 2.

While as for international collaboration, Associate Researcher Dr. Alejandro Maass is the former Director of the Center for Mathematical Modeling (CMM) and current codirector of the CEODOS Chile Mission, an associate program to TARA Ocean. As Dr. Maass is an active member of the CMM and Fellow Ambassador at France's National Agency for Scientific Research (CNRS), we have been able to benefit from his international connections. Thus, Associate Researcher Dr. Beatriz Díez and her students have been involved with TARA Ocean and the Global Ocean System Ecology & Evolution (GO-SEE) program. Also, through 1000 Genomes Chile, we have had permanent communication with the Earth BioGenome Project and Dr. Juliana Vianna, MI-CGR Deputy Director and 1000 Genomes Chile National Coordinator, has participated in their monthly meetings.

6. Outreach and connections with other sectors

a) Outreach and Projection to the External Environment:

Our goal in terms of outreach and science communication is to bring science closer to non-academic audiences. We have been pursuing this goal through the organization of activities that involve real, first-hand science experimentation that is accessible to lay people. As mentioned previously, our focus has been the education ecosystem, where we aim to teach scientific concepts to school children, while also involving the teachers and giving them the tools to continue on their own after the activity is over. Due to technological advances, sequencing nucleic acids (genomes) outside of the lab is feasible and can be a powerful way to engage the citizenry and disseminate knowledge on the power of genomics for human health, environmental protection, and exploration of biodiversity and population genetics.

The reviewer to our 2023 Annual Report suggested that “*the Center should aim at even more activities across the country*”. We had already set this goal for 2024: to broaden the scope of our outreach efforts and to reach unfrequented locations. Chile is one of the longest countries in the world, with 5,415 kilometers separating its most northern and southern cities. Most of our researchers work in Santiago, the capital of the country. In 2024 our outreach team travelled nearly 680 kilometers to the Araucanía Region to carry out an outreach activity that hosted over 400 school children. After that, the team went to Pucón (785 kilometers away from Santiago), where they put together an activity that gathered 40 children from local schools. Then, the team travelled almost 1,336 kilometers to the Antofagasta Region, where they carried out 4 outreach activities that together convened around 500 children. It is worth mentioning that two of the cities we visited, Tocopilla and Taltal, are not usually included in activities of this kind. Lastly, the team traveled approximately 837 kilometers to the Atacama Region to conduct the sequencing of *Cistanthe longiscapa* with school children from Copiapó and Vallenar.

The outreach team together with the Center’s researchers also organized a wide variety of outreach activities in Santiago. These included a science fair for World Penguin Day and DNA Day in March, and a Biotechnology Workshop for high school students. We also were invited to participate in multiple events, such as the National Festival of Science organized by the Ministry of Science, Technology, Knowledge and Innovation, the Science Congress of the National Institute (an emblematic school), the Science Fair of the National Museum of Natural History, among others.

It is important to highlight that in 2024 we published the two pledged products from the 2023 MSI Projection to the External Environment: a [children's book](#) and a [documentary video](#) (freely available on our website), both based on the experience at the Genomic Biodiversity in Extreme Environments Workshop held in San Pedro de Atacama from September 30 to October 6, 2023.

In addition, 1000 Genomes Chile, which we relaunched in 2024, was conceived with a strong element of dissemination and outreach. Before the MI-CRG, 1000 Genomes Chile had organized two versions of the educational program “Chile Sequences Chile” where children from schools across the country participated in the sequencing of the genome of the “*chanchito de tierra*” (land pig) and “*tijeretas*” (earwigs). The latter resulted in a scientific publication that included the school children as coauthors (Kobayashi et al. 2023). In both cases, we held a nationwide competition and selected applications favoring underrepresented populations and regions. School students took part in the collection of the samples, identified the sampled animals, and carried out the sequencing work in their schools in a synchronously coordinated experience. The experience had a significant impact on their motivation, understanding of the science involved, and on their future career choices.

Thus, when we relaunched 1000 Genomes Chile, we articulated a science outreach and education team committed to bringing science to all corners of the nation. Aside from participating in all the activities mentioned above, 1000 Genomes organized a poll open to the public to choose their favorite species and help us select the first species to be sequenced. In the first open vote, with more than 2,000 participants, the *pudú* (*Pudu puda*) was the winner; huemul (*Hippocamelus bisulcus*) took the second place. The *pudú* is the smallest deer species in existence, and the huemul is the southernmost deer in the world; huemul is also on our national shield. In the second open vote, which received almost 17,000 votes, the winner was *Copiapoa cinerea*, a globular cactus characteristic to the North of Chile.

Finally, in 2024 our researchers made 40 appearances in the media. It is worth highlighting that 4 of them were in international media outlets and 5 were in regional media. Also, almost half of these articles covered the 1000 Genomes Chile Project, revealing the high level of public interest in the initiative.

Looking ahead, our goal is to broaden the participation of researchers and students in outreach activities and media engagements. In the past, we often relied on the same individuals, as they were more comfortable and readily available for this type of work. However, since 2024, we have been actively working to involve a more diverse group of researchers and students, and we plan to continue expanding this effort in the following period.

b) **Connections with other sectors:**

As mentioned before, our researchers hold long-standing connections with the productive sector, in particular with representatives from the agriculture and aquaculture industry. In 2024, our research team actively participated in establishing and strengthening connections with other sectors, with 25 activities that included meetings, conferences and panel discussions. Here we highlight some of them:

Associate Researcher Dr. Romina Pedreschi held meetings with agricultural companies like Danper Trujillo (Perú), ProHass (Perú), and Polar Fruit International, to provide technical advice for issues regarding surface browning and discoloration in table grape and plants resilience to climate change. Dr. Pedreschi also met with Gama (company) to prepare an application to a public fund and a project related to climate change adaptation.

Associate Researcher Dr. Ariel Orellana met with the Research and Innovation Center from Concha y Toro vineyard, as he has been collaborating with the Center for many years. Dr. Orellana was also invited by the Ministry of Environment to deliver a conference in Atacama on his work on *Cistanthe longiscapa* in the commemoration of the National Environment Day.

As a well-known expert in genomics, Director Dr. Miguel Allende was invited by the Ministry of Health to present on the state-of-the-art of genomics research in a meeting to discuss the content of a new law. Dr. Allende together with Deputy Director Dr. Juliana Vianna and Adjunct Researcher Dr. Alexandra Galetovic met with Minera Escondida Foundation, that implements outreach programs for school children from the Atacama Region, where the mining company operates. The purpose of the meeting was to obtain their support for our outreach activities. Dr. Vianna was also part of the First Seminar of Wild Fauna Rehabilitation Centers, where she represented 1000 Genomes Chile.

Dr. Juliana Vianna and Outreach Director Milena Murillo led a visit to Rapa Nui in preparation for the MI-CGR Workshop on Genomic Biodiversity in Extreme Environments, that will take place in April-May of 2025. There, they met with the Island's Councilor and the Marine Research Unit. They also met with authorities from the local indigenous community and with the principals of the schools that will participate in the Workshop.

Associate Researcher Dr. Alejandro Maass met with Sticta, a company that designs and optimizes proteins for specific applications, to support the metabolic modeling of porcine cells to improve cultured meat production. Dr. Maass also met with the French Facility for Global Environment (FFEM) for the development of a mathematical-genomic methodology to design plankton protection zones for public policies. Also, Dr. Maass hosted a panel discussion in COP16 titled "New ideas based

on omics-sciences, mathematical modeling and remote sensing for ocean conservation tools”, which gathered experts and representatives from the public sector.

Associate Researcher Dr. Beatriz Díez met the Chief Technology Officer of Zymvol, a Barcelona-based company that combines bioinformatics and molecular modeling to accelerate enzyme discovery and design, as the company expressed interest in Dr. Díez metagenomic samples from thermal and Antarctic systems to search for enzymes with biotechnological potential.

As Director of the SYSTEMIX Center at University of O’Higgins, Adjunct Researcher Dr. Mauricio Latorre met with Minera Valle Central, a mining company with operations in the O’Higgins Region that will collaborate with Dr. Latorre’s Center.

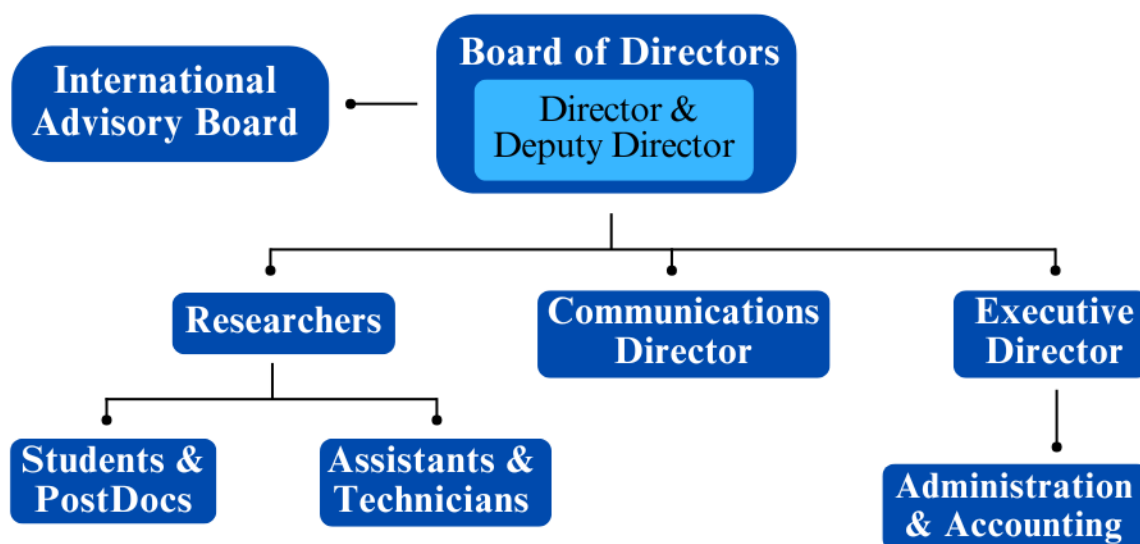
Finally, Adjunct Researcher Dr. Liane Bassini, newly elected Vice president of the Association of Veterinarians Specialized in Aquaculture, held a meeting with SERNAPESCA, the National Service for Fishing and Aquaculture, to align efforts to promote the responsible use of antibiotics, strengthen current and future regulations, and consolidate more sustainable and regulated aquaculture.

7. Administration, Governance and Financial Status

Organization and administration:

2024 was the first year in which the MI-CGR operated as a fully independent organization, managed by the Foundation Center for Genome Regulation created in 2023. The Foundation held four official Board of Directors meetings as mandated by our charter. One of the outcomes of these meetings was the decision to sign employment contracts with the Executive Director and Communications Director. Another decision was to formulate and approve a Code of Conduct and Ethics, and a Good Practices Manual, that include guidance on research misconduct, ethical use of public resources, transparency and evaluation practices, among others.

One of our commitments to the National Agency for Research and Development was to formalize the relationship between our Center and the host institutions—a goal we successfully achieved in 2024. This means that our Center now has a formal collaborative relationship with four of the most important higher education institutions in the country, which will greatly facilitate both our research activities and the training of young researchers. Looking ahead to 2025, our goal is to formalize ties with the three regional institutions to which some of our Adjunct Researchers are affiliated, in order to further expand our collaborative network with universities across the country.



Category	Female	Male	TOTAL
Assistant & Technicians	22	14	36
Administrative Staff	4	2	6
TOTAL	26	16	42

Financial Status:

While the reporting period for this Report is from January 1st to December 31st, our financial year begins at the end of July, when we receive the financial contribution from the Millenium Science Initiative (MSI). This incongruity makes financial reporting quite complicated. Nonetheless, the total amount of funds transferred from MSI to the MI-CGR for the reported period was \$840,000,000 CLP, which is approximately \$869,400 USD. In addition, the MI-CGR received additional funds through a wide variety of projects secured by our Researchers: 25 Fondecyt ANID, 1 ANID Exploration Fund, 3 ANID Fondecy, 2 ANID FONDEF, 2 Regional Centers, 1 INACH (Chilean Antarctic Institute), among other national and international funds. The total yearly amounts per project were adjusted for the reported period, yielding a total of \$308,333,196 CLP for 2024. This is evidence of the competitiveness of our Researchers and their formidable capacity to leverage additional funds.

Additionally, we received funding from the MSI Projection to the External Environment to develop an outreach project in 2025. This will be executed in the MI-CGR Workshop on Genomic Biodiversity in Extreme Environments, that will take place in April-May of 2025 on the Island of Rapa Nui.

Category	Total amount [USD]
Salaries	559,871.27

Infrastructure	11,954.68
Investments	3,620.96
Operational Expenses	320,075.48
Total	895,522.39

Total Funding:

Funds	2024 Sources of Funding	
	Amount [\$]	Percentage of resources used by the Center [%]
MSI	840,000,000	69,53
ANID (Fondecyt)	71,933,196	5,95
ANID (Millenium)	82,000,000	6,79
ANID (Fondequip)	7,500,000	0,62
ANID (Exploration)	57,000,000	4,72
ANID (Regional Centers)	30,000,000	2,48
ANID (Others)	53,000,000	4,39
Other public funds (INACH)	250,000	0,02
Private funds	66,500,000	5,50
TOTAL	1,208,183,196	100

Expenditure structure disaggregated for each of the sub-items:

Type of Expense	Total Amount [\$]
Scientific Staff Personal Científico	165.000.000
Technical Staff Personal Técnico	267.279.255
Administrative Staff Personal Administrativo	59.040.000
Communications Staff Personal de Comunicaciones	27.840.000
Investments Inversiones	3.396.458
Infrastructure Infraestructura	11.213.489
Consulting Consultorias	25.470.798

8. Other achievements [OPTIONAL]

Support to Applications and Researchers

As a Research Center with a well-known reputation and acclaimed Researchers, we strongly believe that we must support the development of new research projects and the promotion of early-career scientists. In 2024, we offered institutional support for two applications to the Regional Fund for Productivity and Development and one to the Salar Research Fund, as well as support for the applications of early-career scientists to competitive funds and academic positions.

9. Negative or positive aspects that you would like to address in order to understand the context in which the center developed its work during the reported period

Relevant Positive and Negative Aspects

Among the positive aspects that we would like to address for the reviewers to understand the context in which the MI-CRG developed its work during 2024, we would like to highlight the efficiency of our executives at ANID, who always responded to our requests and queries on time. We would also like to recognize the efforts of the Agency to improve the conditions in which our Millenium Institutes operate.

Among the negative aspects that we would like to address for the reviewers to understand the context in which the MI-CRG developed its work during 2024, we would like to mention that the high cost of publishing Open Access may prevent publication in this format, even when our Center is committed to the promotion of open science. In the same topic, we would like to refer to the IM-CRG's annual budget, which is provided in Chilean pesos and without adjusting for yearly inflation. In 2024 it was also affected by the rise in the prices of inputs and services for research and administration. For example, in 2023 the yearly budget in US dollars was \$1,050,000 USD, while in 2024 it fell to 869,400 USD. The money provided will continue to lose value and this is detrimental for our research endeavor.

On a different topic, in the 2024 Journal Citation Reports we saw average Journal Impact Factors (JIFs) decline across the board in almost all categories and across almost all publishers. Even when the average impact factor for our 2024 publications did not differ greatly from 2023, the overall decline in JIFs certainly impacted our academic impact.

Finally, we would like to address how research professionals are categorized by our National Agency of Research and Development, and in consequence, in our Center. In other countries, these professionals are dubbed 'scientists' and, in many cases, they do not have a D but are project leaders and have relevant positions in research articles, frequently as main authors. According to our National Agency, these professionals must be categorized as 'technicians' because they are neither researchers nor students. This is the case for many engineers, biochemists, and bioinformaticians in our Center, who make relevant contributions to our research and training objectives. We would like to encourage our National Agency to update its classification system in order to recognize not only these professionals, but also other professionals that are fundamental to the scientific endeavor and currently do not belong in the existing categories.

10. Annexes:**Annex 1.- Research Lines**

Nº	Research Line	Research Line Objectives	Description of Research Line	Researcher	Research Discipline	Starting Date	Ending Date
1	Functional genomics of adaptation and convergent evolution	Use a genomic approach to investigate the independent evolution of similar traits in different lineages.	Convergent evolution generally involves the same genes, and with this line of research we seek to understand the genetic basis of the evolution of similar traits in different	Martín Montecino Leonard. Miguel Allende Connelly. Rodrigo Gutiérrez Ilabaca.	Molecular biology Microbiology. Mathematical sciences	01-07-2022	23-06-2032

			lineages to determine which mutations, either in a gene or in the genetic sequence, are responsible for modifying a particular trait.	Eleodoro Riveras Hernandez.	Cellular Biology		
				Álvaro Glavic Maurer.	Genetics and evolution		
				Alexandra Galetovic Carabantes.	Botanics		
				Violeta Natalia Kallens Meza.	Zoology.		
				Juliana De Abreu Vianna.	Ecology and environmental sciences.		
				Colomban de Vargas .			
				Grace Isabel Armijo.			
				Francisca Díaz Aguirre.			
				Tomás Moyano Yugovic.			
				Rasmus Nielsen Jensen.			
				Carola Cañón Valenzuela.			

				Fabiola Leon Miranda.			
				Emiliano Matías Molina Reyes.			
				Daly Noll Vergara.			
				Sebastián Arredondo Barros.			
				Barbara Casas Atala.			
				Camilo Valdivieso Guerrero.			
2	Interaction networks that govern genome structure in communities of organisms	To investigate how gene regulatory networks interact in the genome of microbial communities.	A gene regulatory network interacts to control a specific cellular function. Gene regulatory networks are important in development, differentiation and response to environmental signals.	Mauricio Latorre Mora. Claudio Latorre Hidalgo. Jacquelinne Acuña Sobarzo. Beatriz Diez Moreno.	Cellular Biology Molecular Biology Population Biology Ecology and environmental sciences	01-07-2022	23-06-1932

				Pablo Vergara Barros.	Genetics and evolution		
				Constanza Schapheer .	Microbiology.		
				Natalia Eugenia Jiménez Tapia.	Analysis		
				Alejandro Maass Sepúlveda.	Mathematical sciences		
				Gloria Coruzzi .	Biogeography		
				Marie France Sagot .	Paleontology.		
				Mauricio González Canales.	Fishery and fish culture		
				Victor Aliaga Tobar.	Immunology.		
					Parasitology.		
				Joaquin Ignacio Rilling Tenorio.			
				Laura Jimenez Jimenez.			
				Jaime Alcorta Loyola.			

				Francisco González Pinilla. Francisco Issotta Contardo. Constanza María Andreani Gerard. José Ignacio Arroyo González. Moises Adolfo Ariel Rojas Navarrete.			
3	Genomics for conservation, ecosystem health and sustainable food production	Analyze genomes and their interaction networks to generate hypotheses related to the impact of climate change on endangered species, and propose solutions for biodiversity conservation, sustainable agriculture and aquaculture.	Conservation genetics is the application of genetics to understand and reduce the risk of extinction of populations and species. From our analysis of genomes, genes and networks, we can generate and test hypotheses related to the impacts of climate change and environmental degradation,	Aurora Gaxiola Alcantar. Claudio Meneses Araya. Romina Pedreschi Plasencia. Ariel Orellana López. Liane Bassini Ney. Gerardo Núñez Lillo.	Molecular Biology. Ecology and environmental sciences. Agronomy Food technology Others in Biology. Genetic Engineering.	01-07-2022	23-06-1932

			and propose biotechnological solutions for biodiversity conservation and sustainable production in agriculture and aquaculture.	Ignacia Hernández Figueroa.	Veterinary Sciences		
				Ana Karina Madriaza Maturana.	Environment		
				Víctor Alfonso García Gutiérrez.	Agriculture production systems		
				Alexis Ignacio Gaete Silva.	Fishery and fish culture.		
				Angélica Reyes Jara.	Biogeography.		
				Verónica Cambiazo Ayala.	Biotechnology.		
					Nutrition		
				Karin Rothkegel Agurto.	Biochemistry.		
				Patricio Olmedo Miraflores.			
				Alvaro Miquel Poblete.			
				Jouseph Gallardo Hidalgo.			

Annex 2.- Institute / Nucleus Researchers

2.1 Summary Table – Center’s Researchers

Category of researcher	Quantity	Average age	Nationality		Distribution Gender		
			National	International	Male	Female	Not stated
Director	1	61	1	0	1	0	0
Alternate Director	1	45	0	1	0	1	0
Principal Researcher	7	57	5	2	4	3	0
Senior Researcher	4	61	0	4	2	2	0
Young Researcher	9	37	9	0	5	4	0
Postdoctoral	24	38	21	3	10	14	0

2.2 Principal Researchers

Full Name	Research Line	Nationality	Gender	Date of birth	Profession	Academic Degree	Affiliation	Current Position	Relation with Center
Miguel Allende Connelly	Functional genomics of adaptation and convergent evolution.	Chilean	M	08-10-1962	Molecular Biology	D	Universidad de Chile	Professor	[2]
Juliana De Abreu Vianna	Functional genomics of adaptation and convergent evolution.	Brazilian	F	09-04-1979	Biology	D	Pontificia Universidad Católica de Chile	Professor	[2]
Rodrigo Gutiérrez Illabaca	Functional genomics of adaptation and convergent evolution.	Chilean	M	30-12-1971	Biochemistry	D	Pontificia Universidad Católica de Chile	Full Professor	[2]
Romina Pedreschi	Genomics for conservation	Italian	F	17-08-	Agronomy	D	Pontificia Universidad Católica	Full Professor	[2]

Plasencia	n, ecosystem health and sustainable food production.			1978			de Valparaíso		
Verónica Cambiazó Ayala	Genomics for conservation, ecosystem health and sustainable food production.	Chilean	F	06-01-1961	Molecular Biology	D	Universidad de Chile	Full Professor	[2]
Beatriz Díez Moreno	Interaction networks that govern genome structure in communities of organisms.	Spanish	F	22-02-1972	Biology	D	Pontificia Universidad Católica de Chile	Full Professor	[2]
Alejandro Maass Sepúlveda	Interaction networks that govern genome structure in communities of organisms.	Chilean	M	11-11-1965	Mathematics	D	Universidad de Chile	Full Professor	[2]
Mauricio González Canales	Interaction networks that govern genome structure in communities of organisms.	Chilean	M	04-12-1964	Molecular Biology	D	Universidad de Chile	Full Professor	[2]
Ariel Orellana López	Genomics for conservation, ecosystem health and sustainable food production.	Chilean	M	01-12-1961	Molecular Biology	D	Universidad Andrés Bello	Full Professor	[2]

2.3 Senior Researchers

Full Name	Research Line	Nationality	Gender	Date of	Profession	Academic Degree	Affiliation	Current Position	Relation with Center
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				birth					
Rasmus Nielsen Jensen	Functional genomics of adaptation and convergent evolution.	American	M	27-01-1970	Biology	D	University of California	Professor	[2]
Gloria Coruzzi	Interaction networks that govern genome structure in communities of organisms.	American	F	28-06-1954	Biology	D	New York University	Full Professor	[2]
Marie France Sagot	Interaction networks that govern genome structure in communities of organisms.	French	F	21-04-1956	Informatics	D	INRIA, Institute for Research in IT and Automation, Université Lyon	Director	[2]
Colomban de Vargas	Functional genomics of adaptation and convergent evolution.	French	M	25-08-1971	Biology	D	CNRS-Sorbonne Université	Senior Researcher	[2]

<u>NOMENCLATURE:</u> [Gender] [M] Male [F] Female [ND] Does not Declare	[Academic Degree] [U] Undergraduate [M] Master [D] Doctoral	[Relation with Center] [1] Full time [2] [2]
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Annex 3.- Publications (Total or partially financed by MSI)

3.1.- WOS Publications or Similar to WOS Standard

3.1.1 Principal Researchers

Nº	Title	Authors	DOI	Quartile	Research Lines	Nº Principal Researchers
1	Functional redundancy	Sauma Sánchez,	10.1093/femsec/fiae157	Q2	Interaction networks that govern genome	1

	buffers the effect of poly-extreme environmental conditions on Southern African dryland soil microbial communities	Tomás; Alcorta, Jaime; Tamayo-Leiva, Javier; Díez, Beatriz; Bezuidenhout, Hugo; Cowan, Don; Ramond, Jean-Baptiste			structure in communities of organisms.	
2	History of Diversification and Adaptation from North to South Revealed by Genomic Data: Guanacos from the Desert to Sub-Antarctica	Fabiola León, Eduardo J Pizarro, Daly Noll, Luis R Pertierra, Benito A Gonzalez, Warren E Johnson, Juan Carlos Marín, Juliana A Vianna	10.1093/gbe/evae085	Q2	Functional genomics of adaptation and convergent evolution.	1
3	Modeling Spinal Muscular Atrophy in Zebrafish: Current Advances and Future Perspectives	David Gonzalez, Constanza Vásquez-Door man, Adolfo Luna, Miguel L Allende	10.3390/ijms25041962	Q2	Functional genomics of adaptation and convergent evolution.	1
4	Associations among MHC genes, latitude, and avian malaria infections in the rufous-collared sparrow (<i>Zonotrichia capensis</i>)	Juan Rivero de Aguilar, Omar Barroso, Elisa Bonaccorso, Hector Cadena, Lucas Hussing, Josefina Jorquera, Javier Martinez, Josué Martínez-de la Puente, Alfonso Marzal, Fabiola León Miranda,	10.1002/ece3.11634	Q2	Functional genomics of adaptation and convergent evolution.	1

		Santiago Merino, Nubia E Matta, Marilyn Ramenofsky, Ricardo Rozzi, Carlos E Valeris-Chacín, Rodrigo A Vásquez, Juliana A Vianna, John C Wingfield				
5	Hox genes control homocercal caudal fin development and evolution	Nicolás Cumplido, Gloria Arratia, Thomas Desvignes, Salome Muñoz-Sánchez, John H. Postlethwait, Miguel L. Allende	10.1126/sciadv.adj5991	Q1	Functional genomics of adaptation and convergent evolution.	1
6	Direct impact of COVID-19 vaccination in Chile: averted cases, hospitalizations, ICU admissions, and deaths	Antoine Brault, Andrew Hart, Paula Uribe, Jorge Prado, Jaime San Martín, Alejandro Maass, Mauricio Canals	10.1186/s12879-024-09304-1	Q2	Interaction networks that govern genome structure in communities of organisms.	1
7	The inhibition of N ₂ fixation by nitrogen is attenuated by the P supply, altering the plant metabolism	Ricardo A Cabeza, Joachim Schulze, Sebastian Salinas-Roco, Amanda Morales-González, Ramón Amigo, Ricardo Pérez-Díaz,	10.1016/j.envxpb.2024.105762	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

		Basilio Carrasco, Rodrigo Contreras-Soto, Carlos Maldonado, Romina Pedreschi, Soledad Espinoza, Alejandro del Pozo				
8	Population structure and connectivity among coastal and freshwater Kelp Gull (<i>Larus dominicanus</i>) populations from Patagonia.	Kasinsky, T., Rosciano, N., Vianna, J.A., Yorio, P., Campagna, L.	10.1371/journal.pone.0301004	Q2	Functional genomics of adaptation and convergent evolution.	1
9	Structure and dispersion of the conjugative mobilome in surface ocean bacterioplankton	Javier Tamayo-Leiva, Jaime Alcorta, Felipe Sepúlveda, Sebastián Fuentes-Alburquenque, José Ignacio Arroyo, José Eduardo González-Pastor, Beatriz Díez	10.1093/ismeco/ycae059	Q1	Interaction networks that govern genome structure in communities of organisms.	1
10	Atmospheric immersion and vacuum impregnation of gallotannins and hydrolysed gallotannins from tara pods (<i>Caesalpinia spinosa</i>) mitigate	David Campos, Rosana Chirinos, Paola Huaraca-Espinoza, Ana Aguilar-Galvez, Diego García-Ríos, Franco	10.1016/j.foodchem.2023.137675	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

	acrylamide and enhances the antioxidant power in potato chips	Pedreschi, Romina Pedreschi				
1 1	A First Omics Data Integration Approach in Hass Avocados to Evaluate Rootstock–Scion Interactions: From Aerial and Root Plant Growth to Fruit Development	Gerardo Núñez-Lillo, Excequel Ponce, Clemens P Beyer, Juan E Álvaro, Claudio Meneses, Romina Pedreschi	10.3390/plants13050603	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1
1 2	Vertically distinct sources modulate stable isotope signatures and distribution of Mesozooplankton in central Patagonia: The Golfo de Penas - Baker Channel connection and analogies with the Beagle Channel	Leonardo R Castro, Samuel Soto-Mendoza, Luciana Riccialdelli, María L Presta, Pamela Barrientos, Humberto E González, Giovanni Daneri, Marcelo Gutiérrez, Paulina Montero, Italo Masotti, Beatriz Díez	10.1016/j.jmarsys.2023.103892	Q2	Interaction networks that govern genome structure in communities of organisms.	1
1 3	Epigenetic regulators controlling osteogenic lineage commitment and bone formation	Parisa Dashti, Eric A Lewallen, Jonathan AR Gordon, Martin A Montecino, James R Davie, Gary S Stein, Johannes PTM van Leeuwen, Bram CJ van	10.1016/j.bone.2024.117043	Q2	Functional genomics of adaptation and convergent evolution.	1

		der Eerden, Andre J van Wijnen				
1 4	Acidithiobacillia class members originating at sites within the Pacific Ring of Fire and other tectonically active locations and description of the novel genus 'Igneaacidithioba cillus'	Dilanaz Arisan, Ana Moya-Beltrán, Camila Rojas-Villalob os, Francisco Issotta, Matías Castro, Ricardo Ulloa, Patricia A Chiacchiarini, Beatriz Díez, Alberto JM Martín, Iván Ñancucheo, Alejandra Giaveno, D Barrie Johnson, Raquel Quatrini	10.3389/fmi cb.2024.136 0268	Q2	Interaction networks that govern genome structure in communities of organisms.	1
1 5	Genomes of the Orestias pupfish from the Andean Altiplano shed light on their evolutionary history and phylogenetic relationships within Cyprinodontifor mes	Pamela Morales, Feliipe Gajardo, Camilo Valdivieso, Moisés A. Valladares, Alex Di Genova, Ariel Orellana, Rodrigo A. Gutiérrez, Mauricio González, Martin Montecino, Alejandro Maass, Marco A. Méndez, Miguel L. Allende	10.1186/s12 864-024-10 416-w	Q2	Functional genomics of adaptation and convergent evolution. Interaction networks that govern genome structure in communities of organisms.	5

16	Phylogenetically diverse wild plant species use common biochemical strategies to thrive in the Atacama Desert	Thomas Dussarrat, Ricardo Nilo-Poyanco, Tomás C Moyano, Sylvain Prigent, Tim L Jeffers, Francisca P Díaz, Guillaume Decros, Lauren Audi, Veronica M Sondervan, Bingran Shen, Viviana Araus, Dominique Rolin, Dennis Shasha, Gloria M Coruzzi, Yves Gibon, Claudio Latorre, Pierre Pétriacq, Rodrigo A Gutiérrez	10.1093/jxb/erae117	Q1	Functional genomics of adaptation and convergent evolution.	1
					Genomics for conservation, ecosystem health and sustainable food production.	
					Interaction networks that govern genome structure in communities of organisms.	
17	Effects of Delaying the Storage of 'Hass' Avocados under a Controlled Atmosphere on Skin Color, Bioactive Compounds and Antioxidant Capacity	Daniela Olivares, Pablo A Ulloa, Cristina Vergara, Ignacia Hernández, Miguel Ángel García-Rojas, Reinaldo Campos-Vargas, Romina Pedreschi, Bruno G Defilippi	10.3390/plants13111455	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1
18	ANTIHYPERTENSIVE AND ANTIDIABETIC PEPTIDES	Rosana Chirinos, Jamerccy Rodriguez-Dia	10.21577/0100-4042.20230126	Q4	Genomics for conservation, ecosystem health	1

	DERIVED FROM IN SILICO SIMULATED GASTROINTESTINAL DIGESTION OF QUINOA (Chenopodium quinoa) GLOBULINS AND MOLECULAR DOCKING STUDY	z, Sebastian Anticona, Ana Aguilar-Galvez, Romina Pedreschi, David Campos			and sustainable food production.	
19	An Open One-Step RT-qPCR for SARS-CoV-2 detection	Ariel Cerda, Maira Rivera, Grace Armijo, Catalina Ibarra-Henriquez, Javiera Reyes, Paula Blázquez-Sánchez, Javiera Avilés, Aníbal Arce, Aldo Seguel, Alexander J Brown, Yesseny Vásquez, Marcelo Cortez-San Martín, Francisco A Cubillos, Patricia García, Marcela Ferres, César A Ramírez-Sarmiento, Fernán Federici, Rodrigo A Gutiérrez	10.1371/journal.pone.0297081	Q1	Functional genomics of adaptation and convergent evolution.	1

20	Nitrogen sensing and regulatory networks: It's about time and space	Carly M Shanks, Karin Rothkegel, Matthew D Brooks, Chia-Yi Cheng, José M Alvarez, Sandrine Ruffel, Gabriel Krouk, Rodrigo A Gutiérrez, Gloria M Coruzzi	10.1093/plcell/koae038	Q1	Functional genomics of adaptation and convergent evolution.	1
21	Are threatened seabird colonies of the pacific ocean genetically vulnerable? The case of the red-tailed tropicbird, <i>Phaethon rubricauda</i> , as a model species	Andrea I Varela, Katherina Brokordt, Juliana A Vianna, María José Frugone, Stefanie MH Ismar-Rebitz, Chris P Gaskin, Nicholas Carlile, Terence O'Dwyer, Josh Adams, Eric A VanderWerf, Guillermo Luna-Jorquera	10.1007/s10531-024-02791-3	Q2	Functional genomics of adaptation and convergent evolution.	1
22	Metabolite profiling and hormone analysis of the synchronized exocarp-mesocarp development during ripening of cv. 'Fuerte' and 'Hass' avocado fruits	Patricio Olmedo, Gerardo Núñez-Lillo, Excequel Ponce, Juan Eugenio Alvaro, Jorge Baños, Esther Carrera, Jorge González-Fernández, José Ignacio	10.1016/j.fbio.2024.104454	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

		Hormaza, David Campos, Rosana Chirinos, Reinaldo Campos-Vargas, Bruno Giorgio Defilippi, Encarna Aguayo, Romina Pedreschi				
2 3	Exploring the molecular basis of diapause I induction in the annual killifish <i>Garcialebias charrua</i> : a transcriptomic approach	N. G. Papa, J. Sotelo-Silveira, L. Inchausti, C. Valdivieso, L. Pereiro, F. Gajardo, A. Di Genova, A. Glavic, C. Chalar, N. Berois, Miguel L. Allende, Maria Jose Arezo	10.1007/s10641-024-01562-x	Q3	Functional genomics of adaptation and convergent evolution.	1
2 4	Biosynthetic gene clusters from uncultivated soil bacteria of the Atacama Desert	Constanza M. Andreani-Gerard, Verónica Cambiazo, Mauricio González	10.1128/msphere.00192-24	Q2	Genomics for conservation, ecosystem health and sustainable food production. Interaction networks that govern genome structure in communities of organisms.	2
2 5	Uncovering phytochemicals quantitative evolution in avocado fruit mesocarp during ripening: A targeted LC-MS	Irene Serrano-García, Carlos Saavedra Morillas, María Gemma Beiro-Valenzuela, Romina	10.1016/j.foodchem.2024.140334	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

	metabolic exploration of Hass, Fuerte and Bacon varieties	Monasterio, Elena Hurtado-Fernandez, Jose Jorge Gonzalez-Fernandez, Jose Ignacio Hormaza, Romina Pedreschi, Lucía Olmo-García. Alegría Carrasco-Pancorbo				
26	Analysis of Maillard reaction precursors and secondary metabolites in Chilean potatoes and neoformed contaminants during frying	Diego García-Ríos, Ignacia Hernández, Juan E. Alvaro, Franco Pedreschi, David Campos, Anita Behn, Romina Pedreschi	10.1016/j.foodchem.2024.140478	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1
27	Diversity and functionality of soil prokaryotic communities in Antarctic volcanic soils: insights from penguin-influenced environments.	Diego Segura, Karen Jordaan, Beatriz Díez, Javier Tamayo-Leiva, Sebastian Doetterl, Daniel Wasner, Jerónimo Cifuentes-Anticevic, Angélica Casanova-Katany	10.21577/0100-4042.20230126	Q3	Interaction networks that govern genome structure in communities of organisms.	1
28	Adaptation strategies of giant viruses to low-temperature marine ecosystems	Marianne Buscaglia, José Luis Iriarte, Frederik	10.1093/ismej/wrae162	Q1	Interaction networks that govern genome structure in communities of organisms.	1

		Schulz, Beatriz Díez				
29	A geometric framework for asymptoticity and expansivity in topological dynamics	Sebastián Donoso, Alejandro Maass, Samuel Petite	10.1090/tran/9269	Q1	Interaction networks that govern genome structure in communities of organisms.	1
30	The Characterization of a Novel PrMADS11 Transcription Factor from <i>Pinus radiata</i> Induced Early in Bent Pine Stem	Tamara Méndez, Joselin Guajardo, Nicolás Cruz, Rodrigo A Gutiérrez, Lorena Norambuena, Andrea Vega, María A Moya-León, Raúl Herrera	10.3390/ijms25137245	Q2	Functional genomics of adaptation and convergent evolution.	1
31	Impact of salmon farming in the antibiotic resistance and structure of marine bacterial communities from surface seawater of a northern Patagonian area of Chile	Javiera Ortiz-Severín, Christian Hodar, Camila Stuardo, Constanza Aguado-Norese, Felipe Maza, Mauricio González, Verónica Cambiazo	10.1186/s40659-024-00556-4.	Q2	Interaction networks that govern genome structure in communities of organisms. Genomics for conservation, ecosystem health and sustainable food production.	2
32	Deciphering the behind blackspot exocarp disorder in avocado cv. Hass through a hormonal, transcriptional and metabolic integration approach	Gerardo Núñez-Lillo, Ignacia Hernández, Patricio Olmedo, Excequel Ponce, Camila Arancibia-Guerra, Laura Sepulveda, Alegría Carrasco-Panc	10.1016/j.potharvbio.2024.113163	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

		orbo, María Gemma Beiro-Valenzuela, Esther Carrera, Jorge Baños, David Campos, Claudio Meneses, Romina Pedreschi				
33	Fruit sugar hub: gene regulatory network associated with soluble solids content (SSC) in <i>Prunus persica</i>	Gerardo Núñez-Lillo, Victoria Lillo-Carmona, Alonso G. Pérez-Donoso, Romina Pedreschi, Reinaldo Campos-Vargas, Claudio Meneses	10.1186/s40659-024-00539-5	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1
34	Dynamic changes in mRNA nucleocytoplasmic localization in the nitrate response of <i>Arabidopsis</i> roots	Alejandro Fonseca, Eleodoro Riveras, Tomás C Moyano, José M Alvarez, Stefanie Rosa, Rodrigo A Gutiérrez	10.1111/pce.15018	Q1	Functional genomics of adaptation and convergent evolution.	1
35	Recent advances in local and systemic nitrate signaling in <i>Arabidopsis thaliana</i>	Laura D Delgado, Valentina Nunez-Pascual, Eleodoro Riveras, Sandrine Ruffel, Rodrigo A Gutiérrez	10.1016/j.pbi.2024.102605	Q1	Functional genomics of adaptation and convergent evolution.	1
36	Climate change and population persistence in a	Roberto F Nespolo, Julian F Quintero-Galvi	10.1098/rspb.2024.0266	Q1	Functional genomics of adaptation and	1

	hibernating marsupial	s, Francisco E Fontúrbel, Francisco A Cubillos, Juliana Vianna, Paulo Moreno-Meynard, Enrico L Rezende, Francisco Bozinovic			convergent evolution.	
37	Nakazawaea atacamensis f.a., sp. nov. a novel non-conventional fermentative ascomycetous yeast species from the Atacama Desert	Araya M, Villarreal P, Moyano T, Santos AR, Díaz FP, Bustos-Jarufe A, Urbina K, Del Pino J, Goenewald M, Gutiérrez RA, Rosa C, Cubillos F	10.1002/yea.3920	Q3	Functional genomics of adaptation and convergent evolution.	1
38	Life on the edge: microbial diversity, resistome, and virulome in soils from the Union Glacier cold desert	Patricio Arros, Daniel Palma, Matias Galvez-Silva, Alexis Gaete, Hugo Gonzalez, Gabriela Carrasco, Jose Coche, Ian Perez, Jorge Gallardo-Cerd a, Eduardo Castro-Nallar, Cristobal Galban, Macarena A Varas, Marco Campos, Jacqueline Acuna, Milko Jorquera, Francisco P Chavez,	10.1016/j.scitotenv.2024.177594	Q1	Interaction networks that govern genome structure in communities of organisms. Genomics for conservation, ecosystem health and sustainable food production.	1

		Veronica Cambiazo, Andres E Marcoleta				
39	Rhizochemistry and soil bacterial community are tailored to natural stress gradients	Thomas Dussarrat, Claudio Latorre, Millena C Barros Santos, Constanza Aguado-Nores e, Sylvain Prigent, Francisca P Díaz, Dominique Rolin, Mauricio González, Caroline Müller, Rodrigo A Gutiérrez, Pierre Pétriacc	10.1016/j.soilbio.2024.109662	Q1	Functional genomics of adaptation and convergent evolution. Interaction networks that govern genome structure in communities of organisms.	2
40	Comparative Genomics Supports Ecologically Induced Selection as a Putative Driver of Banded Penguin Diversification	Fabiola León, Eduardo Pizarro, Daly Noll, Luis R. Pertierra, Patricia Parker, Marcela P. A. Espinaze, Guillermo Luna-Jorquera, Alejandro Simeone, Esteban Frere, Gisele Dantas, Robin Cristofari, Omar E. Cornejo, Rauri C. K. Bowie, Juliana A. Vianna.	10.1093/molecularbiologyandevolution/166	Q1	Functional genomics of adaptation and convergent evolution.	1

4 1	Site-Specific Nutrient Data Reveal the Importance of Soils in Driving the Mycorrhizal Make-Up of Woody Vegetation Worldwide	Xiaobin Hua, Christopher H. Lusk, Ian A. Dickie, Stephen Adu-Bredu, Kathryn J. Allen, Viviana Araus, Laurent Augusto, Pavel Barsukov, David Bauman, Félix Brédoire, David F. R. P. Burslem, James W. Dalling, Leen Depauw, Kyle G. Dexter, Thomas Drouet, John L. Godlee, Roberto Godoy, Rodrigo A. Gutiérrez, Jonathan Ilunga Muledi, Arnaud Jacobs, Robert Kooyman, Claudio Latorre, Jesús López Angulo, Sébastien Macé, Sybryn L. Maes, Francisco Maiato Pedro Gonçalves, Ben Hur Marimon Junior, Manuel Nicolas, Reuben Nilus, Michael	10.1111/geb. 13936		Functional genomics of adaptation and convergent evolution.	1
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		O'Brien, Imma Oliveras Menor, Frida I. Piper, Jennifer Read, Glen Reynolds, Alfredo Saldaña, Beatriz Schwantes Marimon, Kris Verheyen, Mark Westoby, Benjamin Wigley, Ian J. Wright				
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3.2.- SCOPUS Publications or Similar to SCOPUS Standard

3.2.1 Principal Researchers

N°	Title	Authors	DOI	Quartile	Research Lines	N° Principal Researchers
1	TerrANTALife 1.0 Biodiversity data checklist of known Antarctic terrestrial and	Luis R Pertierra, Gilda Varliero, Andrés Barbosa, Elisabeth M Biersma,	10.3897/2FBDJ.12.e106199	Q3	Functional genomics of adaptation and convergent evolution.	1

	freshwater life forms	Peter Convey, Steven L Chown, Don Cowan, Asunción De Los Rios, Pablo Escribano-Alvarez, Diego Fontaneto, Ceridwen Fraser, Mathew Harris, Kevin Hughes, Huw Griffiths, Peter le Roux, Xiaoyue P Liu, Heather Lynch, Roksana Majewska, Pablo A Martinez, Marco Molina-Montenegro, Miguel A Olalla-Tarraga, Lloyd Peck, Antonio Quesada, Cristina Ronquillo, Yan Ropert-Coudert, Leopoldo Sancho,				
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		Aleks Terauds, Juliana Vianna, Annick Wilmotte, Joaquín Hortal, Michelle Greve				
2	Knockdown of tgfb1a partially improves ALS phenotype in a transient zebrafish model	David Gonzalez, Xiomara Cuenca, Miguel L Allende	10.3389/fncel.2024.1384085	Q2	Functional genomics of adaptation and convergent evolution.	1
3	Conventional and ultrasound-assisted extractions of protein from sachu inchi (Plukenetia volubilis) and their impact on the physicochemical and structural characteristics	Rosana Chirinos, Romina Scharff-Salinas, Jamerccy Rodriguez-Diaz, Andres Figueroa-Merma, Ana Aguilar-Galvez, Fanny Guzman, Ingrid Contardo, Romina Pedreschi, David Campos	10.1016/j.afres.2024.100545	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

3.3.- SCIELO Publications or Similar to SCIELO Standard

3.3.1 Principal Researchers

3.4.- Scientific Books and Chapters

3.4.1 Principals Researchers

Nº	Title	Authors	URL/Link	ISBN	Líneas de Investigación	Nº investigadores asociados del centro
1	Modelling the softening behaviour of Chilean ‘Hass’ avocado destined to local and distant markets	Romina Pedreschi, Ignacia Hernández, Claudia Fuentealba, Bruno Defilippi, Reinaldo Campos-Vargas, Claudio Meneses, Maarten Hertog	https://www.ishs.org/ishs-article/1386_6	978-94-6261-204-4	Genomics for conservation, ecosystem health and sustainable food production.	1
2	Zebrafish Larvae Microinjection and Automated Fluorescence Microscopy for Studying Klebsiella pneumoniae Infection and the Host Immune Response	Matías Gálvez-Silva, Macarena A Varas, Miguel L Allende, Francisco P Chávez, Andrés E Marcoletta	https://link.springer.com/protocol/10.1007/978-1-0716-4100-2_12	978-0-387-79053-4	Functional genomics of adaptation and convergent evolution.	1

3.5.- Other Publications

3.5.1 Principals Researchers

3.6.- Other researchers: “WOS Publications or Similar to WOS Standard”, “SCOPUS Publications or Similar to SCOPUS Standard” “SCIELO Publications or Similar to SCIELO Standard”, “Books and chapters in books” y “Other Publications [Other Researchers]”:

Nº	Publication Category	Title	Authors	DOI	Quartile	Research Line	Nº Researchers
1	ISI/WOS or Similar ISI/WOS Standard	A novel pectin methylesterase inhibitor, PME13, in common bean suggests a key role of pectin methylesterification in <i>Pseudomonas</i> resistance	Alfonso G De la Rubia, Asier Largo-Gonsens, Ricardo Yusta, Pablo Sepúlveda-Orellana, Aníbal Riveros, María Luz Centeno, Dayan Sanhueza, Claudio Meneses, Susana Saez-Aguayo, Penélope García-Angulo	10.1093/jxb/erad362	Q1	Genomics for conservation, ecosystem health and sustainable food production.	2
2	ISI/WOS or Similar ISI/WOS Standard	Weighted gene co-expression network analysis reveals immune evasion related genes in <i>Echinococcus granulosus</i> sensu stricto	Ismael Pereira, Gabriela Prado Paludo, Christian Hidalgo, Carroll Stoore, María Soledad Baquedano,	10.3389%2Febm.2024.10126	Q2	Genomics for conservation, ecosystem health and sustainable food production.	1

			Carolina Cabezas, Martín Cancela, Henrique Bunselmeier Ferreira, Macarena Bastías, Aníbal Riveros, Claudio Meneses, Leonardo Sáenz, Rodolfo Paredes				
3	ISI/WO So Similar a ISI/WO S standard	Identification of master regulator genes controlling pathogenic CD4+ T cell fate in inflammatory bowel disease through transcriptional network analysis	José M Jiménez, J Sebastián Contreras-Riquelme, Pía M Vidal, Carolina Prado, Macarena Bastías, Claudio Meneses, Alberto JM Martín, Tomás Perez-Acle, Rodrigo Pacheco	10.1038/s41598-024-61158-4	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1
4	ISI/WO So Similar a ISI/WO S standard	Variovorax sp. strain P1R9 applied individually or as part of bacterial consortia enhances	Jacqueline J Acuña, Joaquín Rilling, Nitza G Inostroza, Qian	10.1038/s41598-024-52535-0	Q1	Interaction networks that govern genome structure in	2

		wheat germination under salt stress conditions	Zhang, Lukas Y Wick, Angela Sessitsch, Milko A Jorquera			communities of organisms.	
5	ISI/WO So Similar a ISI/WO S standard	A retrospective study suggests 55 days of persistence of SARS-CoV-2 during the first wave of the pandemic in Santiago de Chile	Claudio Acuña-Castillo, Mabel Vidal, Eva Vallejos-Vidal, Roberto Luraschi, Carlos Barrera-Avalos, Ailen Inostroza-Molina, Sonia Molina-Cabrera, Daniel Valdes, Kevin Maisey, Mónica Imarai, Rodrigo Vera, Sergio Vargas, Leonel E Rojo, Elías Leiva-Salcedo, Alejandro Escobar, Sebastián Reyes-Cerpa, Alexis	10.1016/j.heliyon.2024.e24419	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

			Gaete, Ricardo Palma-Vejares, Dante Travisany, Claudio Torres, Felipe E Reyes-López, Ana María Sandino				
6	ISI/WO So Similar a ISI/WO S standard	Multiple antibiotic resistance and herbicide catabolic profiles of bacteria isolated from Lake Villarrica surface sediments (Chile)	Milko A Jorquera, Jacqueline J Acuña, Nicole Huerta, Junhong Bai, Ling Zhang, Rong Xiao, Michael J Sadowsky	10.1016/j.envpol.2024.124538	Q1	Interaction networks that govern genome structure in communities of organisms.	1
7	ISI/WO So Similar a ISI/WO S standard	Mycelia Migratory Bacteria in Compost and Compost–Amended Rhizosphere Soil in a Table Grape Orchard	Susett Gonzalez–Gonzalez, Qian Zhag, Jacqueline J Acuña, Michael J Sadowsky, Lukas Y Wick, Milko A Jorquera	10.1007/s42729-024-01862-2	Q2	Interaction networks that govern genome structure in communities of organisms.	1
8	ISI/WO So Similar a ISI/WO	Effects of sustainable agricultural practices on soil microbial diversity,	Pedro Mondaca, Juan L Celis-Díez, Pablo Díaz-Sief	10.1016/j.agee.2024.109053	Q1	Genomics for conservation, ecosystem health	1

	S standard	composition, and functions	er, Natalia Olmos-M oya, Fernanda Montero- Silva, Sofia Molina, Francisco E Fontúrbel, Humberto Aponte, Dinka Mandako vic, Brynelly Bastidas, Eduardo C Arellano, Blas Lavander o, Marcela Carvajal, Aurora Gaxiola			and sustainab le food productio n.	
9	ISI/WO S o Similar a ISI/WO S standard	Identification of bacteria in potential mutualism with toxic Alexandrium catenella in Chilean Patagonian fjords by in vitro and field monitoring	Kyoko Yarimizu, Jorge I Mardones , Javier Paredes- Mella, Ishara Uhanie Perera, So Fujiyoshi, Gonzalo Fuenzalid a, Jacquelin ne J Acuña, Tay Ruiz-Gil,	10.1371/journal.pone.030 1343	Q1	Interactio n networks that govern genome structure in communi ties of organism s.	2

			Marco Campos, Joaquin-Ignacio Rilling, Pedro Calabrano Miranda, Jonnathan Vilugrón, Oscar Espinoza-González, Leonardo Guzmán, Satoshi Nagai, Milko A Jorquera, Fumito Maruyama				
10	ISI/WHO Similar a ISI/WHO standard	A multicenter genomic epidemiological investigation in Brazil, Chile, and Mexico reveals the diversity and persistence of Salmonella populations in surface waters	Zhao Chen, Andrea I Moreno-Switt, Angelica Reyes-Jara, Enrique Delgado Suarez, Aiko D Adell, Celso José Bruno Oliveira, Raquel Regina Bonelli, Xinyang Huang, Eric Brown, Marc Allard,	10.1128/mbio.00777-24	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

			Christoph er Grim, Rebecca Bell, Jianghong Meng, Magaly Toro				
1 1	ISI/WO S o Similar a ISI/WO S standard	Unveiling the genomic landscape of Salmonella enterica serotypes Typhimurium, Newport, and Infantis in Latin American surface waters: a comparative analysis	Zhao Chen, Magaly Toro, Andrea I Moreno-S witt, Aiko D Adell, Enrique J Delgado- Suárez, Raquel R Bonelli, Celso JB Oliveira, Angélica Reyes-Jar a, Xinyang Huang, Brett Albee, Christoph er J Grim, Marc Allard, Sandra M Tallent, Eric W Brown, Rebecca L Bell, Jianghong Meng	10.1128/spectrum.00047- 24	Q2	Genomic s for conservat ion, ecosyste m health and sustainab le food productio n.	1
1 2	ISI/WO S o Similar a ISI/WO	Genomic characterisatio n of the population structure and	Alejandro Piña-Iturb e, Constanza Díaz-Gavi	10.1016/j.lana.2024.1007 11	Q1	Genomic s for conservat ion, ecosyste	1

	S standard	antibiotic resistance of Salmonella enterica serovar Infantis in Chile, 2009–2022	dia, Francisca P Álvarez, Rocio Barron-M ontenegro , Diana M Álvarez-E spejo, Patricia García, Doina Solís, Rodrigo Constenla -Albornoz , Magaly Toro, Jorge Olivares- Pacheco, Angélica Reyes-Jar a, Jianghong Meng, Rebecca L Bell, Andrea I Moreno-S witt			m health and sustainab le food productio n.	
1 3	ISI/WO S o Similar a ISI/WO S standard	Pathogen profile of Baiyangdian Lake sediments using metagenomic analysis and their correlation with environmental factors	Rong Xiao, Yanping Hu, Yaping Wang, Junming Li, Congling Guo, Junhong Bai, Ling Zhang, Kegang Zhang,	10.1016/j.scitotenv.2023. 169628	Q1	Interactio n networks that govern genome structure in communi ties of organism s.	1

			Milko A Jorquera, Jacqueline J Acuña, Wenbin Pan				
14	ISI/WO So Similar a ISI/WO S standard	Structural insights into a functional unit from an immunogenic mollusk hemocyanin	Sebastián M Muñoz, Gabriel Vallejos-Baccellier e, Augusto Manubens , Michelle L Salazar, Andrey FZ Nascimen to, Patricio Tapia-Reyes, Claudio Meneses, Andre LB Ambrosio , María Inés Becker, Victoria Guixé, Victor Castro-Fernandez	10.1016/j.str.2024.02.018	Q2	Genomic s for conservat ion, ecosyste m health and sustainab le food productio n.	1
15	ISI/WO So Similar a ISI/WO S standard	Discovery of functional PRRs for the fungal elicitor Xyn11/eix in Prunus fruit trees	Andree Alvarez, Uri Aceituno-Valenzuela, Meirav Leibman-Markus, Daniela Muñoz,	10.1016/j.stress.2024.100567	Q1	Interactio n networks that govern genome structure in communi ties of	1

			Carlos Rubilar, Franco Figueroa, Manuel Pinto, Mauricio Latorre, Claudia Stange, Adi Avni, Maya Bar, Lorena Pizarro			organisms.	
16	ISI/WO So Similar a ISI/WO S standard	Inorganic polyphosphate : from basic research to diagnostic and therapeutic opportunities in ALS/FTD	Polett Garcés, Armando Amaro, Martin Montecino, Brigitte van Zundert	10.1042/BST20230257	Q2	Functional genomics of adaptation and convergent evolution.	1
17	ISI/WO So Similar a ISI/WO S standard	Microbial hotspots in a relict fog-dependent Tillandsia landbeckii dune from the coastal Atacama Desert	Andrea Jaeschke, S Matthias May, Anna Hakobyan, Ramona Mörchen, Olaf Bubenzer, Stefano M Bernasconi, Enno Schefuß, Dirk Hoffmeister, Claudio Latorre, Martina Gwozdz,	10.1016/j.gloplacha.2024.104383	Q1	Interaction networks that govern genome structure in communities of organisms.	1

			Janet Rethemeyer, Claudia Knief				
18	ISI/WHO So Similar a ISI/WHO S standard	Population dynamics and cultural niche construction during the Late Holocene in a mediterranean ecosystem (central Chile, 32° S– 36° S)	Carolina Godoy-Aguirre, Matías Frugone-Álvarez, Eugenia M Gayo, Roberto Campbell, Mauricio Lima, Antonio Maldonado, Claudio Latorre	10.1177/09596836231225722	Q3	Interaction networks that govern genome structure in communities of organisms.	1
19	ISI/WHO So Similar a ISI/WHO S standard	New uses for ancient middens: bridging ecological and evolutionary perspectives	Katie M Becklin, Julio L Betancourt, Joseph Braasch, Olivier Dézerald, Francisca P Díaz, Angélica L González, Robert Harbert, Camille A Holmgren, Angela D Hornsby, Claudio Latorre, Marjorie D Matocq,	10.1016/j.tree.2023.12.003	Q1	Interaction networks that govern genome structure in communities of organisms.	2

			Felisa A Smith				
20	ISI/WHO So Similar a ISI/WHO S standard	Evaluating the isotopic composition of leaf organic compounds in fog-dependent <i>Tillandsia landbeckii</i> across the coastal Atacama Desert: Implications for hydroclimate reconstructions at the dry limit	Andrea Jaeschke, Christoph Böhm, Jan H Schween, Enno Schefuß, Marcus A Koch, Claudio Latorre, Sergio Contreras, Janet Rethemeyer, Holger Wissel, Andreas Lücke	10.1016/j.gloplacha.2024.104393	Q1	Interactio n networks that govern genome structure in communi ties of organism s.	1
21	ISI/WHO So Similar a ISI/WHO S standard	The first peoples of the Atacama Desert lived among the trees: A 11,600-to 11,200-year-old grove and congregation site	Paula C Ugalde, Delphine Joly, Claudio Latorre, Eugenia M Gayo, Rafael Labarca, Mikhaela Simunovic, Virginia McRostie, Vance T Holliday, Jay Quade, Calogero M Santoro	10.1073/pnas.2320506121	Q1	Function al genomics of adaptatio n and converge nt evolution .	1
22	ISI/WHO So Similar	The extinct <i>Notiomastodon platensis</i>	Erwin González-Guarda,	10.1016/j.quascirev.2024.108957	Q2	Function al genomics	1

	a ISI/WO S standard	(proboscidea, Gomphoteriid ae) inhabited mediterranean ecosystems during the Late Pleistocene in north-central Chile (31° S–36° S)	Ricardo A Segovia, Matías Valenzuela, Lidiane Asevedo, Natalia Villavicencio, Carlos Tornero, Iván Ramírez-Pedraza, Sebastián Ortega, José Capriles, Rafael Labarca, Claudio Latorre			of adaptation and convergent evolution.	
2 3	ISI/WO S o Similar a ISI/WO S standard	Molecular systematics of chinchilla rats and taxonomic assessment of the Abrocoma cinerea species complex	Francisco J González-Pinilla, Claudio Latorre, R Eduardo Palma	10.1093/jmammal/gyae095	Q2	Interaction networks that govern genome structure in communities of organisms.	2
2 4	SCIELO o Similar a SCIELO standard	Antecedentes sobre la historia natural de la becacina grande Gallinago stricklandii (Gray 1845): ¿un ave residente en cabo de Hornos?	Barroso, O., C. Cañón, F. Novoa, M. J. Jorquera, S. Luarte Tranamil, R. Jara, R. Vásquez & R. Rozzi.	10.22352/aip202452004	S/C (Sin Cuartil)	Functional genomics of adaptation and convergent evolution.	1

25	ISI/WHO So Similar a ISI/WHO S standard	Genetic Population Structure of Jumbo Squid (<i>Dosidicus gigas</i>) in the Southeastern Ocean and Its Implication for Fisheries Management	M. Cecilia Pardo-Gandarillas, Pamela Morales, Jennifer Catalán, Sergio A. Carrasco, Sebastián Hernández, Pablo A. Oyarzún, Rodrigo Wiff, Christian M. Ibáñez	10.1111/fme.12782	Q2	Functional genomics of adaptation and convergent evolution .	1
26	ISI/WHO So Similar a ISI/WHO S standard	Comparative morphology of the rhinarium and upper lip in sigmodontine rodents: Refined nomenclature, intertribal variation in a phylogenetic framework, and functional inferences	Ulyses Pardiñas, J. Brito, E. Cuéllar Soto & C. Cañón	10.1002/jmor.21760	Q2	Functional genomics of adaptation and convergent evolution .	1
27	SCIELO o Similar a SCIELO standard	Roedores nativos de la Reserva de Biosfera Cabo de Hornos en el extremo sur de Chile: avances en su conocimiento y conservación	Carola Cañón, O. Barroso, F. Novoa, G. D'Elia, R. Vásquez & R. Rozzi	10.22352/aip202452007	S/C (Sin Cuartil)	Functional genomics of adaptation and convergent evolution .	1

28	ISI/WHO So Similar a ISI/WHO S standard	Perspective of soil carbon sequestration in Chilean volcanic soils	Francisco Matus, Osvaldo Salazar, Felipe Aburto, Denisse Zamorano, Francisco Nájera, Radmila Jovanović, Catalina Guerra, Luis Reyes-Rojas, Oscar Seguel, Marco Pfeiffer, José Dörner, Susana Valle, Sergio Radic-Schilling, Efraín Duarte	10.1038/s44296-024-00038-4	Q2	Interaction networks that govern genome structure in communities of organisms.	0
29	ISI/WHO So Similar a ISI/WHO S standard	GWAS meta-analysis of resistance against <i>Piscirickettsia salmonis</i> in Atlantic salmon	Rodrigo Marín-Nahuelpi, Baltasar F Garcia, Agustin Piña-Elgueta, Jouseph Gallardo-Hidalgo, Paulina López, Daniela Cichero, Thomas Moen,	10.1016/j.aquaculture.2023.740249	Q1	Genomics for conservation, ecosystem health and sustainable food production.	1

			Jørgen Ødegård, José M Yáñez				
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3.7.- Collaborative publications:

Category of Publication	1 researcher		2 researchers		3 researchers		4 or more	
	Nº	%	Nº	%	Nº	%	Nº	%
ISI/WOS Publications or Similar to ISI/WOS Standard	37	49,33%	19	25,33%	7	9,33%	4	5,33%
SCOPUS Publications or Similar to SCOPUS Standard	3	4,00%	0	0,00%	0	0,00%	0	0,00%
SCIELO Publications or Similar to SCIELO Standard	2	2,67%	0	0,00%	0	0,00%	0	0,00%
Books and chapters	1	1,33%	1	1,33%	0	0,00%	0	0,00%
Other Publications	0	0,00%	0	0,00%	0	0,00%	0	0,00%
Total of publications	43	57,33%	20	26,67%	7	9,33%	4	5,33%

Annex 4.- Education and capacity building

Annex 4.- Short-term Traineeships of MSI students

4.1 List of Internships

Student Name	Institution	Country	Advisor	Project Description	Starting Date	Ending Date
Gabriel Ignacio Galvez Jimenez	Houston Methodist Research Institute	Estados Unidos de America	Diana Panesso	Investigación en microbiología de bacterias de relaves mineros	14-04-2024	21-08-2024

4.2 List of External Internships

Intern Type	Intern Name	Academic Degree	Home Institution	Destination Institution	Country	Project Description	Starting Date	Ending Date
Student	María Esperanza Letelier Correa	U	Universidad de Chile	Pontificia Universidad Católica de Chile	Chile	Apoyar en la elaboración de material digital de divulgación	02-09-2024	28-02-2025
Student	Ana Karina Madriaza Maturana	D	Centro de Investigaciones Energéticas, Medioambientales y Tecnológicas	Pontificia Universidad Católica de Chile	Spain	Proyecto Long Term Iberoamerican study on nitrogen deposition (LIASONd). Estudio de	28-10-2024	

						la contaminaci on de nitrogeno en el agua lluvia en iberoameric a		
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Annex 5- Networking and other collaborative work

5.1. Formal Collaboration networks

Network Name	Network Scope	Researchers				Institutions
		From the Center		External		
		Researchers	Postdocs / Students	Researchers	Postdocs / Students	
Go-See	I	4	2	30	10	CNRS, University of Arizona, Imperial College London
INRIA-Équipe Associé	I	4	2	3	2	CNRS-Rennes; INRIA-Bordeaux
1000 Genomas Chile	N	10	1	43	0	Instituto Milenio Centro de Regulación del Genoma, Instituto Milenio de Biología Integrativa, Centro Avanzado de Enfermedades Crónicas, Instituto Milenio de Ecosistemas Antárticos y

						Subantárticos, Centro de Modelamiento Matemático, Centro InterN Cabo de Hornos, Instituto de Ecología y Biodiversidad
Consortio de secuenciación del genoma del SARS-CoV-2	N	3	0	60	0	Ministerio de Ciencias, Universidad de Chile, Pontificia Universidad Católica, Universidad Mayor, Universidad Andrés Bello, Universidad de Valparaíso, Centro de Modelamiento Matemático, Instituto Milenio IBio, Proyecto 1000 Genomas, Universidad Austral de Chile-sede Puerto Montt; Faculty of Renewable Natural Resources, Arturo Prat University, Iquique and Universidad de Antofagasta, Antofagasta

Earth Biogenome Project	I	3	0	50	0	Universidad de Chile; Dalhousie University; Revive & Restore; University of Sydney; Spacetime Ventures; Australian Museum; Universidad N Autonoma de Mexico; University of Oslo; Center for Translational Biodiversity Genomics
Proyecto Europeo Bluetools	I	1	1	14	1	Universidad Autonoma de Madrid, Universidad De Alicante, Centro Astrobiologia Madrid
Tara Ocean	I	4	2	10	3	Fundacion Tara Ocean
Red IM-CRG - Centro SYSTEMIX	N	1	8	0	0	IM-CRG y Centro SYSTEMIX
Red IM-CRG - CR2	N	3	14	0	0	IM-CRG y CR2
Red IM-CRG - CMM	N	2	2	0	0	IM-CRG y CMM
Red IM-CRG - iBio	N	6	10	0	0	IM-CRG e iBio
Red IM-CRG - BASE	N	4	13	0	0	IM-CRG y BASE.
Red IM-CRG - IEB	N	5	14	0	0	IM-CRG e IEB
Red IM-CRG - ACCDIS	N	9	0	0	0	IM-CRG y ACCDIS

Red IM-CRG - Núcleo Milenio de Neuroepigenética y Plasticidad EpiNeuro	N	1	4	0	0	IM-CRG y EpiNeuro
Red IM-CRG - CHIC	N	6	0	0	0	IM-CRG y CHIC
Red IBT-UNALM - PUCV	I	1	1	0	0	IBT-UNALM y PUCV
Red con el Instituto de Biología Molecular y Celular de Plantas CSIC– Universidad Politécnica de Valencia (España)	I	1	3	0	0	Instituto de Biología Molecular y Celular de Plantas CSIC– Universidad Politécnica de Valencia (España)
Red IM-CRG - Centro BIOSAV	N	1	8	0	0	IM-CRG y Centro BIOSAV
Red IM-CRG - U. Bordeaux	I	4	3	0	0	IM-CRG y U. de Bordeaux
MeBioS – Katholieke Universiteit Leuven (Bélgica)	I	1	3	0	0	Katholieke Universiteit Leuven (Bélgica)
Instituto de Investigaciones Agropecuarias – INIA La Platina	N	1	3	0	0	Instituto de Investigaciones Agropecuarias – INIA La Platina

NOMENCLATURE:**[Network Scope]**

[N] National [I] International [LA] Latin American

Annex 5.2.- Collaboration Networks

Activity Name	Objective	Description	Co-Participants Institutions	Number of Research from the Center	Number of Postdocs/Students from the Center	Product
NLHPC	Free access to supercomputing time and high-performance mass storage capacity to analyze complex scientific data with massive computing power, high-speed analysis, and flexibility.	The IM-CRG maintains an account in the NLHPC that allows for data analysis and storage using high-performance computing (HPC). Supercomputers can play multiple roles in the field of genomics, such as helping to organize and recognize patterns in data and identify functional elements throughout a	NLHPC	1	10	4, Publicaciones y tesis

		genome sequence. Modern HPC systems provide a platform with massive data storage and management capabilities specifically designed to handle the vast amounts of data generated by the life sciences.				
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Annex 6. - Outreach

6.1. Outreach activities throughout the period

Event Title	Type of Event	Target Audience	Region	N° of Student from the Center	Participating Researchers
Secuenciación del genoma de la pata de guanaco - Vallenar	Interactive workshop	High school students and teachers	Región de Atacama	1	Ariel Orellana López. Miguel Allende Connolly.
ExpoCiencias FECI 2024	Conference	General public	Región Metropolitana de Santiago		Álvaro Glavic Maurer. Emiliano Matías Molina Reyes.
Congreso Futuro 2024	Citizen participation	General public	Región Metropolitana de Santiago		Juliana De Abreu Vianna.
Laboratorio Móvil	Public space intervention	Primary and high school students	Región de la Araucanía	2	

					Jacquelinne Acuña Sobarzo.
ExpoCiencias FECI 2024	Citizen participation	General public	Región Metropolitana de Santiago	5	Emiliano Matías Molina Reyes. Álvaro Glavic Maurer.
Día del Pingüino y del ADN	Other	University students and professors	Región Metropolitana de Santiago	11	Juliana De Abreu Vianna.
Festival Cazadores de Genes - Antofagasta	Otra	Primary and high school students and teachers	Región de Antofagasta	7	Alexandra Galetovic Carabantes. Miguel Allende Connelly.
Festival Cazadores de Genes - Antofagasta	Otra	Primary and high school students and teachers	Región de Antofagasta	7	Juliana De Abreu Vianna. Alexandra Galetovic Carabantes. Miguel Allende Connelly.
Festival Cazadores de Genes - Antofagasta	Other	Primary and high school students and teachers	Región de Antofagasta	7	Alexandra Galetovic Carabantes. Juliana De Abreu Vianna. Miguel Allende Connelly.

Festival Cazadores de Genes - Araucanía	Other	Primary and high school students and teachers	Región de la Araucanía	6	Jacquelinne Acuña Sobarzo. Miguel Allende Connelly. Alexis Ignacio Gaete Silva. Daly Noll Vergara.
Festival Cazadores de Genes - Antofagasta	Other	Primary and high school students and teachers	Región de Antofagasta	7	Alexandra Galetovic Carabantes. Miguel Allende Connelly. Juliana De Abreu Vianna.
Congreso de Ciencias del Instituto Nacional	Conference	High school students	Región Metropolitana de Santiago	0	Miguel Allende Connelly.
Festival Ladera Sur	Interactive Workshop	General public	Región Metropolitana de Santiago	2	Alexis Ignacio Gaete Silva. Daly Noll Vergara.
Experiencia Práctica Biotecnología Liceo Manuel de Salas	Interactive Workshop	High school students	Región Metropolitana de Santiago	4	Álvaro Glavic Maurer.
Clases de Biotecnología Liceo Manuel de Salas	Workshop	High school students	Región Metropolitana de Santiago	4	Álvaro Glavic Maurer.
Semana de la Ciencia de la	Other	High school students	Región Metropolitana de Santiago	0	Alejandro Maass Sepúlveda.

Embajada de Francia					
Feria de Ciencias Colegio Trehwela's de Colina	Otra	High school students Primary school students	Región Metropolitana de Santiago	3	Miguel Allende Connelly.
Secuenciación del genoma de la pata de guanaco - Vallenar	Interactive Workshop	High school students and teachers	Región de Atacama	1	Ariel Orellana López. Miguel Allende Connelly.
Temporales de Ciencia Chiloé	Conference	General public	Región de los Lagos		Ana Karina Madriaza Maturana.
Feria de Ciencias del Museo Nacional de Historia Natural	Contest	Primary and high school students	Región Metropolitana de Santiago		Ana Karina Madriaza Maturana.
Entrega de Libros IEB a biblioteca escolar	Workshop	Primary and high school students	Región Metropolitana de Santiago	1	Ana Karina Madriaza Maturana.

6.2.- Articles and Interviews

Type of Media and Scope	Local / Regional		National		International		Total
	Nº Interviews	Nº Articles	Nº Interviews	Nº Articles	Nº Interviews	Nº Articles	
Written	0	2	3	11	0	1	17
Internet	0	3	3	9	0	3	18
Audiovisual	0	0	3	0	1	0	4
Total	0	5	9	20	1	4	39

6.3 Products of Projection to the External Environment (PME) (OPTIONAL)

N°	Date	Product	Objective	Researchers	Target audience	Type	Scope
1	04-11-2024	Documental “Exploradores del Desierto de Atacama”	Register the experience of the 2024 Workshop on Genomics Biodiversity	19	General public	Audiovisual	National
2	29-10-2024	Libro “ADN Explorador”	Educate children on basic concepts of genomics	19	School students	Book	National

Annex 7. - Connections with other sectors

Activity	Type of Activity	Institution Country	Agent Type	Economic Sector
Presentación inicial en una reunión de trabajo sobre el estado del arte de la investigación con genoma en Chile y cuáles son los beneficios y también los riesgos que se deberían prever en una propuesta normativa .	[4]	Chile	[2]	Medicine and human health
Charla y mesa de conversación sobre "Desincronización de color en paltos" en la 8va Conferencia Redagráfica	Other	Chile		Agriculture
Primer Seminario de Centros de Rehabilitación de Fauna Silvestre de Chile	[4]	Chile	[2]	Environment
Reunión con Danper Trujillo SAC	[1]	Perú	[1]	Agriculture
Reunión en el Centro de Investigación e Innovación de Concha y Toro	[4]	Chile	[1]	Wine market
Reunión con equipo Sticta	[1]	Chile	[1]	Biotechnology
Reunión SERNAPESCA-MEVEA	[4]	Chile	[2]	Aquaculture
Charla "10 años de estudio en la genómica de la Pata de Guanaco" en Seminario	Seminario científico de CONAF Atacama	Chile	[2]	Forestry

"Biodiversidad marino y terrestre de la Región de Atacama"				
Reunión con Seremi de Ciencia, Conocimiento, Tecnología e Innovación de la Macrozona Centro - Sr. Rodrigo González Rebeco	Visita de autoridad	Chile	[2]	Public
Reunión Polar Fruit International	[1]	Chile	[1]	Fruticulture
Reunión ProHass Perú	[4]	Perú	[1]	Fruticulture
COP 16 - New ideas based on omics-sciences, mathematical modeling and remote sensing for ocean conservation tools		Colombia		Environment
Reunión FFME	[1]	Francia	[2]	Environment
Reunión Gama Ltda	[4]	Chile	[1]	Fruticulture
Reunión Zymvol (Barcelona)	[4]	España	[1]	Biotechnology
Reunión con Fundación Minera Escondida	[4]	Chile	[1]	Mining
Reunión con Tuki Ludo y Tukave Pakomio, Consejo Directivo	[1]	Chile		Environment
Reunión con Sebastián Yancovic y Marcela Hey	[1]	Chile		Other
Reunión con Rector Colegio Católico de Rapa Nui	[1]	Chile	[3]	Education
Reunión con Consuelo Labra (Comisión de Desarrollo) y Nancy Rivera (Unidad de Investigación Marina)	[1]	Chile	[2]	Public
Reunión con Concejala Maria Ika	[1]	Chile	[2]	Public
Reunión con Rectora Colegio San Sebastián de Rapa Nui	[1]	Chile	[3]	Education
Reunión con representante de Colegio La Aldea de Rapa Nui	[1]	Chile	[3]	Education
Charla "La Importancia de la Metrología en la Genómica para un Desarrollo Sostenible en Conservación de la biodiversidad, Agricultura y Pesca en Chile"	[3]	Chile	[3]	Education
Reunion de colaboración con Minera Valle Central	[4]	Chile	Industria	Mining

NOMENCLATURE:

[Type of Activity] [1] Development of Studies [2] Project Implementation [3] Training [4] Prospective Activity [5] Scientific Training [6] Installation of Scientists [7] Others (specify at the table foot other types of activity)

[Agent Type] [1] Industry and Services [2] Organizations and Public Services [3] Educational Sector

Annex 8.- Relevant materials, products and activities carried out by the center. OPTIONAL:

Letter from the Institute's Director

As Director of the Institute, I complement our official report with a few comments and thoughts about the progress of our project.

The year 2024 was exceptionally productive and fruitful from many perspectives, especially those that have to do with the consolidation of an administrative and organizational structure within the CGR. We have incorporated a highly motivated team to tackle the administrative tasks of the Institute which include an Executive Director aided by two financial administrators, lightening the burden of the scientists in these areas. We also have a dedicated Communications Director whose responsibilities involve positioning the Institute in the national and international media and coordinating our outreach efforts. Both persons have been formally hired (i.e., with contracts) by the Institute's Foundation which puts us into compliance with national labor laws. We have also held regular meetings of the Foundation's Board of Directors, which includes all Associate Investigators and a representative from each of the participating universities. The Board approves all major decisions of the Foundation and oversees its compliance with the legal requirements of these types of institutions in the country. Thus, we have produced annual reports for the Ministry of Justice, and we have generated policies, procedures and protocols for issues like ethics, diversity and inclusion, safety and intellectual property, all of which are in line with established good practices for non-profit

Foundations. We have also signed agreements with the universities harboring our researchers to establish the scope and limits of the institutions' responsibilities. Since many of the issues are not familiar to us scientists, we have hired a legal team for consultation. Overall, our Institute has become a well-managed organization, with an efficient operation and excellent relationships with the harboring universities and the funding agency. Our financial reports have been approved with little or no observations, and the procedures for expenditures are carried out rapidly and with minimal perturbation of the scientific enterprise.

Importantly, we have been successful in the scientific and dissemination aspects where we have surpassed all of the baseline metrics that we reported during the first year including number of published articles, co-authored articles, trained students, and outreach activities. Part of our funding has been set aside for collaborative projects within the CGR, focusing on the adjunct faculty, which has had the effect of increasing our joint publications and theses. It is noteworthy that since 2010, our center has shown a steady increase in the average impact factor values it has reached as well as the number of yearly citations of its researchers.

In terms of training, it is important to note that the CGR contributes to the Chilean scientific community with highly trained young scientists, in the areas of genomics, bioinformatics and systems biology. Importantly, we have impact not only in the traditional undergraduate and graduate schools at our universities but also in the professional development of other affiliated personnel such as engineers, medical doctors, agronomists, veterinarians, chemists and other specialists. The know-how of the CGR is unique in the country and we have numerous requests from colleagues to support or sponsor their projects or funding applications making our Institute an invaluable asset for these institutions and projects.

At the beginning, we incorporated 4 Senior Researchers to assist us in expanding our international ties with world class research centers of excellence. We also proposed various evaluations by this International Advisory Board to assess our Center in the scientific dimension. These were meant to be at years 2 and 4 for the first period, and 7 and 9 for the second. The evaluation in year 2 was not possible due to scheduling conflicts, but we are making an effort to have it in year 4 (2025).

Finally, I want to highlight the highly impactful outreach and educational activities we have embarked in, especially related to the 1000 Genomes Chile initiative. We have taken genomics into the classroom and other public venues all over the country, influencing the education of thousands of young minds. Activities in the Antofagasta, Araucanía, Valparaíso and Metropolitan regions have been very successful and a very worthwhile use of resources and personnel. We are in a time of crisis, when science has been undervalued or ignored by large segments of society. In part, this is our failure, as we have not been able to influence policy and educational standards to accept evidence as the basis for decisions and opinion. It is our responsibility to change this perception and work towards a higher level of scientific literacy and comprehension of our role in society. Thus, we view this aspect of our efforts as crucial, urgent and ethically necessary.



Miguel L. Allende Connelly
MI-CGR Director

Our year in pictures



MI-CGR Deputy Director Dr. Juliana Vianna was invited as a speaker in Congreso Futuro 2024. The event was held from January 15th to the 20th and had over 115 speakers from 20 countries.



Relaunching of the Chilean 1000 Genomes Project in April 2024 with nearly 1000 attendees and keynote speaker Dr. Camila Mazzoni from the European Reference Genome Atlas.



In June 2024, we travelled to the Araucanía Region to carry out an outreach activity that had almost 400 visitors, mainly school children and their teachers. This activity was supported by MI-CGR students and Postdoctoral Researchers and hosted by Adjunct Researcher Dr. Jacqueline Acuña from the University of La Frontera.



Nanopore Day Santiago in July 2024. MI-CGR Deputy Director Dr. Juliana Vianna and Associate Researcher Dr. Ariel Orellana (right) were speakers at the event. Also in attendance were Adjunct Researcher Dr. Liane Bassini (left) and former MI-CRG D student Dr. Alex Di Genova.



MI-CGR Scientific Meeting in Pucón, Araucanía Region, in August 2024. 9 Associate Researchers and 9 Adjunct Researchers participated.



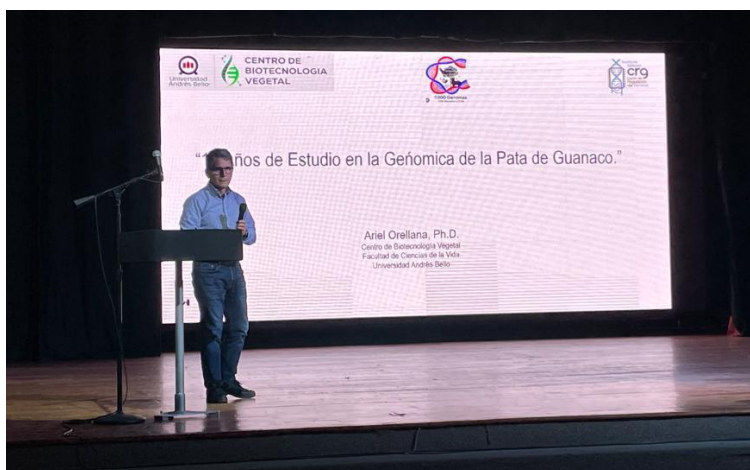
As Vice president of the Association of Veterinarians Specialized in Aquaculture, Adjunct Researcher Dr. Liane Bassini (left) led a meeting with SERNAPESCA, the National Service for Fishing and Aquaculture, in August 2024.



Meeting with authorities from the University of Antofagasta in September 2024. We also offered a presentation of the Chilean 1000 Genomes Project to students from the university. In the same trip we visited three schools and one cultural center for outreach activities. We also held a meeting with Minera Escondida Foundation. These activities were hosted by Adjunct Researcher Dr. Alexandra Galetovic from the University of Antofagasta.



MI-CGR Director Dr. Miguel Allende and Deputy Director Dr. Juliana Vianna at the radio station in Antofagasta for an interview about the Chilean 1000 Genomes Project.



Associate Researcher Dr. Ariel Orellana was invited to the celebration of the National Environment Day in Atacama in October 2024. The event was organized by the National Forestry Corporation and the University of Atacama.



Associate Researcher Dr. Alejandro Maass (right) was part of the scientific delegation that accompanied the presidents of Chile and France, Gabriel Boric and Emmanuel Macron, respectively, on their visit to the AGB 46 ship Almirante Viel in Valparaíso in November 2024.



Adjunct Researcher Dr. Martin Montecino (left) was invited to discuss the “big scientific discoveries of 2024” by La Tercera Board in November 2024.



Dr. Anton Nekrutenko, Dorothy Foher Huck and J. Lloyd Huck Chair in Genomics at PennState, taught a workshop on Galaxy for nearly 30 students in November 2024. This workshop was organized by the Chilean 1000 Genomes Project.



MI-CGR Director Dr. Miguel Allende and Associate Researcher Dr. Ariel Orellana, together with three students, travelled to the Atacama Region in November 2024, where they guided two practical experiences on the sequencing of the genome of *Cistanthe longiscapa* in two different schools.

