Industry-Academia Collaborations in Bioinformatics

General information
(distribute freely)
July 2025

GeneVia Technologies

Prof. Matti Nykter, Founder, Chief Scientific Officer

Prof. Nykter also leads the Computational Biology Group at Tampere University, Finland, focusing on computational cancer research (tumor evolution, treatment resistance, circulating tumor DNA)

Dr. Matti Nykter
Professor, Tampere University
CSO, Genevia Technologies

- Selected publications
  - Sipola, J. et al. (2025). **Plasma Cell-Free DNA Chromatin Immunoprecipitation Profiling Depicts Phenotypic and Clinical Heterogeneity in Advanced Prostate Cancer**. *Cancer research*, 85(4), 791–807. https://doi.org/10.1158/0008-5472.CAN-24-2052
  - Kiviaho, A. et al. (2024). **Single cell and spatial transcriptomics highlight the interaction of club-like cells with immunosuppressive myeloid cells in prostate cancer**. *Nature communications*, 15(1), 9949. https://doi.org/10.1038/s41467-024-54364-1
  - Nurminen, A. et al. (2023). **Cancer origin tracing and timing in two high-risk prostate cancers using multisample whole genome analysis: prospects for personalized medicine**. *Genome medicine*, 15(1), 82. https://doi.org/10.1186/s13073-023-01242-y
  - Herberts, C. et al. (2022). **Deep whole-genome ctDNA chronology of treatment-resistant prostate cancer**. *Nature*, 608(7921), 199–208. https://doi.org/10.1038/s41586-022-04975-9
  - Vandekerkhove, G. et al. (2021). **Plasma ctDNA is a tumor tissue surrogate and enables clinical-genomic stratification of metastatic bladder cancer**. *Nature communications*, 12(1), 184. https://doi.org/10.1038/s41467-020-20493-6
  - Dufva, O. et al. (2020). **Immunogenomic Landscape of Hematological Malignancies**. *Cancer cell*, 38(3), 380–399.e13. https://doi.org/10.1016/j.ccell.2020.06.002
  - Woodcock, D. J. et al. (2020). **Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy**. *Nature communications*, 11(1), 5070. https://doi.org/10.1038/s41467-020-18843-5
  - Latonen, L. et al. (2018). **Integrative proteomics in prostate cancer uncovers robustness against genomic and transcriptomic aberrations during disease progression**. *Nature communications*, 9(1), 1176. https://doi.org/10.1038/s41467-018-03573-6
  - Annala, M. et al. (2018). **Circulating Tumor DNA Genomics Correlate with Resistance to Abiraterone and Enzalutamide in Prostate Cancer**. *Cancer discovery*, 8(4), 444–457. https://doi.org/10.1158/2159-8290.CD-17-0937
  - Gao, Q. et al. (2018). **Driver Fusions and Their Implications in the Development and Treatment of Human Cancers**. *Cell reports*, 23(1), 227–238.e3. https://doi.org/10.1016/j.celrep.2018.03.050
  - Wyatt, A. W. et al. (2017). **Concordance of Circulating Tumor DNA and Matched Metastatic Tissue Biopsy in Prostate Cancer**. *Journal of the National Cancer Institute*, 109(12), djx118. https://doi.org/10.1093/jnci/djx118
  - Urbanucci, A., et al. (2017). **Androgen Receptor Deregulation Drives Bromodomain-Mediated Chromatin Alterations in Prostate Cancer**. *Cell reports*, 19(10), 2045–2059. https://doi.org/10.1016/j.celrep.2017.05.049
  - Wyatt, A. W., et al. (2016). **Genomic Alterations in Cell-Free DNA and Enzalutamide Resistance in Castration-Resistant Prostate Cancer**. *JAMA oncology*, 2(12), 1598–1606. https://doi.org/10.1001/jamaoncol.2016.0494
  - Cancer Genome Atlas Research Network (2015). **The Molecular Taxonomy of Primary Prostate Cancer**. *Cell*, 163(4), 1011–1025. https://doi.org/10.1016/j.cell.2015.10.025
  - Gundem, G. et al. (2015). **The evolutionary history of lethal metastatic prostate cancer**. *Nature*, 520(7547), 353–357. https://doi.org/10.1038/nature14347

GeneVia Technologies

Genevia Technologies

What we do best:

1. Analysis of NGS, mass spectrometry and other omics data

2. Data integration (multi-omics analysis, machine learning)

3. Supporting academic biomedical researchers from idea stage to publication

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Genevia Technologies

Relevant experience:

- 14 years of service
- 18 PhD computational biologists
- 170 client organisations in 20+ countries
- Hundreds of publications (company H-index: 81)
- See more: https://geneviatechnologies.com/

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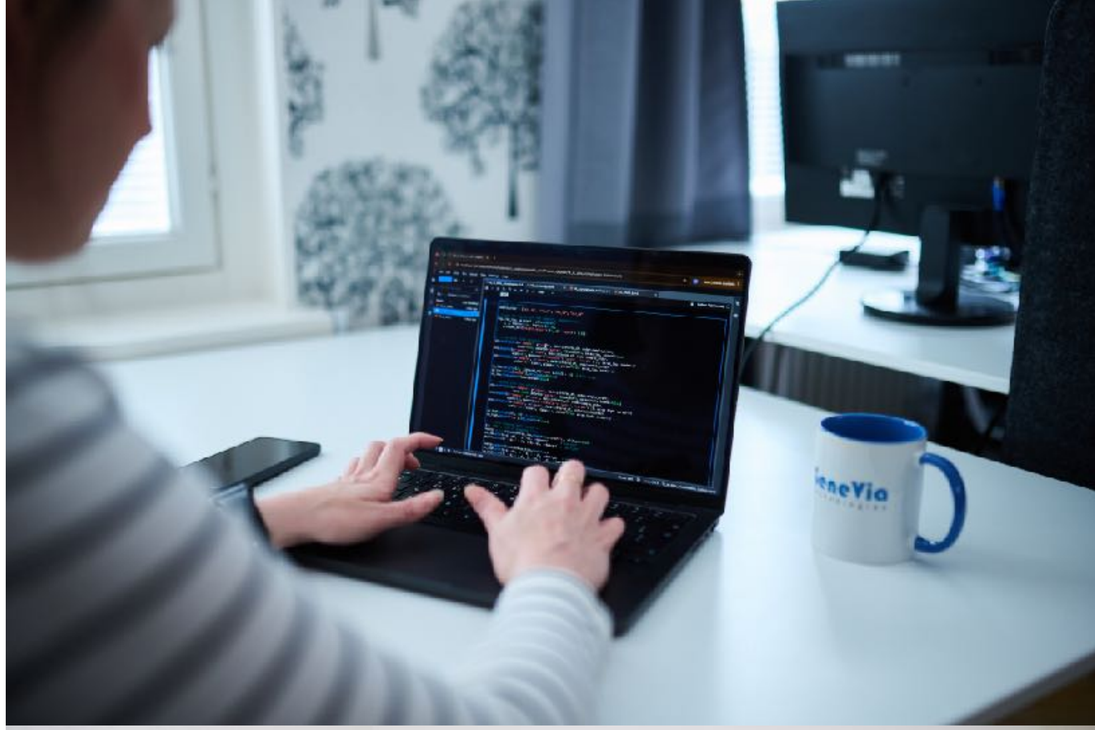
Your bioinformatics core

You choose the content

- Support my grant application
- Advise on experiment design / data generation
- Teach, consult & co-supervise my student / postdoc
- Analyse *any* type of omics data:
  - Conduct primary analysis with gold standard protocols
  - Integrate multiple levels of data
  - Interpret results and innovate downstream analyses
  - Draft visually stunning figures and crisp text
- Identify, re-analyse or integrate public data sets
- Develop re-usable bioinformatics pipelines
- Conceptualise & co-author manuscripts with my researchers



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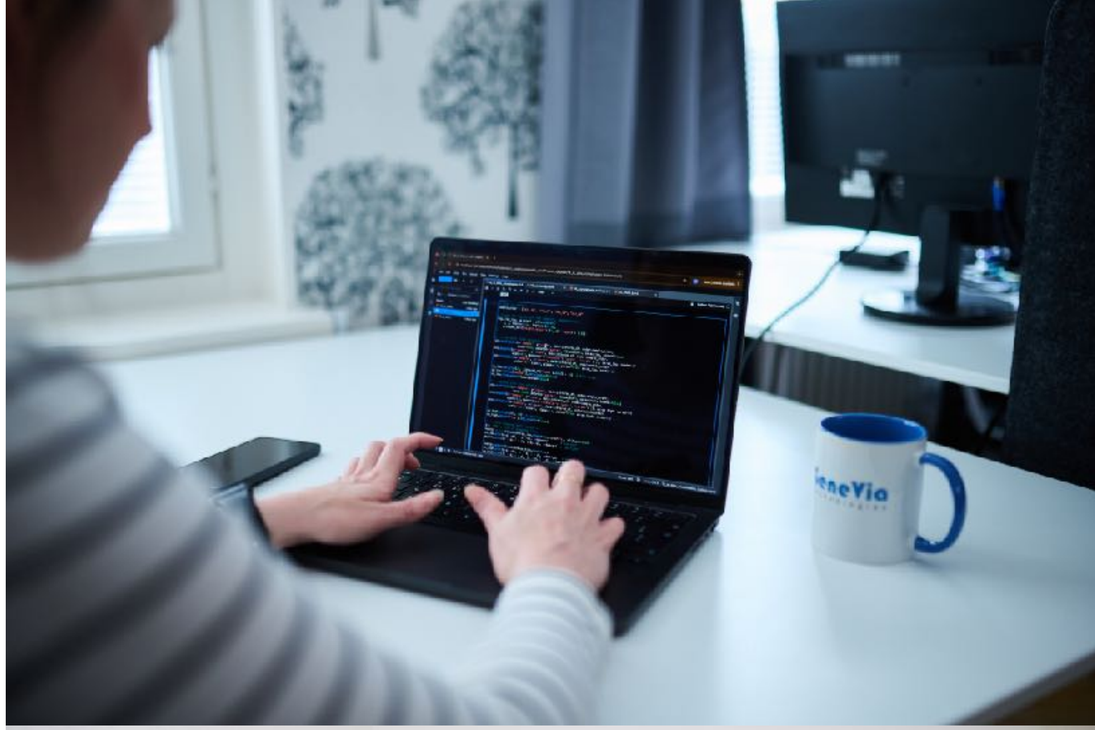
Your bioinformatics core

You choose how you want to work

- Start when you want, pause when you want, wrap up when you want
- Schedule when, how and how often you want to talk to our scientists
- Switch experts to get the best support for each parts of your project
- Stick with one expert for consistency and convenience
- Choose how much time will they reserve for you



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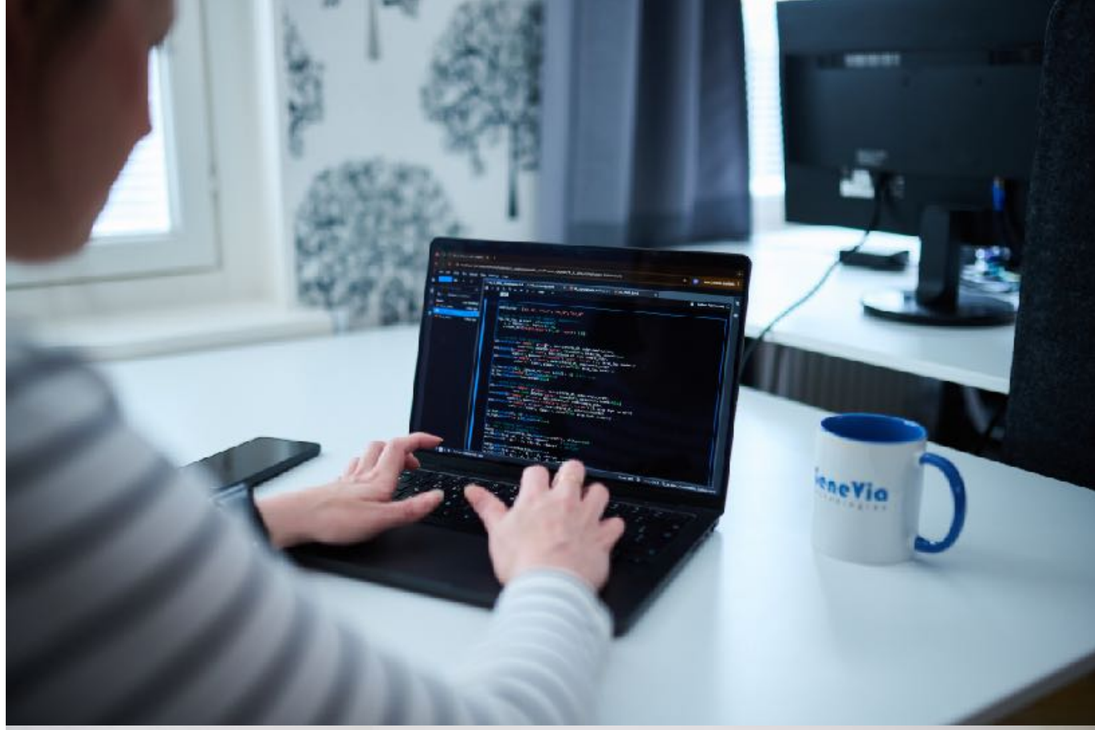
Your bioinformatics core

You choose your deliverables

- Figures, tables & text
- Files, data & pipelines
- Ideas, interpretation & insight
- Support, supervision & data submission
- Report, presentation & publication



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We make it happen!

Have our international team of experts support you at the scale your need:

- Small hourly consulting (min. 10h)
- One full project / data set (min. 1 month)
- All the projects in your group (6-12 mo / 0.25 - 0.75 FTE)
- All the groups in your department (min. 12 mo / 1+ FTE)

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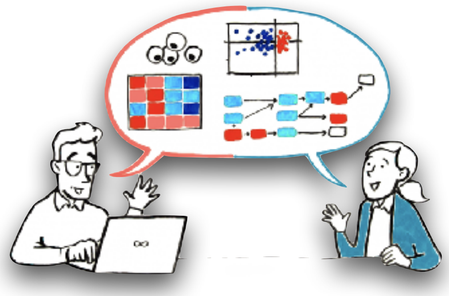
Modes of collaboration

Fee-per-service

Our full team and services at your disposal when and how you want



Joint grant funding

We can join your grant application as a co-applicant or subcontractor

mac 4me

Genevia Grants

Apply for our bioinformatics mini grants for academic researchers

Seminars & Workshops

We are delighted to support science events of our customers

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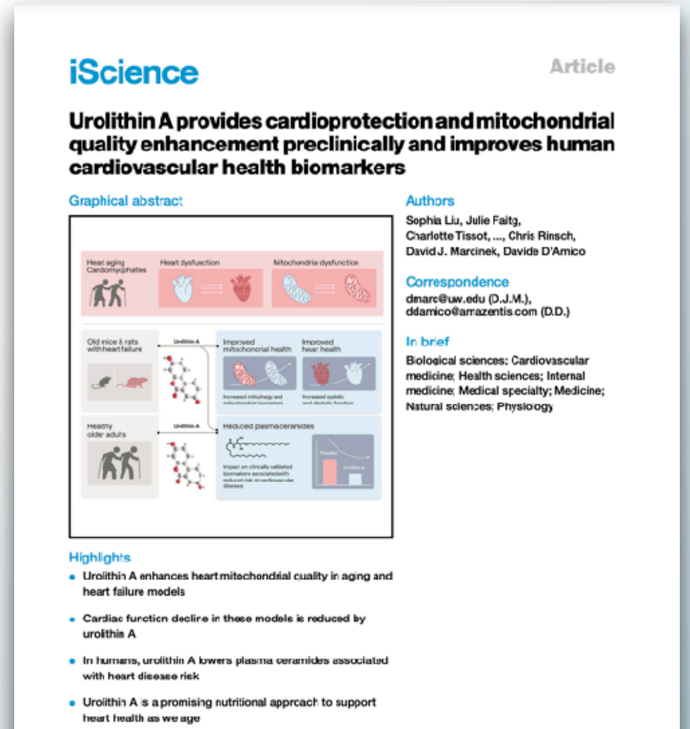
Case: Amazentis

- The client
  - A Swiss biotech conducting preclinical and clinical research on a postbiotic, Urolithin A
- Omics analysis for clinical trials
  - Transcriptomic, proteomic & metabolomic data
  - Aims: mechanism of action, "molecular endpoints”
- Papers
  - **iScience 2025** https://doi.org/10.1016/j.isci.2025.111814
  - **medRxiv (preprint) 2023** https://doi.org/10.1101/2023.06.16.23291378
  - **Cell Rep Med 2022** https://doi.org/10.1016/j.xcrm.2022.100633

“We really like the flexibility of Genevia’s approach. They go beyond being a simple service provider to give a scientific input that is comparable to a top academic collaboration.”

Dr. Davide D’Amico
R&D Group Leader, Amazentis

Full interview: **geneviatechnologies.com/references/cases/tailored-bioinformatics-support-for-a-clinical-trial/**


iScience

Article

Urolithin A provides cardioprotection and mitochondrial quality enhancement preclinically and improves human cardiovascular health biomarkers

Graphical abstract

Authors

Sophia Liu, Julie Faitg, Charlotte Tissot, ..., Chris Rinsch, David J. Marcinek, Davide D'Amico

Correspondence

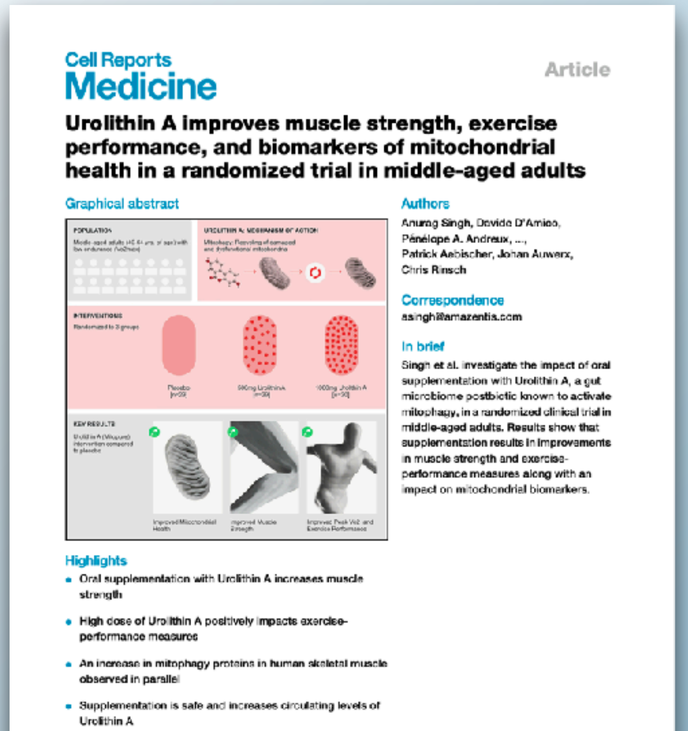
dmarc@uw.edu (D.J.M.), ddamico@amazentis.com (D.D.)

In brief

Biological sciences: Cardiovascular medicine; Health sciences; Internal medicine; Medical specialty; Medicine; Natural sciences; Physiology

Highlights

- Urolithin A enhances heart mitochondrial quality in aging and heart failure models
- Cardiac function decline in these models is reduced by urolithin A
- In humans, urolithin A lowers plasma ceramides associated with heart disease risk
- Urolithin A is a promising nutritional approach to support heart health as we age


Cell Reports Medicine

Article

Urolithin A improves muscle strength, exercise performance, and biomarkers of mitochondrial health in a randomized trial in middle-aged adults

Graphical abstract

Authors

Anurag Singh, Davide D'Amico, Pénélope A. Andreux, ..., Patrick Aebischer, Johan Auwerx, Chris Rinsch

Correspondence

asingh@amazentis.com

In brief

Singh et al. investigate the impact of oral supplementation with Urolithin A, a gut microbiome postbiotic known to activate mitophagy, in a randomized clinical trial in middle-aged adults. Results show that supplementation results in improvements in muscle strength and exercise-performance measures along with an impact on mitochondrial biomarkers.

Highlights

- Oral supplementation with Urolithin A increases muscle strength
- High dose of Urolithin A positively impacts exercise-performance measures
- An increase in mitophagy proteins in human skeletal muscle observed in parallel
- Supplementation is safe and increases circulating levels of Urolithin A

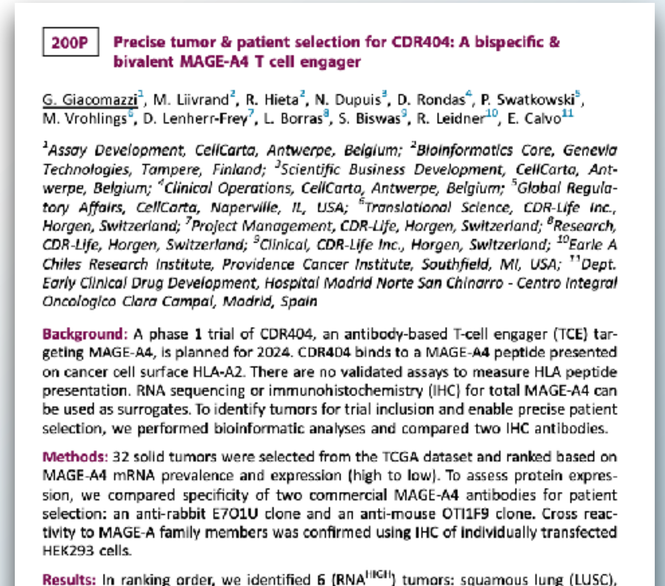
Case: CDR-Life

- The client
  - A Swiss biotech developing anti-cancer T-cell engagers
- Public omic data analysis
  - Characterizing target expression across tumor types to identify indications to include in a clinical trial
  - Biomarker discovery (molecular correlates of target expression)
- Abstracts
  - **ASCO 2024** https://doi.org/10.1200/JCO.2024.42.16_suppl.e20024
  - **ESMO 2023** https://doi.org/10.1016/j.annonc.2023.09.2923

"As is typical in scientific exploration, initial findings frequently resulted in new questions, steering our investigation in different directions. Genevia seamlessly navigated these pivots."

Dr. Melissa Vrohlings
Translational Science Leader, CDR-Life

Full interview: **geneviatechnologies.com/references/cases/characterizing-a-cancer-immunotherapy-target-with-genomic-data/**



200P **Precise tumor & patient selection for CDR404: A bispecific & bivalent MAGE-A4 T cell engager**

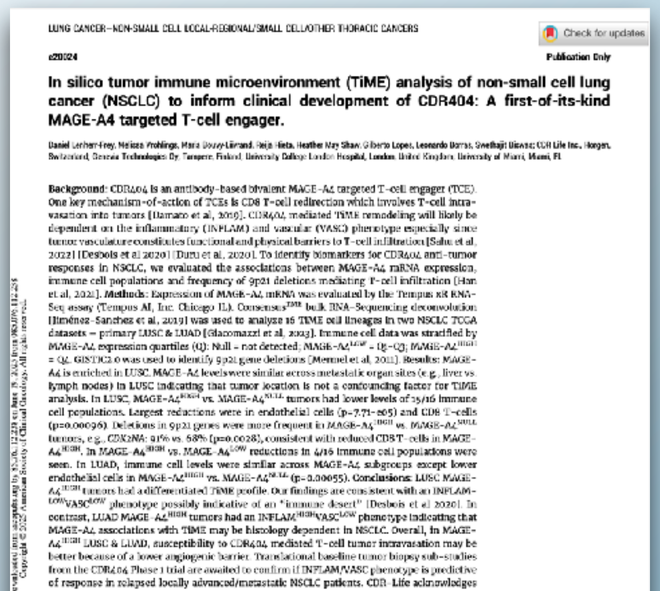
G. Giacomazzi[1], M. Liivrand[2], R. Hieta[2], N. Dupuis[3], D. Rondas[4], P. Swatkowski[5], M. Vrohlings[6], D. Lenherr-Frey[7], L. Borras[8], S. Biswas[9], R. Leidner[10], E. Calvo[11]

[1]Assay Development, CellCarta, Antwerpe, Belgium; [2]Bioinformatics Core, Genevia Technologies, Tampere, Finland; [3]Scientific Business Development, CellCarta, Antwerpe, Belgium; [4]Clinical Operations, CellCarta, Antwerpe, Belgium; [5]Global Regulatory Affairs, CellCarta, Naperville, IL, USA; [6]Translational Science, CDR-Life Inc., Horgen, Switzerland; [7]Project Management, CDR-Life, Horgen, Switzerland; [8]Research, CDR-Life, Horgen, Switzerland; [9]Clinical, CDR-Life Inc., Horgen, Switzerland; [10]Earle A Chiles Research Institute, Providence Cancer Institute, Southfield, MI, USA; [11]Dept. Early Clinical Drug Development, Hospital Madrid Norte San Chinarro - Centro Integral Oncologico Clara Campal, Madrid, Spain

Background: A phase 1 trial of CDR404, an antibody-based T-cell engager (TCE) targeting MAGE-A4, is planned for 2024. CDR404 binds to a MAGE-A4 peptide presented on cancer cell surface HLA-A2. There are no validated assays to measure HLA peptide presentation. RNA sequencing or immunohistochemistry (IHC) for total MAGE-A4 can be used as surrogates. To identify tumors for trial inclusion and enable precise patient selection, we performed bioinformatic analyses and compared two IHC antibodies.

Methods: 32 solid tumors were selected from the TCGA dataset and ranked based on MAGE-A4 mRNA prevalence and expression (high to low). To assess protein expression, we compared specificity of two commercial MAGE-A4 antibodies for patient selection: an anti-rabbit E7O1U clone and an anti-mouse OTI1F9 clone. Cross reactivity to MAGE-A family members was confirmed using IHC of individually transfected HEK293 cells.

Results: In ranking order, we identified 6 (RNA^{HIGH}) tumors: squamous lung (LUSC),



LUNG CANCER—NON-SMALL CELL LOCAL-REGIONAL/SMALL CELL/OTHER THORACIC CANCERS

e20024 Publication Only

In silico tumor immune microenvironment (TiME) analysis of non-small cell lung cancer (NSCLC) to inform clinical development of CDR404: A first-of-its-kind MAGE-A4 targeted T-cell engager.

Daniel Lenherr-Frey, Melissa Vrohlings, Mara Bouzy-Liivrand, Reija Hieta, Heather May Shaw, Gilberto Lopes, Leonardo Borras, Sivathajit Biswas; CDR Life Inc., Horgen, Switzerland; Genevia Technologies Oy, Tampere, Finland; University College London Hospital, London, United Kingdom; University of Miami, Miami, FL

Background: CDR404 is an antibody-based bivalent MAGE-A4 targeted T-cell engager (TCE). One key mechanism-of-action of TCEs is CD8 T-cell redirection which involves T-cell intravasation into tumors [Hamano et al, 2019]. CDR404 mediated TiME remodeling will likely be dependent on the inflammatory (INFLAM) and vascular (VASC) phenotype especially since tumor vasculature constitutes functional and physical barriers to T-cell infiltration [Sahu et al, 2022] [Desbois et al 2020] [Datta et al, 2020]. To identify biomarkers for CDR404 anti-tumor responses in NSCLC, we evaluated the associations between MAGE-A4 mRNA expression, immune cell populations and frequency of 9p21 deletions mediating T-cell infiltration [Han et al, 2021]. **Methods:** Expression of MAGE-A4 mRNA was evaluated by the Tempus xR RNA-Seq assay (Tempus AI, Inc. Chicago IL). Consensus^{TME} bulk RNA-Sequencing deconvolution [Jiménez-Sánchez et al, 2019] was used to analyze 16 TiME cell lineages in two NSCLC TCGA datasets – primary LUSC & LUAD [Giacomazzi et al, 2023]. Immune cell data was stratified by MAGE-A4 expression quartiles (Q): Null – not detected; $MAGE\text{-}A4^{LOW}$ – 1st-Q; $MAGE\text{-}A4^{HIGH}$ = Q4. GISTIC2.0 was used to identify 9p21 gene deletions [Mermel et al, 2011]. **Results:** MAGE-A4 is enriched in LUSC. MAGE-A4 levels were similar across metastatic organ sites (e.g., liver vs. lymph nodes) in LUSC indicating that tumor location is not a confounding factor for TiME analysis. In LUSC, $MAGE\text{-}A4^{HIGH}$ vs. $MAGE\text{-}A4^{NULL}$ tumors had lower levels of 15/16 immune cell populations. Largest reductions were in endothelial cells ($p=7.7\text{-}e05$) and CD8 T-cells ($p=0.00096$). Deletions in 9p21 genes were more frequent in $MAGE\text{-}A4^{HIGH}$ vs. $MAGE\text{-}A4^{NULL}$ tumors, e.g., *CDKN2A*: 41% vs. 58% ($p=0.0228$), consistent with reduced CD8 T-cells in $MAGE\text{-}A4^{HIGH}$. In $MAGE\text{-}A4^{HIGH}$ vs. $MAGE\text{-}A4^{LOW}$ reductions in 4/16 immune cell populations were seen. In LUAD, immune cell levels were similar across MAGE-A4 subgroups except lower endothelial cells in $MAGE\text{-}A4^{HIGH}$ vs. $MAGE\text{-}A4^{NULL}$ ($p=0.00655$). **Conclusions:** LUSC $MAGE\text{-}A4^{HIGH}$ tumors had a differentiated TiME profile. Our findings are consistent with an $INFLAM^{LOW}VASC^{LOW}$ phenotype possibly indicative of an "immune desert" [Desbois et al 2020]. In contrast, LUAD $MAGE\text{-}A4^{HIGH}$ tumors had an $INFLAM^{HIGH}VASC^{LOW}$ phenotype indicating that MAGE-A4 associations with TiME may be histology dependent in NSCLC. Overall, in $MAGE\text{-}A4^{HIGH}$ LUSC & LUAD, susceptibility to CDR404 mediated T-cell tumor intravasation may be better because of a lower angiogenic barrier. Translational baseline tumor biopsy sub-studies from the CDR404 Phase 1 trial are awaited to confirm if INFLAM/VASC phenotype is predictive of response in relapsed locally advanced/metastatic NSCLC patients. CDR-Life acknowledges

Case: Herantis Pharma

- The client
  - A Finnish biotech company developing a peptidomimetic molecule (based on CDNF) to treat Parkinson's disease
- Spatial and bulk transcriptomic data analysis
  - To study the mechanisms of action in preclinical disease models

"She [Genevia's bioinformatician] is able to explain the technical side very well to us non-bioinformaticians and has been very patient with our questions. This is very important in this kind of interface where we understand the biology and she has the bioinformatics and methodological knowledge"

Dr. Henri Huttunen
CSO, Herantis Pharma

Full interview: **geneviatechnologies.com/references/cases/investigating-the-mechanism-of-action-of-a-disease-modifying-treatment-for-parkinsons-disease-using-bulk-and-spatial-transcript/**

GeneVia Technologies

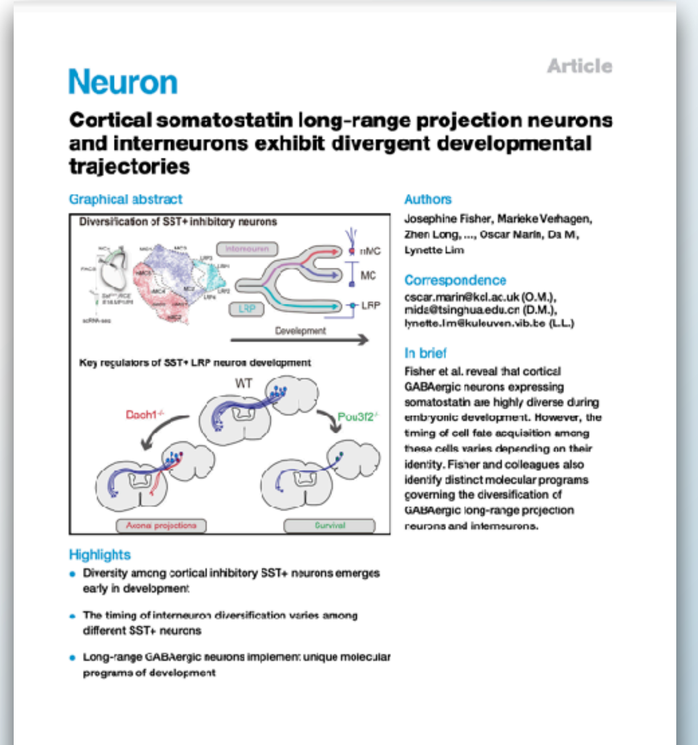
Case: VIB / KU Leuven

- The client
  - A developmental neurobiology group
- Analysis and integration of single-cell datasets
  - Aims: build neuronal single-cell atlas, study developmental trajectories
- Papers
  - **biorXiv (preprint) 2025** https://doi.org/10.1101/2025.02.19.636192
  - **Neuron 2024** https://doi.org/10.1016/j.neuron.2023.11.013

"The keyword here is collaboration. Typically, when contracting a service, you specify what you want, and the next interaction occurs months later -- with Genevia, it's different."

Dr. Lynette Lim
Group Leader, VIB / KU Leuven

Full interview: **geneviatechnologies.com/references/cases/building-a-neuronal-atlas-with-single-cell-technologies/**


Neuron

Article

Cortical somatostatin long-range projection neurons and interneurons exhibit divergent developmental trajectories

Graphical abstract

Diversification of SST+ inhibitory neurons

Key regulators of SST+ LRP neuron development

Authors

Josephine Fisher, Marieke Verhagen, Zhen Long, ..., Oscar Marin, Da M, Lynette Lim

Correspondence

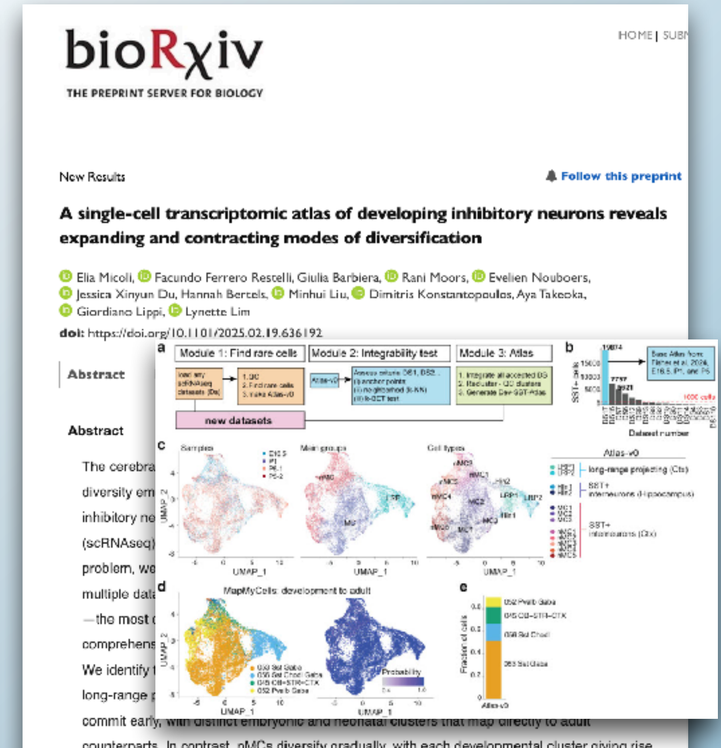
oscar.marin@kcl.ac.uk (O.M.), nida@tsinghua.edu.cn (D.M.), lynette.lim@kuleuven.vib.be (L.L.)

In brief

Fisher et al. reveal that cortical GABAergic neurons expressing somatostatin are highly diverse during embryonic development. However, the timing of cell fate acquisition among these cells varies depending on their identity. Fisher and colleagues also identify distinct molecular programs governing the diversification of GABAergic long-range projection neurons and interneurons.

Highlights

- Diversity among cortical inhibitory SST+ neurons emerges early in development
- The timing of interneuron diversification varies among different SST+ neurons
- Long-range GABAergic neurons implement unique molecular programs of development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A single-cell transcriptomic atlas of developing inhibitory neurons reveals expanding and contracting modes of diversification

doi: https://doi.org/10.1101/2025.02.19.636192

Abstract

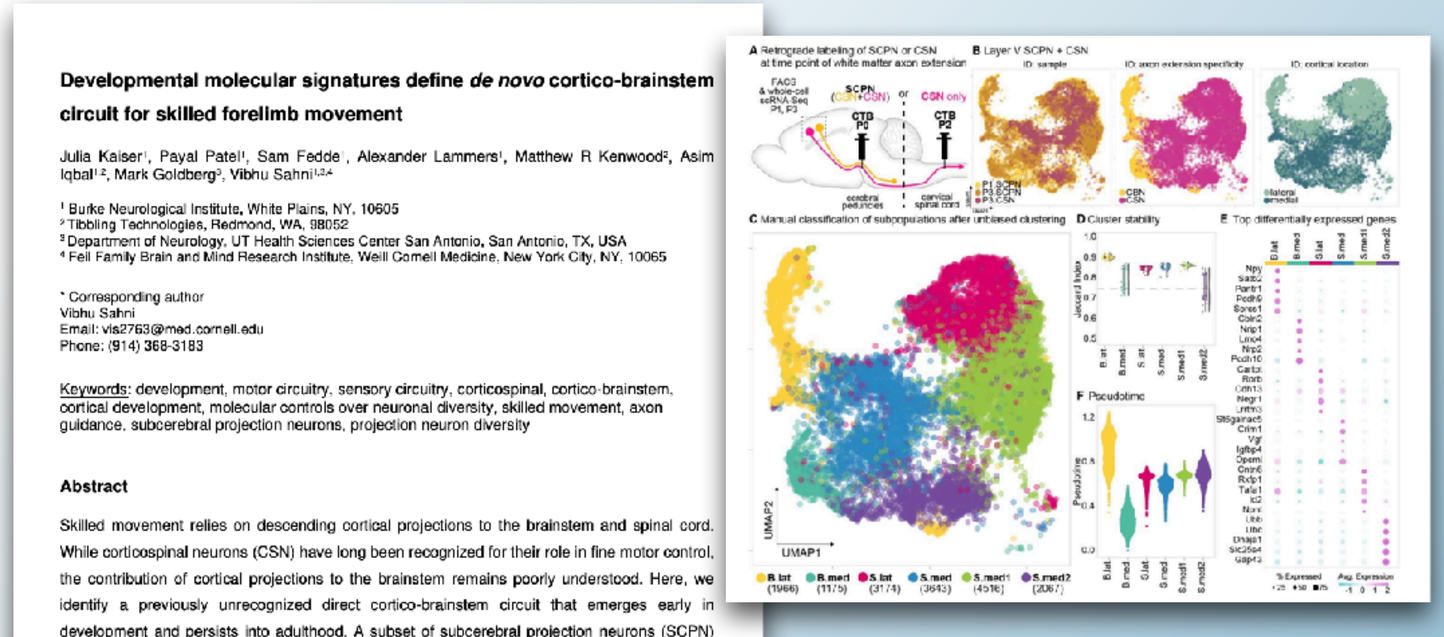
Case: Weill Cornell Medical College

- The client
  - A developmental / regenerative neurobiology group
- Single-cell RNA-seq data analysis
  - Aims: molecular characterization of cortico-brainstem neurons (CBN) vs corticospinal neurons (CSN)
- Papers
  - **Res Sq (preprint) 2025** https://doi.org/10.21203/rs.3.rs-6150344/v1

"I really appreciate the way he [Genevia's bioinformatician] took it upon himself to take the lead."

Dr. Vibhu Sahni
Group Leader, Weill Cornell Medical College

Full interview: **geneviatechnologies.com/references/cases/studying-neural-circuit-development-with-single-cell-rna-sequencing/**



Developmental molecular signatures define *de novo* cortico-brainstem circuit for skilled forelimb movement

Julia Kaiser[1], Payal Patel[1], Sam Fedde[1], Alexander Lammers[1], Matthew R Kenwood[2], Asim Iqbal[1,2], Mark Goldberg[3], Vibhu Sahni[1,2,4]

[1] Burke Neurological Institute, White Plains, NY, 10605
[2] Tibbling Technologies, Redmond, WA, 98052
[3] Department of Neurology, UT Health Sciences Center San Antonio, San Antonio, TX, USA
[4] Feil Family Brain and Mind Research Institute, Weill Cornell Medicine, New York City, NY, 10065

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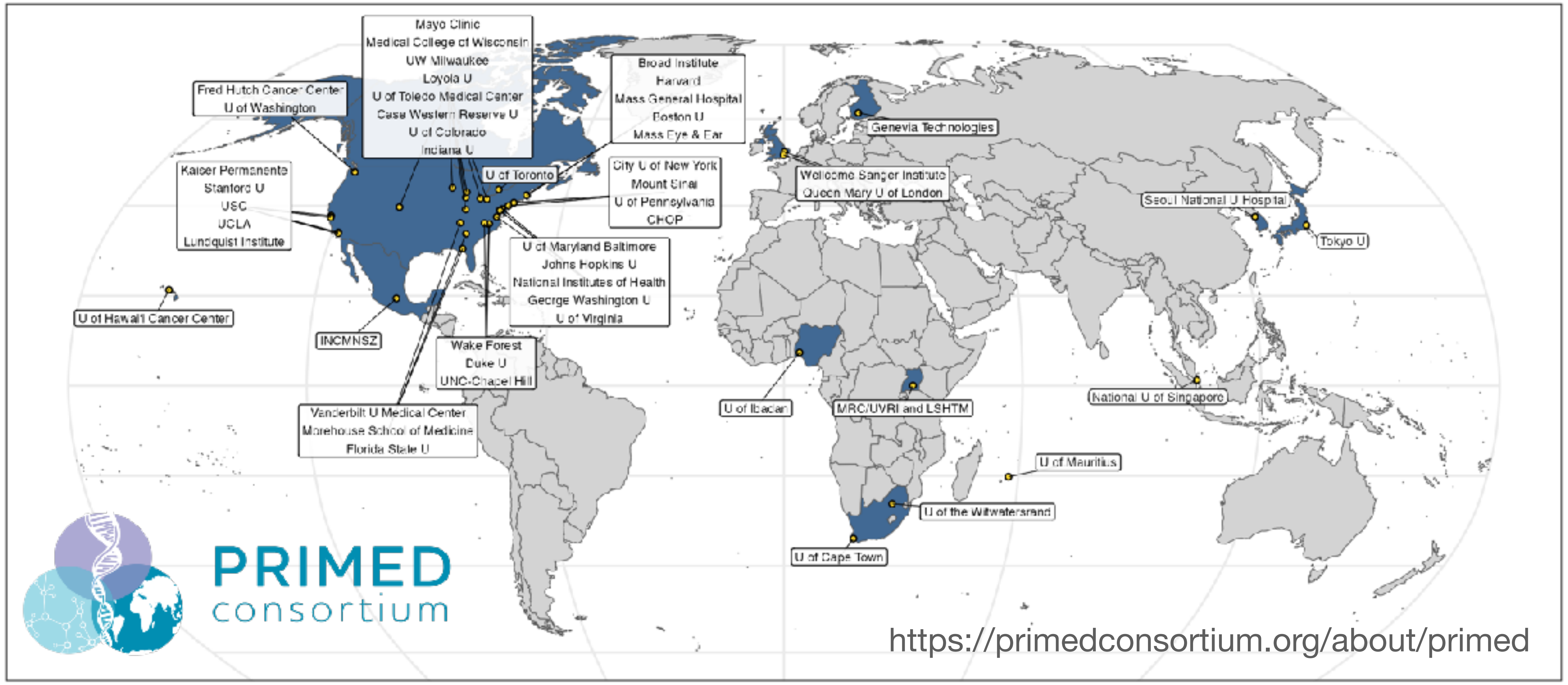
Keywords: development, motor circuitry, sensory circuitry, corticospinal, cortico-brainstem, cortical development, molecular controls over neuronal diversity, skilled movement, axon guidance, subcerebral projection neurons, projection neuron diversity

Abstract

Skilled movement relies on descending cortical projections to the brainstem and spinal cord. While corticospinal neurons (CSN) have long been recognized for their role in fine motor control, the contribution of cortical projections to the brainstem remains poorly understood. Here, we identify a previously unrecognized direct cortico-brainstem circuit that emerges early in development and persists into adulthood. A subset of subcerebral projection neurons (SCPN)

Case: University of Maryland

- The client
  - A genetic epidemiology group
- Population genetics
  - GWAS and PRS analysis for cardiovascular and HPV-related endpoints in African cohorts
- Papers
  - **Obesity 2024** https://doi.org/10.1002/oby.24123
  - **European journal of human genetics 2024** https://doi.org/10.1038/s41431-023-01521-7



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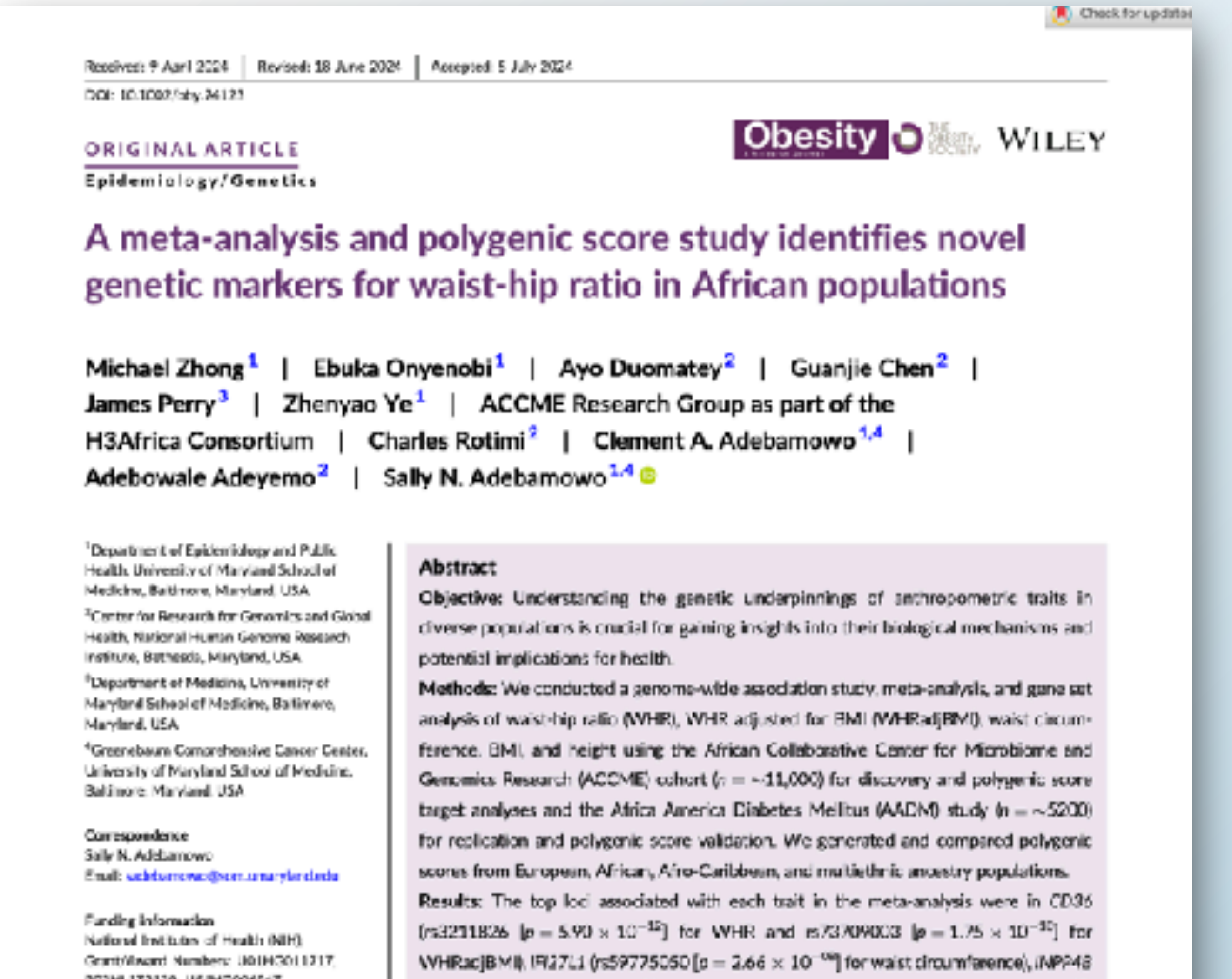

Received: 9 April 2024 | Revised: 18 June 2024 | Accepted: 5 July 2024

ORIGINAL ARTICLE
Epidemiology/Genetics

Obesity WILEY

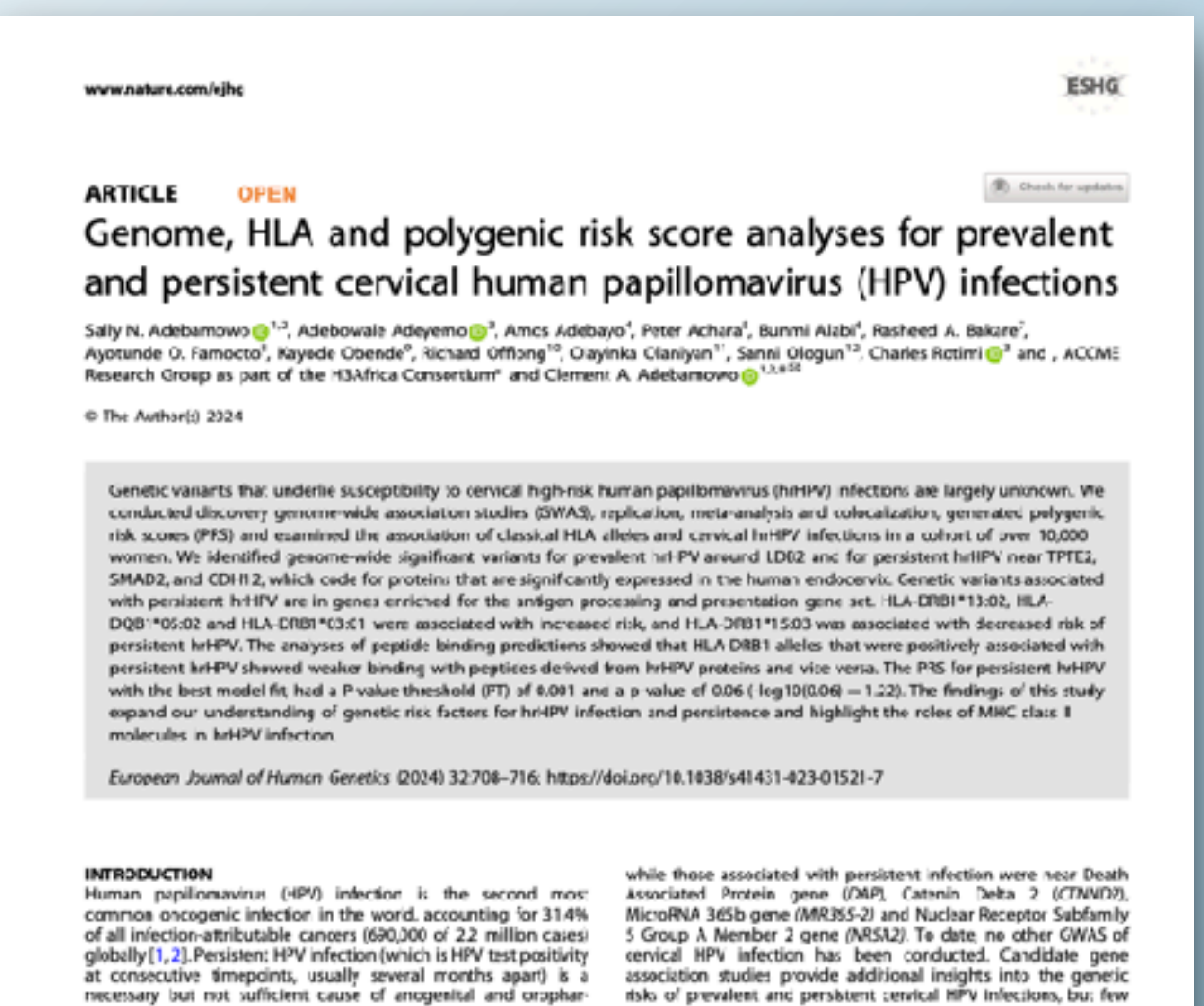
A meta-analysis and polygenic score study identifies novel genetic markers for waist-hip ratio in African populations

Michael Zhong | Ebuka Onyenobi | Ayo Duomatey | Guanjie Chen | James Perry | Zhenyao Ye | ACCME Research Group as part of the H3Africa Consortium | Charles Rotimi | Clement A. Adebamowo | Adebowale Adeyemo | Sally N. Adebamowo

Abstract

Objective: Understanding the genetic underpinnings of anthropometric traits in diverse populations is crucial for gaining insights into their biological mechanisms and potential implications for health.

Methods: We conducted a genome-wide association study, meta-analysis, and gene set analysis of waist-hip ratio (WHR), WHR adjusted for BMI (WHRadjBMI), waist circumference, BMI, and height using the African Collaborative Center for Microbiome and Genomics Research (ACCME) cohort ...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Genome, HLA and polygenic risk score analyses for prevalent and persistent cervical human papillomavirus (HPV) infections

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INTRODUCTION

“The keyword here is collaboration”

“It’s a whole different level of professionalism; a service, but on an academic level.”

Dr. Robert Hänsel-Hertsch
University of Cologne

“It’s not just somebody doing what I ask them to do and then emailing me a report – it’s collaborative.”

Dr. Rhoel Dinglasan
University of Florida

“I would, without a doubt, recommend Genevia – this collaboration has been just easy and great in many ways.”

Dr. Henri Huttunen
Herantis Pharma

“With a company like Genevia, there is a team with a range of different competencies, and you can trust that they are always up to date.”

Dr. Eric Feraille
University of Geneva

“Data safety and security are paramount for Genevia -- I feel more secure compared to certain previous collaborations.”

Dr. Michaela Lucas
University of Western Australia

“I think Genevia’s service definitely was an asset, and I highly recommend it: every time I give a talk somewhere I talk about Genevia.”

Dr. Vibhu Sahni
Weill Cornell Medical College

“I really appreciate the regular meetings, being kept up to date, and having very easy access to everything.”

Dr. Laura Stone
University of Minnesota

“The keyword here is collaboration. Typically, when contracting a service, you specify what you want, and the next interaction occurs months later -- with Genevia, it’s different.”

Dr. Lynette Lim
VIB / KU Leuven

“IInitial findings resulted in new questions, steering our investigation in different directions. Genevia seamlessly navigated these pivots.”

Dr. Melissa Vrohlings
CDR-Life

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