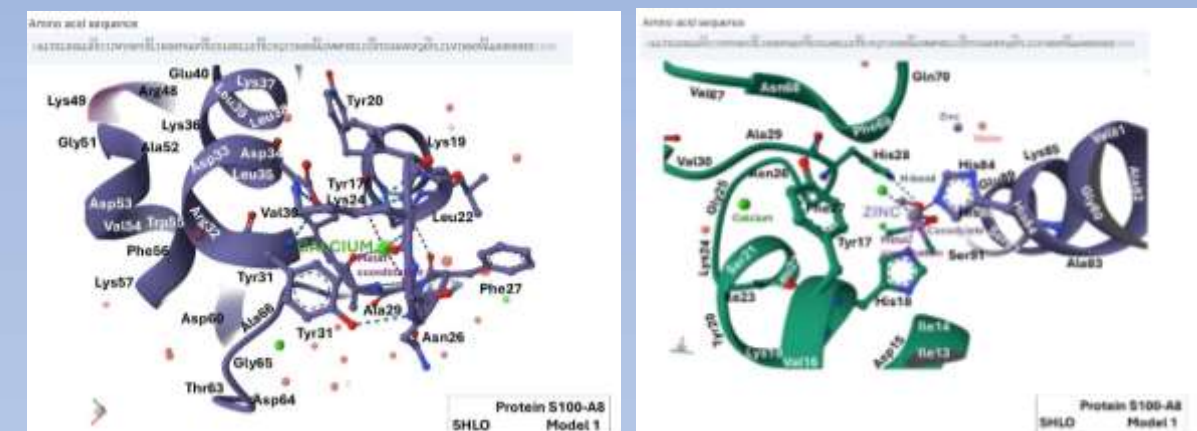


Official Journal of the Global Newborn Society and 52 allied organizations
International Society for Marginalized Lives
Dr. Mozib Newborn Foundation
The Carlo GNS Center for Saving Lives at Birth
Vishwa Mahesh Parivaar
Autism Care Network Foundation

And

GNS Down Syndrome Foundation
Newborn Foundation of Azerbaijan
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Uruguayan Neonatal Association
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Anatolian Midwives Association
GNS Western Australia
Perinatal Society of Singapore
Pioneers - looking for sustainable ways to reduce infant mortality
Bhutan Neonatal Care Forum
Global Newborn Society Iran Chapter
National Federation of Neonatologists of Mexico
College of Neonatologists of the State of Jalisco, Mexico
The Skylar Project
International Society for Marginalized Lives
Friends Aid Africa, Bukedea, Uganda
Society of Bacteriophage Research and Therapy
GNS Center for Computational Scientific Methodology
GNS International Association of Neonatal POCUS
SABREE Enrichment Academy: Empowering Ability
The Caribbean Association for Hematology and Oncology
First Breath of Life
GNS Neonatal Radiology Forum
Global Newborn Society, Orthopedic Surgery Section



Calprotectin: An Overview

Figure shows Ca⁺⁺ and Zn⁺⁺ ions inside the S100A8 peptides



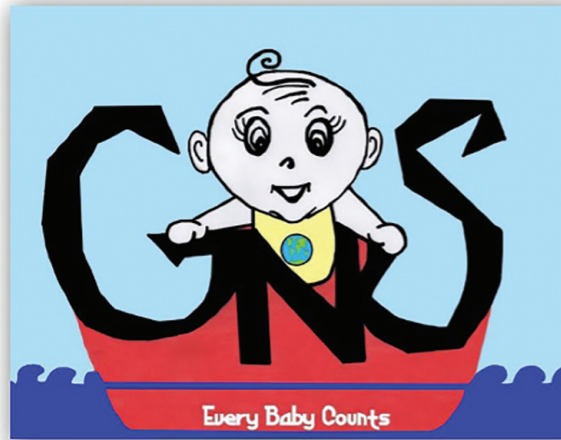
Other highlighted articles:

Impact of the Ukrainian Conflict on Mothers and Young Infants Who Have Had to Migrate to Poland
Meckel diverticulum

Also available online at

<https://www.globalnewbornsociety.org/our-scientific-journal-newborn>

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Global Newborn Society

Each time we lose an infant, we lose an entire life and its potential!

Newborn is the official journal of the [Global Newborn Society \(GNS\)](#), a globally active, non-profit organization that is registered as a 501(c)(3) non-profit formation in the United States and is currently being listed as an analogous charity in many other nations. The aim is to enhance research in newborn medicine, understand epidemiology (risk factors) of disease, train healthcare workers, and promote social engagement. The GNS was needed because despite all improvements in medical care, infants remain a high-risk patient population with mortality rates similar to 60-year-olds. We need to remind ourselves that *Every Baby Counts*, and that *Each Time We Lose an Infant, We Lose an Entire Life and its Potential*.

Our logo above, a hand-drawn painting, graphically summarizes our thought-process. There is a lovable little young infant exuding innocent, genuine happiness. The curly hair, shape of the eyes, long eyelashes, and the absence of skin color emphasize that infants need care all over the world, irrespective of ethnicity, race, and gender. On the bib, the yellow background reflects happiness, hope, and spontaneity; the globe symbolizes well-coordinated, worldwide efforts. The age-related vulnerability of an infant, with all the limitations in verbal expression, is seen in being alone in the boat.

The unexpressed loneliness that many infants endure is seen in the rough waters and the surrounding large, featureless sky. However, the shades of blue indicate that the hope of peace and tranquility is not completely lost yet. The acronym letters, GNS, on the starboard are made of cast metal and are pillars of strength. However, the angular rough edges need continued polishing to ascertain adequacy and progress. The red color of the boat symbolizes our affection. The expression "*Every Baby Counts*" seen on the boat's draft below the waterline indicates our commitment to philanthropy, and if needed, to altruism that does not always need to be visible. The shadow behind the picture shows that it has been glued on a solid wall, one built out of our adoption and commitment.

Design of the Journal Cover

The blue color on the journal cover was a careful choice. Blue is the color of flowing water, and symbolizes the abnormalities of blood vascular flow that are seen in many neonatal illnesses. There is a gradual transition in the shades of blue from the top of the cover downwards. The deeper shades of blue on the top emphasize the depth, expertise, and stability, which the renowned authors bring. Light blue is associated with health, healing, tranquility, understanding, and softness, which their studies bring. The small letter “n” in the title of the journal, *newborn*, was chosen to emphasize the little size of a newborn baby. The issue editors chose three articles to be specifically highlighted; the two pictures and two titles below reflects an order suggested by them.

Instructions to Authors

The journal welcomes original articles and review articles. We also welcome consensus statements, guidelines, trials methodology, and core outcomes relevant to fetuses/young infants in the first 1000 days. A detailed set of instructions to authors can be seen online at <https://www.globalnewbornsociety.org/intructions-for-authors>. The manuscripts can be submitted via the [online manuscript submission system](#).

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A Combination of Human Wisdom and Artificial Intelligence will Win the Game

There is concern in academia about how artificial intelligence (AI) will change learning, and our society.¹⁻³ We have a different view. As mentioned in earlier editorials, we see advancing AI not as an artificial change but as a combination of supplementary and supplemental intelligence.⁴ As shown in **Figure 1**, we have highlighted that a combination of human qualities and AI together could/will be a winning strategy. Humans will bring creativity, ethical judgment, clinical insight, and contextual understanding, and electronic processing will provide speedy calculations, pattern recognition, and the ability to quickly/efficiently analyze massive datasets. This synergistic model will bring speed—machines will likely enhance, not replace human decision-making. We will no longer have the guilt about breaks for meals and personal needs, and may actually gain time to dream, think, and plan orbital jumps in our goals. Advances from organizations such as DeepMind and developments in systems like AlphaFold illustrate how human–AI collaboration can solve complex scientific problems that neither could address alone.⁵⁻⁹ In the following paragraphs, we expand on the reasons for our thinking based on extensive discussions with our colleagues engaged in the development of AI algorithms:

- 1. Pattern recognition and hidden structures:** AI enables the identification of complex, multidimensional patterns within large datasets that might have been difficult to detect using conventional statistical approaches.¹⁰⁻¹² Machine learning algorithms can recognize subtle correlations, nonlinear relationships, and hierarchical structures across thousands or millions of variables simultaneously.¹³⁻¹⁷ Deep learning systems developed by DeepMind, such as AlphaFold, have shown how AI can uncover intricate biological patterns from massive protein sequence datasets.¹⁸ By revealing hidden structures in data, AI can transform raw information into meaningful insights.^{19,20}
- 2. Scalability and high-throughput data processing:** Large-scale scientific technologies generate enormous volumes of data that exceed the capacity of manual analysis.^{21,22} AI provides scalable computational frameworks capable of processing high-throughput sequencing data, continuous physiological monitoring streams, and large imaging repositories efficiently and consistently.²³⁻²⁷ Automated pipelines powered by AI reduce human error, enhance reproducibility, and enable real-time analysis.^{28,29} This scalability allows researchers to move beyond small datasets and engage with population-level or genome-wide investigations.^{30,31}
- 3. Predictive modeling and forecasting:** AI inspires data analysis by shifting focus from descriptive interpretation to predictive insight.^{32,33} Through supervised learning techniques, models can be trained on historical data to forecast outcomes, classify disease states, or estimate risk probabilities.^{34,35} These predictive capabilities are particularly powerful in clinical research, where AI can anticipate complications, stratify patients based on risk, and support personalized decision-making.^{12,36} By modeling nonlinear and high-dimensional relationships, AI often achieves greater predictive accuracy than traditional regression-based approaches.^{37,38}
- 4. Unsupervised discovery and hypothesis generation:** Beyond prediction, AI supports exploratory analysis through unsupervised learning methods that identify natural groupings or latent structures without predefined labels.^{39,40} Clustering algorithms, dimensionality reduction techniques, and network-based analyses reveal new subtypes, biological pathways, or evolutionary

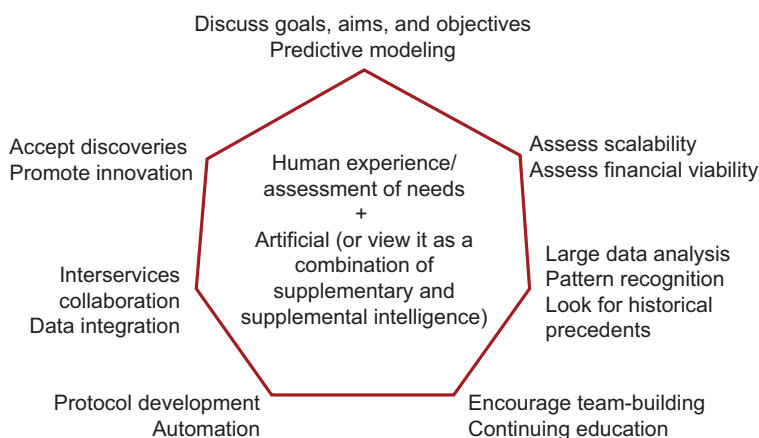


Fig. 1: We need to recognize possible advantages of combining human wisdom with artificial intelligence (AI). We have mentioned in earlier issues of the journal – is AI even the right word – should we not view these advances as a combination of supplemental and supplementary intelligence? In this heptagon, we have highlighted that a combination of human qualities and AI together would be a winning strategy. Humans will bring creativity, ethical judgment, clinical insight, and contextual understanding, and electronic processing will provide speedy calculations, pattern recognition, and the ability to quickly/efficiently analyze massive datasets. This synergistic model will bring speed - machines will likely enhance, not replace human decision-making. We will no longer have the guilt about breaks for meals and personal needs, and may actually gain time to dream, think, and plan orbital jumps in our goals. Advances from organizations such as DeepMind and developments in systems like AlphaFold illustrate how human–AI collaboration can solve complex scientific problems that neither could address alone. Ultimately, the future of innovation is likely to depend on integrating human reasoning with adaptive AI. Let float and swim in this stream – we will enjoy it

relationships.⁴¹ This capacity for unbiased discovery encourages hypothesis generation and supports innovative research directions.⁴² Rather than testing only predetermined assumptions, AI may help in formulation of new questions.^{43,44}

5. **Integration of heterogeneous data sources:** Modern research frequently involves integrating diverse data types, including genomic sequences, imaging data, electronic health records, and environmental variables.⁴⁵ AI provides frameworks capable of combining these heterogeneous datasets into unified analytical models. Such integrative analysis enables the identification of cross-domain relationships that may not be evident when datasets are examined independently.⁴⁶ By synthesizing multiple layers of information, AI promotes systems-level understanding of complex biological and clinical phenomena.⁴⁷
6. **Automation and efficiency enhancement:** AI reduces the burden of repetitive and computationally intensive tasks, including feature extraction, anomaly detection, image segmentation, and sequence alignment optimization.³⁶ Automation can accelerate research workflows and improve consistency across analyses.⁴⁸ As a result, researchers will likely be able to allocate more time to interpretation, critical thinking, and theoretical development.⁴⁹
7. **Continuous learning and adaptation:** Unlike static analytical methods, AI systems can continuously learn from new incoming data and refine their models over time.^{12,50} Adaptive algorithms improve performance as datasets expand, making them particularly suitable for dynamic environments such as clinical monitoring systems or evolving epidemiological studies.^{51,52} This ability to update knowledge in real time can provide updated insights that will remain responsive to new evidence.

To conclude, the integration of human intelligence with AI represents a transformative and highly effective approach to large-scale data analysis.¹⁰ While AI offers unparalleled computational capacity, scalability, and advanced pattern recognition, human expertise provides contextual understanding, ethical judgment, creativity, and critical interpretation.^{53,54} Together, this can be synergistic partnership.

In each issue of this journal, our editorial team highlights the achievements of one of our partnering members. Here, we present the Instituto Nacional de Perinatología Isidro Espinosa de los Reyes, which is associated with the National Health Institutes of México (NHIM), in Mexico City.⁵⁵ It was founded in 1977 by Dr. Eduardo Jurado Garcia, who led the facility as its first Director.⁵⁶ The three main activities are identified as healthcare, education, and research. The NHIM is a renowned referral center for women and neonatal health care, with facilities for high-risk gynecology, reproductive health, maternal-fetal medicine with fetal surgery, fetal cardiology, neonatology, genetics, and oncology (Fig. 2). The newborn center includes an intensive care unit with 75 beds; 16 are earmarked for specialized ventilation, surgery, neurosurgery, hypothermia, and areas for rooming-in. It is equipped for high-frequency ventilation, inhaled nitride oxide, neonatal infrared spectroscopy, incubators for magnetic resonance, equipment for hypothermia, and a specifically equipped neonatal ambulance for transport. There is an associated human milk bank. There is a well-recognized follow-up program. The facility is attached with largest neonatologist training center in Mexico, which collaborates with the Universidad Nacional Autónoma de México (National Autonomous University of Mexico) and graduates about 30 new neonatologists each year.

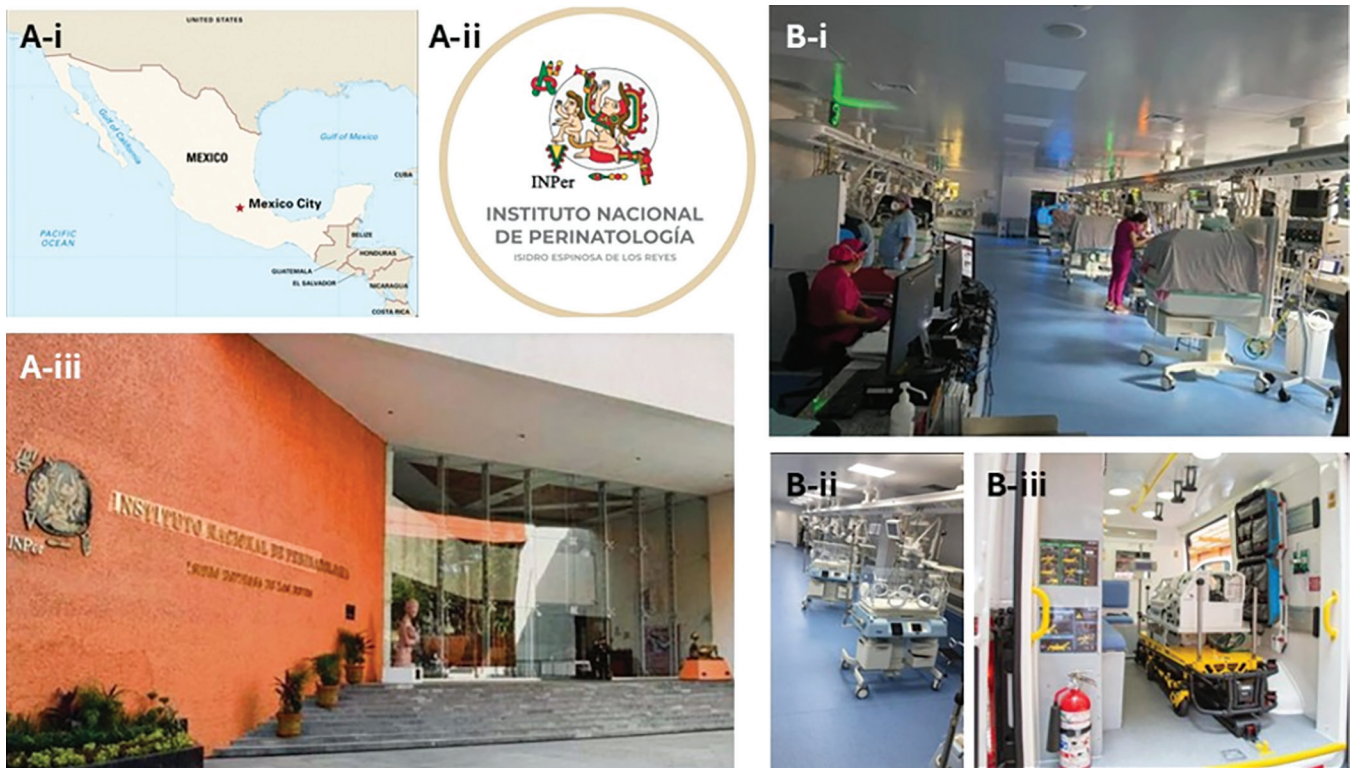


Fig. 2: Instituto Nacional de Perinatología Isidro Espinosa de los Reyes, which is associated with the National Health Institutes of México (A-i) located in Mexico City; (A-ii) The logo of the Institute, Princesa 3 Pederal (Princess 3 Flintstone), comes from Codex Nutall found in the región of Oaxaca; (A-iii) The hospital entrance. Figures B (i–iii) show the neonatal intensive care unit, facilities, and the transport service, respectively

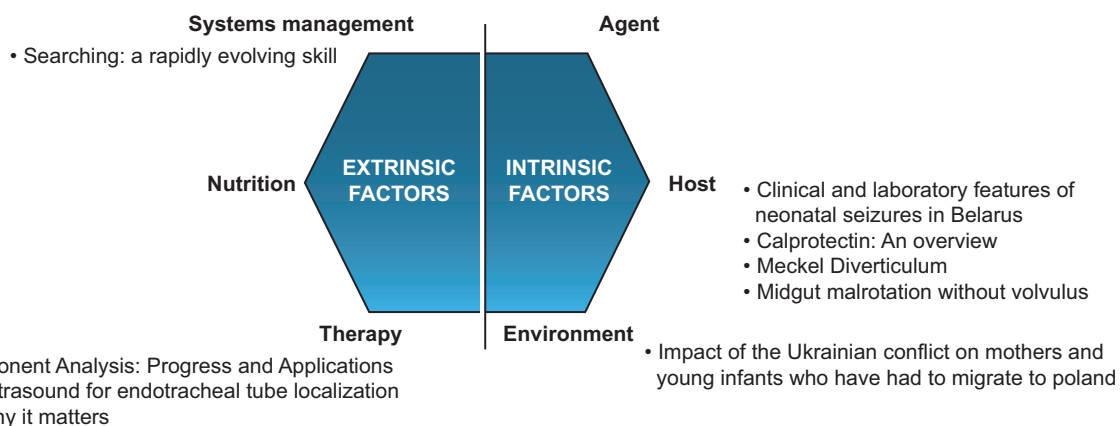


Fig. 3: Areas of focus in the newborn, Volume 5, Issue 1. We have expanded the traditional agent-host-environment trinodal disease model to a hexagonal system. The three additional foci represent extrinsic factors that can affect health - those originating in therapy, nutrition, and systems management are shown. This issue covers 3 nodes, with articles focused on host factors, therapy/monitoring systems, and systems management.

This journal aims to cover fetal/neonatal problems that begin during pregnancy, at the time of birth, or during the first 1,000 days after birth. As in our previous issues, we present 8 articles here (Fig. 3). Pratasevich described the clinical and laboratory features of neonatal seizures in Belarus.⁵⁷ Although Belarus has now one of the lowest neonatal mortality figures in the world,⁵⁸ seizures continue to be seen in infants. The authors reviewed the clinical features of 75 neonates with seizures in the Grodno region. Hypoxic-ischemic encephalopathy, perinatal infections, metabolic disorders, and intracranial hemorrhages were the leading causes. Seizures were seen most often in term infants in the early neonatal period. The authors continue to develop the cohort in a prospective fashion. As requested by the readers, we, as editors, are also introducing consistent series focused on imaging⁵⁹ and procedures.⁶⁰

Frydrysiak-Brzozowska and her colleagues⁶¹ have reported the impact of the war in Ukraine on pregnant mothers and their infants who have had to relocate to Poland. There has been widespread destruction, displacement, and humanitarian crises across Ukraine.⁶² Over 2 million people had to flee Ukraine within 2 weeks and there have been many more border crossings.⁶³ In this article, the authors have focused on the social impact of population migration, with particular attention to its effects on perinatal outcomes. Thousands of Ukrainian women were pregnant when the war began and the conflict affected their care with lack of access to medical facilities and high levels of stress. Their infants also need care. The arrival of large numbers of refugees has changed Poland's social landscape.⁶⁴ However, the Polish government and society have responded to these population movements by offering all-possible protection and wide-ranging support.⁶⁵ The country deserves global recognition and gratitude.

In an important review article, Maheshwari, Mohammadabadi, and Michie have described our current understanding of the biological/clinical importance of calprotectin, a heterodimeric calcium- and zinc-binding innate immunity-related protein.^{66,67} Neonates rely on innate immunity for survival and can show higher calprotectin levels than older children and adults.⁶⁸⁻⁷⁰ Serum calprotectin levels are increased during systemic inflammation, further highlighting its important contribution to immune responses.⁷¹ In gut disorders, fecal calprotectin is a useful noninvasive marker that can help differentiate inflammatory bowel conditions from functional gastrointestinal disorders, assess the severity of disease activity, and monitor therapeutic responses.⁷¹ It is a valuable diagnostic and monitoring tool that can enhance decision-making while reducing reliance on invasive investigations.⁷²

Khare has reviewed the embryology, clinical features, and management of Meckel diverticulum (MD).⁷³ These are congenital 'pouches' located on the antimesenteric border of the distal ileum, seen worldwide in about 2% of all infants.^{74,75} The etiopathogenesis is not clear. There can be three possible variants of MDs: (a) a cyst with the rest of the omphalomesenteric duct (OMD) seen as a terminal fibrous band connecting with the umbilicus; (b) the whole OMD remains patent; and (c) an umbilical cyst, a fluid-filled remnant in a part of the ductal pathway.^{74,76} Asymptomatic patients may be closely followed with conservative management. However, for symptomatic cases, surgical management with a diverticulectomy or a segmental ileal resection may have to be considered.⁷⁷

Maheshwari and colleagues⁷⁸ formed a team with authors from all continents to review how Principal Component Analysis (PCA) is done/understood in the analysis of high-throughput arrays.⁷⁹ This work is important because of the existing/needed interface between clinicians and computer software experts because of differing areas of expertise. Simply put, PCA is a statistical technique used to reduce the dimensionality of large datasets while preserving as much important information as possible.⁷⁹ Gene expression data typically contain thousands of variables, something strikingly different from the clinical thought process. PCA reduces this high dimensionality into a smaller set of variables.⁸⁰ Progress in these sections can help researchers better visualize complex expression patterns, identify clusters of samples, detect outliers, and uncover underlying biological differences between health and diseased states.

Anil Rao has contributed a pictorial essay of plain and contrast-enhanced gastrointestinal images from an infant with intestinal malrotation.^{59,81} Gut malrotation is a congenital condition in which the intestines become fixed in an abnormal position during fetal development and do not rotate further.⁸² This condition presents most frequently during infancy with symptoms of intestinal obstruction, although some individuals may remain asymptomatic until later in childhood or adolescence. The diagnosis is typically made using imaging studies, and treatment usually involves surgical correction to prevent serious complications. The pathophysiology of malrotation is not well known, although mutations or altered expression of some genes involved in laterality and gut morphogenesis

are now being discovered.^{83,84} The management of these infants involves supportive management and surgical intervention to prevent life-threatening complications such as midgut volvulus.^{85,86}

Michie and Maheshwari⁸⁷ discuss on how our methods for online search for topics are changing. With the advent of artificial intelligence (AI) neural networks, the debate about the convenience and accuracy of medical or scientific information obtained from published material, search engines, and AI tools is becoming ever stronger.⁸⁸⁻⁹⁰ A new era of questioning - 'why', 'how' and 'what if' - the Socratic approach seems to be appearing again.^{91,92} We not only need careful validation of AI large language models, but there are also concerns that the ease of computation-enabled linear thinking could limit serendipity.⁹³⁻⁹⁵

Finally, we are developing a few series of procedure-focused articles to standardize the approach all over the world. Monika Kaushal from the United Arab Emirates has provided a brief summary of the sonographic confirmation of endotracheal tube (ETT) position in newborn infants.⁶⁰ In neonatal intensive care units, ETT malposition is a frequently encountered difficulty in management of critically ill infants.⁹⁶ Chest radiography still remains the gold standard for confirmation of correct positioning of the ETT, but it is limited by temporal delays, radiation exposure, and workflow inefficiencies.⁹⁷ Point-of-care ultrasound (POCUS) offers a rapid, radiation-free, and reliable alternative for confirming the position of the ETT at the bedside. This review summarizes the clinical rationale, scanning technique, available evidence, and practical strategies for using POCUS for ETT localization in neonates.

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Editors

Ling He, MD, PhD⁹⁸

Professor, University of Arizona, Tucson, USA

Academic interest in mechanisms of cellular energy production and utilization

Sonji Fatima (Daniel) Harold, EdD⁹⁹

St Louis, Missouri, USA

Author, Educationist, Social Service, Mother

Adrianna Frydrysiak – Brzozowska, MSc¹⁰⁰

Dean, Faculty of Health Sciences, The Mazovian University in Płock, Poland

Interest in academic administration, nursing profession, infant care

Searching, a Rapidly Evolving Skill

Colin Michie¹⁻⁵, Akhil Maheshwari⁵⁻²⁴

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ABSTRACT

With the advent of artificial intelligence (AI) neural networks, their capacity to deliver answers to searches for medical or scientific information is rapidly taking over from search engines and publishers. This should empower searches based on thoughtful questions, including “why,” “how,” and “what if” – the Socratic approach. Outputs from AI large language models (LLMs) require careful validation, and it is likely they will limit serendipity.

Keywords: Agentic AI systems, Alexa, Algorithmic biases, Anthropic’s Claude, Creativity, Fabrications, Filter bubbles, Hallucinations, Health information seeking behavior, Index Medicus, Infant, Large language models, Mothers, National Library of Medicine, Newborn, Occam’s razor, OpenAI’s Chat GPT, Personalized algorithms, PubMed, Searching, Serendipity, Siri, Socratic questions, Team consultations, Voice assistants.

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KEY POINTS

- Searching for information online relating to health is moving onto artificial intelligence (AI) platforms.
- Artificial intelligence is likely to deliver most search results to the public and professionals in the future.
- Caution is required when employing AI systems because their outcomes require validation.
- We need to understand better how our patients use their personal healthcare search results.
- Artificial intelligence’s personalization will change how we search.

We share a common habit.^{1,2} We often question, explore, and search for answers^{3,4} using a mobile, laptop, or vocal assistant.^{5,6} This core pursuit, searching for health information, is changing dramatically, search processes are becoming volatile.⁷⁻⁹ “Traditional” search engine traffic is falling and publishers predict this decrease will continue.^{10,11} Search engines are being overtaken by a range of AI systems. Assistants such as Siri or Alexa, OpenAI’s Chat GPT, and Anthropic Claude can provide answers vocally or written, to help everyone search.^{12,13} ChatGPT is possibly the fastest growing application ever, now with over 800 million users each week.^{10,14}

The printed page transformed societies in Western Europe steadily from the 15th century.¹⁵ Large scale printing disseminated new skills of reading and calculation, literacies, and knowledge.¹⁶ It generated novel patterns of enquiry, teaching, and writing.^{16,17} However, this did not improve the impact for all researchers.^{18,19} Robert Hooke wrote in 1679: “Twill be much better to embrace the influence of Providence.”²⁰ In 1879, “Index Medicus” was launched by the National Library of Medicine, compiled manually for a monthly publication.²¹ Medical textbooks and journals became progressively more affordable, popular, and routine occupants of a clinician’s office.¹⁹ Museums, radio, television and newspapers recorded, documented, indexed, and curated archives that enriched searching the fields of health and social care.²² Patients and potential patients used all these too to seek out information about their health.²³ In the 1980s, their telephone calls to the newly opened Cancer Information Service were studied, before internet searches were available.²⁴⁻²⁶ Freimuth and colleagues outlined a pentagonal frame of determinants for search: Prior knowledge;

¹Department of Population, Policy and Practice Research and Teaching Department, University College, London, Great Ormond Street Institute of Child Health, United Kingdom

²American Canadian School of Medicine, Dominica, Caribbean

³Excellence in Pediatrics, Copenhagen, Denmark

⁴British Paediatric Society for the History of Paediatrics and Child Health, United Kingdom

⁵Global Newborn Society, Harrison, New York, United States of America

⁶Department of Pediatrics/Neonatology, Boston Children’s Health Physicians Group at the Maria Fareri Children’s Hospital, New York Medical College, Valhalla, New York, United States of America

⁷GNS Forum for Transgenerational Inheritance, New York, United States of America

⁸Mongolian Association of Obstetrics, Gynecology, and Neonatology, Ulaanbaatar, Mongolia

⁹Department of Neonatology, Institute of Maternal and Child Health, Matuil, Dhaka, Bangladesh

¹⁰Bangladesh Neonatal Foundation, Dhaka, Bangladesh

¹¹Dr. Mozib Newborn Foundation, Dhaka, Bangladesh

¹²Pioneers – looking for sustainable ways to reduce infant mortality, Oslo, Norway

¹³Banaras Hindu University Institute of Excellence, Varanasi, Uttar Pradesh, India

¹⁴S.A.B.R.E.E. Enrichment Academy, Saint Louis, Missouri, United States of America

¹⁵The Skylar Project, Daphne, Alabama, United States of America

¹⁶International Society for Marginalized Lives, Harrison, New York, United States of America

¹⁷PreemieWorld Foundation, Springfield, Virginia, United States of America

¹⁸Carlo GNS Center for Saving Lives at Birth, Birmingham, Alabama, United States of America

¹⁹Autism Care Network Foundation, India

²⁰Neonatology-Certified Foundation, Brooksville, Texas, United States of America

²¹GNS Infant Nutrition Education Program, Harrison, New York, United States of America

²²International Prader-Willi Syndrome Organization, Cambridge, United Kingdom

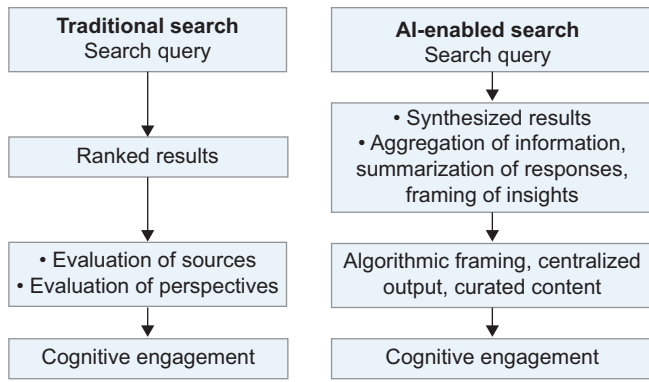


Fig. 1: Differences between traditional and AI-enabled search systems. The figure contrasts searching with conventional processes with AI-enabled paradigms. In traditional search, users submit a query and receive a ranked list of possible answers, which require evaluation of sources and perspectives, followed by manual synthesis of information for knowledge construction. In contrast, AI-enabled search systems generate a synthesized response by aggregating and summarizing information from diverse data sources (LLMs) before tailoring it and presenting it to the user. This approach reduces cognitive load and may increase efficiency, but it centralizes information curation, framing, and prioritization employing an unknown algorithm. This comparison highlights the shifts in information access, exposure to diverse viewpoints, and perceived epistemic authority in AI-mediated environments

understanding of goals and time frames; cost-benefit analysis of search; actual undertaking of the search; evaluation of the information for adequacy, credibility, and applicability; and finally, appraisal of the decision as to its adequacy.²⁷⁻²⁹

Following the launch of the internet, “PubMed” replaced “Index Medicus” as an online resource.³⁰ Today, “PubMed” hosts millions of general medical searches through its website each day, as well as automated traffic searches.^{31,32} It houses approximately 36 million peer-reviewed articles, increasing by approximately a million a year.³³ In addition, clinicians search using a diversity of other search engines including intelligent textbooks, best-practice journals, national guidelines, and specialized resources from Universities, Colleges and Societies.^{31,34}

Artificial intelligence search systems are delivering evolutionary, revolutionary transformations (Fig. 1).³⁵ Large language models (LLMs), trained with self-supervised machine learning from vast numbers of documents reduce unnecessary browsing, guiding greater focus.^{36,37} Indeed the stated aim of Google Zero is to reduce the number of clicks you would normally employ by providing you with a single instant synthesis, a complete answer.³⁸ This limitation means rigorous searchers may require several separate questions to examine evidence or apply critical thinking in diverse ways to their searches.³⁹⁻⁴⁰

Some users describe AI chatbots as supporting their creativity, just as in simulation training.³⁹ Specialized AI searches can be tailored to work in the areas of evidence-based practice, genomics, or by linking concepts and mechanisms to explore connections.^{33,39} The “Consensus” AI system offers to search 250 million peer-reviewed articles with powerful tools to provide evidence-based summaries and citations.⁴⁰ In the care of newborn infants, AI holds promise as a research tool in the searching and analysis of vast amounts of data that could be collected from continuous monitoring.^{41,42}

²³First Breath of Life, Shreveport, Louisiana, United States of America
²⁴GNS Forum for Big Data Analytics and Machine Learning, Bengaluru, India

Corresponding Author: Colin Michie, Department of Population, Policy and Practice Research and Teaching, University College; Great Ormond Street Institute of Child Health, London, United Kingdom; American Canadian School of Medicine, Dominica, Caribbean; Excellence in Pediatrics, Copenhagen, Denmark; British Paediatric Society for the History of Paediatrics and Child Health, London, United Kingdom; Global Newborn Society, Harrison, New York, United States of America, e-mail: c.michie@ucl.ac.uk

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Digital provenance is required before relying on the results of AI searches.⁴³ Although we no longer require the “pleases,” “thank-you’s” or promises of a lunch out – as were once needed for medical school librarians – AI outputs require careful checking.⁴⁴ Incorrect responses or fabrications are not always detectable. Large language models can produce incorrect responses or fabrications, often referred to as hallucinations.^{34,45} Racial, socioeconomic, and sexual biases can influence search outputs.⁴⁶ There are many geographic disparities too. Large language models have a richer training background in the West but are still being developed in the peri-equatorial/tropical economies such as in Africa or India, regions with larger numbers of mothers and infants.⁴⁷ India’s strengths in computational software systems may bring global solutions to this issue.^{48,49} Artificial intelligence bots collect information continuously as they trawl the internet; the realities and limitations of these inputs cannot be ignored.^{50,51}

Artificial intelligence systems are widely used by patients, applying strategies similar to those used with telephone services forty years ago: Social habits have persisted across a generation!^{52,53} Some very human-centered techniques can be observed.⁵⁴ Users typically employ multiple search tools, applying those outcomes that best match their perception of their situations, time-frames, and understanding. Suboptimal advice may be preferred and applied, even though the source technology is not understood.^{55,56} Gratifyingly, it seems people still prefer to speak to a human professional regarding their health and that of their infants. However, it is conceivable that in future more approachable or convenient vocal AI systems, for instance, could challenge this norm.^{57,58}

Artificial intelligence-enabled searches may subtly change our intellectual environments by removing serendipity.⁵⁹ In the past many scientific discoveries have been the result of unexpected “accidents.” Now it might be more likely for searchers to uncover unexpected, but beneficial material (Fig. 2).⁶⁰ We might not fortuitously run into a useful title when browsing for a book on a shelf. Or perhaps derive inspiration from the page next to the targeted one in an encyclopedia or website. Personalized algorithms designed to target information to us based on our internet use can inadvertently create intellectual “filter bubbles” that restrict the diversity of outcomes provided to a researcher.⁶¹ Will personalized AI searches and workflows limit our “Eureka” moments? Will we end up rationing the providence commended by Hooke, or limiting a neonatologist’s application of Occam’s razor?⁶²



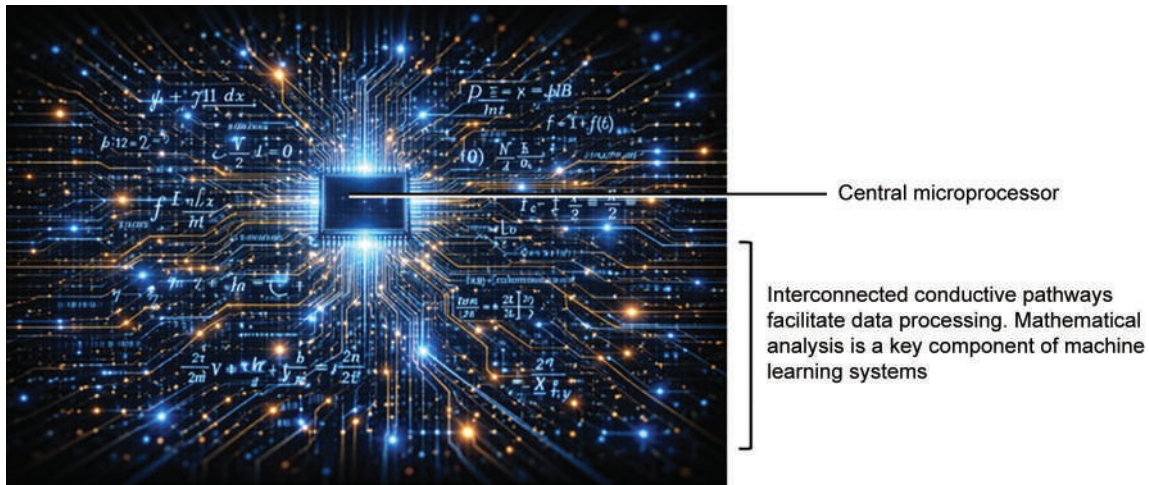


Fig. 2: Schematic representation of an AI-inspired computational circuit. In AI hardware, a central microprocessor is often embedded within an intricate network of conductive pathways, which facilitate data flow for information processing. Artificial intelligence is fundamentally built upon mathematical expressions and analytical formulas that enable machines to process data, recognize patterns, and make informed decisions. Core mathematical disciplines such as linear algebra, calculus, probability, and statistics form the backbone of AI algorithms. Matrices and vectors are used to represent data and neural network parameters, calculus for optimization through techniques like gradient descent, and probability theory-based inferences in predictive modeling and estimation of uncertainty. Analytical formulas can be used to define loss functions, activation functions, and model evaluation metrics, allowing systems to iteratively adjust parameters and improve performance. Together, these mathematical foundations make AI capable of learning from data, generalizing patterns, and solving complex real-world problems. For instance, to prepare this figure we first drafted a legend and then fed serial versions with minor modifications into ChatGPT (OpenAI 2026. ChatGPT version 5. <https://chat.openai.com>) until a desired illustration was obtained

Artificial intelligence tools are powerful, speedy, appealing, and even seductive.⁶³ To apply them effectively to searches we need to think, review, and modify our personal exploring habits, pushing back on over-simplifications.⁶⁴ Joint consultations within clinical groups, for example using Socratic, open-ended questions, can help develop secret sauces; methods for searches. Teams are stronger than an individual for hunting or tracking! Our researches, care of patients and clinical services must not be run, or overrun, by expanding AI agents.⁶⁵

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Clinical and Laboratory Features of Neonatal Seizures in Belarus

Tatsiana S Pratasevich¹, Nadzeya Yankouskaya², Natalya Dzianisik³, Volga Onehina⁴, Anhelina Palkhouskaya⁵

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ABSTRACT

Introduction: Seizures are the most frequently-seen neurological emergency in neonates. The first weeks of life are a time of heightened risk for seizures due to age-dependent risk factors. Neonatal seizures are harmful to the developing brain; early and accurate diagnosis is critical.

Methods: We reviewed the clinical course of 75 infants serially admitted for convulsive seizures during the period 2016–2021 in the Grodno region of Belarus. All information relevant to the course of pregnancy and childbirth, gestational age, characteristics of seizures and data from laboratory and instrumental research methods were recorded.

Results: Most patients in our cohort were full-term (52/75, 69.3%). There was a history of severe obstetric complications in 69/75 (92%). A risk of miscarriage and acute respiratory viral infection had been recorded in the mother in 25/75 (33%) each. The main causative factors for seizures were hypoxic-ischemic encephalopathy (64/75, 85.3%), perinatal infections (52/75, 70%), metabolic disorders (24/75, 32%), and intracranial hemorrhages (20/75, 26.7%). Seizures were seen most often in the early neonatal period (61/75, 81.3%; $p < 0.001$). Motor automatisms (36/75, 48%) and clonic convulsions (30/75, 40%) were seen frequently.

Conclusion: Our team was able to identify motor seizures more frequently. The main causes of seizures were hypoxic-ischemic encephalopathy, perinatal infections, metabolic disorders, and intracranial hemorrhages but the etiology could not be identified in many cases. Further work is needed for timely identification of cause as etiology is a leading predictor of outcome.

Keywords: Clonic convulsions, Focal cerebral ischemia, Fosphenytoin, Grodno, Hypoxia, Hypoxic-ischaemic encephalopathy, Leukomalacia, Motor automatisms, Neonatal seizures, Neurological emergency, Neuronal excitation, Phenobarbital, Tandem mass spectrometry.

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KEY POINTS

- Seizures are the most frequently-seen neurological emergency in neonates.
- We reviewed the clinical course of 75 infants who were admitted continuously with convulsive seizures during the period 2016–2021 in the Grodno region of Belarus.
- Maternal history of severe obstetric complications and acute respiratory viral infection had been recorded in nearly a third of all patients. Most infants were born at full term and developed seizures in the early neonatal period.
- In our cohort, most patients had early-onset seizures caused by hypoxic-ischemic encephalopathy, perinatal infections, metabolic disorders, and intracranial hemorrhages. The etiology could not be identified in many. Further work is needed for a timely identification of cause because the etiology is a leading predictor of outcome.

BACKGROUND

Seizures are the most common neurological emergency in neonates, and this age group also has the highest incidence of seizures compared with any other period of life. The first weeks of life are a time of heightened risk for seizures due to physiological features of the developing brain that lead to increased neuronal excitation and decreased inhibition. Usually, seizures in neonates are a symptom of an acute brain injury; seizures are only rarely due to neonatal-onset epilepsy syndromes.

Neonatal seizures are harmful to the developing brain; early and accurate diagnosis is critical.^{1–3} Seizures occur in 1–5 per 1,000

^{1,2}Department of Pediatrics, Grodno State Medical University, Grodno, Belarus

³2nd Pediatric Department for Newborns and Premature Babies, Grodno Regional Clinical Children's Hospital, Grodno, Belarus

⁴Department of Neurology, Grodno Regional Clinical Children's Hospital, Grodno, Belarus

⁵Department of Intensive Care Unit, Republican Scientific and Practical Center for Pediatric Oncology, Hematology and Immunology, Minsk, Belarus

Corresponding Author: Tatsiana S Pratasevich, Department of Pediatrics, Grodno State Medical University, Grodno, Belarus, Phone: +375295684359, e-mails: tprotas16@gmail.com; tatprat@mail.ru

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live births; incidence increases in preterm infants and in low-birth-weight infants. Seizures in the neonatal period differ considerably from those observed later in life with respect to their etiological profile and clinical presentation. In addition, the etiological profile in preterm infants is different from that seen in term infants. Hypoxic-ischemic encephalopathy is the most frequent cause of neonatal seizures in term babies followed by focal ischemia (stroke), cerebral malformations and metabolic disturbances.^{4–7} A maternal infection in the prenatal period, congenital infections, diabetes, hypoglycemia, and a history of difficult birth are key indicators of potential perinatal asphyxia. The characteristics of other individuals

in the family should be examined for familial epileptic syndromes. Differences in etiology have been observed according to the level of national development.⁴ Biochemical abnormalities occur either as an underlying cause or as an associated abnormality. Therefore, biochemical anomalies should be excluded in every case of neonatal seizure, despite the presence of other causes of neonatal seizures. In preterm neonates, intraventricular hemorrhage (IVH) and infections cause most of the seizures reported in this group. Better, prompt clinical and neuroimaging evaluations have reduced the number of undiagnosed cases, and the institution of newer neuroprotective strategies has improved the outcomes.^{4,5,8}

Early recognition and treatment of these biochemical disturbances are essential for optimal management and satisfactory outcomes.⁹ In this study, we examined the clinical course of 75 infants with convulsive seizures, admitted serially, who had complete records during the period 2016–2021 in the Grodno region of Belarus. Data relevant to the course of pregnancy and childbirth, gestational age, characteristics of seizures and data from laboratory and instrumental research methods were recorded. We present our findings in this brief report.

METHODS

This study was designed as a retrospective review of risk factors for the development of convulsive syndrome in newborns in the Grodno region, as well as to analyze clinical characteristics and the results of laboratory and instrumental diagnostic tests. The total population of this region is estimated to be about 350,000. The infants were selected based on availability of complete records; five cases had to be excluded due to incomplete records. The study was approved by the institutional review board.

The following objectives were set for this study:

- To analyze complaints and leading clinical symptoms of seizure syndrome in children in Grodno and the Grodno region for the period 2016–2021.
- To assess the characteristics of the mothers' pregnancy and childbirth.
- To determine the most common causes of seizure syndrome in newborns. A total of 75 patients with neonatal seizures were included in the study for the period 2016–2021.

Clinical Evaluation

Special attention was paid to the course of pregnancy and childbirth, gestational age, characteristics of seizures, and data from laboratory and instrumental research methods. In the infants, the severity of organ-specific dysfunction was quantified as follows:

Encephalopathy

The diagnosis of neonatal encephalopathy was based on the main and additional criteria:¹⁰

Main Criteria

The presence of one of the following signs in the early neonatal (adaptation) period:

- Apgar score <5 at 5 minutes after birth;
- Need for resuscitation after birth or in the first 72 hours after birth;
- The presence of stable or progressive hypertensive-hydrocephalic syndrome;
- Impaired sucking and/or swallowing;

- Recurrent seizures;
- Coma;
- Organic changes revealed by cranial ultrasound, X-ray (if trauma is suspected), and magnetic resonance imaging (MRI) of the brain.

Presence of several (≥ 3) signs after the early neonatal adaptation:

- Absence or minimal expression of the concentration response;
- Central nervous system (CNS) arousal or depression;
- Minimal facial expressions, monotonous and unmodulated voice;
- Marked reduction or absence of the following reflexes: defensive, Babkin, support and automatic gait, Bauer crawl, upper and/or lower grasping;
- Spontaneous myoclonus.

Additional Criteria (risk factors for damage to the nervous system)

- Adverse medical history: A complicated obstetric history, chronic maternal illnesses, occupational exposure, and the age of the parents, especially the mother (under 18 or over 35 for primiparous women).
- Abnormal pregnancy: Threatened miscarriage, medication use and various medical interventions, acute maternal illnesses, etc.
- Abnormal labor: Prolonged or rapid, use of obstetric assistance or surgical interventions, Apgar score within 6–7 points.

Additional risk factors can be used in the diagnosis of neonatal encephalopathy in cases where neurological disorders are minimal and are on the borderline between normal and pathological.

Respiratory Distress

Respiratory failure in newborns is graded by clinical severity, typically mild (<3), moderate (4–6), and severe (>7) using the Silverman-Anderson or Downes' scores.¹¹ Increased work of breathing is associated with tachypnea, cyanosis, and grunting.

Post-hypoxic Cardiac Dysfunction

Inclusion criteria included a history of perinatal hypoxic-ischemic damage to the CNS such as cerebral ischemia and post-hypoxic cardiovascular disorders of the perinatal period [International classification of diseases (ICD)-X code P29], based on objective and/or instrumental examination data. Data from the cardiovascular system, such as impaired repolarization, altered cardiac rhythms and conduction disturbances on electrocardiograms, and impaired myocardial contractility with cardiac dilatation on echocardiography on postnatal days 4–6, was noted. In our intensive care units, we classify cardiac dysfunction using established grading systems.^{12,13} In the respiratory system, based on gestational age, tachypnea, retractions, coughing, oliguria, lethargy, feeding difficulties, and insufficient weight gain may be observed. Some term infants develop signs of cardiorespiratory failure with hepatomegaly and/or splenomegaly.

Other Information

We also add the following information to our statistical models:

- ICD-10 code for unspecified perinatal infections;
- Signs of systemic inflammatory response syndrome. This code is when a newborn exhibits signs of inflammation without an identified pathogen or clear localization.



- ICD-10 code P36.3 for sepsis in the newborn due to other and unspecified staphylococci
- P36.8 sepsis in the newborn due to other bacterial agents
- P36.2 sepsis in the newborn due to *Staphylococcus aureus*

Laboratory Findings

To confirm infection as a possible cause, a blood count and acute phase reactants were examined, and a lumbar puncture was performed to evaluate the cerebrospinal fluid (CSF). Blood gas profiles, serum lactate and amino acids, urine organic acids, and a tandem acylcarnitine profile were examined if a metabolic disorder was suspected. Magnetic resonance imaging is accepted as the gold standard imaging modality.

In our laboratory, normal total white blood cell (WBC) counts are $14 (9.6\text{--}17.8) \times 10^9/\text{L}$. The range of segmented neutrophils was 51 (34–63)%, band neutrophils 4 (2–6)%, lymphocytes 31 (20–43)%, monocytes 9 (7–11)%, eosinophils 2 (1–4)%, and basophils 1 (1–1)%. An immature-to-total neutrophil (I:T) count > 0.2 is noted.

We define normal serum sodium levels as 132–146 mmol/L and hypocalcemia as <2 mmol/L in full-term and <1.75 mmol/L in preterm infants. Procalcitonin concentrations (enzyme immunoassay) of 0.1–0.5 ng/mL may indicate a low risk of a clinically-significant bacterial infection requiring antibiotic treatment, 0.5–2 a low risk of sepsis or septic shock, and >2 ng/mL indicates a risk of severe sepsis or septic shock.

Tandem mass spectrometry is usually performed for neurological disorders with disturbances of consciousness (lethargy, coma), focal/generalized seizures, changes in muscle tone, opercular automatism, pedaling movements of the lower extremities, etc. Hereditary disorders of amino acid and organic acid metabolism and mitochondrial β -oxidation defects are the largest groups of hereditary disorders (more than 100 nosological entities). Most of these diseases manifest in early childhood and are characterized by an acute onset with neurological manifestations.

Reference values for leukocytes in CSF analysis: WBC counts of $0\text{--}30 \times 10^6/\text{L}$; 5–35% lymphocytes, 50–90% monocytes, and 0–8% neutrophils.

Imaging

In our protocols, we perform CNS imaging to diagnose hypoxic-ischemic changes in the brain when the following changes are seen:

Cranial Sonography

In full-term newborns:

- Parasagittal ischemic necrosis
- Ischemic lesions of the basal ganglia and thalamus
- Subcortical leukomalacia
- Diffuse hypoxic-ischemic changes in the acute period
- Cerebral edema
- Multicystic encephalomalacia (total cystic degeneration)
- Focal ischemic brain lesions.

In premature infants:

- Periventricular leukomalacia (PVL)
- Diffuse leukomalacia (PVL + subcortical leukomalacia)
- Periventricular hemorrhagic infarction.

Computed tomography (CT)/magnetic resonance imaging (MRI) of the brain is performed based on clinical decisions, considering the patient's severity of illness and the possibility of structural

Table 1: Clinically-relevant findings in pre- and perinatal records

Findings	Number
Delivery	
Vaginal	44 (58.7%)
Cesarean section	31 (41.3%)
Primigravida	31 (41.3%)
Second pregnancy	17 (22.7%)
Third or later pregnancy	27 (36%)
Prior complicated obstetric history	69 (92%)***
Antepartum records	2 (2.7%)
Acute respiratory viral infections	28 (37.3%)
Threatened miscarriage	27 (36%)
Anemia	13 (17.3%)
Findings suggestive of acute fetal hypoxia during delivery	12 (16%)
Prolonged (>18 hours) premature rupture of membranes (<36 weeks' gestation); PPROM with an anhydrous period >12 hours	8 (10.7%)
Weak labor	6 (8%)
Umbilical cord prolapse	2 (2.7%)
Umbilical cord entanglement	15 (20%)

** $p < 0.01$, *** $p < 0.001$. PPROM, preterm prelabor rupture of membranes

pathology of the brain, cerebral hemorrhages, and malformations of the cerebral cortex.

Treatment

We use diazepam as a first-line drug for emergency care. However, a number of limitations often necessitate the selection and administration of alternative therapies for both controlling the seizures and providing maintenance therapy. Phenobarbital monotherapy is effective in no more than half of all infants with seizures.

Statistical Analysis

Data were processed using traditional methods of variation statistics with the application software packages "STATISTICA 10.0" and "EXCEL". Non-parametric data were shown as percentages or as median/interquartile ranges and analyzed using the Mann-Whitney/Kruskal-Wallis tests.^{14–16} When comparing groups with a limited number of observations, the two-tailed Fisher test was used.^{16,17}

RESULTS

Obstetric records showed that 44 (58.7%) infants were born vaginally, and 31 (41.3%) were born by cesarean section. Thirty-one (41.3%) mothers were primigravidae; 17 (22.7%) had this as a second pregnancy, and 27 (36%) were in their third and subsequent pregnancies. Findings suggestive of a complicated maternal clinical course are listed in Table 1.

In our cohort, 52/75 (69.3%) infants were born at full-term at a gestational age (median, range) of 39^{+2} (39–40) weeks. Preterm infants were born at 35 ($32^{+1}\text{--}36^{+6}$) weeks, $p < 0.0001$. The clinical features are summarized in Table 2.

Table 2: Clinical findings of infants with seizures

Findings	Number
Gestational age (median, IQR) weeks; 75 infants	37.2 (33 ⁺³ –39) weeks
Term; 52 infants (69.3%)	39 ⁺² (39–40) weeks
Preterm; 23 infants (30.7%)	35 (32 ⁺¹ –36 ⁺⁶) weeks***
Birth weight (median, IQR)	3150 (2700–3800) grams
Length (median, IQR)	51 (49–54) cm
Gender	
Males	43 (57.3%)
Females	32 (42.7%); difference not significant
Birth asphyxia	21 (28%)
Multisystem support with assisted ventilation	49 (65.3%)**
Neonatal encephalopathy	64 (85.3%)***
Culture-positive invasive perinatal infections	9/75 (12%)***
Blood	3 (4%)
CSF	2 (2.7%)
Endotracheal tube	4 (5.3%)
Respiratory failure	50 (66.7%)***
Grade I	6 (8%)
Grade II	18 (2%)
Grade III	26 (34.7%)***
Cardiac dysfunction	16 (21.3%)

p* < 0.01, *p* < 0.001. IQR, interquartile range; CSF, cerebrospinal fluid

Table 3: Seizures

Findings	Number
Types of seizures	
Clonic contractions	30 (40%)
Tonic spasms	21 (28%); neck hyperextension in 11
Myoclonus in hypernatremia	20 (26.7%)
Subtle seizures	
Convulsions of diaphragm	18 (24%)
Motor automatisms	36 (48%)
Oral automatisms	17 (22.7%)
Rowing arm movements, pedaling with legs	12 (16%)
Ocular (such as nystagmus)	7 (9.3%)
Atypical movements	12 (16%)
Apnea with desaturation	8 (10.7%)
Vegetative movements	4 (5.3%)
Mydriasis	2 (2.7%)
Transient skin redness	1 (1.3%)
Gagging	1 (1.3%)

Most seizures occurred within the first 48 hours after birth (<48 hours: 46 (61.3%; postnatal days 3–7: 15 (20%); and >7 days: 14 (18.7%; *p* = 0.00001). Table 3 lists the types of seizures.

Table 4: Laboratory findings

Findings	Number
Altered WBC counts	
Leukocytosis	25 (33.3%)
Leukopenia	10 (13.3%)
Bandemia with I:T >0.2	39 (52%)
Biochemical abnormalities	24 (32%)
Serum Na range (median, IQR)	128.4 (124.1–129.3) mmol/L
Hyponatremia (median, IQR)	6 (8%); 128.4 (124.1– 129.3) mmol/L
Hypernatremia	1 (151.1 mmol/L)
Serum Ca range (median, IQR)	1.8 (1.5–1.9) mmol/L
Hypocalcemia	16 (21.3%)
Hypoglycemia (blood glucose ≤1.5 mmol/L)	1 (0.13%)
Increased C-reactive protein	27 (36%)
Increased procalcitonin	6 (8%). Measured 6.43 (0.82–37.3) ng/mL

IQR, interquartile range; I:T, immature:total neutrophil counts

Table 5: Findings on cranial ultrasonography

Findings	Number
Intracranial hemorrhages	20 (26.7%)
Intraventricular hemorrhage	8 (10.7%)
Grade II	3 (4%)
Grade III	5 (6.7%)
Epidural hemorrhage	2 (2.7%)
Subdural hemorrhage	2 (2.7%)
Subarachnoid hemorrhage	6 (8%)
Epidural hemorrhage	2 (2.7%)
Intracerebral hemorrhage in 2	2 (2.7%)
Ventricular dilatation	36 (48%)
Hypoxic-ischemic changes	17 (22.7%)

Laboratory findings are summarized in Table 4. Tandem mass spectrometry data showed decreased free carnitine levels in 1 (1.3%) infant. Cerebrospinal fluid showed neutrophilic pleocytosis in 20 (26.7%) newborns, and increased red blood cells (hemorrhage) in 25 (33.3%).

Microbiology records showed positive cultures from invasive sites in 9/75 (12%): endotracheal tube [4 (5.3%)], blood [3 (4%)], and CSF [2 (2.7%)]. Most infections involved Gram-positive bacteria: Staphylococci [48% (*Staphylococcus haemolyticus*, *Staphylococcus epidermidis*, *Staphylococcus aureus*, *Staphylococcus lentus*, and *Staphylococcus warneri*)] and Streptococci (9.3%). A few showed Gram-negative bacteria [*Klebsiella pneumoniae* (8%), *Escherichia faecium* (8%), and *Escherichia coli* (2.7%)].

In our protocols, we routinely perform CNS imaging to evaluate encephalopathic changes. Cranial ultrasonography was performed on all 75 infants. The findings are shown in Table 5.

Magnetic resonance imaging was performed in 31 (41.3%). The findings are shown in Table 6.



Table 6: Findings on MRI. Percentages are expressed in the cohort of 75

Findings	Number
Cystic-gliar transformation	6 (8%)
Post-ischemic leukomalacia (periventricular leukomalacia)	4 (5.3%)
Subcortical dysmetabolic changes (T2-hyperintense signals, white matter lesions, or volumetric reductions in thalamus and caudate nucleus)	2 (2.7%)
Congenital defects	8 (10.7%)
Dandy-Walker malformation type 1	2 (2.7%)
Deviated internal carotid artery	2 (2.7%)
Hypoplasia of the septum pellucidum	1 (1.3%)
Aneurysm of the lateral villous artery	1 (1.3%)
Hypoplasia of the cerebellar hemispheres	1 (1.3%)
Dural arteriovenous fistula	1 (1.3%)

Table 7: Findings on EEG

Findings	Number
Indirect signs of immaturity of brain structures	3 (4%)
Severe disorganization of the bioelectrical activity of the brain	2 (2.7%)
Diffuse changes in cortical rhythms	1 (1.3%)
Flat EEG	4 (5.3%)
No abnormalities	9 (12%)

EEG, electroencephalography

We use electroencephalography (EEG) for monitoring infants with encephalopathy.^{2,18–20} In this cohort, 19 (25.3%) patients were monitored (Table 7).

To treat seizures, we use intravenous diazepam as the first-line drug. If necessary, phenobarbital is then prescribed for maintenance therapy. In the analyzed group, diazepam was used in 56 (74.7%) newborns, phenobarbital in 48 (64%), and Depakine in 11 (14.7%). Sodium oxybutyrate was used in 8 (10.7%). Eighteen (24%) infants continued to have seizures after diazepam. In 30 (49%), a recurrence was observed in within 24 hours after stopping diazepam. Seizures stopped spontaneously in 8 (10.7%) infants. Maintenance therapy with phenobarbital was carried out at a dose of 5 mg/kg/day. In 11 cases, due to phenobarbital's ineffectiveness, Depakine was prescribed.

DISCUSSION

The first weeks of life represent a period of heightened vulnerability to seizures because of age-dependent physiological characteristics of the developing brain.^{21,22} During the neonatal period, neuronal networks are intrinsically more excitable due to an increased density and activity of excitatory glutamatergic receptors and an immature inhibitory γ -aminobutyric acid (GABA) system.^{23,24} During early development, GABA can exert depolarizing (excitatory) rather than inhibitory effects because of elevated intracellular chloride levels, further promoting neuronal excitation.²⁵ Additionally, incomplete myelination, enhanced synaptic plasticity, and evolving cortical connectivity contribute to an imbalance between excitation and inhibition.^{26,27} Together, these factors create a neurobiological environment in which seizures are more easily initiated and propagated during the first weeks of life.²⁸

Neonatal health in Belarus is considered strong by global standards, with one of the lowest neonatal mortality rates in Eastern Europe.²⁹ Over the past three decades, the country has achieved a substantial decline in deaths within the first 28 days of life, largely due to universal access to facility-based deliveries, a well-structured three-tier perinatal care system, and high coverage of skilled birth attendants.³⁰ Comprehensive prenatal screening programs, early ultrasound assessments, and effective referral networks for high-risk pregnancies have further improved outcomes. Advances in neonatal intensive care have increased survival among preterm and very low birth weight infants. Despite demographic challenges such as declining birth rates, the overall organization of maternal and newborn healthcare services continues to support favorable neonatal outcomes nationwide.

As in other parts of the world, neonatal seizures are defined in Belarus as sudden, abnormal electrical discharges in the brain occurring in the first 28 days of life.³¹ These are recognized as an important acute neurological condition in newborn care and are covered in national clinical guidance for neonatal medicine. A clinical protocol from the Republican Centre for Health Development (Ministry of Health of Belarus) lists "seizures of the newborn" (ICD-10 code P90) as a specific neonatal condition requiring structured diagnosis and management within perinatal and neonatal services, with standardized approaches to evaluation and treatment outlined at different levels of health care.³² We are still compiling precise Belarus-specific prevalence data.³³ International pediatric neurology literature indicates that neonatal seizures occur in roughly 1–5 per 1,000 term infants and significantly more often among preterm babies. Major causes include hypoxic-ischemic encephalopathy (HIE), intracranial hemorrhage, infections, and metabolic disturbances associated with acute CNS dysfunction.^{4–7,9}

Seizures due to an intracranial process vs. those due to systemic disorders cannot always be reliably distinguished by clinical manifestations (such as focal or generalized seizures).³⁴ Neuroimaging methods can help in investigating these cases.^{35,36} Transfontanelle ultrasonography, v-cEEG, CT, and MRI can be helpful.³⁷ In experienced hands, ultrasound is an outstanding tool to detect brain abnormalities in preterm and full-term infants, to follow the progression of these lesions, and to describe the maturation of the infant brain.¹⁸ Video-continuous EEG has also been shown to be useful and should be initiated as soon as is feasible, in order to evaluate for events of concern, screen for subclinical seizures, and assess the EEG background.¹⁶ The goal is to confirm diagnosis, identify etiology, and guide treatment. These can manifest with subtle or focal movements that are difficult to distinguish from other neonatal behaviors, making EEG monitoring particularly important.³⁸ The management and outcomes vary with the underlying cause, gestational age, and severity; some seizures resolve with treatment of the provoking condition, whereas others may portend longer-term neurological sequelae such as epilepsy or developmental impairment, especially in preterm infants or those with severe brain injury.^{39,40}

In our study, 92% of pregnant women had a complicated obstetric history; one-third had an acute respiratory viral infection and another third a threatened miscarriage. Nearly 60% experienced episodes of intrapartum hypoxia. Factors associated with neonatal seizures were HIE (85.3%), infections (69.3%), metabolic disorders (32%), and intracranial hemorrhages (26.7%). Seizures were seen most often in the early neonatal period (81.3%). Even though the cohort was selected based on clinically-obvious seizures, nearly

half also showed subtle signs. Acute symptomatic seizures in many newborns can be caused by yet unidentified factors, calling for further investigation.

Neonatal sepsis was not a leading cause of neurological morbidity in our series. Most of the isolates were Gram-positive bacteria, and the spectrum differed from those in other countries. Staphylococci appeared most frequently, as noted in previous reports from Eastern Europe.⁴¹ Group B streptococci were not observed as frequently. *Staphylococcus haemolyticus* is a coagulase-negative staphylococcus (CoNS) - a Gram-positive, catalase-positive bacterium that is part of the normal skin flora but acts as an opportunistic pathogen, commonly associated with hospital-acquired infections and biofilm formation on medical devices.⁴² It is known for high levels of antibiotic resistance.⁴² Similar to other parts of the world, we also need protocols to reduce variability in maternal screening, infection control measures, and antimicrobial stewardship programs.⁴³ Strengthening perinatal prevention strategies and neonatal intensive care unit (NICU) infection control will help in reducing disease burden.⁴⁴

Seizures are common in neonates, but there is considerable variability in clinical management. According to the literature, phenobarbital is used as the first-line antiseizure medication regardless of etiology.^{4,7,45,46} It is seen to be more effective than levetiracetam and easier to administer than fosphenytoin, and there are some data suggest it might even be safe to discontinue the phenobarbital after the acute seizures resolve, prior to hospital discharge.⁶ However, in our experience, phenobarbital monotherapy is effective in only about half of all infants with seizures. Identification and correction of transient metabolic disturbances improve outcomes, but about a third of all patients still require combination therapy.⁴⁷ A standardized pathway is still needed for clinical management. We have also developed educational materials to inform parents and guardians about the diagnosis and initial treatment options.⁴⁵

Prognosis depends on the etiology: long-term outcomes of neonatal seizures are variable, ranging from no neurologic abnormalities to developmental delay, intellectual disability, and epilepsy.⁴ Most neonates with seizures due to a transient electrolyte disturbance, such as hypocalcemia and hyponatremia, do well when seizures resolve after the disturbance is reversed and long-term antiseizure medications are not required.²⁸ However, those with severe intraventricular hemorrhage show high morbidity and mortality.⁴⁸ For idiopathic seizures or seizures due to brain malformations, earlier onset is associated with worse neurodevelopmental outcomes.³⁹ The outcomes of newborns impacted by non-metabolic neonatal seizures can improve with comprehensive clinical and laboratory evaluation and appropriate therapy.⁹

Similar to other parts of the world, neonatal seizures are viewed as a neurological emergency in Belarus. These call for prompt recognition and structured management. We need standardized clinical protocols and access to specialized neonatal services to support early diagnosis, appropriate treatment, and timely referral of high-risk infants. As survival of preterm and critically-ill newborns continues to improve, ongoing emphasis on neurocritical monitoring, timely etiologic evaluation, and long-term neurodevelopmental follow-up will remain essential to minimize adverse outcomes and further strengthen neonatal neurological care in Belarus.⁴⁹

ORCID

Tatsiana S Pratasevich  <https://orcid.org/0000-0002-7810-3611>

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Meckel Diverticulum

Atul K Khare

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ABSTRACT

Meckel diverticulum (MD) is a congenital pouch on the antimesenteric border of the distal ileum. It is a remnant of the omphalomesenteric (vitelline) duct. These anomalies are seen all over the world with a fairly consistent prevalence of 0.2–4%. There is no strong evidence for genetic factors. There can be seen three possible variants: (1) an MD with the rest of the omphalomesenteric duct (OMD) seen as a terminal fibrous band connecting with the umbilicus; (2) the whole OMD remains patent; and (3) an umbilical cyst, a fluid-filled remnant in a part of the ductal pathway. The cause is unknown; no single gene mutation has been consistently associated with MDs, but new information is emerging about the pathogenesis of gut heterotopias. Some of these diverticula are seen in patients with trisomy 13, trisomy 18, trisomy 21, or with broader patterns of multiple congenital anomalies, including the Vertebral, Anal, Cardiac, tracheoesophageal, Renal, Limb anomalies (VACTERL) association. Meckel diverticulums can be associated with fibrous peritoneal bands, which can be associated with mechanical intestinal obstruction by kinking, compressing, or entrapping small bowel loops. Symptomatic cases may be diagnosed with a nuclear medicine technetium-99m pertechnetate Meckel scan that detects gastric tissue. Asymptomatic patients may be closely followed with conservative management. However, for symptomatic cases, a diverticulectomy is performed, and the fibrous bands or adhesions are released. If the base is broad, a segmental ileal resection is considered.

Keywords: Antimesenteric border, Auerbach, Bone morphogenetic protein, Calprotectin, Congenital pouch, Diverticulectomy, Ectopic gastric tissue, Ectopic pancreatic tissue, Eosinophilia, Fibroblast growth factors, Fibrous peritoneal bands, Homeobox gene, Infant, Meckel scan, Meissner, Neonate, Newborn, Nod-like receptor family CARD domain containing 4, Nod-like receptor pathway, Omphalomesenteric duct, Segmental ileal resection, Sonic hedgehog pathway, Technetium-99m pertechnetate, Trisomy 13, Trisomy 18, Trisomy 21, Umbilical cyst, VACTERL association, Vitelline duct, Volvulus, Wnt/ β -catenin signaling, Yolk sac.

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KEY POINTS

- Meckel diverticulum (MD) is a congenital pouch on the antimesenteric border of the distal ileum. It is a remnant of the omphalomesenteric (vitelline) duct.
- Meckel diverticulum is seen all over the world with a fairly consistent prevalence of 0.2–4%. There is no strong evidence for genetic factors.
- Meckel diverticulums can be seen in three possible variants: (1) an MD with the rest of the omphalomesenteric duct (OMD) seen as a terminal fibrous band connecting with the umbilicus; (2) the whole OMD remains patent; and (3) an umbilical cyst, a fluid-filled remnant in a part of the ductal pathway.
- No single gene mutation has been found to be consistently associated with MDs. Sometimes these diverticulae are seen in patients with trisomy 13, trisomy 18, trisomy 21, or with broader patterns of multiple congenital anomalies, including the Vertebral, Anal, Cardiac, tracheoesophageal, Renal, Limb anomalies (VACTERL) association.
- Meckel diverticulums can be associated with fibrous peritoneal bands, which can be associated with mechanical intestinal obstruction by kinking, compressing, or entrapping small bowel loops.
- Symptomatic cases may be diagnosed with a nuclear medicine technetium-99m pertechnetate Meckel scan that detects gastric tissue.
- Asymptomatic patients may be closely followed with conservative management. However, for symptomatic cases, a diverticulectomy is performed. If the base is broad, a segmental ileal resection is considered. Surgical release of fibrous bands or adhesions may also be necessary.

Department of Pediatric Surgery, Sawai Man Singh Medical College, Jaipur, Rajasthan, India

Corresponding Author: Atul K Khare, Department of Pediatric Surgery, Sawai Man Singh Medical College, Jaipur, Rajasthan, India, Phone: +91 8839523630, e-mail: dratulkhare@gmail.com

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INTRODUCTION

An MD is a congenital pouch on the antimesenteric border of the distal ileum. It is a remnant of the OMD (vitelline duct) that connects the developing embryo with the yolk sac, and its location corresponds to the terminal portion of the midgut.^{1–3} The MD is frequently described using a rule of 2;⁴ it is seen in 2% of the population, often presents before age 2, and may contain two types of ectopic tissue (gastric or pancreatic). In adults with a persisting MD, the diverticulum is about 2 inches long and is located 2 feet from the ileocecal valve. In many patients, these diverticula do not cause symptoms. However, others can present with peptic ulceration, bleeding, inflammation, gastrointestinal dysmotility, obstruction, volvulus, or intussusception.^{2,3,5–8}

In this review, we present a synopsis of our current understanding of the pathophysiology, clinical features, diagnosis, and management of MD. We have combined some data from our own preliminary studies with an extensive literature search in Embase, PubMed, and Scopus. To avoid bias in identification of

studies, keywords were short-listed *a priori* from PubMed's Medical Subject Headings (MeSH) thesaurus.

EPIDEMIOLOGY

Meckel diverticula are seen all over the world with a fairly consistent prevalence of 0.2–4%.^{1,3,6,9} There is no strong evidence for increased risk due to ethnic/racial factors, maternal nutrition, or environmental toxins. However, a few series have noted higher numbers in males with male-to-female ratios as high as 2:1.¹⁰ Some hospital-based studies from Europe and North America have reported slightly higher frequencies than in the rest of the world, but these also might be related to study methods, access to imaging, rates of surgery, and autopsy rates, rather than to true genetic or environmental differences.^{7,11}

NORMAL GUT MORPHOGENESIS—POSSIBLE INSIGHTS INTO THE DEVELOPMENT OF MDs

During development, the primitive gut continues to communicate with the yolk sac through the OMD.¹² Normal gut morphogenesis and apoptosis, which are controlled by multiple genes and signaling pathways, include:

- Homeobox (HOX) genes, which regulate anteroposterior patterning of the gut. Abnormal HOX expression can affect midgut differentiation and vitelline duct regression;^{13,14}
- Sonic hedgehog (SHH) pathway is critical for intestinal epithelial-mesenchymal signaling and proper midgut development;^{15,16}
- Fibroblast growth factors (FGFs) are involved in gut elongation and rotation; disturbances may interfere with duct involution;^{17,18}
- Bone morphogenetic protein (BMP) signaling contributes to apoptosis and regression of transient embryonic structures, including the vitelline duct;^{19,20} and
- Wnt/ β -catenin signaling that regulates intestinal stem cell proliferation and differentiation to indirectly affect midgut remodeling.^{15,21}

The pathogenesis of gastric heterotopia in MD is likely rooted in incomplete obliteration of the vitelline duct during embryonic development and misplaced gastric/pancreatic tissue within the diverticulum.^{3,22} Meckel diverticulum results from the failure of involution of the OMD; these aberrations may result from abnormal apoptotic signaling, genetic defects, or mechanical factors that affect gut folding and positioning.^{3,23}

Meckel diverticula are true congenital diverticula composed of all layers of the intestinal wall and do not inherently have a tendency to become fibrotic.³ These may show ectopic presence of embryonic cells that differentiate into gastric mucosa (50%), pancreatic cells (15%), and others, such as duodenal/colonic mucosa in others.⁵ In some cases, fibrous vitelline or omphalomesenteric bands can persist as straps connecting the diverticulum to the umbilicus or abdominal wall.

GENETICS

Meckel diverticulum has been associated with chromosomal abnormalities such as trisomy 13, trisomy 18, and trisomy 21. However, no specific genes have been identified as causative. These associations are thought to reflect the high prevalence of multiple congenital anomalies, including gastrointestinal malformations, cardiac defects, and craniofacial anomalies. Some

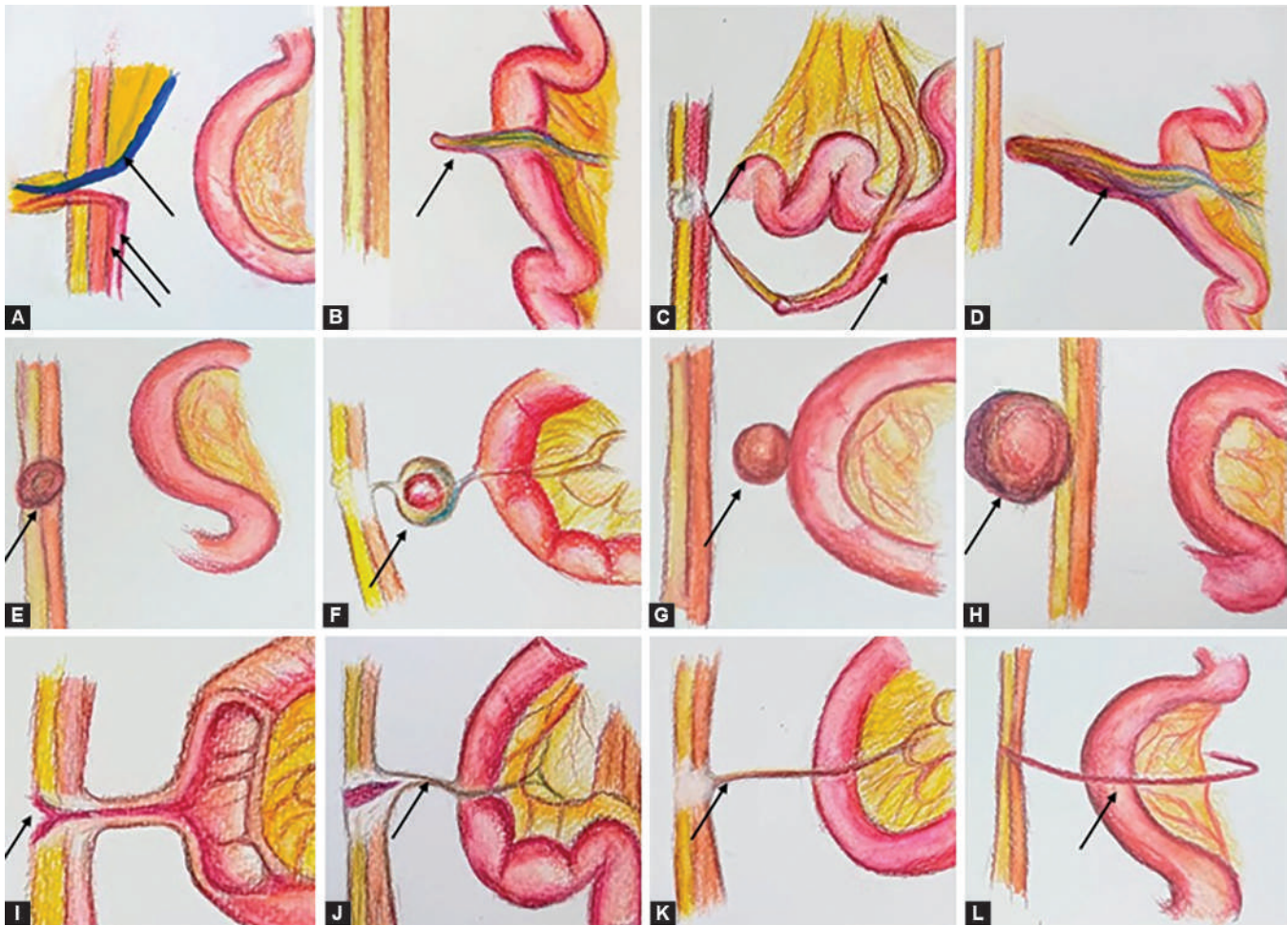
patients show cecal duplication cysts in addition to MD.²⁴ It has also been associated with the broader patterns of multiple congenital anomalies, including the VACTERL association, omphalocele, gastroschisis, intestinal atresia, malrotation, and congenital cardiac defects such as ventricular and/or atrial septal defects, and less frequently, conotruncal anomalies.³ Overall, MD is considered congenital but not genetically inherited, where the associations reflect disrupted embryologic development rather than a defined hereditary syndrome.

The heterotopia seen in MD does not have a clear relationship with specific Mendelian genes but may be related to developmental mis-patterning of the foregut-midgut boundary.^{12,22} Gastric heterotopia has been associated with increased expression of the SRY-related HMG-box (SOX) 2, a key foregut transcription factor vital for maintaining stomach tissue identity and function.^{25–27} Other gastric epithelial markers, such as mucin (MUC) 5AC in foveolar cells, MUC6 in pyloric glands, the alpha and beta subunits of the gastric H⁺/K⁺-ATPase (ATP4A, ATP4B), and pepsinogen in fundic-type heterotopia, are also notable in parietal and chief cell differentiation.^{28–32} Current information links SOX2 expression with the presence of gastric characteristics, such as the presence of gastric mucins MUC5AC and MUC6, and its loss/ectopic expression with non-gastric mucosal patterning, metaplasia, or heterotopia.^{33–35} The gel-like mucin glycoproteins are characteristically present in the stomach, duodenum, and pancreas, where these shield the epithelium from acid, proteases, and pathogens.^{36,37} The gastric H⁺/K⁺-ATPases are the proton pumps in stomach parietal cells; these enzymes pump hydrogen ions (H⁺) into the stomach lumen in exchange for potassium ions (K⁺), creating the highly acidic environment needed for digestion.^{32,38}

SRY-related HMG-box 2 expression shows a high-to-low anterior–posterior gradient within the foregut endoderm; the strongest expression is seen in the esophagus and stomach with a progressive downregulation toward the foregut–midgut junction.^{39,40} This graded SOX2 expression helps establish foregut identity, promoting gastric and esophageal epithelial differentiation while actively repressing intestinal fate.^{41,42} It suppresses intestinal gene programs by antagonizing *CDX2*; these changes are modulated by regional Wnt/ β -catenin, BMP, FGF, and retinoic acid signaling gradients.^{43,44} Disruption or persistence of SOX2 expression beyond its normal domain can shift epithelial patterning toward a gastric phenotype, contributing to developmental anomalies such as gastric heterotopia in the intestine.^{43,44}

In contrast to SOX2, the gene *CDX2* likely promotes intestinal epithelial identity.^{45,46} It induces hallmark intestinal genes such as *MUC2*, *villin (VIL1)*, sucrase-isomaltase (SI), and *KLF4* gene Krüppel-like factor 4 (*KLF4*, which encodes a transcription factor vital for cell proliferation, differentiation, and stem cell maintenance).^{47,48} Consequently, *CDX2* represses gastric lineage factors such as SOX2 and drives goblet cell formation and intestinal-type architecture, reinforcing the phenotypic switch.^{45,46,49}

Meckel diverticula can show considerable inflammation. Genes implicated in inflammatory pathways, such as those in the toll-like receptor (TLR) and nod-like receptor (NLR) activation, have been examined. Toll-like receptors are not involved in the formation of MD, but these might be important in the exaggerated immune responses to bacterial or inflammatory stimuli.^{1,3} Similarly, the NLR pathway mediators do not seem to be directly involved.^{1,3} Nod-like receptor family CARD domain containing 4 (NLRC4), a known regulatory gene in the inflammasome-mediated immune



Figs 1A to L: (A) The normal umbilicus at birth is best recognized for its vascular connections. There are two umbilical arteries (red) ascending along the anterior abdominal wall (arrows). These carry blood from the internal iliac arteries in the pelvis and pass through the umbilicus to the placenta. After birth, the obliterated remnants of these arteries can be seen as the subperitoneal medial umbilical ligaments. The umbilical vein runs along the free edge of the falciform ligament, a bilayered, sickle-shaped fold of peritoneum that extends from the anterior abdominal wall to the inferior border and anterior surface of the liver. The vein undergoes fibrosis and can be seen later as the ligamentum teres hepatis (round ligament of the liver); (B–L) An MD and some other congenital defects in the umbilicus. The key findings in all the figures are marked by arrows: (B) Meckel diverticulum, a blind, isolated pouch is a remnant of the OMD that arises on the small intestine (ileum) and usually does not open into the umbilicus; (C) An MD with an associated fibrous cord that extends from the peritoneum to the umbilicus; (D) Meckel diverticulitis, with inflammation in the outpouching due to infection or enzymatic damage; (E) Umbilical polyp; (F) Fibrous umbilical cord with intra-abdominal cyst; (G) Duplication cyst from the small intestine. The neck is smaller than typically seen; (H) A large umbilical granuloma (these are usually <1 cm in size); (I) Umbilical-intestinal fistula (patent vitellointestinal duct); (J) Umbilical cord sinus; (K) Fibrous cord between the umbilicus and the small intestine; and (L) Remnant of umbilical vessel

responses, has been examined.⁵⁰ Its mutations have been implicated in autoinflammatory diseases like infantile enterocolitis; it could enhance inflammation in MD, but does not have a causative role. At the cellular level, macrophage activation can similarly enhance the local inflammatory responses.⁴

PATHOPHYSIOLOGY

After birth, the OMD usually gets obliterated by 5 weeks of age. Meckel diverticula have been seen associated with many related abnormalities: (1) an MD with the rest of the OMD seen as a terminal fibrous band connecting with the umbilicus. This fibrous connection can be complicated by intestinal obstruction, volvulus, or internal hernia; (2) the whole OMD remaining patent, seen as a fistulous

connection from the ileum to the umbilicus with fecal discharge from the umbilicus; and (3) an umbilical cyst, a fluid-filled remnant in a part of the ductal pathway.^{51–55} These, an inflamed MD, and a few other umbilical anomalies are shown in Figure 1.

CLINICAL FEATURES

Meckel diverticulum is a true congenital outpouching of the ileum that arises from incomplete involution of the vitelline duct, not due to abnormal intestinal innervation.⁶ Hence, many patients can remain completely asymptomatic. The diverticulum contains all layers of the intestinal wall, including the myenteric (Auerbach) and submucosal (Meissner) plexuses, so its intrinsic innervation is generally normal and should not be a primary cause of dysmotility.³

Considering that these congenital diverticula contain all layers of the intestinal wall, they should also not have an inherent tendency for scarring.³

In other patients, MD can be associated with other abnormalities (Fig. 1) and present with clinical complications. In some cases, remnants of the OMD can evolve over time into linear cord-like structures that connect the diverticulum to the umbilicus or abdominal wall.^{53,55} These can alter gut motility by kinking, compressing, or entrapping loops of small bowel.⁵³ Many patients may show clinical features suggestive of inflammation, dysmotility, obstruction, volvulus, or intussusception, with the diverticulum acting as the lead point.^{2,3,6,56,57} They may present with nausea, vomiting, low-grade fever, right lower quadrant abdominal pain, and painless rectal bleeding.⁶⁻⁸ In some cases, chronic inflammation may lead to localized fibrosis and adhesions. Recognition of these bands is important, as surgical removal of the MD along with the band is typically required to prevent recurrent obstruction.⁵³

The ectopic gastric tissue in many MDs secretes acid, and can cause peptic ulceration, bleeding, and inflammation (diverticulitis) within the diverticulum or in the nearby bowel.⁵ These MDs frequently show visible/histopathological signs of inflammation (Figs 1B and D);^{58,59} this condition, known as Meckel diverticulitis, can show clinical features similar to those of acute appendicitis.⁶⁰ Inflammation may also cause stasis of bowel contents within the diverticulum.

There is no direct link between MD and peripheral eosinophilia. However, secondary eosinophilia may occasionally occur if the diverticulum becomes inflamed or if there is ulceration from ectopic gastric tissue, leading to a local inflammatory response that can slightly elevate eosinophil counts.^{61,62} Rarely, if the diverticulum contains ectopic pancreatic or other heterotopic tissue, it could provoke a localized immune reaction. Some infants show hypersensitivity-type reactions in the diverticular tissue.^{3,62}

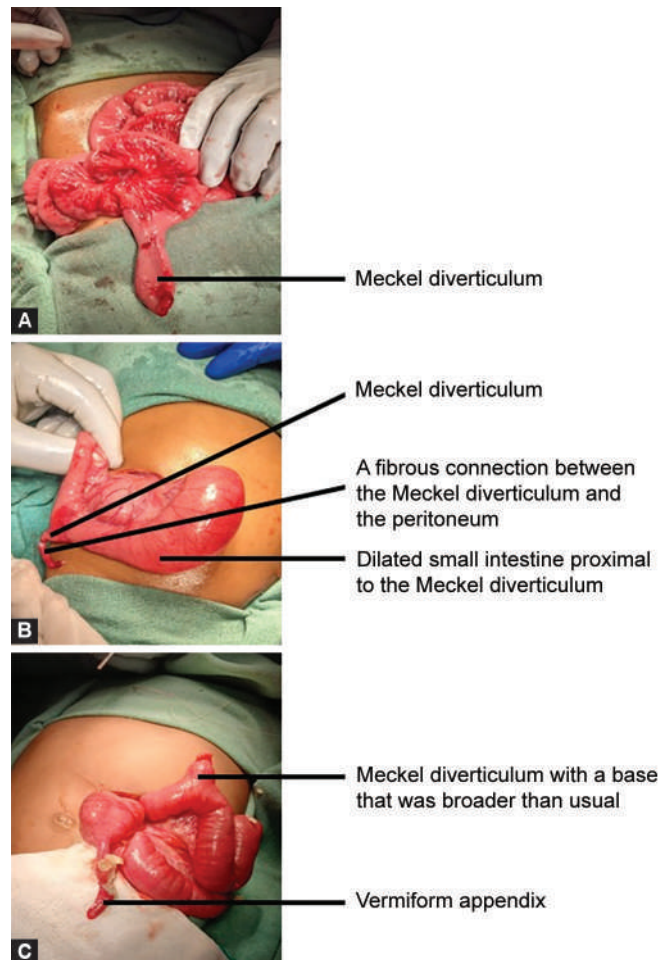
Fecal calprotectin is a biomarker of intestinal inflammation.⁶³ In MD, fecal calprotectin is not typically elevated unless there is complicated inflammation such as Meckel diverticulitis or ulceration from ectopic gastric tissue.^{64,65}

DIAGNOSIS

Meckel diverticula are often found incidentally. Nuclear Meckel scans using intravenously administered technetium-99m pertechnetate, which is selectively taken up by true/ectopic gastric mucosal cells, can help in detecting gastric tissue.⁶⁶⁻⁶⁸ This scan is useful in infants/children presenting with painless rectal bleeding or suspected ulceration due to acid secretion from ectopic gastric tissue.⁶⁷ Sensitivity rates of 85–90% have been documented in children. However, in adults, lower detection rates of about 60% have been seen because of smaller/inactive ectopic tissue.⁶⁸ There may be false positives in patients with intestinal inflammation or duplication cysts.^{69,70} Others, those without gastric mucosa, show a false negative.⁷⁰ Overall, Meckel scans are considered the diagnostic test of choice for identifying symptomatic MDs with gastric mucosa.⁶⁸ In many cases, the diagnosis is often confirmed only after surgery with histopathological examination of the excised tissues.^{5,71}

TREATMENT

Asymptomatic patients may be closely followed with conservative management.⁷² However, for MDs discovered incidentally during



Figs 2A to C: Intraoperative findings seen in three different infants with Meckel diverticula

a laparotomy or in symptomatic cases, including those with bleeding, obstruction, inflammation (diverticulitis), or perforation, a diverticulectomy is performed.⁷²⁻⁷⁵ If the base is broad or there is associated ulceration or inflammation of the adjacent ileum, a segmental ileal resection is considered.^{72,73} These procedures can be performed via open laparotomy or laparoscopically, depending on the clinical situation and the surgeons' experience.⁷⁵ In children presenting with bleeding, removal of the diverticulum usually resolves the problem.⁷⁵ However, while in cases with obstruction, surgical release of fibrous bands or adhesions may also be necessary.⁵⁵ Postoperative outcomes are generally excellent, with low recurrence and resolution of symptoms.^{6,72}

Figure 2 shows the gross morphology of a newly resected MD from three different infants. Histopathological examination of these tissue samples typically shows gastric heterotopia with mucus-producing goblet cells and acid-producing parietal cells (Fig. 3).

There is no direct link between MD and neurodevelopmental disorders, and it does not inherently affect brain development or cognitive function.^{6,76} However, in rare cases where MD occurs as part of chromosomal abnormalities or syndromic conditions, such as trisomy 13, 18, or 21, or VACTERL association, there may be associated neurodevelopmental delays or intellectual disabilities, but these outcomes are due to the underlying syndrome rather than the diverticulum itself.⁷⁶

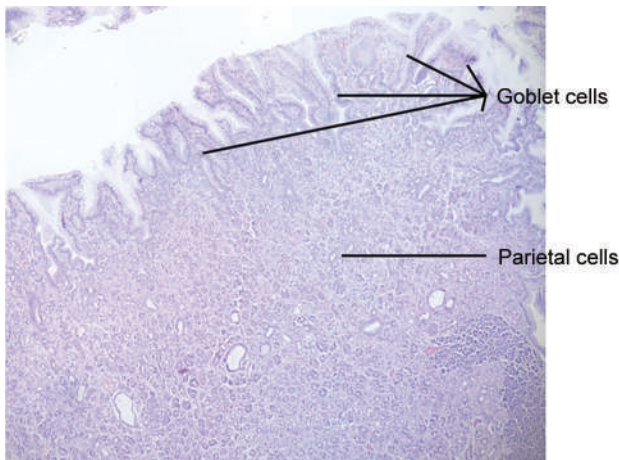


Fig. 3: Histopathological findings (hematoxylin-eosin, 20 \times) in a tissue section of an MD. Gastric heterotopia was seen with mucus-producing goblet cells and acid-producing parietal cells

CONCLUSION

Meckel diverticulum is one of the most common congenital gastrointestinal malformations all over the world. However, it still poses a diagnostic challenge in many infants due to its diverse clinical presentations, ranging from incidental findings to life-threatening complications. Its embryological origin explains the presence of ectopic tissue, which contributes to complications such as bleeding, inflammation, and intestinal obstruction. Advances in imaging and surgical techniques have improved outcomes, but timely diagnosis still remains important. A thorough understanding of its embryologic origin, clinical manifestations, and management strategies is essential for optimizing patient care.

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Principal Component Analysis: Progress and Applications

Akhil Maheshwari^{1–20}, Jayanta K Das^{2,20}, Brunetta Guaragni²¹, Somashekhar Nimbalkar²², Naief Alghnime²³, Jubara Allah²⁴, Moises Quiles-Corona^{2,25}, Yashas N Basavapatna^{2,20}

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ABSTRACT

Principal component analysis (PCA) is a statistical technique used to reduce the dimensionality of large datasets while preserving as much important information as possible. It performs a mathematical rotation of the data to create a new set of uncorrelated variables called principal components (PCs), which are ordered by the amount of variance explained in the data and are orthogonal (uncorrelated) to each other. Principal component analysis is used for analysis because such data typically involves thousands of gene expression variables measured across a relatively small number of samples. As each gene represents one dimension, a dataset could potentially represent a 10,000–30,000-dimensional space. Principal component analysis then reduces this high dimensionality by transforming the original gene expression variables into a smaller set of PCs that capture the majority of variation in the data. This helps researchers visualize complex expression patterns, identify clusters of samples, detect outliers, and uncover underlying biological differences between healthy and diseased states. Principal component analysis also helps reduce noise and redundancy in microarray datasets, making downstream statistical analysis and classification more reliable and efficient. In this review, the authors have reviewed current information on the generation of PCs and then subsequent use/analysis of data generated from microarray or similar large data sources.

Keywords: Background correction, Correlation matrix, Covariance matrix, Data centering, Data noise, Dimensionality, Eigenvalues, Eigenvectors, Exponential normalization, Gene expression, GEO matrices, High-throughput datasets, Infant, Log₂ transformation, Machine learning, Microarray, Neonate, Newborn, Normalization, Outliers, Preprocessing, Preprocessing of data, Principal component scores, Quantile normalization, Redundancy, Robust multi-array averages, Variation.

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KEYPOINTS

- Principal component analysis (PCA) is a statistical technique used to reduce the dimensionality of large datasets while preserving as much important information as possible.
- In microarray data, PCA is used for analysis because such data typically involves thousands of gene expression variables measured across a relatively small number of samples.
- Principal component analysis compresses data from thousands of genes to a handful of components, where the computed principal components (PCs) represent a progressively decreasing degree of variation.
- This article provides a review of current methods of generation of principal components, including preprocessing of data with normalization, log₂ transformation, and, if needed, scaling. Information is also included about centering of data, computation of covariance or correlation matrices, calculation of eigenvalues and eigenvectors, selection of PC, and analysis of results.

INTRODUCTION

Principal component analysis is a statistical technique used to reduce the dimensionality of large datasets while preserving as much important information as possible.^{1–8} It performs a mathematical rotation of the data to create a new set of uncorrelated variables called PCs, which are ordered by the amount of variance explained in the data and are orthogonal (uncorrelated) to each other.^{8,9} The PCs are ordered by the degree of variance that is explained by each.³ By keeping only the top PCs, PCA simplifies complex datasets, reduces noise, improves visualization, and can

¹Department of Pediatrics/Neonatology, Boston Children's Health Physicians Group at the Maria Fareri Children's Hospital, New York Medical College, Valhalla, New York, United States of America

²Global Newborn Society, Harrison, New York, United States of America

³GNS Forum for Transgenerational Inheritance, New York, United States of America

⁴Mongolian Association of Obstetrics, Gynecology, and Neonatology, Ulaanbaatar, Mongolia

⁵Department of Neonatology, Institute of Maternal and Child Health, Matuil, Dhaka, Bangladesh

⁶Bangladesh Neonatal Foundation, Dhaka, Bangladesh

⁷Dr. Mozib Newborn Foundation, Dhaka, Bangladesh

⁸Pioneers - Looking for Sustainable Ways to Reduce Infant Mortality, Oslo, Norway

⁹Banaras Hindu University Institute of Excellence, Varanasi, Uttar Pradesh, India

¹⁰S.A.B.R.E.E. Enrichment Academy, Saint Louis, Missouri, United States of America

¹¹The Skylar Project, Daphne, Alabama, United States of America

¹²International Society for Marginalized Lives, Harrison, New York, United States of America

¹³PreemieWorld Foundation, Springfield, Virginia, United States of America

¹⁴Carlo GNS Center for Saving Lives at Birth, Birmingham, Alabama, United States of America

¹⁵Autism Care Network Foundation, India

¹⁶Neonatology-Certified Foundation, Brooksville, Texas, United States of America

make machine learning models faster and more effective without significantly losing information.^{10,11}

In microarray/other high-throughput physiological data, PCA is used for analysis because such information typically carries thousands of gene expression variables measured across a relatively small number of samples.^{5,6,12–14} As each gene represents one dimension, and therefore, a dataset could possibly represent a 10,000–30,000-dimensional space.¹⁵ Principal component analysis reduces this high dimensionality by transforming the original gene expression variables into a smaller set of PCs that captures the majority of variation in the data.¹² This helps researchers visualize complex expression patterns, identify clusters of samples, detect outliers, and uncover underlying biological differences between health and diseased states.^{9,13,16} Additionally, PCA helps reduce noise and redundancy in microarray datasets, making downstream statistical analysis and classification more reliable and efficient.¹⁷

After the collection of a large number of data points, PCA then compresses all the information to a handful of components, where the computed PCs represent a progressively decreasing degree of variation.^{7,12,13} PC1 + PC2 can explain 30–60% of total variance, and the first 5–10 PCs capture most of the biologically-meaningful variation.⁸ Thus, the PCA compresses the data from thousands of genes to a small, manageable number of variables. In this review, we have attempted to explain the process by which PCs are generated and then used for the analysis of data generated from microarray or similar large data sources. We have combined some data from our own preliminary studies with an extensive literature search in Embase, PubMed, and Scopus.^{18,19} To avoid bias in the identification of studies, keywords were short-listed *a priori* from PubMed's Medical Subject Headings (MeSH) thesaurus.²⁰

GENERATION OF PRINCIPAL COMPONENTS

Principal component analysis is a standard exploratory step used to understand global patterns in high-throughput data such as those from microarray experiments, which might include changes in the expression of thousands of genes.^{8,12–14,17,21} By reducing the dimensionality of the data, PCA can help identify dominant patterns of gene expression, detect outliers, and reveal underlying biological variation such as differences between experimental conditions or sample groups.^{5,22,23} Principal component analysis reduces these high-dimensional data into a few principal components that capture the largest sources of variation, allowing researchers to visualize sample similarities and differences.^{5,22,23} Overall, these analytical steps can help differentiate true biological signals from experimental noise, making it an essential quality-control and exploratory step before downstream steps.^{1,8,11} Principal component analysis can also help in visualizing complex high-throughput datasets in 2–3 dimensions, making it easier for interpretation of results, assessment of data quality, and reduction of noise before applying further statistical or machine learning analyses.^{10,24}

Principal Component Analysis (PCA)

The main steps in PCA are as follows:^{1,3–5,14,21,23}

(a) Generation of principal components:

- Preprocessing of the data: Normalization, \log_2 transformation, and, if needed, scaling.
- Center the data: Subtraction of the mean of each variable.
- Compute covariance or correlation matrix: Measure relationships between variables.

¹⁷GNS Infant Nutrition Education Program, Harrison, New York, United States of America

¹⁸International Prader-Willi Syndrome Organization, Cambridge, United Kingdom

¹⁹First Breath of Life, Shreveport, Louisiana, United States of America

²⁰GNS Forum for Big Data Analytics and Machine Learning, Bengaluru, India

²¹Children's Hospital ASST Spedali Civili of Brescia, Brescia, Italy

²²Department of Pediatrics, All India Institute of Medical Sciences (AIIMS), Deogarh, Jharkhand, India

²³Department of Orthopedics, King Salman Armed Forces Hospital, Tabuk, Saudi Arabia

²⁴Department of Neonatology, King Saud bin Abdulaziz University for Health Sciences, Jeddah, Saudi Arabia

²⁵Department of Neonatology/Pediatrics, University of Guadalajara, Guadalajara, Mexico

Corresponding Author: Akhil Maheshwari, Boston Children's Health Physicians at New York Medical College/Maria Fareri Children's Hospital, Valhalla, New York, United States of America, Phone: +1-708-910-8729, e-mail: akhil@globalnewbornsociety.org

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- Calculate eigenvalues and eigenvectors: Identify directions of maximum variance.

(b) Selection of principal components: Choose components with the largest eigenvalues.

(c) Projection of data: Transform the original data into the principal component space.

(d) Interpretation of results: Analyze score and loading plots to understand patterns.

Generation of Principal Components

To transform the original variables in a dataset into PCs, the first step is to standardize the data so that each variable has a mean of zero and a standard deviation of one. This ensures that variables measured on different scales contribute equally.^{3,25} Next, the covariance (or correlation) matrix of standardized data is computed to understand how variables vary together.

- (a) Preprocessing of raw microarray data helps remove technical noise and make gene expression measurements comparable across samples.^{26,27} It typically includes background correction to eliminate non-specific signal, normalization to adjust for systematic differences between arrays, and \log_2 transformation to stabilize variance across expression levels.²⁸ Additional steps may involve probe summarization and filtering out low-quality or low-expressed genes.²⁹ Proper preprocessing ensures that downstream analyses such as PCA and differential gene expression reflect true biological variation, not artifacts introduced during sample preparation, hybridization, or scanning.^{12,30}



Table 1: Impact of background correction on PCs

<i>Without background correction</i>	<i>With background correction</i>
PCs dominated by noise	PCs reflect biology
Poor replicate clustering	Improved clustering
Artificial outliers	Reduced false outliers

PCs, principal components

Table 2: Effect of normalization on PCA results

<i>Without normalization</i>	<i>With normalization</i>
PCs dominated by intensity	PCs reflect condition differences
Replicates poorly cluster	Replicates cluster tightly
Artificial batch effects	Reduced batch effects

PCs, principal components; PCA, principal component analysis

(b) Background correction can help because raw data often contain technical noise, biases, and measurement errors that can distort the true structure of the dataset.¹¹ Background correction, along with normalization and scaling, helps ensure that the observed variation reflects meaningful biological or experimental differences rather than artifacts.³¹ Applying PCA after these preprocessing steps allows the principal components to capture genuine patterns in the data, leading to more accurate dimensionality reduction, clearer visualization, and more reliable interpretation of results (Table 1).^{3,5}

(c) Normalization is essential before performing PCA on high-throughput data.^{3,32} Principal component analysis is variance-driven, and consequently, technical inconsistency between arrays could overtake biological variation if normalization is skipped or done improperly.^{3,33} It is also needed because of potential problems arising from irregularities in labeling, scanner sensitivity, and hybridization (Table 2).^{3,22,33,34}

Exponential normalization using negative controls (NEQC) is a frequently-used preprocessing method for background correction and normalization.^{11,32} It uses the signal from negative control probes to estimate and remove background noise more accurately than simple subtraction methods. After background correction, NEQC typically applies \log_2 transformation and quantile normalization to make expression values comparable across samples.^{35,36} This approach improves data quality by reducing technical variation, stabilizing variance, and ensuring that downstream analyses such as PCA reflect true biological differences rather than experimental artifacts.

Normalization with robust multi-array averages (RMAs) can further help with technical noise, background signals, and systematic biases that can distort the true biological variation.^{9,37,38} Robust multi-array average preprocessing corrects for background, normalizes across arrays, and summarizes probe-level data into expression measures, making the data consistent and comparable.^{39,40} Conducting PCA on such preprocessed and normalized data helps detect genuine biological patterns, improves visualization, and supports more accurate clustering and downstream analyses.^{41,42}

Quantile normalization is another normalization method; it adjusts the data so that all samples have the same overall distribution of expression values, making these comparable.^{43,44} Performing PCA on normalized data ensures that the PCs capture

true biological variation rather than technical artifacts, leading to more accurate dimensionality reduction, better visualization, and reliable interpretation of patterns and relationships in the dataset.⁴⁵ Quantile normalization may need to be avoided if there are global, biologically meaningful shifts in expression or highly unbalanced experimental designs.⁴⁶ However, this situation is not seen frequently.

(d) \log_2 transformation is often combined with PCA in the analysis of gene expression data.⁴⁷ It stabilizes the variance across a wide range of expression values and reduces the impact of extreme values or skewed distributions.⁴⁸ The data become more symmetric in a normal-like distribution, which is important because PCA relies on variance to identify principal components.^{48,49} \log_2 transformation makes PCA analyses more accurate in identifying the underlying biological patterns, shows better clustering, and prevents highly-expressed outlier genes from dominating the principal components.^{47,48}

Background correction can possibly be skipped in very high-quality arrays, preprocessed data such as in public GEO matrices, or when correction increases variance in low-expression probes.⁵⁰ However, skipping background correction is generally discouraged because PCA emphasizes variance, and noise inflates variance disproportionately.³

(e) Centering of the data: For centering data, the mean of each variable is subtracted from all its values so that each variable has a mean of zero.⁸ Ensuring that a PCA will capture the variance around the average, not the absolute values, allows the analysis to focus on patterns of variation and relationships between variables instead of their raw magnitudes.⁸

(f) Covariance or correlation matrices: These are computed to quantify how variables vary together across observations.^{3,45} The covariance matrix is used when variables are on the same scale, while the correlation matrix is preferred when variables have different scales.^{3,45} The covariance matrix summarizes how pairs of variables vary together after the data have been mean-centered.⁵¹ Each diagonal element represents the variance of a variable, while off-diagonal elements represent the covariance between variables.⁵² The covariance matrix is used to compute eigenvalues and eigenvectors, which determine the principal components and the amount of variance each component explains.^{3,53}

A correlation matrix measures the standardized relationships between variables after mean-centering and scaling.^{3,53} It is particularly useful for variables measured on different scales, ensuring each variable contributes equally to the analysis. The correlation matrix is then used to compute eigenvalues and eigenvectors, which help define the PCs and measure variance.^{3,54}

(g) Eigenvalues and eigenvectors: Principal component analysis uses linear algebra to transform data into PCs. It finds these by calculating eigenvectors (directions) and eigenvalues (importance) from the covariance matrix.^{3,53} Principal component analysis selects the top components with the highest eigenvalues and projects the data onto them to simplify the dataset.

The prefix “eigen” indicates a value or direction that is characteristic of a particular transformation or matrix.⁵³ An eigenvalue is a scalar value in a square matrix; it indicates how much the direction of its corresponding eigenvector is stretched or scaled when a linear transformation is applied.^{3,53} In mathematical terms, for a matrix A , an eigenvalue λ , and a non-zero eigenvector v satisfy the equation $Av = \lambda v$.^{3,53}

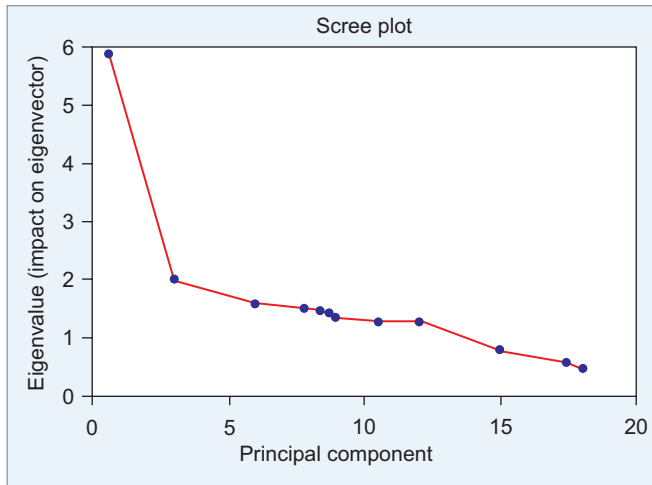


Fig. 1: Principal component analysis is an unsupervised machine learning technique that seeks to find PCs, predictor variables that explain the variation in a dataset. A scree plot shows the potency of each PC in terms of the change in the angle of the eigenvector. The prefix “eigen” indicates a scalar unit value that measures a particular vectorial transformation.

Eigenvalues are important because they reveal key properties of a transformation or dataset, stability in systems, and patterns in many scientific applications.^{3,45}

An eigenvector defines a direction of change when a linear transformation is applied to it.^{3,45,55} For a square matrix A , the equation $Av = \lambda v$ is the product of the eigenvalue λ and the direction of change defined by eigenvector v , λv , should be valid.^{55,56} In data science, eigenvectors represent the directions of maximum variance.³ The principal components are the top selected eigenvectors.^{3,17,45,53}

Selection of Principal Components

Principal component analysis should ideally be applied to background-corrected, normalized, and log-transformed data, as technical noise can otherwise unduly dominate the principal components.^{11,28} At this stage, the data are clean, comparable, and centered, allowing PCA to accurately capture meaningful patterns and sources of variation in the dataset.

Principal components are selected for the largest eigenvalues, as these selected variables should explain the greatest amount of variance in the data (Fig. 1).^{3,45} The original data are transformed into the principal component space by multiplying them with the selected eigenvectors, resulting in principal component scores that represent the data in a reduced-dimensional form.^{3,45}

Principal component scores are the coordinates of the original observations (samples) in the new PC space.^{3,57} These are obtained by projecting the impact of selected eigenvectors on centered (and possibly scaled) data.^{3,45,57} These scores summarize each observation in terms of the PCs, allowing visualization, clustering, and analysis of patterns in a lower-dimensional space while retaining most of the original variance (Fig. 2).^{3,9,22,45,57}

Principal component analysis can help filter low-expression or low-variance genes by highlighting the genes that contribute most to the variation in the dataset.^{12,58} In a gene expression analysis, genes with very low expression or little variation across samples often add noise rather than meaningful information.¹² In PCA, these

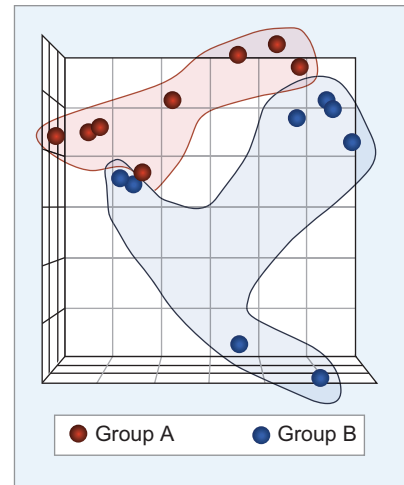


Fig. 2: Microarray profiles of two groups, A and B ($n = 8$ animals in each group). The graph is a scatter plot of the values of three PCs based on the correlation matrix of the total normalized array intensity data; each point represents one animal.

genes typically contribute very little to the principal components, making it easier to identify and focus on high-variance genes that drive biological differences. This filtering improves downstream analyses, enhances visualization, and increases the reliability of clustering or classification results.⁵⁹

CONCLUSION

Continued progress of PCA over the last several years underscores its importance in data analysis and machine learning. As datasets grow larger and more complex, PCA remains a reliable method for reducing dimensionality while preserving meaningful patterns. It is a critical tool for extracting valuable insights from high-dimensional data.

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Impact of the Ukrainian Conflict on Mothers and Young Infants Who have had to Migrate to Poland

Adrianna Frydrysiak-Brzozowska¹, Srijan Singh², Olga Adamczyk-Gruszka³, Kinga Piórkowska⁴, Adrianna Józwiak⁵

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ABSTRACT

The war in Ukraine has led to a major dislocation of the population into neighboring Poland. The conflict began in February 2014 with Russia's annexation of Crimea and escalated dramatically on February 24, 2022, when Russia launched a full-scale invasion of Ukraine. There has been widespread destruction, displacement, and humanitarian crises across the country. Millions of Ukrainians have fled their homes; over 2 million people had to flee Ukraine within 2 weeks and there have been more than 9.4 million border crossings. In this article, we have focused on the social impact of population migration, with particular attention to its effects on perinatal outcomes. Broad estimates suggest that around 2,65,000 Ukrainian women were pregnant when the war began and approximately 80,000 were expected to give birth in the first 3 months of the conflict. The Ukrainian conflict significantly affected the care of pregnant mothers—many experienced suboptimal antenatal care, underwent high levels of stress, and saw considerable uncertainty during displacement. Their infants had high needs for medical care. The arrival of large numbers of Ukrainians has led to noticeable changes in Poland's social landscape. The Polish government and society have responded to population movements from Ukraine by offering all-possible protection and wide-ranging support. Poland has received global recognition for its efforts to support Ukrainian mothers and children during the refugee crisis.

Keywords: Crimea, Donetsk, Humanitarian crises, Kharkiv, Kherson, Luhansk, Newborn, Population dislocation, Russians, Zaporizhzhia.

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KEY POINTS

- The war in Ukraine has led to a major dislocation of the population into neighboring Poland. This population movements from Ukraine to Poland can be ascribed to geographic proximity, a long-shared border, and cultural and linguistic similarities.
- In this article, we have focused on the social impact of population migration, with particular attention to its effects on perinatal outcomes. The large-scale movement of people has placed significant pressure on healthcare systems, social services, and community support networks.
- The exact figures for the number of pregnant Ukrainian women who migrated to Poland are not readily available. Broad estimates suggest that around 265,000 Ukrainian women were pregnant when the war began and approximately 80,000 were expected to give birth in the first 3 months of the conflict.
- The Ukrainian conflict has significantly affected the care of pregnant mothers. Many pregnant women experienced disrupted antenatal care, high levels of stress, and uncertainty during displacement, increasing risks for both maternal and fetal health.
- The arrival of large numbers of Ukrainians has led to noticeable changes in Poland's social landscape. The Polish government and society responded to population movements from Ukraine by offering temporary protection and wide-ranging support. Poland has received global recognition for its efforts to support Ukrainian mothers and children during the refugee crisis.

INTRODUCTION

The war in Ukraine has led to a major dislocation of the population into neighboring Poland. The conflict began in February 2014 with Russia's annexation of Crimea and escalated dramatically on February 24, 2022, when Russia launched a full-scale invasion of Ukraine.¹ There has been widespread destruction, displacement, and humanitarian crises across the country.

¹Faculty of Health Sciences, Collegium Medicum, The Masovian University in Płock, Poland; Polish Nursing Association, Płock, Poland; Global Newborn Society, Harrison, New York, United States of America

²Global Newborn Society, Harrison, New York, United States of America; Department of Neonatology, Yashoda Medicity, Ghaziabad, Uttar Pradesh, India; GNS Forum for Transgenerational Inheritance

³Department of Gynecology and Obstetrics, Collegium Medicum, Jan Kochanowski University in Kielce, Poland

^{4,5}Faculty of Health Sciences, Collegium Medicum, The Masovian University in Płock Poland

Corresponding Author: Adrianna Frydrysiak-Brzozowska, Faculty of Health Sciences, Collegium Medicum, The Masovian University in Płock, Poland; Polish Nursing Association, Płock, Poland; Global Newborn Society, Harrison, New York, United States of America, Phone: +24 3665414(216), e-mail: a.frydrysiak-brzozowska@mazowiecka.edu.pl

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Millions of Ukrainians have fled their homes; over 2 million people had to flee Ukraine within 2 weeks and there have been more than 9.4 million border crossings (Fig. 1).² There are more than 1.5 million registered refugees, of which 90% are women, children, and elderly people; the primary reasons were to escape violence, destruction, and insecurity. The war has affected civilians, infrastructure, and essential services, creating urgent needs for food, shelter, healthcare, education, and protection.^{3–5}

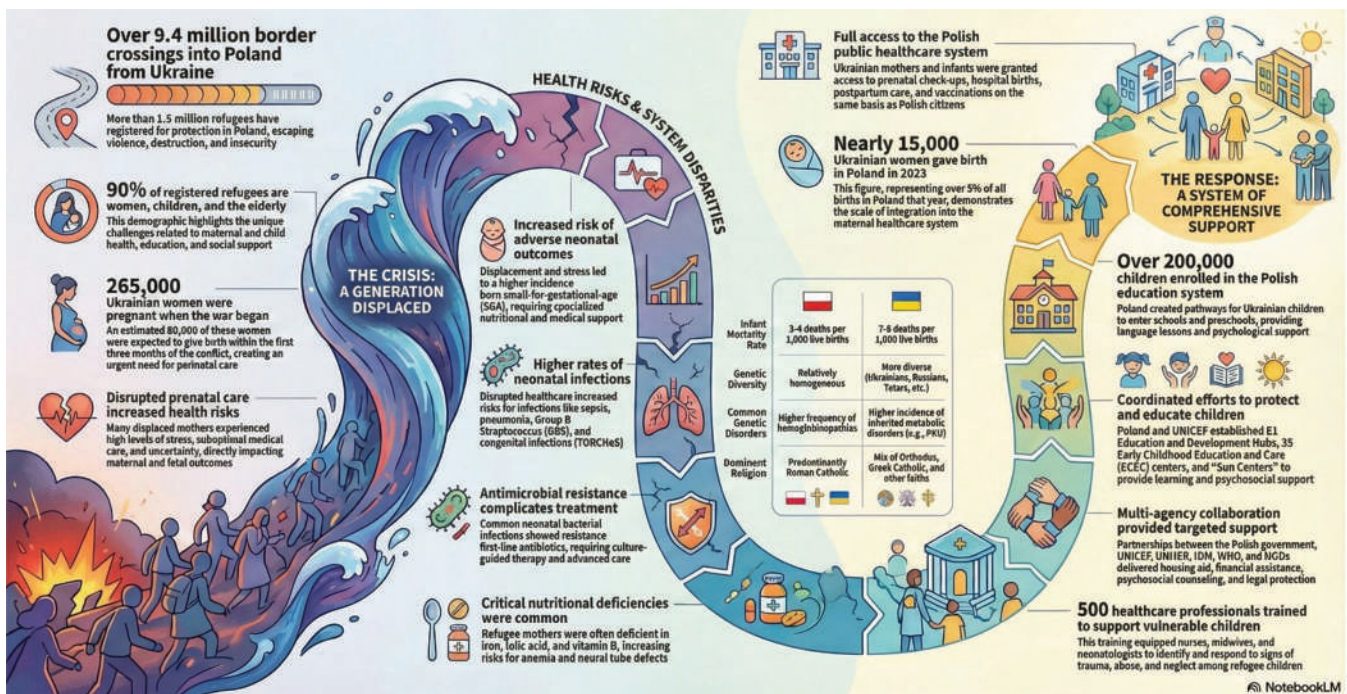


Fig. 1: Hope in displacement: Supporting Ukrainian mothers and infants in Poland. This figure has been prepared with NotebookLM (Google)

International organizations, governments, and humanitarian agencies have mobilized to provide emergency aid, support displaced populations, and respond to the social, economic, and health impacts of the conflict.

The population movements from Ukraine to Poland can be ascribed to geographic proximity, a long-shared border, and cultural and linguistic similarities. Poland is one of Ukraine's closest neighbors, allowing people to cross the border quickly and safely, often with minimal travel costs. The shared border made large-scale movement possible even in emergency conditions. In addition, similarities in language, history, and cultural traditions helped Ukrainians adapt more easily to life in Poland, reducing feelings of displacement. These factors, combined with existing Ukrainian communities in Poland, made Poland a natural and practical destination for many people leaving Ukraine. The migrants have come from multiple regions, particularly those most affected by conflict and insecurity. Many refugees originated from eastern and southern Ukraine, including areas such as Donetsk, Luhansk, Kharkiv, Zaporizhzhia, and Kherson, where military activity has been intense.⁶⁻⁸ Large numbers also left central and northern regions, including Kyiv and surrounding oblasts, due to threats of attacks or occupation. People from western regions, which were initially less affected, sometimes moved as well to join family or seek economic opportunities. The flow from these diverse regions reflects both immediate safety concerns and longer-term considerations for work, education, and family reunification. Figure 2 shows emergency mass shelter facilities established in sports halls in Poland during the initial influx of refugees from Ukraine.

In this article, we have focused on the social impact of population migration, with particular attention to its effects on perinatal outcomes. The large-scale movement of people has placed significant pressure on healthcare systems, social services, and community support networks. Understanding these effects

is essential for shaping effective health, social, and protection responses for migrant mothers and infants. Figure 3 shows the key factors influencing perinatal and neonatal outcomes among Ukrainian mothers and young infants displaced to Poland during the ongoing conflict.

Maternal Factors and Impact on Perinatal Outcomes

Migration of Pregnant Women

The exact figures for the number of pregnant Ukrainian women who migrated to Poland are not readily available. During the initial months after Russia's full-scale invasion in 2022, many of the refugees entering Poland were women of reproductive age, and a significant share were pregnant when they fled. Broad estimates suggest that around 2,65,000 Ukrainian women were pregnant when the war began and approximately 80,000 were expected to give birth in the first 3 months of the conflict.^{9,10} All these women did not stay in Poland or were counted locally, and so the statistics may not be readily usable for healthcare planning. However, nearly 15,000 Ukrainian women gave birth in Poland in 2023, constituting more than 5% of all births in the country that year, showing that many pregnant refugees accessed maternal care after arriving.^{11,12}

Care of Pregnant Mothers

The Ukrainian conflict has significantly affected the care of pregnant mothers, particularly those who were forced to flee their homes and seek safety in countries such as Poland. Many pregnant women experienced disrupted antenatal care, high levels of stress, and uncertainty during displacement, increasing risks for both maternal and fetal health. In Poland, pregnant Ukrainian women were granted access to prenatal services, including routine check-ups, ultrasounds, and hospital-based maternity care within the public health system. With support from United Nations Children's Fund (UNICEF), non-governmental organizations (NGOs), and





Fig. 2: Emergency mass shelter facilities established in sports halls in Poland during the initial influx of refugees from Ukraine (2022). Large-capacity gymnasiums and sports arenas were rapidly repurposed to accommodate displaced families, with rows of temporary camp beds and basic bedding arranged to provide short-term shelter and essential support services

Sources: Hall at ul. Sowińskiego, Szczecin (Gazeta Wyborcza Szczecin); Hall at ul. Dożynkowa, Poznań (Poznań University of Economics and Business); Wrocław (Gazeta Wroclawska)

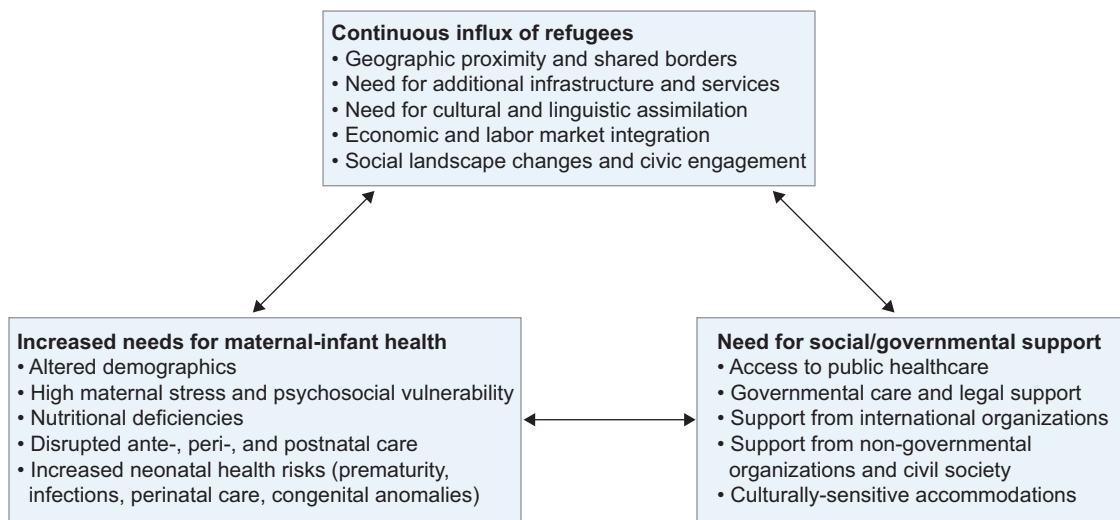


Fig. 3: Key factors influencing perinatal and neonatal outcomes among Ukrainian mothers and young infants displaced to Poland during the ongoing conflict

local authorities, services such as psychosocial support, health education, and language assistance were provided to help ensure safe pregnancies and improve maternal outcomes.¹³

The Ukrainian conflict increased the average maternal age among displaced pregnant women. Women who were already pregnant or who chose to continue planned pregnancies during displacement were often in their late twenties or thirties, reflecting

pre-existing trends of delayed childbearing in Ukraine. Younger women were more likely to postpone pregnancy due to insecurity, separation from partners, and economic uncertainty, while older women were more likely to proceed with pregnancy despite the conflict.¹⁴ As a result, healthcare providers in host countries observed a higher proportion of pregnancies among older mothers, with implications for prenatal monitoring and maternal care needs.

Maternal Health Factors

Polish and Ukrainian societies differ in several ethnic and cultural aspects. Poland is ethnically more homogeneous with most identifying themselves as ethnic Poles; Ukraine is more diverse, with significant populations of Russians, Belarusians, Crimean Tatars, and other minority groups. Language is another key difference: Polish, a West Slavic language, dominates in Poland. In Ukraine, most people speak Ukrainian, an East Slavic language, and some use Russian. Religious composition also varies; Poland is predominantly Roman Catholic. On the other hand, Ukraine has a mix of Orthodox, Greek Catholic, and other faiths.

The health statistics show considerable differences. The infant mortality rates (IMRs) are quite dissimilar between Poland and Ukraine, reflecting variations in healthcare systems and living conditions. In Poland, the IMR has been about 3–4 deaths per 1,000 live births, thanks to well-developed prenatal and neonatal care, widespread vaccination, and effective public health programs.¹⁵ In contrast, Ukraine has had a higher IMR of around 7–8 deaths per 1,000 live births, with some regions experiencing even greater challenges due to limited healthcare access, economic constraints, and the impact of conflict.^{16,17} These differences underscore the additional health risks faced by displaced Ukrainian infants in Poland, who may arrive with complications linked to disrupted prenatal care and stressful living conditions.

Poland and Ukraine differ in their levels of genetic diversity due to historical migration patterns, population size, and ethnic composition. Poland is relatively homogeneous, with the majority of the population being ethnic Poles with limited genetic variation. Ukraine, in contrast, is more genetically diverse, reflecting its larger number of ethnic groups; the society is comprised of several subgroups including Ukrainians, Russians, Belarusians, Crimean Tatars, and other minorities. There is also a history of migrations and interactions with neighboring regions. This greater genetic diversity in Ukraine can influence susceptibility to certain inherited conditions, disease prevalence, and responses to medical interventions, whereas Poland's more homogeneous population may exhibit more uniform genetic traits across the majority population.¹⁸

In both Poland and Ukraine, several genetic disorders are observed with varying frequency, influenced by population genetics, ethnic composition, and healthcare screening practices. Cystic fibrosis, congenital hypothyroidism, and phenylketonuria (PKU) are seen in both countries. Hemoglobinopathies such as beta-thalassemia, sickle cell disease, and other abnormal hemoglobin variants are seen more frequently in Poland. Ukraine has a higher incidence of inherited metabolic disorders such as phenylketonuria, galactosemia, and various amino acid, organic acid, and fatty acid oxidation disorders.¹⁹ Both countries have implemented neonatal screening programs to detect these conditions early, enabling timely interventions and improving long-term health outcomes for affected infants.

Socioeconomic Needs

The demographics of Ukrainian pregnant mothers who arrived in Poland reflect a wide range of ages, educational backgrounds, and family circumstances; most women of reproductive age are typically in their late-twenties to mid-thirties. Many were married or partnered, but a significant proportion were single or separated from family due to the conflict. Poland has provided broad acceptance and integration for these women, granting access to public healthcare, prenatal services, and social support on the same basis as Polish citizens. Combined with assistance from NGOs and

international organizations like UNICEF, this inclusive approach has helped ensure that Ukrainian pregnant mothers receive medical care, psychosocial support, and practical resources despite the challenges of displacement.

The Ukrainian conflict has heightened the vulnerability of pregnant mothers, particularly single mothers, who often arrived in Poland without family or partner support. Separation from relatives, the stress of displacement, and limited social networks increased the emotional and practical challenges of pregnancy, including childcare, healthcare access, and daily living needs. To address these gaps, Polish authorities, NGOs, and international organizations such as UNICEF provided targeted support, including counseling, social services, peer networks, and community programs to assist single mothers. These measures helped reduce isolation, ensured access to healthcare and social protection, and offered essential guidance for managing pregnancy under the difficult circumstances of displacement.

Ukrainian mothers in Poland often face difficulties such as limited access to transportation needed to reach medical centers. During displacement, many women faced long journeys, border crossings, and limited availability of safe or affordable transport, which delayed or disrupted antenatal care.²⁰ In Poland, newly-arrived pregnant women often struggled with unfamiliar transport systems, language barriers, and mobility constraints, especially in the later stages of pregnancy. To address these challenges, local authorities, NGOs, and international organizations helped arrange transportation to hospitals and clinics, provided information on public transport, and offered outreach services closer to refugee communities. Improving transport access was essential to ensuring timely prenatal check-ups, safe deliveries, and emergency obstetric care.

Nutritional Needs

Refugee mothers were at increased risk of specific nutritional deficiencies due to displacement, stress, and disrupted access to adequate food during pregnancy. Common deficiencies included iron, folic acid, and vitamin D, which are critical for maternal health and fetal development. In response, Polish healthcare providers, in coordination with NGOs and UNICEF, implemented programs to assess nutritional status, provide supplementation, and offer dietary counseling tailored to the needs of pregnant Ukrainian women.^{21,22} These interventions helped reduce risks such as anemia, neural tube defects, and poor fetal growth, supporting healthier pregnancy outcomes despite the challenges posed by conflict and displacement.

Economic Needs

Ukrainian pregnant mothers have received targeted economic support in Poland to help meet the costs associated with displacement and pregnancy. The Polish government, in coordination with local authorities and NGOs, provided financial assistance, including cash benefits, maternity allowances, and support for housing and essential needs.²³ Additional support from international organizations like UNICEF helped cover healthcare-related expenses, transport to medical facilities, and access to prenatal services. These measures have been critical in reducing financial stress, enabling pregnant mothers to access proper care, and ensuring the health and well-being of both mothers and their unborn children during the challenging circumstances of displacement.



Cultural Preferences

Immigrant mothers from Ukraine brought with them diverse religious beliefs that sometimes influenced their preferences for medical care.³ Most Ukrainian refugees identify as Orthodox or Greek Catholic, and others follow Roman Catholicism, Protestantism, or are non-religious. These beliefs affected decisions around prenatal and perinatal care, childbirth practices, and acceptance of certain medical interventions. Polish healthcare providers, supported by NGOs and organizations like UNICEF, worked to ensure culturally and religiously sensitive care, offering respectful communication, accommodation of spiritual needs, and guidance aligned with both medical standards and mothers' values. This approach helped build trust, improve healthcare access, and support positive maternal and neonatal outcomes among displaced Ukrainian mothers.

Some of these Ukrainian mothers expressed a preference regarding the religion of their healthcare providers, often seeking caregivers who shared their Orthodox, Greek Catholic, or Roman Catholic faith.²⁴ A very small proportion expressed avoidance of Jewish healthcare providers, reflecting personal, cultural, or historical sensitivities. Mostly, preferences were influenced not by religion but by comfort, trust, and the desire for culturally and spiritually sensitive care. Polish healthcare facilities, in collaboration with NGOs and organizations like UNICEF, have worked to accommodate these preferences where possible, while ensuring that all medical decisions remain guided by professional standards. By respecting maternal considerations alongside evidence-based care, providers were able to foster trust, reduce stress, and improve maternal and neonatal outcomes among displaced Ukrainian families.

Among Ukrainian mothers displaced to Poland, cultural and personal preferences regarding fetal gender have occasionally influenced pregnancy expectations, though such preferences vary widely by family and region. While most mothers prioritize the health and safety of the child above all, some may express a preference for a particular gender due to family composition, cultural traditions, or personal reasons. Polish healthcare providers, together with NGOs and organizations like UNICEF, have respected these preferences while emphasizing unbiased medical care, ensuring that fetal monitoring, prenatal support, and counseling remain focused on the well-being of both mother and child. By combining sensitivity to personal or cultural expectations with professional care standards, healthcare teams have supported positive outcomes for Ukrainian mothers and their newborns.

Risk of Prenatal Infections

The Ukrainian conflict has increased the risk of prenatal infections among pregnant mothers, largely due to disrupted healthcare services, delayed antenatal visits, and challenging living conditions during displacement.²⁵ Interruptions in routine screening and treatment for infections such as hepatitis, human immunodeficiency virus (HIV), syphilis, and other preventable conditions posed risks to both maternal and fetal health.²⁶ In host countries like Poland, pregnant Ukrainian women were integrated into prenatal care systems, where screening, treatment, and preventive services were provided according to national guidelines.²⁷ Support from international organizations and NGOs helped strengthen early detection, continuity of care, and health education, reducing the potential impact of prenatal infections on pregnancy and neonatal outcomes.

Medical Terminations of Pregnancy

Reliable, detailed figures on the number of Ukrainian medical terminations of pregnancy for medical vs other reasons during the conflict period are not systematically reported in publicly available official data. However, national health statistics from Ukraine during the full-scale invasion period provide some context. According to the Ukrainian Ministry of Health's Public Health Center, Ukrainian women underwent approximately 90,000 abortions over the first 2 years of the full-scale invasion (2022–2023), based on registered procedures. This figure includes both spontaneous pregnancy losses (miscarriages) and medically-performed terminations, whether for health indications or other reasons.²⁸ These numbers total represents a decline compared with prewar years but reflects ongoing reproductive health needs amid war disruptions. In 2023, there were about 45,000 abortions were recorded in Ukraine, down slightly from 2022, though experts caution that official data may undercount procedures due to population displacement, disrupted health services in conflict zones, and unregistered or out of country procedures not captured in Ukrainian statistics.²⁹ These statistics do not break down terminations by specific medical indication, and there is no comprehensive international dataset that isolates conflict related medical terminations (such as those due to fetal anomaly or maternal health risk) separately from routine reproductive care. The available totals reflect all legally recorded terminations and spontaneous losses during the war affected years rather than a distinct count of conflict driven medical terminations.

Number of Ukrainian Women Who Gave Birth in Poland

In 2023, nearly 15,000 Ukrainian women gave birth in Poland, making Ukrainian births a significant portion of all live births that year.^{12,30} These figures reflect births after arrival rather than the specific count of neonates transported into Poland immediately after birth, they show that a substantial number of Ukrainian infants have been part of the refugee flows and have entered the Polish healthcare and protection systems as newborns or young children.

Maternal Postpartum Care

The Ukrainian conflict has had a notable impact on maternal postpartum care in Poland, as many displaced mothers arrived shortly before or after giving birth. Disruption, stress, and separation from family support networks increased the need for comprehensive postpartum services, including medical follow-up, mental health support, and guidance on infant care.³¹ Poland's healthcare system provided Ukrainian mothers with access to postpartum check-ups, breastfeeding support, and neonatal care on the same basis as Polish citizens. With additional support from UNICEF and NGOs, services such as psychosocial counseling, parenting education, and community-based support were strengthened to address the complex physical and emotional needs of mothers during the postpartum period.

IMPACT OF PERINATAL FACTORS ON NEONATAL OUTCOMES

Need for Neonatal Transportation to Better-equipped Hospitals

There are no comprehensive official figures specifically on the number of Ukrainian neonates transported into Poland as

newborns, but related data on births to Ukrainian refugee mothers in Poland provides a useful context. From the start of the war in February 2022 through the first part of the refugee response, thousands of Ukrainian infants were born in Polish hospitals after their mothers arrived as refugees. For example, between February 24, 2022 and August 31, 2022, approximately 4,537 newborns were reported born in Poland to Ukrainian mothers, and other estimates put the number of Ukrainian newborns born in Polish hospitals in that period at several thousand.¹²

Needs for Neonatal Intensive Care

Most publicly available transport statistics focus broadly on medical evacuations or refugee flows. Data on medical evacuation programs, such as Ukraine's MedEvac initiative have reported that over 5,000 patients were transported abroad for specialized care but these figures are not broken down by specific medical conditions.^{32,33} This initiative is a humanitarian medical evacuation program designed to provide urgent care to critically-ill patients who cannot access necessary treatment locally due to the conflict. Individual cases of highly vulnerable infants being moved for urgent treatment have been reported but no comprehensive official statistics are available about transports for serious conditions such as prematurity, birth asphyxia, sepsis, or congenital anomalies. Some individual cases of infants with complex multisystem congenital conditions being evacuated have been reported as part of humanitarian and medical coordination efforts, but these reports still remain anecdotal and have not yet been formally counted.

The Ukrainian conflict has affected the incidence of infants born small-for-gestational age (SGA) among the refugee populations. Displacement, stress, disrupted prenatal care, and limited access to adequate nutrition and medical monitoring during pregnancy increased the risk of growth restriction *in utero*.^{34,35} Upon arrival in Poland, many infants were assessed through neonatal and pediatric services, where early detection of SGA allowed for timely interventions, including nutritional support and monitoring for potential complications. Support from Polish healthcare providers, UNICEF, and NGOs has been essential in addressing these risks, ensuring that affected infants receive appropriate care to promote healthy growth and development despite the challenges of displacement.¹³

Neonatal Infections

Among Ukrainian infants, especially those displaced to Poland, certain neonatal infections have been frequently observed due to disrupted prenatal care, stressful living conditions, and limited early healthcare access. Common infections include sepsis and bloodstream infections, respiratory infections such as pneumonia, gastrointestinal infections, skin, and soft tissue infections.

Group B streptococcus (GBS) has been identified as a significant cause of neonatal infections among Ukrainian infants, particularly in those born prematurely or with low birth weight.^{36–39} Group B streptococcus can lead to serious conditions such as sepsis, pneumonia, and meningitis, contributing to morbidity and mortality in newborns. Although exact country-specific statistics for Ukrainian infants during the conflict are limited, studies from similar Eastern European populations suggest that GBS is one of the leading bacterial pathogens in neonatal infections, accounting for a substantial proportion of early-onset sepsis cases. In Poland, healthcare providers caring for displaced Ukrainian infants have prioritized GBS screening, early antibiotic treatment,

and preventive protocols to reduce the risk and impact of these infections.

Neonatal bacterial infections among Ukrainian infants have shown concerning levels of antimicrobial resistance, complicating treatment and increasing the risk of severe outcomes. Common pathogens such as *Escherichia coli*, *Klebsiella* species, and *Staphylococcus aureus*, including methicillin-resistant staphylococcus aureus (MRSA) strains, have been reported with resistance to first-line antibiotics. Contributing factors include disrupted healthcare systems, limited access to timely prenatal and neonatal care, and prior inappropriate or incomplete antibiotic use during displacement. In Poland, clinicians caring for displaced Ukrainian neonates have emphasized culture-guided therapy, infection control measures, and close monitoring, often in collaboration with pediatric infectious disease specialists, to effectively manage resistant infections while minimizing the spread of drug-resistant bacteria.

Some infants may need to be tested for congenital infections such as the Toxoplasmosis, Rubella, Cytomegalovirus, Herpes, and Syphilis (TORCHeS). Premature and low-birth-weight infants are particularly vulnerable.^{40,41} Polish healthcare providers, with support from UNICEF and NGOs, have focused on early screening, timely treatment, and preventive measures such as hygiene promotion, breastfeeding support, and vaccination to reduce the incidence and complications of these infections.

The medical needs of premature Ukrainian infants in Poland often differ from those of locally-born Polish preterm infants due to the effects of displacement and disrupted prenatal care. Many Ukrainian infants experienced limited or interrupted maternal healthcare, higher rates of maternal malnutrition, and exposure to stress or infections during pregnancy, increasing the risk of low birth weight, growth restriction, and neonatal complications. They may also have incomplete vaccination and higher susceptibility to sepsis or other infections.⁴² As a result, Ukrainian premature infants frequently require additional screening, infection prevention, nutritional support, and specialized follow-up care compared with Polish infants, even though both groups share core needs such as respiratory support, thermoregulation, and monitoring for prematurity-related complications.

Congenital Anomalies

The neonatal congenital anomalies such as cardiac defects, neural tube defects, cleft lip and palate, and musculoskeletal malformations are broadly similar between both countries. Poland has established a comprehensive prenatal screening and neonatal diagnostic programs, enabling early detection through ultrasound, genetic testing, and newborn examinations. Early identification allows timely medical or surgical interventions, counseling, and long-term management, which significantly improve outcomes for affected infants. Public health initiatives, including folic acid supplementation and maternal care programs, have also contributed to reducing the incidence of certain preventable congenital anomalies in the population.

Primary Care for Infants

The Ukrainian conflict has significantly affected access to primary care for infants in Poland, as large numbers of displaced families entered the country with urgent health needs. Many Ukrainian infants required immediate registration with primary healthcare providers to access routine check-ups, vaccinations, and developmental monitoring. Poland integrated refugee children



into its public healthcare system, granting them access to primary care on the same basis as Polish citizens. With support from UNICEF and NGOs, primary care services were expanded through outreach, language assistance, and training for healthcare workers. These measures helped ensure continuity of care for infants, despite the increased demand on Poland’s healthcare system.

Neonatal Vaccine Coverage

The Ukrainian conflict has had a significant impact on vaccination coverage for infants and young families in Poland. Many Ukrainian children arrived with disrupted or incomplete immunization schedules due to the breakdown of healthcare services during the war and displacement. In response, Polish health authorities, in collaboration with UNICEF and other partners, integrated refugee children into the national vaccination program, providing free access to routine and catch-up immunizations.¹³ Outreach campaigns, information in Ukrainian, and support from local health centers helped parents understand vaccination schedules and overcome barriers such as language and system unfamiliarity.⁴³ These efforts were essential in protecting infants and young children from vaccine-preventable diseases and maintaining public health in host communities.

YOUNG UKRAINIAN FAMILIES HAVE NEEDED CONSIDERABLE SOCIAL SUPPORT

Many young migrant families need support. Under temporary protection arrangements, they were allowed to stay legally in the country without applying for traditional asylum. They were given rights to work, access healthcare, enroll children in schools, and receive social assistance. Registration systems helped Ukrainians obtain identification numbers, which were essential for accessing services and employment. These protections reduced vulnerability and helped displaced people achieve a level of stability and safety while living in Poland.

Ukrainians who moved to Poland were provided with access to public services and community support (Fig. 4). They were entitled to healthcare on the same basis as Polish citizens, including emergency treatment, primary care, and specialist services. Psychological support was also offered to help people cope with trauma caused by war and displacement. In addition, social care services supported vulnerable groups. Alongside state services, non-governmental organizations and volunteers played an important role in providing everyday care, guidance, and assistance to Ukrainians adjusting to life in Poland.



Fig. 4: Reception, coordination, and community support services for displaced Ukrainian families in Poland (2022). (Top left) Crowded railway station concourse adapted to receive newly arrived refugees, with volunteer registration and information desks; (Top right) On-site assistance point displaying “Solidarni z Ukrainą” (“Solidarity with Ukraine”) signage, providing guidance, transportation coordination, and humanitarian information; (Bottom left) Designated child-friendly space within a reception facility offering supervised play and psychosocial support; (Bottom right) Volunteer-run donation and distribution center organizing clothing, toys, and essential supplies for displaced families. These images illustrate the rapid mobilization of civil society, municipal authorities, and humanitarian organizations to provide immediate reception, protection, and basic services during the acute phase of displacement

Sources: Hall at ul. Sowińskiego, Szczecin (Gazeta Wyborcza Szczecin); Hall at ul. Dożynkowa, Poznań (Poznań University of Economics and Business); Wrocław (Gazeta Wroclawska)

Young siblings in these families were given access to formal education within the Polish school system. Poland has developed pathways for more than 2,00,000 Ukrainian children to enroll in formal schools and preschools.^{44–46} These pathways include preparatory classes, Polish language lessons, and support from teaching assistants to help children adapt to the curriculum.¹³ Schools have also offered psychological and social support to address the emotional impact of displacement. By creating flexible and inclusive education programs, Poland has ensured that Ukrainian children can continue their learning, maintain a sense of normalcy, and integrate more easily into Polish society. Nearly 2,60,000 children have been supported with specialized early childhood development, Polish language learning or digital learning in dedicated hubs for children have helped, including children with disabilities. Nearly 5,000 Polish teachers and assistants have been trained. About 17,000 digital tablets and 1,400 computers have been provided to bridge learning gaps. Over 3,50,000 children in 2,220 education institutions, including schools, community centers, daycares, and preschools, have been supported with learning materials. These investments in the Polish system have been provided to whole classrooms, schools, and preschools, meaning Polish children have also benefitted in addition to their Ukrainian peers. Universities also opened opportunities for Ukrainian students by offering fee waivers, scholarships, and flexible admission procedures. These measures aimed to reduce disruption to education and support the long-term integration of Ukrainian learners in Poland.

Housing support was provided through both government programs and community initiatives. At the beginning of the crisis, many were accommodated in reception centers, sports halls, and temporary shelters. The Polish government later introduced financial assistance for host families and subsidies to help Ukrainians rent private accommodation. Local authorities worked to match refugees with available housing, while charities and volunteers helped find longer-term solutions. Although housing shortages remained a challenge, this support helped many Ukrainians secure safe and stable places to live in Poland.

Polish courts have appointed temporary guardians for unaccompanied Ukrainian children to ensure their safety and well-being. These guardians, often volunteers, or social workers, were legally responsible for protecting the children's rights, making decisions about their care, and helping them access education, healthcare, and social services. This system provided essential oversight for children who arrived without parents or adult relatives, preventing neglect or exploitation. By assigning temporary guardians, Poland aimed to offer a stable and supportive environment for vulnerable young refugees while longer-term solutions were arranged.⁴⁷

IMPACT ON POLISH SOCIAL AND ECONOMIC NEEDS

The arrival of large numbers of Ukrainians has led to noticeable changes in Poland's social landscape. Ukrainian communities now form an important component of Polish cities and towns, influencing everyday life through language, culture, and traditions. Schools, workplaces, and public services have become more diverse, requiring greater emphasis on inclusion and integration. At the same time, Polish society has seen strong civic engagement, with volunteers and organizations working to support newcomers. While challenges such as housing pressure and service demand

have emerged, the increased diversity has also strengthened social ties and cultural exchange within Poland.

The arrival of large numbers of Ukrainians has changed Poland's economic landscape in several ways. Many Ukrainians have entered the labor market, helping to address labor shortages in sectors such as construction, manufacturing, healthcare, and services. Their participation has increased overall workforce supply and contributed to economic activity and tax revenues. At the same time, government spending on social support, housing, and public services has risen, creating short-term financial pressure. In the longer term, the integration of Ukrainians into the workforce has the potential to support economic growth and strengthen Poland's economy.^{48,49}

The influx of Ukrainian people has placed considerable pressure on Poland's public services and infrastructure. Hospitals, schools, housing systems, and transportation networks now face increased demands, requiring rapid adaptation and expansion. Local governments have had to allocate additional funds and resources to meet the needs of refugees, while social services and NGOs worked to provide immediate support. The sudden population rise also created challenges in employment, language access, and community integration. Despite these pressures, Poland has managed a large-scale humanitarian response, balancing urgent needs with longer-term planning with some success.

MOVEMENT OF POLISH IMMIGRANTS BACK TO UKRAINE OR TO OTHER SCHENGEN AREAS

Some Ukrainians who moved to Poland have since returned to Ukraine or relocated to other European countries. As conditions in certain parts of Ukraine stabilized, some people chose to go back to reunite with family or rebuild their lives. Others moved on to other Schengen countries such as Germany, Czechia, or Italy in search of better job opportunities, long-term housing, or family connections. Changes in personal circumstances, employment prospects, and levels of support across Europe have influenced these decisions, leading to a more fluid pattern of movement rather than permanent settlement in one country.

The Polish government and society responded to population movements from Ukraine by offering temporary protection and wide-ranging support. Ukrainians arriving in Poland were granted legal status that allowed them to stay, work, and access public services. The government provided access to healthcare, education for children, and social benefits, while local authorities helped with accommodation and registration. At the same time, Polish citizens, charities, and volunteer groups played a major role by offering housing, food, transportation, and donations. This combined state and community response helped millions of Ukrainians settle more safely and quickly in Poland during the crisis.

Poland has worked closely with UNICEF to support Ukrainian children affected by displacement. Together, they have focused on ensuring access to education, healthcare, and psychosocial support for young refugees. United Nations Children's Fund has helped provide learning materials, safe spaces, and programs to address trauma and emotional well-being. Coordination with Polish authorities has also strengthened child protection systems, including assistance for unaccompanied and vulnerable children. This collaboration has been essential in helping Ukrainian children adapt to life in Poland and continue their development despite the disruption caused by conflict. Around 1,38,000 aid packages have been provided to individuals and families through our joint work with municipalities and local NGOs.^{13,50}



GLOBALY-COORDINATED EFFORTS

Poland has received global recognition for its efforts to support Ukrainian mothers and children during the refugee crisis. The country's comprehensive response, including access to healthcare, education, housing, and social services, has been recognized by international organizations and governments. Poland's policies ensured that mothers and children could find safety, maintain their well-being, and continue their daily lives despite displacement. Collaborative initiatives with organizations such as the UNICEF and local NGOs have further strengthened this support.

United Nations Children's Fund has helped the Polish government and NGOs to establish 61 Education and Development Hubs across the country. These hubs provide Ukrainian children with access to formal and non-formal education, language support, and psychosocial services.^{13,51} They serve as safe spaces where children can continue learning, participate in creative and recreational activities, and receive guidance to help them integrate into Polish schools. By combining government resources, NGO expertise, and UNICEF support, these hubs have helped displaced children maintain their education and well-being during the crisis.

Early Childhood Education and Care (ECEC) centers have helped support Ukrainian children affected by displacement. At present there are 35 such centers; these provide preschool-aged children with safe learning environments, early education programs, and opportunities for social interaction.^{13,51} They also offer language support, psychosocial care, and activities that help children cope with the stress of displacement. By expanding early childhood services, Poland has helped ensure that young Ukrainian children can continue their development, build essential skills, and adapt more smoothly to life in a new country.

Poland has developed several models to support Ukrainian pregnant mothers, focusing on education, development, therapy, and psychosocial well-being. These programs provide prenatal care, guidance on maternal and child health, and access to medical services. They also offer psychosocial support, including counseling, stress management, and peer support groups, to help mothers cope with the challenges of displacement. Educational workshops and parenting programs help expectant mothers prepare for childbirth and early child-rearing in a new environment. By combining health, learning, and emotional support, these initiatives aim to protect the well-being of both mothers and their children.

United Nations Children's Fund-supported Sun Centers currently support about 10,000 children in Krakow. These provide safe and welcoming spaces for Ukrainian children and families displaced by the conflict. These centers offer educational activities, psychosocial support, and recreational programs that help children cope with trauma and maintain a sense of normalcy.⁵⁰ They also provide guidance and resources for parents, including information on healthcare, schooling, and social services. By combining learning, play, and emotional support, the Sun Centers help Ukrainian families adjust to life in Poland while promoting children's well-being and development.

EFFORTS OF THE POLISH GOVERNMENT

Ukrainian children escaping conflict are particularly vulnerable to violence, exploitation, and abuse, making specialized care essential. In response, Poland has trained around 500 healthcare professionals—including nurses, midwives, and neonatologists—across the country. This training equips medical staff to identify and respond to signs of trauma, abuse, or neglect, while providing age-

appropriate healthcare and psychosocial support. By strengthening the skills of healthcare workers, Poland aims to protect displaced children, ensure their well-being, and provide safe, informed care during a highly vulnerable time.

The Polish government worked closely with municipalities in areas with high concentrations of refugees to reach out to the Ukrainian population. Local authorities helped coordinate registration, access to healthcare, education, housing, and social services, ensuring that displaced families received timely assistance. Municipalities also collaborated with NGOs, volunteers, and international organizations to provide information, support, and resources, helping refugees integrate into local communities and access essential services efficiently.

In spring–summer 2022, the Polish government and UNICEF reached out to more than 5,000,000 Ukrainian refugees to promote immunization, child health, and overall well-being. Working in partnership with local municipalities and NGOs, they provided information on vaccination schedules for poliomyelitis and hepatitis A, access to healthcare services, and guidance on preventive care. These efforts helped ensure that displaced children received necessary immunizations, regular check-ups, and medical support despite the disruption caused by conflict. By combining government resources, UNICEF expertise, and community networks, Poland strengthened public health protection for a large refugee population.⁵⁰

Polish governmental bodies, institutions, local administrations, and grassroots civil society organizations have collaborated with the UN to strengthen policies and systems supporting Ukrainian mothers and infants. This partnership focused on improving access to healthcare, education, psychosocial services, and social protection for displaced families. Efforts included developing care programs, training healthcare professionals, and creating safe spaces for mothers and children. These activities were particularly prominent in major cities such as Krakow, Warsaw, and Gdansk, where large numbers of refugees arrived, ensuring coordinated support and effective delivery of essential services.

The Polish Ministry of Family and Social Policy and the Ministry of Education and Science (MoES) collaborated with UNICEF to ensure the protection, education, and health of Ukrainian mothers and infant refugees.^{52,53} This partnership focused on providing access to healthcare services, early childhood education, and psychosocial support, as well as safeguarding children from exploitation and abuse. By coordinating policies, programs, and resources, the ministries and UNICEF strengthened systems to meet the specific needs of displaced families, ensuring that mothers and infants could receive comprehensive care and support during their time in Poland.

Poland worked jointly with United Nations High Commissioner for Refugees (UNHCR) and a local NGO Empowering Children Foundation (Fundacja Dajemy Dzieciom Siłę) to support the Child Protection Working Group. This collaboration aimed to strengthen systems and policies to protect Ukrainian children from violence, exploitation, and abuse.⁵⁴ Through coordinated efforts, the group provided guidance, training, and resources to frontline workers, while ensuring that child protection services were accessible and responsive. By combining international expertise, local knowledge, and government support, the initiative enhanced the safety and well-being of displaced children across Poland.

Polish organizations work closely with UNICEF to support the Basic Needs and Health Sectors, aiming to harmonize the country-

wide response for refugee infants and children. Their efforts focus on ensuring access to quality, inclusive education within the national school system, as well as through informal education initiatives. At the same time, they strengthen social protection mechanisms to address children's health, safety, and overall well-being. By coordinating services across education, health, and social sectors, these partnerships have helped create a comprehensive and consistent support system for Ukrainian refugee children.

Poland has worked closely with UNICEF to respond to the urgent needs of Ukrainian refugees and to scale up emergency responses. Together, they have expanded access to healthcare, education, child protection, and psychosocial support, while providing emergency supplies and resources to families in crisis. This collaboration also involves training frontline workers, strengthening national systems, and coordinating with local authorities, NGOs, and community networks. By scaling up these efforts, Poland and UNICEF have been able to deliver timely and effective assistance to a large number of displaced children and families across the country.

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In other efforts, the Polish government has also facilitated coordination between various government entities and the UNHCR, International Organization for Migration (IOM), World Health Organization (WHO), and International Rescue Committee (IRC). By creating clear communication channels, joint planning mechanisms, and shared operational frameworks, the government ensured that resources, information, and services were effectively coordinated. This collaboration minimized duplication, improved efficiency, and allowed humanitarian organizations to complement state-led initiatives, providing comprehensive support in areas such as protection, health, education, and social services for Ukrainian refugees.

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GUIDANCE FROM VARIOUS MULTINATIONAL ORGANIZATIONS

The European Union (EU)'s legal and regulatory framework, combined with Poland's country-specific practices, required a thorough understanding of the rules of engagement and the operational context for the refugee response. Humanitarian actors, government agencies, and NGOs needed to navigate EU asylum policies, temporary protection directives, and national regulations to provide effective support. This included understanding eligibility for services, legal status, and protection rights for refugees, as well as coordinating across multiple institutions and sectors. A clear grasp of both EU-wide and local procedures was essential to ensure social assistance, for healthcare, education, and social protection, was delivered efficiently and in compliance with legal requirements.

United Nations Children's Fund has been able to tap into the capacity of the Polish national and regional governments, combining it with its own technical expertise to strengthen the refugee response. By working alongside government institutions, it has helped design and implement programs in education, health, child protection, and social services. This approach has helped scale up emergency programs, such as access to schools, early childhood care, vaccinations, and psychosocial support, while leveraging the capacity and expertise of local authorities. Using the state's service delivery systems ensured that refugee assistance was integrated, sustainable, and aligned with national structures. This collaboration has also promoted efficient use of existing infrastructure, personnel, and administrative systems. The partnership has ensured that interventions were both locally feasible and aligned with international standards, maximizing the impact of assistance for Ukrainian children and families in Poland.

United Nations Children's Fund Poland have partnered with 12 municipalities that host around 75% of the total Ukrainian refugee population in the country.⁵⁶ Through this collaboration, UNICEF supported local authorities in providing education, healthcare, psychosocial services, and child protection programs. The partnership helped municipalities coordinate resources, train staff, and create safe spaces for children and families. By focusing on areas with the highest concentration of refugees, these initiatives maximized impact and ensured that displaced Ukrainians received timely and effective support.

United Nations Children's Fund Poland has also scaled up the delivery of humanitarian support to meet the urgent needs of Ukrainian refugees. This included strengthening the capacities of frontline responders, providing emergency supplies, and mobilizing



human resources to assist children and families. United Nations Children's Fund worked to support national systems, ensuring that healthcare, education, and social services could cope with increased demand. These efforts were carried out in close coordination with the Polish government, other UN agencies, the Polish National Committee (NatCom), as well as youth and community networks. By combining resources, expertise, and local knowledge, UNICEF helped deliver timely and effective assistance to those most affected by the crisis.¹³

Facilitated coordination between various units of the Polish government has helped streamline the efforts in refugee response with leading organizations such as UNHCR, IOM, WHO, and IRC. By creating clear communication channels, joint planning mechanisms, and shared operational frameworks, the government ensured that resources, information, and services were effectively coordinated. This collaboration minimized duplication, improved efficiency, and allowed humanitarian organizations to complement state-led initiatives, providing comprehensive support in areas such as protection, health, education, and social services.

GOVERNMENTAL BUDGETARY PRIORITIZATION FOR MOTHER-INFANT CARE

Poland allocates a substantial portion of its national health budget to maternal and child health, including prenatal care, neonatal services, vaccinations, and specialized care for premature or high-risk infants, ensuring broad access and high-quality services. In contrast, Ukraine's healthcare budget for infants has historically been more limited, with fewer resources for prenatal screening, neonatal intensive care, and preventive programs, and the ongoing conflict has further strained funding and service delivery. These differences mean that while Polish infants generally benefit from well-supported healthcare systems, Ukrainian infants, particularly those in conflict-affected areas, face greater challenges in accessing timely and comprehensive medical care.

EPILOGUE

The arrival of Ukrainian infants and young families in Poland has highlighted both the resilience of displaced populations and the strength of coordinated humanitarian and healthcare responses. Despite the immense challenges posed by conflict, displacement, and disrupted prenatal and neonatal care, Polish authorities, healthcare providers, NGOs, and international organizations such as UNICEF have worked together to provide comprehensive support—ranging from medical care, vaccination, and neonatal interventions to psychosocial, educational, and social services.⁵⁷ Ukrainian infants, including those born prematurely or with congenital or infectious conditions, have benefited from timely interventions, specialized care, and protective services that have mitigated many of the risks associated with displacement. While ongoing efforts are needed to ensure continuity of care and long-term development, the experience underscores the importance of preparedness, collaboration, and culturally sensitive approaches in safeguarding the health and well-being of the youngest and most vulnerable refugees.

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Calprotectin: An Overview

Akhil Maheshwari^{1–20}, Taherah Mohammadabadi^{2,21}, Colin Michie^{2,22–25}

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ABSTRACT

Calprotectin is a heterodimeric calcium- and zinc-binding protein comprised of two calcium-binding peptides, *S100A8* and *S100A9*. It is expressed mainly in activated neutrophils and macrophages and serves as a sensitive biomarker of inflammation. It promotes innate immunity by limiting microbial growth through depletion of essential metals such as zinc and manganese, and by activating signaling pathways involving the toll-like receptor 4 (TLR4) and the receptor for advanced glycation end (RAGE) products. Neonates depend to a great extent on innate immunity for survival and can show higher calprotectin levels than older children and adults. In addition to the gastrointestinal tract, calprotectin is detectable in all anatomical compartments, whenever and wherever neutrophils or activated macrophages are recruited. High circulating levels of calprotectin are detectable during systemic inflammatory response syndrome, further highlighting its important contribution to immune responses. In patients with gut disorders, fecal calprotectin is a useful noninvasive marker that can help differentiate inflammatory bowel conditions from functional gastrointestinal disorders, assess the severity of disease activity, and monitor therapeutic responses. Calprotectin has been viewed as a highly conserved component of the innate immune system for over 500 million years. Clinically, it is a valuable diagnostic and monitoring tool that enhances decision-making while reducing reliance on invasive investigations. In this article, we present our current understanding of calprotectin expression, evolution, and clinical importance. We have added data from our own preclinical studies to an extensive review of the literature using the databases PubMed, EMBASE, and Scopus.

Keywords: Adenine complex ATP-binding cassette, Alarmins, ATP-binding cassette, *Calgranulin-A*, *Calgranulin B*, Citrullination, Cytosolic protein, CzcD, EF-hand, Electrostatic interactions, Filaggrin, Heterodimer geometry, High mobility group box 1, Hydrophobic interactions, Inflammatory stimuli, Manganese transport protein H, Myeloid-related protein-14, Myeloid-related protein-8, Neonatal intensive care unit, Neonate, Neutrophil extracellular trap, Paralogous proximity, Periplasmic binding protein, Pneumococcal surface antigen B, C, and A, Pseudopaline, Receptor for advanced glycation end products, *S100A8*, *S100A9*, *Salmonella* iron transporter ABCD, Siderophores, Transition metal sequestration activity, Zinc uptake regulator, Zincophores, Zinc uptake ATP-binding box complex.

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KEYPOINTS

- Calprotectin is a multifunctional cytosolic protein complex expressed in neutrophils, monocytes, macrophages, dendritic cells, keratinocytes, and squamous mucosal epithelial cells and is upregulated in response to inflammatory stimuli.
- Calprotectin is a heterodimeric protein complex comprised of two calcium-binding protein components, *S100A8* and *S100A9*. It promotes innate immunity by limiting microbial growth by depleting essential metals such as zinc and manganese, and inducing inflammatory responses by activating the toll-like receptor 4 (TLR4) and the receptor for advanced glycation end (RAGE) products.
- The antimicrobial activity of calprotectin has at least three mechanisms: (1) metal sequestration; (2) electrostatic interactions between its cationic surface regions and the anionic phospholipids in microbial membranes; and (3) hydrophobic interactions with microbial membranes.
- Calprotectin is a highly conserved component of the innate immune system originating from an ancestral protein in jawless fish about 500 million years ago.
- Neonates typically have higher serum ($0.79 \pm 0.33 \mu\text{g/mL}$) and fecal calprotectin ($0.34 \pm 0.68 \text{ mg/gm stool}$) concentrations than those seen in adults. Levels gradually decrease with age and stabilize as the immune system undergoes maturation. Infants with sepsis, necrotizing enterocolitis (NEC), hypoxic stress, or infection show higher calprotectin levels in blood and stool.

¹Department of Pediatrics/Neonatology, Boston Children's Health Physicians Group at the Maria Fareri Children's Hospital, New York Medical College, Valhalla, New York, United States of America

²Global Newborn Society, Harrison, New York, United States of America

³GNS Forum for Transgenerational Inheritance, New York, United States of America

⁴Mongolian Association of Obstetrics, Gynecology, and Neonatology, UlaanBaatar, Mongolia

⁵Neonatology, Institute of Child Health, Matuil, Dhaka, Bangladesh

⁶Bangladesh Neonatal Foundation, Dhaka, Bangladesh

⁷Dr. Mozib Newborn Foundation, Dhaka, Bangladesh

⁸Pioneers—Looking for Sustainable Ways to Reduce Infant Mortality, Oslo, Norway

⁹Department of Neonatology/Pediatrics, Tufts University School of Medicine, Boston, Massachusetts, United States of America

¹⁰Banaras Hindu University Institute of Excellence, Varanasi, Uttar Pradesh, India

¹¹S.A.B.R.E.E. Enrichment Academy, Saint Louis, Missouri, United States of America

¹²The Skylar Project, Daphne, Alabama, United States of America

¹³International Society for Marginalized Lives, Harrison, New York, United States of America

¹⁴PreemieWorld Foundation, Springfield, Virginia, United States of America

¹⁵Carlo GNS Center for Saving Lives at Birth, Birmingham, Alabama, United States of America

INTRODUCTION

Calprotectin is a multifunctional cytosolic protein complex expressed variably across different cell types.^{1–4} It is expressed in neutrophils, monocytes, macrophages, dendritic cells, keratinocytes, and squamous mucosal epithelial cells, and is upregulated in response to inflammatory stimuli.⁵ There are two calcium-binding protein components: (1) soluble in 100% saturated ammonium sulfate solution-A8 (*S100A8*) [named variously as *calgranulin-A*, migration inhibitory factor-related protein-8, or myeloid-related protein-8 (MRP8)] and (2) *S100A9* (*calgranulin B* or MRP14).^{6–10} The two genes are highly conserved across all vertebrates, reflecting strong underlying evolutionary pressures to maintain metal-binding and antimicrobial functions; both are crucial for maintaining the innate immune and intestinal inflammatory responses.^{11,12} *S100A8* and *S100A9* encode proteins with calcium-binding motifs and residues critical for transition metal sequestration, which together enable calprotectin to form functional heterodimers and heterotetramers.^{13–16} And genetic variation, such as single-nucleotide polymorphisms, can influence calprotectin levels and activity.^{17–19}

Calprotectin promotes innate immunity by (1) limiting microbial growth by depleting essential metals such as zinc (Zn) and manganese (Mn) and (2) inducing inflammatory responses by activating the TLR4 and the RAGE products.^{20–24} It also works synergistically with various alarmins that carry damage-associated molecular patterns (DAMPs), such as the high mobility group box 1 (HMGB1; Fig. 1).^{25–28} Not surprisingly, as an antimicrobial peptide, calprotectin inhibits the growth of many gram-positive and gram-negative bacteria, and fungi such as *Candida* spp.²⁹ Neonates, who depend on innate immunity for survival, often show higher calprotectin levels than older children and adults; the median calprotectin levels in neonatal stool can be 200–2,000 µg/gm and can rise further with mucosal inflammation.³⁰ In this article, we present our current understanding of calprotectin expression, evolution, and clinical importance. We have added data from our own preclinical and peer-reviewed studies to an extensive review of the literature using the databases PubMed, EMBASE, and Scopus.^{31,32}

STRUCTURE OF CALPROTECTIN

Calprotectin is a heterodimeric protein complex comprised of an *S100A8* (MRP8) and another *S100A9* (MRP14) subunit.^{33,34} Both protein motifs have been visualized with a thumb (end digit, E) and a forefinger (F) joined in a distal palm-like shape, the “EF-hand.”^{13,15} This distal palm is a short loop of about 12 amino acids and holds a “marble,” a Ca⁺⁺ ion (Fig. 2).³⁵ The presence of calcium ions induces conformational changes in the protein complex and exposes specific domains that can sense intracellular calcium fluctuations.^{35,36}

- N-terminal EF-hand: A “pseudo” or *S100*-specific loop typically consisting of 14 amino acids, with a relatively limited Ca⁺⁺ affinity.³⁷
- C-terminal EF-hand: A “canonical” or classical EF-hand loop consisting of 12 amino acids, which exhibits higher calcium affinity.³⁸

The properties of the calprotectin protein are detailed in Figure 3.^{39–42} The protein is relatively water-soluble, and the hydrophobic amino acids are buried inside the core, away from the surface (Figs 3A and B).^{24,43} The secondary structure (Fig. 3C), the

¹⁶Autism Care Network Foundation, Chandigarh, India

¹⁷Neonatology-Certified Foundation, Brooksville, Texas, United States of America

¹⁸GNS Infant Nutrition Education Program, Harrison, New York, United States of America

¹⁹International Prader-Willi Syndrome Organization, Cambridge, United Kingdom

²⁰First Breath of Life, Shreveport, Louisiana, United States of America

²¹Faculty of Animal Science and Food Technology, Agricultural Sciences and Natural Resources University, Iran

²²Department of Population, Policy and Practice Research and Teaching, University College, Great Ormond Street Institute of Child Health, London, United Kingdom

²³American Canadian School of Medicine, Dominica, Caribbean

²⁴Excellence in Pediatrics, Copenhagen, Denmark

²⁵British Paediatric Society for the History of Paediatrics and Child Health, United Kingdom

Corresponding Author: Akhil Maheshwari, Department of Pediatrics/ Neonatology, Boston Children's Health Physicians Group at the Maria Fareri Children's Hospital, New York Medical College, Valhalla, New York, United States of America, Phone: +1-708-910-8729, e-mail: akhil@globalnewbornsociety.org

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three-dimensional distribution of various amino acids (Fig. 3D), and the relative proximity to Ca⁺⁺ ions are reasonably well-characterized (Fig. 3E).^{24,44} In the presence of Ca⁺⁺ ions, calprotectin can form heterotetramers or higher-order oligomers, which can further enhance its stability and metal-binding capacity (Fig. 4).⁴⁵ The binding sites with Ca⁺⁺ and other transitional metals such as Zn⁺⁺ (Fig. 5) and Mn⁺⁺ ions are known.^{24,46,47} We know that the combination of Ca⁺⁺-induced conformational flexibility and metal sequestration underlies its antimicrobial effects, as these expose hydrophobic surfaces, allowing the protein to interact with various enzymes and ion channels.^{48,49}

S100A8 and *S100A9* are expressed in neutrophils, monocytes, and activated macrophages, where these induce cytokine expression, activate leukocytes, and enhance antimicrobial activity as mediators of innate immunity and inflammation.^{45,50–52} In addition to the gastrointestinal tract, these can be identified in the lungs, liver, skin, joints, and cardiovascular system, whenever and wherever neutrophils or activated macrophages are recruited.⁵³ These contribute to local antimicrobial defense, metal sequestration, and pro-inflammatory signaling.⁹ Circulating calprotectin is detectable during systemic inflammatory response syndrome, further highlighting its important role in immune responses and inflammatory diseases.²¹

Tertiary/Quaternary Protein Structure

- Transition metal-binding sites: Mutations in the sequence for histidine, aspartate, or cysteine residues involved in sequestration of Zn and Mn can compromise nutritional immunity, diminishing antimicrobial activity against bacteria and fungi.⁵⁴

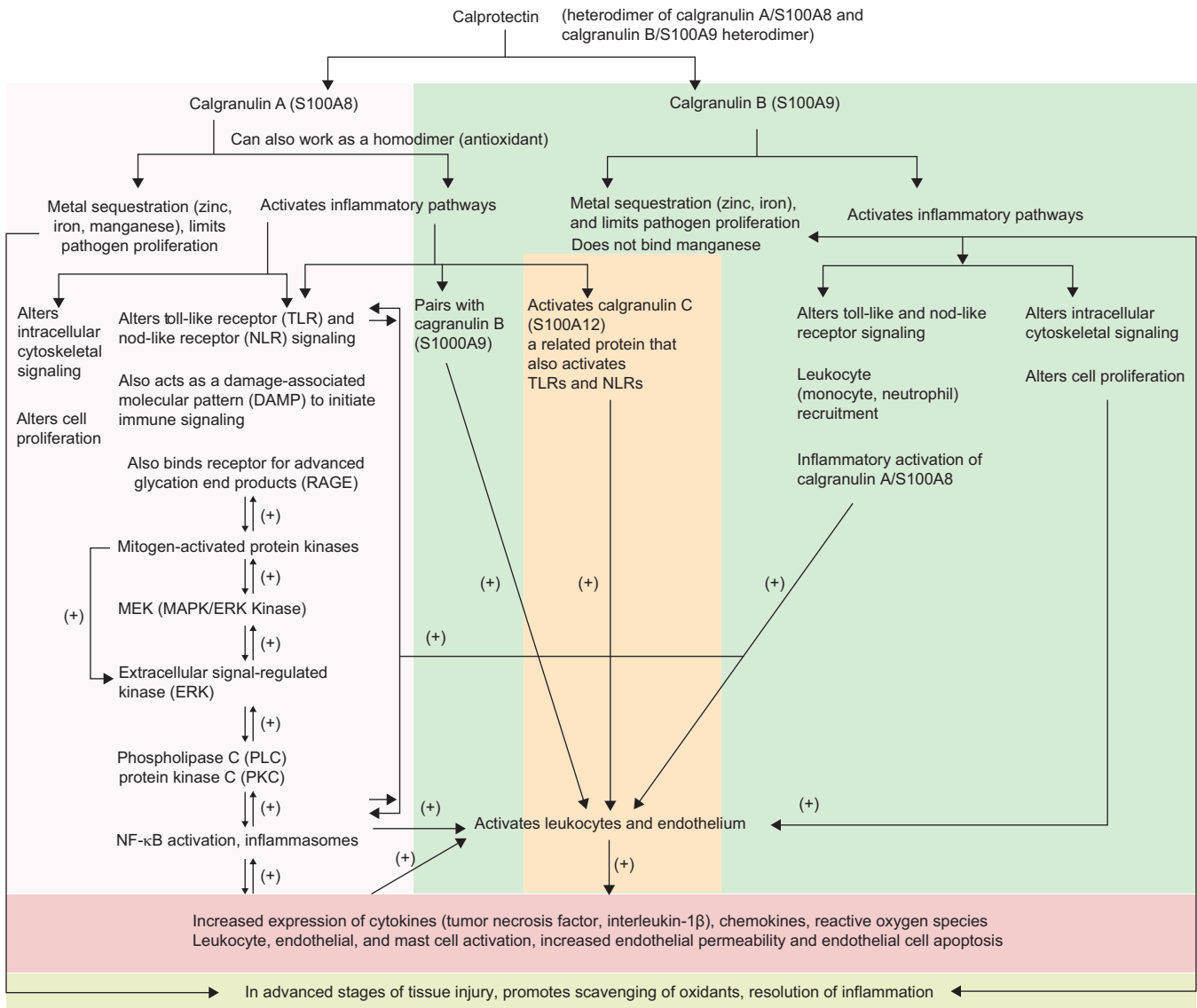


Fig. 1: Calprotectin is an important mediator in innate immunity; it is expressed predominantly in neutrophils and monocytes, where it contributes to early host defense against infection. Calprotectin is composed of *calgranulin A (S100A8)* and *calgranulin B (S100A9)* proteins. This complex promotes calcium-related signaling and immune function. Ca^{2+} binding induces conformational changes such as dimerization, increases its stability, its interaction with target molecules, and association with cell membranes during inflammation. In this calcium-bound state, calprotectin sequesters transition metals such as zinc and manganese more effectively, strengthening its antimicrobial activity and role in innate immune defense. Calprotectin is released at sites of inflammation and exerts antimicrobial activity by sequestering essential metal ions such as zinc and manganese and thereby limiting microbial growth (nutritional immunity). In addition to its antimicrobial role, calprotectin also functions as a DAMP, activating pattern recognition receptors and amplifying inflammatory signaling. Through these mechanisms, calprotectin helps coordinate innate immune responses and serves as a sensitive biomarker of inflammation

- Protein–protein interaction surfaces: Changes at the *S100A8/S100A9* interface in calprotectin may alter the tertiary/quaternary structure.⁴⁵ Appropriate heterodimerization is critical for the stability and function of calprotectin. The heterodimers develop with specific hydrophobic and electrostatic interactions, and are needed for the stability of the protein complex, sequestration of metal ions, and interaction with microbial membranes.^{5,20,55} These effects are particularly relevant in neonates and during development, where subtle differences at the interface may modulate calprotectin activity and influence early gut colonization and immune defense.⁵⁶
- Interaction with metallic ions: Heterodimerization positions the histidine- and aspartate-coordinated metal-binding sites at the subunit interface for chelation of Zn, Mn, and other transition metals.⁴⁴ Alterations at the interface due to mutations, post-translational modifications, or structural instability can distort the heterodimer and its metal-binding sites.^{20,57} This effect is important in the neonates, where it might influence host–microbe interactions.
- Interactions with microbial membranes: The *S100A8/S100A9* interface is critical for interactions with microbial membranes.⁴⁶ Proper heterodimerization positions key hydrophobic and



KEY STRUCTURAL ELEMENTS

S100A8

Cytosolic protein, no signal peptides: Forms a heterodimer with S100A9 to perform metal sequestration, antimicrobial activity, and pro-inflammatory signaling via receptors like RAGE and TLR4.

Secreted via the endoplasmic reticulum–Golgi pathway. Non-classical release from leukocytes via non-classical secretion such as passive release during cell activation/necrosis or via microvesicles/exosomes.

Two EF-hand domains:

- N-terminal EF-hand (pseudo-EF-hand): 14-residue motif, low-affinity calcium binding, overall structural stability. Asp10, Asp12, and Glu14 coordinate calcium with lower affinity.
- C-terminal EF-hand (canonical-EF-hand): 12-residue motif, higher-affinity calcium binding with conformational change. Asp57, Asp59, Glu62, and Glu66 coordinate calcium with high affinity, driving conformational changes.

Calcium-binding residues: aspartate (Asp), glutamate (Glu), and sometimes asparagine (Asn) residues, which coordinate the calcium ion in a pentagonal bipyramidal geometry. Calcium binding leads to an 'open' conformational change to expose a hydrophobic surface and heterodimerization with S100A9 and enabling interactions with target proteins. "Closed" S100A8 is largely inactive.

EF-hand loops contain conserved acidic residues, aspartate and glutamate, which coordinate the calcium ion in a pentagonal bipyramidal geometry. Calcium binding in S100A8 induces a structural rearrangement in S100A9, exposing hydrophobic surfaces that allow heterodimerization to form calprotectin and facilitate interactions with receptors such as RAGE and TLR4. Without calcium, S100A9 remains largely inactive. These cation-binding sites are essential for its immune and inflammatory functions.

Zinc-binding sites needed for antimicrobial activity. Zinc coordination occurs at interface regions when S100A8 forms a heterodimer with S100A9. Zinc-binding residues include conserved histidine (His) and aspartate (Asp) residues; in S100A8, residues such as His17, His27, and Asp30 participate in metal ion coordination at the heterodimer interface with S100A9, enabling nutritional immunity.

There is a heterodimer requirement; zinc binding is more stable when S100A8 pairs with S100A9 to form calprotectin, creating a tetrahedral coordination site at the dimer interface. This metal-chelating activity inhibits microbial growth through nutritional immunity.

Antimicrobial activity: Zinc-binding sites contribute to antimicrobial activity through metal ion sequestration and structural interactions within the calprotectin heterodimer.

- N-terminal EF-hand has lower calcium affinity but stabilizes the overall fold of the protein. Antimicrobial activity is mediated at the heterodimer interface, where conserved histidine and aspartate residues from S100A8 coordinate zinc and manganese ions. These changes deprive pathogens of essential metals and provide nutritional immunity.
- C-terminal EF-hand domain in S100A8 binds calcium and exposes hydrophobic surfaces needed for heterodimerization with S100A9. These metal-binding regions, combined with the conformational flexibility conferred by the EF-hand domains, define the functional domains of S100A8 that are critical for its direct antimicrobial effects and innate immune defense.

Dimerization and structural stabilization: Residues within the hydrophobic surface exposed upon calcium binding, including portions of the C-terminal EF-hand, are critical for heterodimer formation with S100A9 and proper structural integrity.

Functional motifs: Conserved motifs in both EF-hands contribute to receptor interaction (such as RAGE, TLR4) and pro-inflammatory signaling.

Active site: the term is used in the context of metal-binding and functional activity, rather than enzymatic catalysis, because S100A8 is not an enzyme:

- **Two EF-hand domains:** N-terminal pseudo-EF-hand (low-affinity) that contributes to structural stability; and C-terminal canonical EF-hand (high-affinity) that undergoes conformational changes upon calcium binding, exposing hydrophobic surfaces that enable heterodimerization with S100A9.
- **Transition metal-binding site (zinc/manganese):** located at the heterodimer interface with S100A9. Key residues include His17, His27, and Asp30, which coordinate zinc or manganese ions; site crucial for **nutritional immunity**, as it sequesters essential metals from pathogens.
- **Functional Interface for immune signaling:** calcium-induced structural changes expose surfaces that allow interaction with receptors such as RAGE and TLR4, mediating pro-inflammatory signaling.

Sequence splicing: process for removal of introns; exons are joined in the pre-mRNA transcript and the mature mRNA is then translated.

S100A8 gene shows 3 exons and 2 introns. Canonical splicing produces the full-length protein, including both EF-hand calcium-binding domains necessary for structural stability, heterodimerization with S100A9, and antimicrobial activity.

Alternative splicing appears to be rare or minimal. Proper splicing is crucial because any mis-splicing or exon skipping could disrupt the EF-hand domains or the metal-binding interface, impairing calcium and zinc binding, heterodimer formation, and overall innate immune function.

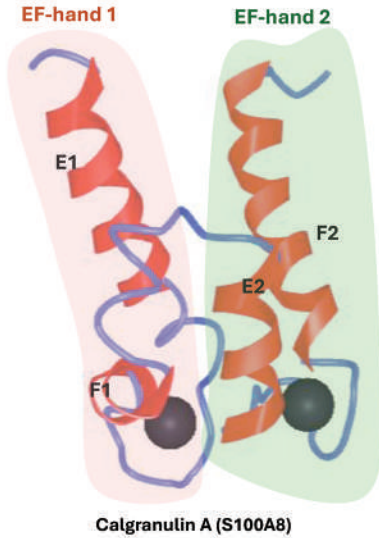
Post-translational modifications: several amino acid residues undergo such changes and affect its structure, activity, and interactions. Key modified residue positions include:

- **Cysteine residues:** Cys42 is prone to oxidation, forming disulfide bonds or sulfenic/sulfinic acids under oxidative stress. This modification can influence protein stability and pro-inflammatory activity.
- **Serine/threonine residues:** Ser100 (numbering may vary by species) can undergo phosphorylation, which modulates calcium-dependent conformational changes and interaction with S100A9 or other target proteins.
- **Methionine residues:** Certain methionines may undergo oxidation, which can alter the protein's redox state and antimicrobial function.
- **Other modifications:** Acetylation and nitrosylation at exposed lysine or cysteine residues have been reported in inflammatory contexts, affecting immune signaling and receptor interactions.

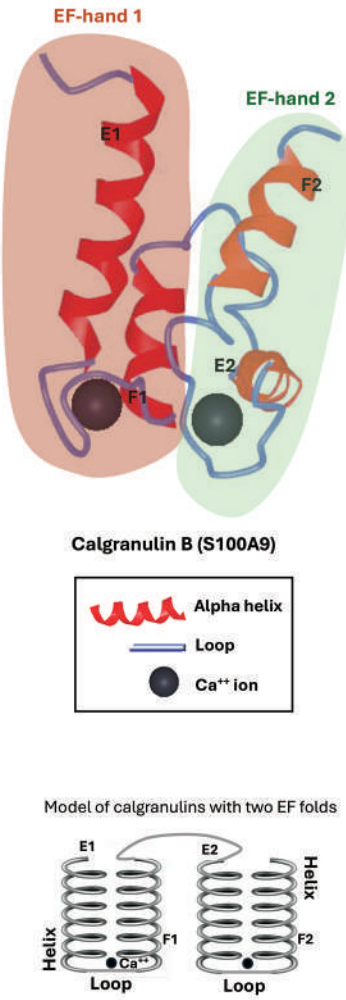
Genetic alterations:

Two non-coding or regulatory mutations, rs3795391 (A > G) and rs3806232 (A > G) located upstream of the encoding gene, have been associated with increased plasma levels of S100A8 and systemic inflammation.*

Specific minor allele frequencies (MAFs) vary by population, though precise numeric frequencies are not known. These SNPs are common enough to be counted in association studies across ethnic groups.



(Contd...)



KEY STRUCTURAL ELEMENTS

S100A9

Cytosolic protein, no signal peptides; cytosolic protein released from cells through non-classical secretion pathways rather than the ER–Golgi route. Compact gene with 3 exons and 2 introns, spliced to encode the full-length protein. Alternative splicing of S100A9 appears to be rare.

Secreted during cell activation, stress, or necrosis, and can also be packaged into exosomes or microvesicles. Forms a heterodimer with S100A8, which is crucial for metal sequestration, antimicrobial activity, and activation of inflammatory pathways via RAGE or TLR4.

Two EF-hand domains:

- N-terminal EF-hand (pseudo-EF-hand): 14-residue motif, low-affinity calcium binding, overall structural stability
- C-terminal EF-hand (canonical EF-hand): 12-residue motif, higher-affinity calcium binding with conformational change.

As mentioned above, antimicrobial function is mainly mediated at the heterodimer interface with its conserved histidine and aspartate residues that coordinate zinc and manganese ions, effectively sequestering these metals from invading microbes. These metal-binding regions, together with the calcium-induced conformational flexibility of the EF-hand domains, define the domains in S100A9 that are critical for nutritional immunity, pathogen growth inhibition, and innate immune defense.

Several specific amino acid positions serve critical structural and functional roles, particularly in calcium binding, heterodimerization with S100A8, and antimicrobial activity:

Calcium-binding residues:

- N-terminal pseudo-EF-hand: Asp20, Asp22, and Glu24 contribute to low-affinity calcium binding and stabilize the protein fold.
- C-terminal canonical EF-hand: Asp85, Asp87, Glu90, and Glu94 coordinate high-affinity calcium binding, inducing conformational changes necessary for activity.

Zinc- and manganese-binding residues: His91, His95, and His103 form part of the metal-binding site at the heterodimer interface with S100A8, critical for nutritional immunity.

Dimerization and structural stabilization: Residues in the hydrophobic interface exposed upon calcium binding are essential for heterodimer formation with S100A8, structural stability, and functional activation.

Functional motifs for immune signaling: Conserved regions in both EF-hand domains facilitate interaction with receptors like RAGE and TLR4, mediating pro-inflammatory signaling.

Active site: Calcium-binding EF-hand motifs, including the N-terminal pseudo-EF-hand (low-affinity) and C-terminal canonical EF-hand (high-affinity).

Two EF-hand domains: N-terminal pseudo-EF-hand (low-affinity) that contributes to structural stability; and C-terminal canonical EF-hand (high-affinity) that undergoes conformational changes upon calcium binding, exposing hydrophobic surfaces that enable heterodimerization with S100A8.

Transition metal-binding site (zinc/manganese): Located at the interface of the S100A8/A9 heterodimer. His91, His95, and His103 coordinate zinc or manganese ions. This site mediates nutritional immunity, depriving microbes of essential metals.

Functional interface for immune signaling: Calcium-dependent conformational changes expose surfaces that interact with receptors such as RAGE and TLR4, promoting pro-inflammatory signaling in innate immunity.

Sequence splicing: process by which the pre-mRNA transcript of the S100A8 gene is processed to remove introns and join exons, generating a mature mRNA that can be translated into the functional protein.

Compact gene with 3 exons and 2 introns, spliced to encode the full-length protein. Alternative splicing of S100A9 appears to be rare.

Post-translational modifications: Most genetic alterations are single-nucleotide polymorphisms (SNPs), in non-coding regulatory regions (such as upstream promoter regions), which alter the expression of S100A9, not its amino-acid sequence.

Genetic alterations:

Several mutations have been described:

- **rs3014866:** an SNP in the 5'-upstream regulatory region (promoter) associated with increased plasma levels of S100A9 and risk of type 2 diabetes and metabolic traits. Carriers of the TT genotype may show varied effects on insulin sensitivity.
- **rs3014866:** C allele and CC genotype were linked to higher plasma S100A9 levels, increased risk and earlier onset of Parkinson's disease.
- **rs3014866:** lower risk of stroke in a Southern Chinese cohort.
- **rs1063933:** a coding SNP (lysine → glutamate, K96E) of S100A9. Functional effects unclear.

Associations with clinical phenotypes suggest that regulatory variation at S100A9 may affect disease risk by modulating inflammatory gene expression.

* The "rs" nomenclature identifies single nucleotide polymorphisms (SNPs) in the human genome. The prefix "rs" stands for "Reference SNP cluster ID" (<https://www.ncbi.nlm.nih.gov/snp/>). These name specific mutations and genomic positions but not the type, such as transition, transversion, insertion, or deletion.

Fig. 2: Calgranulin A and B are both comprised of two helix-loop-helix EF hands. The two helices are visualized as digits: a thumb (end digit, E) and a forefinger (F). These digits are joined on an imagined palm, a short loop of about 12 amino acids, which holds a Ca^{++} ion. A low-affinity calcium-binding site is also seen at the N-termini on the helices and a high-affinity site at the C-termini. Calcium binding induces a conformational change with helical rotation, exposing a hydrophobic surface for interaction with target proteins such as RAGE products

cationic regions that interact with negatively charged bacterial membranes.⁴⁶ Altered conformation can reduce the binding with the microbial membranes and its antimicrobial activity.²⁹

Functional defects in calprotectin could theoretically increase susceptibility to infections or inflammation, though naturally occurring human mutations are not widely reported.⁵⁸ One reason for the genetic mutations not being widely reported in a clinical context is that calprotectin is usually marked as a biomarker for inflammation and measured for concentrations, not function.⁶

METAL-BINDING DOMAINS

Ca^{++} ions bind EF-hand motifs in calprotectin and induce conformational changes that stabilize it and promote dimer/tetramer formation, indirectly enhancing its transition metal sequestration activity.²⁴ There are two metal-binding sites at the interface of the S100A8/S100A9 heterodimer, involving histidine (His) and aspartate (Asp) residues from both subunits:¹⁴ (1) a high-affinity

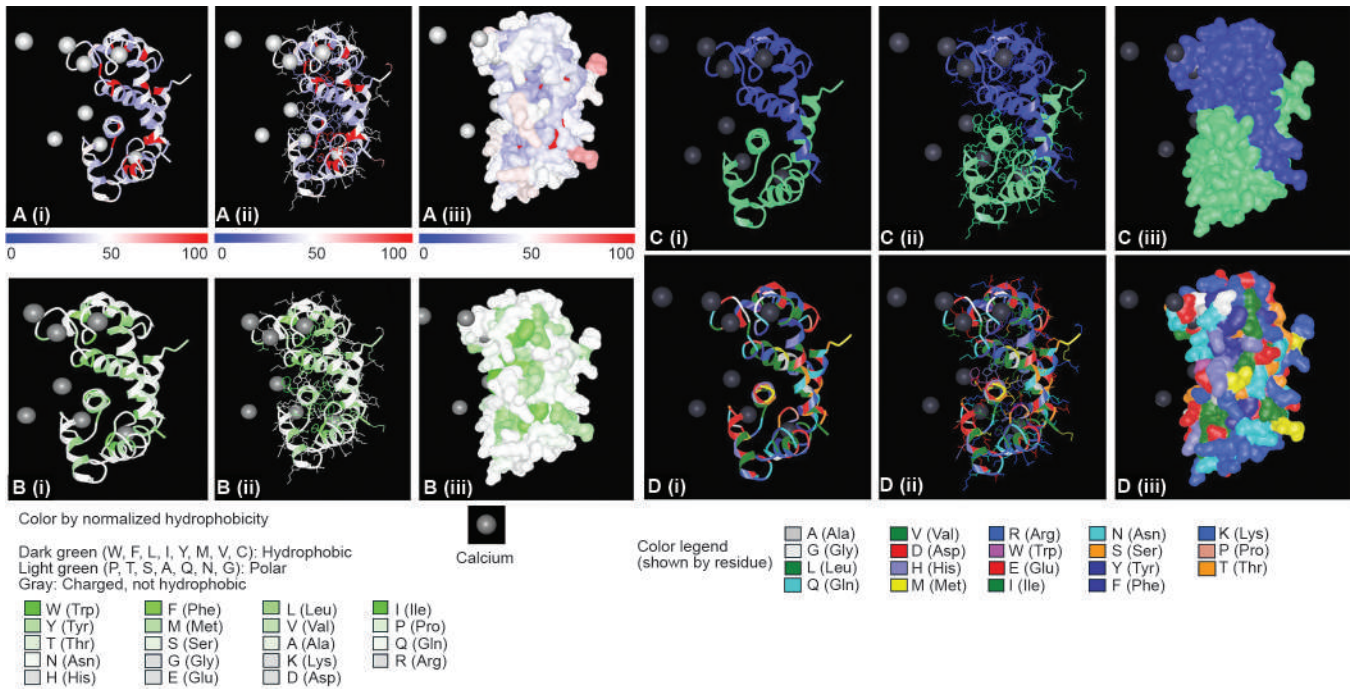
multi-His motif binds divalent metal ions such as Zn^{++} ; Fig. 5B), Mn^{++} , ferrous (Fe^{++}), and nickel (Ni^{++});¹⁴ and (2) a combination of His and Asp residues sequesters Zn^{++} .²⁰ These metals stabilize the heterodimer geometry and enhance the affinity and specificity of metal sequestration in a feed-forward process.^{20,24}

Metal ions are central to the structure and function of calprotectin.⁵⁹ As mentioned above, Ca^{++} -enhanced inhibition of microbial enzymes and cellular survival.⁴⁷ Metal binding also promotes protein oligomerization and may facilitate membrane destabilization, further enhancing antimicrobial effects.⁶⁰ Thus, metal ions are both structural cofactors and functional effectors, enabling calprotectin to regulate microbial growth and contribute to host defense.²⁰

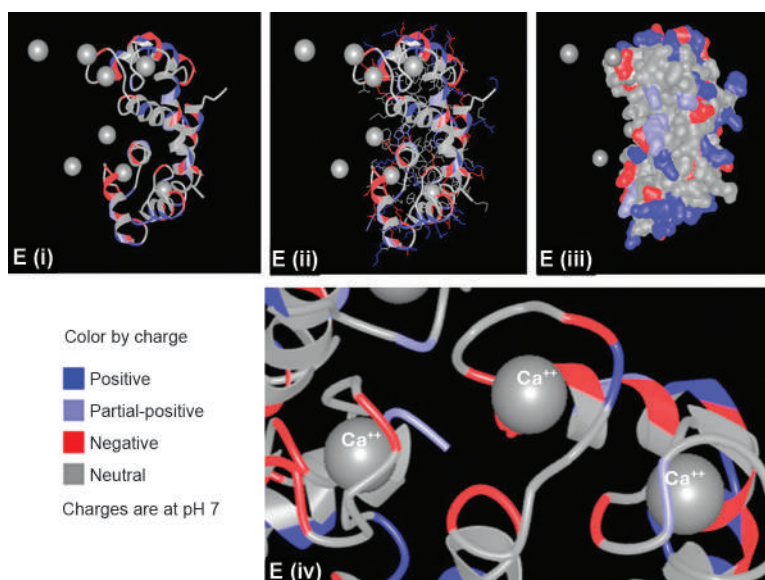
MECHANISMS OF SECRETION

Calprotectin is secreted primarily by activated neutrophils and monocytes/inflammatory macrophages.⁶¹ It lacks a signal peptide, and





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Figs 3A to E: This figure shows three sequential illustrations of the calprotectin molecule from left-to-right: (i) primary ribbon structures with folds show the organization of the protein backbone; (ii) structure with side chains; and (iii) molecular surface. (A) Solvent accessibility. Color change from blue-to-white-to-red indicates increasing solvent accessibility. The average accessible surface of residues in most folded proteins is around relative to an unfolded state. A value of suggests that the protein's surface is well-hydrated; (B) Hydrophobicity. Predicted solvent-accessible surface area (SASA), shown in a scale ranging from a deep green color at its low end to high white: (i–ii) primary ribbon structure and the structure with side-chains shows the green and white color residues as evenly distributed; (iii) solvent-accessible space-filling model predicts these surfaces as much whiter and hence, the hydrophobic residues green residues are buried away from the surface inside the core of the protein. We have used the SASA method to produce this illustration. Relative solvent accessible area (RSA)/SASA are standard measures to describe the degree of residue exposure in the protein surface. There are many methods for the estimation of RSA/SASA that focus on the Ca atom-distance matrix and use deep learning methods; some of the existing RSA estimators are based on coordination numbers, half-sphere exposure, and SphereCon, one of the recognized RSA-estimation algorithms; (C) Calprotectin is a heterodimer of *calgranulin A* (*S100A8*, blue) and *calgranulin B* (*S100A9*, green); (D) Amino acid composition of the calprotectin heterodimer molecule. The amino acid color-coding is as shown below. (E) The amino acid structure (i–ii) showed a good overall balance of positively and negatively charged amino acid residues. However, (iii) the surface of the protein molecules showed more neutral/positively charged regions. Inside the molecule, (iv) most calcium ions (Ca^{++}) were located close to negatively charged glutamic acid, aspartic acid, asparagine, and glycine residues. Zinc (Zn^{++}) is seen at specific interfacial sites, coordinated by Histidine (H) and Cysteine (C) residues such as the His-X-X-His motifs on both *S100A8* and *S100A9* subunits (not shown here). The presence of Ca^{++} may enhance Zn-binding, which is crucial for the antimicrobial functions. In the EF-hand motif, the glutamic and aspartic acids in the loop region provide the negatively charged oxygen atoms, which enhance the effect of the positively charged Ca^{++} ions. Here, Ca^{++} may induce a significant conformational and charge alteration to promote sequestration of transition metals and self-association into a tetramer. Each calprotectin subunit (*S100A8* and *S100A9*) has two EF-hands; the C-terminal EF-hand is considered "canonical" and has a higher negative charge and a stronger affinity for Ca^{++} ions. The N-terminal EF-hand is "non-canonical," with a lower number of negatively charged residues and binds Ca^{++} with lower affinity

Source: The base structure was adopted from: <https://www.ncbi.nlm.nih.gov/Structure/icn3d/full.html?&mmdbid=35490&bu=1&showanno=1&source=full-feature>. This structure was derived from the iCn3D (short for "I see in 3D") format, a web-based interactive tool for analysis of three-dimensional macromolecular structures. This has been developed using the Web Graphics Library, a JavaScript Application Programming Interface to render 3D graphics in web browsers without requiring plugins. A JavaScript control and a shader code have been executed on the graphics processing unit for high-performance interactive graphics. These illustrations were prepared using data/tools provided on the web portals of the RCSB and NCBI PDBs, MMDB, GenBank, RefSeq, TPA, UniProtKB/Swiss-Prot database, PIR, PRF, and Microsoft PowerPoint, Microsoft Illustrator, and/or Adobe Photoshop

hence, the secretory mechanisms are largely non-classical and do not involve the conventional endoplasmic reticulum–Golgi pathway.^{5,29} Calprotectin is released passively during cell death, especially during neutrophil necrosis or neutrophil extracellular trap (NET) formation, where it associates with DNA/histones into the extracellular space to trap microbes. The molecule is produced actively via cytoskeleton-dependent pathways involving membrane translocation and vesicle shedding.⁶² In neutrophils, inflammatory activation mobilizes calprotectin to the cytosol and plasma membrane, followed by release through microvesicles or exocytosis-like processes.⁶³ During NET formation, calprotectin is expelled along with chromatin.⁶⁴ Once released, extracellular calprotectin contributes to a DAMP signal, amplifying inflammatory

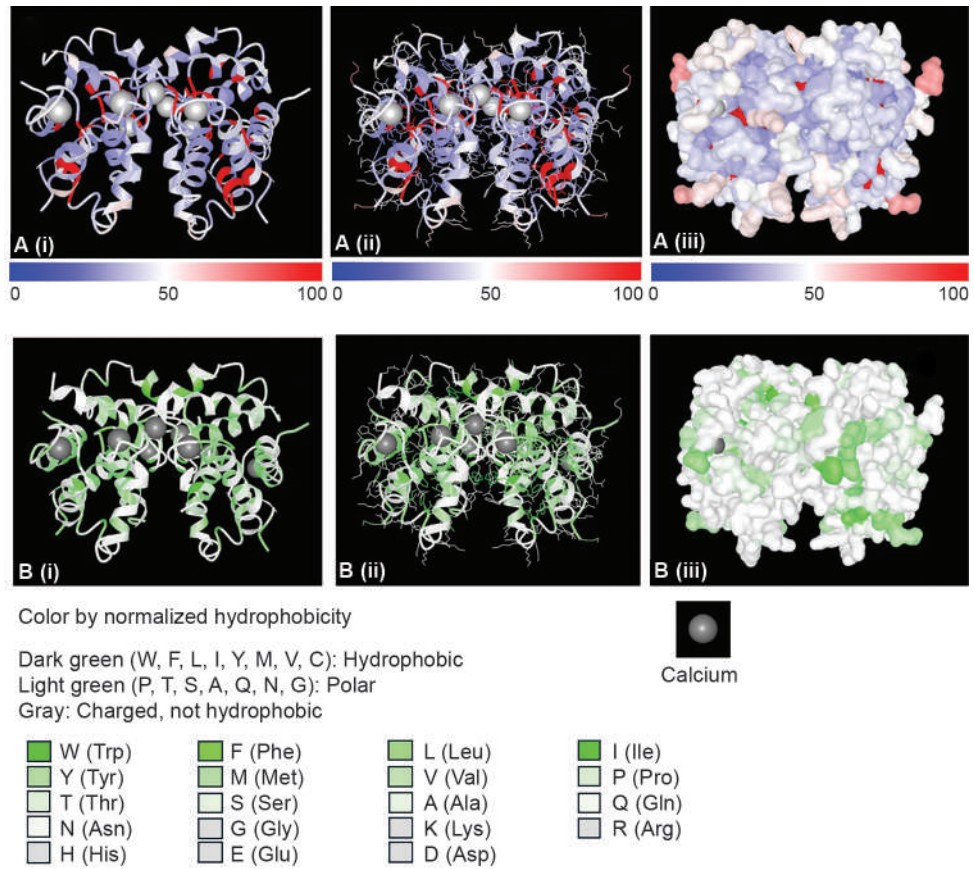
cascades by engaging pattern recognition receptors such as TLR4 and RAGE.⁵ Levels of calprotectin, by whatever mechanism, show considerable variation between different individuals.

HOST DEFENSE

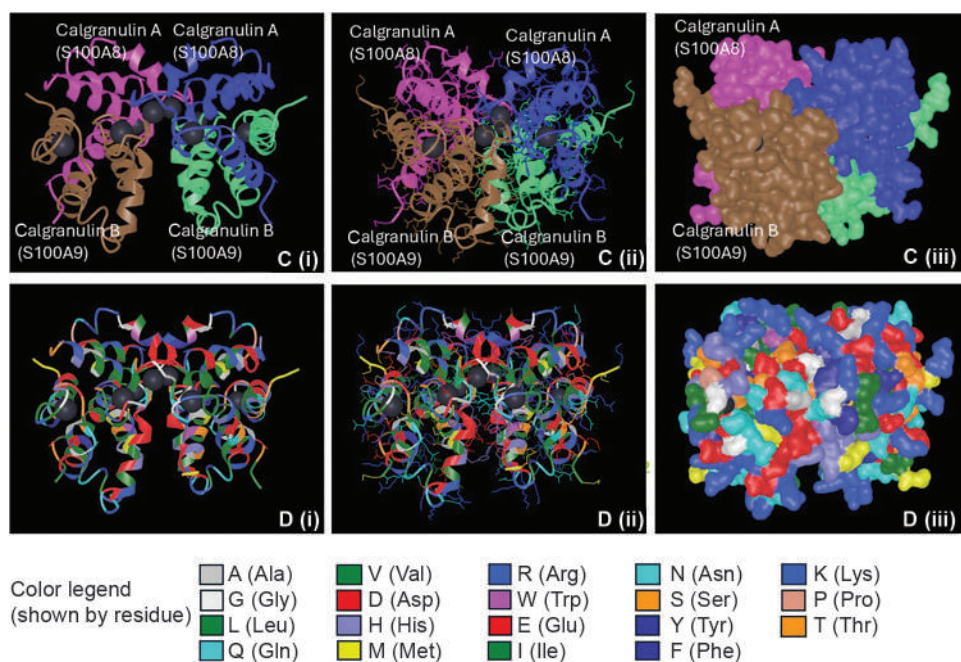
Calprotectin shows innate antimicrobial activity by at least three mechanisms:⁵

- Metal sequestration.
- Electrostatic interactions between its cationic surface regions and the anionic phospholipids in microbial membranes.⁶⁵ These interactions alter the local charge distribution, weakening lipid–lipid interactions and can reduce membrane stability, increase





(Contd...)



Figs 4A to D: In the presence of high concentrations of Ca^{++} ions, calprotectin heterodimers usually join to form heterotetramers composed of two *calgranulin A* (S100A8) and *calgranulin B* (S100A9) subunits. The illustrations here show the heterotetramers in the same sequence as in earlier figures. From left to right, we show: (i) primary ribbon structures with folds in the protein backbone; (ii) a structure with side chains; and (iii) the molecular surface. (A) Solvent accessibility. Color change from blue-to-white-to-red indicates increasing solvent accessibility. Value of $\geq 35\%$ suggests that the protein surface is well-hydrated; (B) Hydrophobicity. Predicted solvent-accessible surface area (SASA), shown in a scale ranging from a deep green color at its low end to high white: (i–ii) primary ribbon structure and the structure with side-chains shows the green and white color residues as evenly distributed; and (iii) solvent-accessible space-filling model show a predominance of white surfaces, suggesting that hydrophobic green residues are buried in the core of the protein. Here, the SASA method shows that the protein surface is relatively solvent accessible; (C) Heterotetramers of two *calgranulin A* (S100A8) and *calgranulin B* (S100A9); (D) Amino acid composition of the calprotectin heterotetramer. The amino acid color-coding is shown below the figure

Source: The base structure was adopted from: <https://www.ncbi.nlm.nih.gov/Structure/icn3d/full.html?&mmdbid=35490&bu=1&showanno=1&source=full-feature>. This structure was derived from the iCn3D (short for “I see in 3D”) format, a web-based interactive tool for analysis of three-dimensional macromolecular structures. This has been developed using the Web Graphics Library, a JavaScript Application Programming Interface to render 3D graphics in web browsers without requiring plugins. A JavaScript control and a shader code have been executed on the graphics processing unit for high-performance interactive graphics. These illustrations were prepared using data/tools provided on the web portals of the RCSB and NCBI PDBs, MMDB, GenBank, RefSeq, TPA, UniProtKB/Swiss-Prot database, PIR, PRF, and Microsoft PowerPoint. Microsoft Illustrator, and/or Adobe Photoshop

permeability, and compromise membrane-associated processes essential for microbial viability.⁶⁶

- Hydrophobic interactions with microbial membranes, which can expose nonpolar surface residues associated with lipid acyl chains.⁴⁹ These hydrophobic contacts can possibly facilitate partial insertion of calprotectin into the phospholipid bilayer, altering lipid packing and membrane organization, and ultimately, disrupting the microbial membranes.¹⁶

These membrane changes can also enhance the bactericidal efficacy of innate immune cells by making pathogens more vulnerable to phagocytosis and intracellular killing.

BACTERIAL MOLECULAR TARGETS

Calprotectin targets the following molecular systems in bacteria:

Zinc Uptake Systems

- Zinc uptake ATP-binding box complex (ZnuABC) transporter in gram-negative bacteria:⁶⁷ many gram-negative pathogens rely heavily on the ZnuABC transporter under Zn-depleted conditions; it is a high-efficiency bacterial Zn uptake regulator composed of

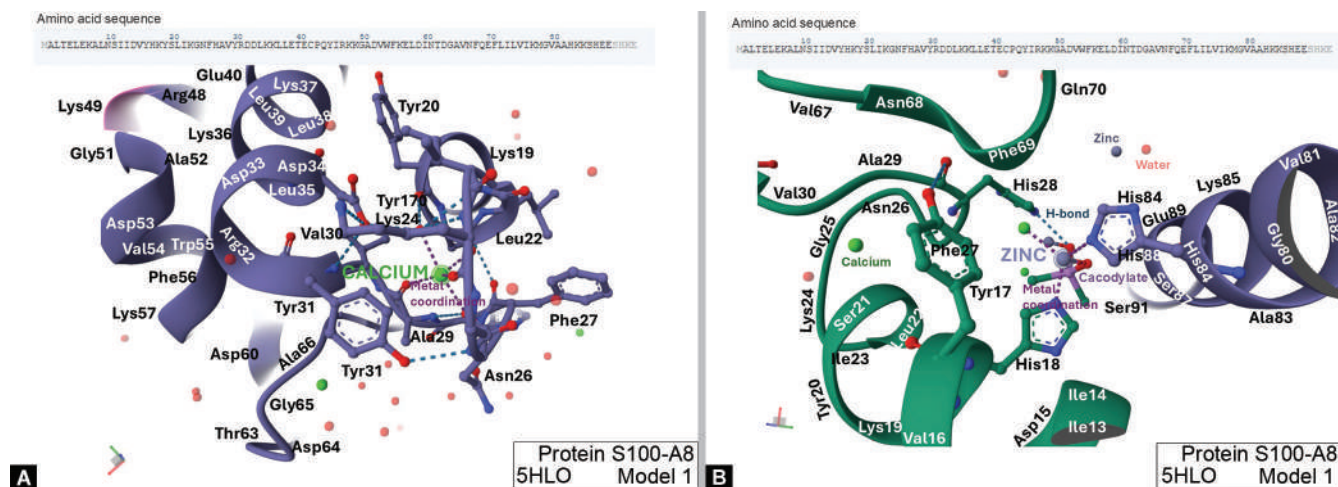
a periplasmic binding protein (ZnuA), a transmembrane protein (ZnuB), and an ATPase (ZnuC).⁶⁸

- Zinc uptake regulator (Zur) regulon is a set of bacterial genes, including ZnuABC, involved in high-affinity Zn acquisition.⁶⁹ It allows bacteria to partially overcome calprotectin-mediated metal starvation, maintaining essential enzymatic activities and supporting survival.
- Adenine complex ATP-binding cassette (AdcABC) system is a high-affinity Zn-uptake complex in *Streptococcus pneumoniae* (*S. pneumoniae*).⁷⁰ It is comprised of the AdcA Zn-binding lipoprotein with AdcB and AdcC permeases. When calprotectin causes Zn depletion, the bacterial AdcABC genes help maintain essential enzymatic functions and cellular processes.⁷¹

Manganese Uptake Systems

- Manganese transport protein H (MntH) is a proton-dependent divalent metal transporter of the natural resistance-associated macrophage protein (NRAMP) family; it helps bacteria overcome calprotectin-mediated metal starvation by importing Mn^{++} and some Fe^{++} .^{72,73} The NRAMPs are evolutionarily conserved metal transporters found in bacteria, fungi, plants, and animals.





Figs 5A and B: Human *S100A8* (Protein databank entry 5HLO). (A) Calcium binding site. Ca^{++} binds to EF-hand motifs present in the *S100* subunits (*S100A8* and *S100A9*). It induces conformational changes to promote dimer/tetramer formation; (B) A zinc-binding site containing several histidine residues in the vicinity. A cacodylate ion is also seen; it is a water-soluble organoarsenic compound $[(\text{CH}_3)_2\text{AsO}_2\text{H}]$ of hitherto uncertain function. The term *S100* signifies that these proteins are soluble in 100% ammonium sulfate at neutral pH. The full name *S100A8* contains the serial number A8 of the protein in this series. Ala, Alanine; Arg, arginine; Asp, aspartate; Asn, asparagine; Glu, glutamate; Gly, glycine; H-bond, hydrogen bond; His, histidine; Ile, isoleucine; Leu, leucine; Lys, lysine; Phe, phenylalanine; Ser, serine; Tyr, tyrosine; Val, valine; 5HLO, crystal structure of calcium and zinc-bound human *S100A8* in space group C222₁. Based on the crystallography results, the space group (Hermann-Mauguin symbol) is labeled as C222₁ in a C-centered orthorhombic crystal system. There is a two-fold rotation axis along the crystallographic axes, and a third 2₁ screw axis is also seen

- Pneumococcal surface antigen B, C, and A (PsaBCA) transporter is a high-affinity Mn uptake system in *S. pneumoniae*.^{74–76} The PsaABC is a crucial ATP-binding cassette comprised of PsaA (metal-binding lipoprotein), PsaB (ATPase), and PsaC (permease) components encoded within the psbCA operon. It helps these bacteria salvage Mn^{++} from the extracellular environment; even trace amounts of Mn can help the bacteria maintain vital enzymatic functions, oxidative stress defense, and overall cellular homeostasis.⁷⁷
- *Salmonella* iron transporter ABCD (SitABCD) is an ATP-binding cassette found in *Salmonella enterica* serovar Typhimurium and other pathogenic enterobacteria.^{78,79} It promotes ATP hydrolysis-driven transport of substrates across biological membranes. Despite its name labeling it as an iron transporter, it is primarily a Mn^{++} transporter that can transport some iron (Fe^{++}) and help these bacteria survive in calprotectin-rich environments.⁸⁰ When extracellular Mn is depleted by calprotectin, bacteria upregulate SitABCD expression, enabling efficient scavenging of trace Mn from the host environment.⁸¹ This allows essential enzymatic processes, oxidative stress defense, and cellular metabolism to continue despite metal restriction.

Many pathogens combine metal uptake with efflux systems to fine-tune intracellular levels of Zn and Mn, avoiding both starvation and toxicity.

- Bacteria can upregulate high-affinity metal uptake systems, such as ZnuABC, PsaBCA, SitABCD, and AdcABC, and also coordinate metal efflux systems such as cation diffusion facilitators, resistance-nodulation-cell division transporters, and P-type ATPases to maintain optimal intracellular metal concentrations.⁸² In *S. pneumoniae*, the zinc effluxer cadmium, cobalt, and zinc/ H^+ - K^+ antiporter (CzcD) is upregulated during zinc stress.⁸³ This

- dual strategy allows these pathogens to efficiently scavenge trace metals from the environment.
- Some pathogens can sequester Zn and Mn by expressing zincophore or metallophore proteins.^{84,85} These small, high-affinity molecules chelate trace metals from the host environment, effectively competing with calprotectin and other host proteins for essential nutrients.⁸⁶ The Zn-binding siderophores, the zincophores, chelate zinc in a host microenvironment.⁸⁷ Zinc is an essential micronutrient required for numerous bacterial enzymes and regulatory proteins, but its availability is restricted during infection by host metal-sequestering proteins such as calprotectin.⁸⁸ The best known zincophores include staphylopin in *Staphylococcus aureus* and pseudopaline in *Pseudomonas aeruginosa*; these molecules belong to a broader family of metallophores capable of binding multiple divalent metals, including Zn, Ni, and cobalt.^{89–91} After chelating Zn, the zincophore–metal complex is transported into the bacterial cell.⁹² These proteins play an important role in bacterial survival and virulence.
- Siderophores are small, high-affinity molecules secreted by bacteria, fungi, and some other microorganisms to scavenge iron from the environment, essential for their growth and metabolism.⁹³ In the host, iron with the host is tightly bound to proteins like transferrin, lactoferrin, and ferritin, making it largely inaccessible to invading pathogens.⁹⁴ Siderophores overcome this limitation by binding iron with extremely high affinity and transporting it back into microbial cells via specific receptors.⁹⁵ In host–pathogen interactions, siderophores play a critical role in microbial survival and virulence, and the host immune system counters them through nutritional immunity.⁹⁶ Proteins such as calprotectin and lipocalin-2 sequester metals or intercept siderophores, thereby limiting microbial proliferation.²⁰

GENETICS

Calprotectin mutations are uncommon; major mutations often lead to early resorption of the embryo.⁹⁷ Many single-nucleotide polymorphisms associated with altered inflammatory responses have been identified (Fig. 2).^{17,18,98–100} Variations, including *S100A9* dimers and truncated forms, have been recognized.¹⁰¹

EPIGENETICS

Calprotectin isoforms and their expression patterns differ between neonates and adults, although the core heterodimer (*S100A8/S100A9*) is the same.¹⁰² In the perinatal period, some post-translational modifications can alter stability, metal-binding capacity, and antimicrobial activity.¹⁰³

- Phosphorylation:
 - *S100A9* is phosphorylated on serine and threonine residues, which can influence heterodimer stability, subcellular localization, and interactions with other proteins.¹⁰⁴
 - Phosphorylation may enhance inflammatory activity and higher-order oligomers.¹⁰⁵
- Oxidation:
 - Methionine and cysteine residues in both subunits can be oxidized.¹⁰⁶
 - Oxidation can alter metal-binding, antimicrobial activity, and TLR4 activation.¹⁰⁷
- Proteolytic processing:

Partial proteolysis of *S100A8* or *S100A9* can generate fragments with altered chemotactic or antimicrobial activity.⁹
- Citrullination:

Arginine to citrulline conversion can modulate inflammatory signaling.¹⁰⁸ These reactions usually involve enzymes known as peptidylarginine deiminases.¹⁰⁹

These PTMs alter the capacities of calprotectin as an antimicrobial, metal-sequestering, and proinflammatory agent, depending on the tissue environment, oxidative stress, and developmental stage.

EVOLUTION OF CALPROTECTIN

Calprotectin is a highly conserved component of the innate immune system. Similarly, a number of structural elements, such as the EF-hand Ca^{++} -binding motifs and high-affinity transition metal-binding sites, have been retained across the vertebrates.^{5,21} There has been a strong evolutionary pressure to preserve its antimicrobial functions employing membrane destabilization and nutritional immunity (by sequestering local reserves of essential metals).^{16,110–112} These non-specific defense mechanisms are crucial elements of vertebrate innate immunity.

About 500 million years ago, an ancestral protein with EF motifs developed in jawless fish (Agnatha).^{113,114} This sequence then evolved into an *S100* gene with simple regulatory and structural features (Table 1).¹¹⁵ Some of these *S100* genes differentiated into an *S100A* subfamily in cartilaginous fish via duplication events.¹¹⁶ To recollect, a gene can evolve into (1) orthologous homologs with retained sequences and function over time in different species; and/or (2) paralogous genes that arise from duplication within a genome, producing copies that can diverge in sequence, regulation, or function over time.¹¹⁷ Many *S100* paralogs can be seen in present-day cartilaginous fish (sharks and rays), bony fish, and amphibians.¹¹⁶ These genes began to show functional

diversification with specialized roles in innate immunity, inflammation, and cellular signaling.¹¹⁸ It is difficult to establish a clear one-to-one ortholog relationship with all modern human *S100* genes, except for a few related to *S100B*, a crucial calcium-binding protein in the nervous system.¹¹⁶ Later in evolution, the *S100A* subfamily grew further via gene duplication and pathogen-driven positive selection, and the paralogs underwent functional diversification for roles in innate immunity, inflammation, and cellular signaling.¹¹⁹

The *S100A8* (*calgranulin A*) and *S100A9* (*calgranulin B*) genes are believed to have evolved in mammals through duplication within the *S100* gene family, not from speciation.^{120,121} Genomic, phylogenetic, and functional evidence suggest that these are paralogs, but pathogen-driven positive selection has shaped the regulatory regions and protein sequences.^{118,122} The two proteins form a stable heterodimer, calprotectin; this co-dependence reflects coevolution after duplication.⁶¹ Calprotectin is expressed by activated neutrophils, monocyte-derived/tissue-resident inflammatory macrophages, and other cells; the baseline expression is low in macrophages, but it is readily inducible during inflammation.⁶¹

In humans, *S100A8* and *S100A9* are located next to each other in the *S100* gene cluster on chromosome 1q21;^{123,124} this chromosomal segment is known to have expanded through repeated tandem duplications and copy-number variation.^{125,126} Other than the *S100* gene family, there are others such as the filaggrin/FLG-related genes and other epidermal differentiation and immune-related genes.^{127,128} There is some supporting evidence of segmental duplications, repetitive elements, and recombination hotspots, which promote unequal crossing-over and recurrent duplication events.¹²⁹ This chromosome has played a major role in the expansion of gene families involved in immunity, inflammation, and barrier function, although this instability also makes it susceptible to deletions and duplications associated with disease.¹³⁰

Even though *S100A8* and *S100A9* gene subsets are typically viewed as paralogs that arose from a duplication in an ancestral *S100A* gene early in mammalian evolution, we cannot confidently exclude the possibility that the *S100A9* gene may have appeared much later during evolution than *S100A8* (Fig. 6A).^{45,131,132} The appearance of a paralogous proximity between the two could well have alternative explanations, such as sequence divergence events, gene conversion, and/or lineage-specific gene losses.^{133–140} In addition, further rounds of duplication within the gene family can create paralogs of different evolutionary ages.¹⁴¹ These paralogs could appear to have “evolved” at different time-points, when in reality their functional innovation or regulatory specialization happened long after their shared duplication event.^{131,142} *S100A8* genes show more evolutionary divergence than *S100A9* (Figs 6B and C); the two genes likely experienced asymmetric evolutionary constraints after duplication, leading to different selective pressures.^{120,143,144}

The evolutionary analysis shown above was developed using the software suite MEGA 12.¹⁴⁵ The phylogeny was inferred using the maximum likelihood method and the Jones–Taylor–Thornton (1992) model of amino acid substitutions, and the tree with the highest log likelihood (–9,220.17) is shown.¹⁴⁶ The initial tree for the heuristic search was selected by choosing one with superior log-likelihood from the Neighbor-Joining and maximum parsimony (MP) algorithms.¹⁴⁷ The chosen MP tree had the shortest length in



Table 1: Evolution of *S100A8* and *S100A9* genes

Evolutionary stage	Timeline	Evolution of <i>S100</i> genes	Evolution of <i>S100A8</i> / <i>S100A9</i> genes	Calprotectin (<i>S100A8</i> - <i>S100A9</i> heterodimer)	Evolutionary events
Early vertebrates (jawless fish; agnatha)	500 mya	Basic structure, ancestral EF hand proteins	None	None	
Cartilaginous fish (sharks, rays)	400 mya	Expanding groups of <i>S100</i> proteins	None	None	Some <i>S100</i> proteins now developing anti-microbial properties
Bony fish (teleosts)	380 mya	Expanding groups of <i>S100</i> proteins	Absent or distant homologs	None	
Amphibians and reptiles	320 mya	Expanding groups of <i>S100</i> proteins	Distant <i>S100A</i> -like genes	None	First signs of innate immunity
Early mammals	225 mya	Nearly full <i>S100A</i> family of proteins	<i>S100A8</i> and <i>S100A9</i> emerge via duplication <i>S100A8</i> and <i>A100A9</i> dimers form	Present	Functional calprotectin heterodimer forms; innate immunity begins to mature
Primates and humans	55 mya	Conserved <i>S100A8</i> / <i>S100A9</i>	Highly expressed, divergent <i>S100A8</i>	Present	<i>S100A8</i> diverges faster; <i>S100A9</i> more conserved; calprotectin develops in leukocytes and plays important antimicrobial and anti-inflammatory roles

Mya, million years ago

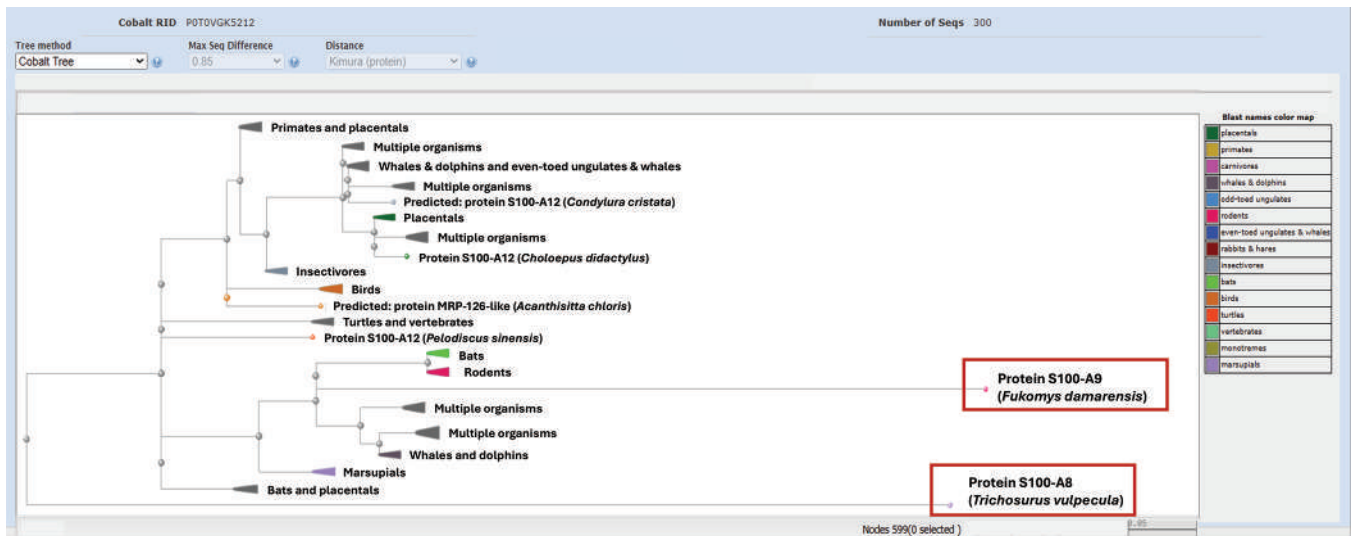
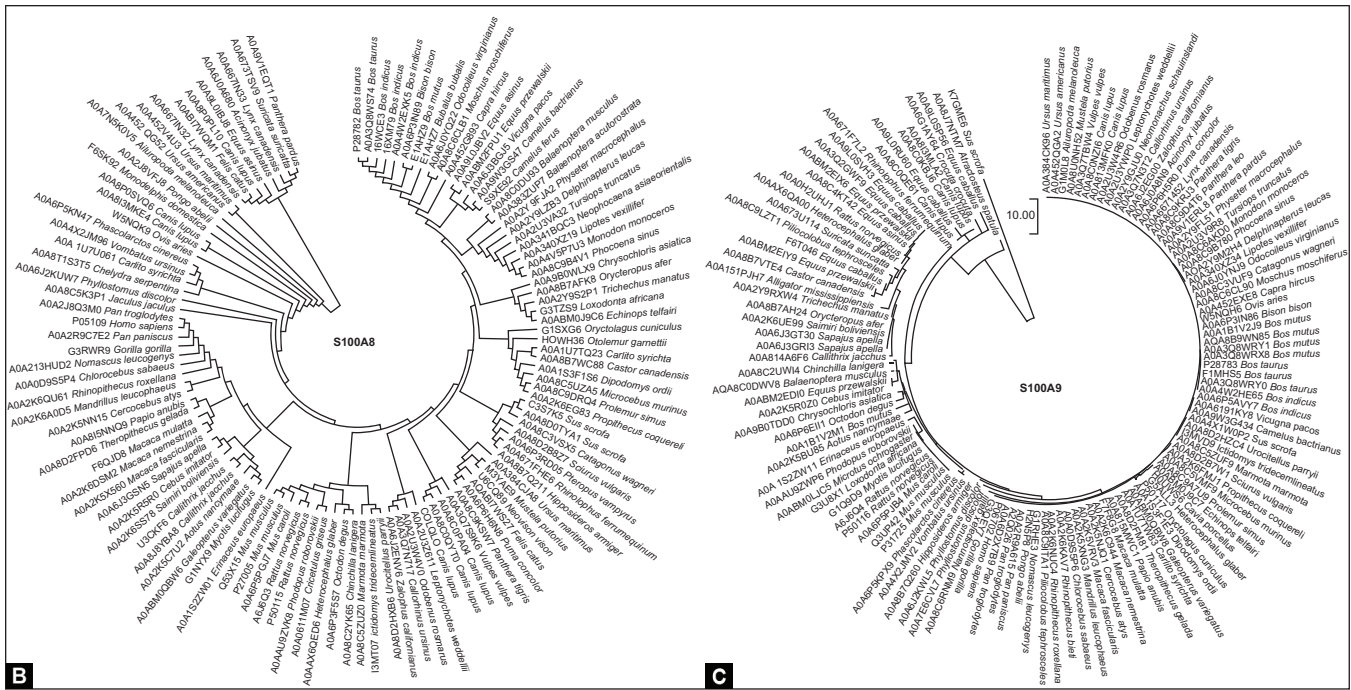


Fig. 6A: (A) Neighbor-joining (NJ) phylogenetic trees showing aerial views of the evolution of human *S100A8* and *S100A9*. These proteins each contain a calcium-binding site in the EF-hand motifs present in the *S100* subunits (*S100A8* and *S100A9*); calcium binding induces conformational changes to promote dimer/tetramer formation. A histidine-rich zinc-binding site is seen in the vicinity. There is also a cacodylate ion, a water-soluble organoarsenic compound $[(CH_3)_2AsO_2H]$ of hitherto uncertain function. The NJ tree is an unrooted, distance-based depiction of iterative clustering of the most closely related taxa (species/sequences). This method minimizes the total branch length in estimating evolutionary divergence; the distance matrix is seen as input. There is some correction for unequal evolutionary rates. The branch lengths are proportional to evolutionary distance. *S100A8* was first seen in *Trichosurus vulpecula*, the common brushtail possum. It diverged in marsupials during the Pliocene era, around 5–2.6 million years ago. *S100A9* appeared more recently in *Fukomys damarensis*, the Damaraland mole-rat, within the last million years. The term *S100* signifies that these proteins are soluble in 100% ammonium sulfate at neutral pH. The full name *S100A8* contains the serial number A8 of the protein in this series. Ala, alanine; Arg, arginine; Asp, aspartate; Asn, asparagine; Glu, glutamate; Gly, glycine; H-bond, hydrogen bond; His, histidine; Ile, isoleucine; Leu, leucine; Lys, lysine; Phe, phenylalanine; Ser, serine; Tyr, tyrosine; Val, valine; 5HLO, crystal structure of calcium and zinc-bound human *S100A8* in space group C222₁. Based on the crystallography results, the space group (Hermann-Mauguin symbol) is labeled as C222₁ in a C-centered orthorhombic crystal system. There is a two-fold rotation axes along the crystallographic axes, and a third 21 screw axis is also seen. The phylogenetic tree was drawn using tools available on the TreeView site: https://www.ncbi.nlm.nih.gov/blast/treeview/treeView.cgi?request=page&cobaltRID=POTOVGK5212&request=page&checkStatus=on&link_loc=alignPage&screenWidth=1536&screenHeight=864



Figs 6B and C: (B) Evolution of human *S100A8*: A detailed pie-chart phylogram is shown down to the species level, constructed with currently available data. The large number of branches could be an artifact arising from the inclusion of more taxa, but may also indicate rapid evolutionary splitting and adaptive radiation due to new ecological opportunities/environmental changes. Branch lengths are still an estimation of the evolutionary changes, but the tips/nodes simultaneously display both divergence and distribution patterns; (C) Evolution of human *S100A9*: Human *S100A8* and *S100A9* likely evolved through duplication and diversification in the vertebrate *S100* gene family (chromosome 1q21), which expanded under strong immune-related selective pressures. *S100A9* shows less evolutionary divergence than *S100A8*

10 searches, each of which was started with a randomly generated baseline. The analytical procedure encompassed 117 amino acid sequences with 299 positions in the final dataset.

The regulatory evolution of *S100A8* may also have contributed. There is more adaptive variability in promoter/enhancer regions and gene sequence, allowing amino-acid changes without compromising heterodimer formation.⁹⁸ These could provide some explanation for lineage-specific differences in expression timing and magnitude. Overall, *S100A8* has shown a flexible modulatory role and has heterodimerized with the *S100A9* genes that displayed a core structural and stabilizing role.⁴⁵ This coupling provided a strong purifying selection to preserve the newly evolved dimer, implying that changes in one copy must be compensated by changes in the other to preserve overall function.^{148,149} After duplication, paralogs are known to diverge in sequence and regulation, but if these form heterodimers, multiprotein complexes, or participate in tightly linked pathways, mutations in one gene that affect binding, stability, or activity can create selective pressures on the other to adapt correspondingly.^{140,150,151} This interdependent evolution ensures proper complex formation, activity, or regulation, allowing the paralogs to specialize or acquire new functions while maintaining essential interactions.¹⁴⁰ Coevolution is particularly common in immune proteins, signaling molecules, and structural partners, where coordinated changes are critical for biological function.¹⁵²

The regulatory elements of *S100A8* may also have contributed to asymmetric evolutionary constraints, leading to different selective pressures. There is greater adaptive variability in promoter/enhancer regions and gene sequence, allowing amino-acid changes

without compromising heterodimer formation.^{153–155} Consequently, there have been more lineage-specific differences in expression timing and magnitude.^{50,156} These show a flexible modulatory role and heterodimerize with the *S100A9* genes that displayed a core structural and stabilizing role.⁴⁵ This coupling has provided selection pressures to preserve the newly evolved dimer.^{45,120}

In a panoramic view, *S100A8* may have been a mammal-specific innovation in leukocyte-based innate immunity.¹⁵³ It then heterodimerized with *S100A9* to form calprotectin and took on specialized roles in inflammation and antimicrobial defense. Over time, *S100A8* has adapted to host–pathogen interactions and undergone sequence and regulatory divergence. *S100A9* also arose in the *S100A* subfamily and contributed to innate immunity. It stabilizes the calprotectin heterodimer and contributes to metal-chelating antimicrobial activity.

There is a possibility of functional asymmetry that followed duplication in the two gene sets. *S100A8* has shown more amino-acid changes, particularly in surface-exposed and regulatory regions. There is also greater divergence in promoter and enhancer elements, leading to more lineage-specific expression patterns. *S100A9* has maintained core structural and functional roles in the calprotectin heterodimer, imposing stronger purifying selection. Compared to *S100A8*, *S100A9* has remained relatively conserved in sequence, reflecting strong purifying selection to maintain its structural and functional roles in inflammation. Recent data show that *S100A9* may exist in more than one isoform, one that is full-length and a shorter variant, *S100A9**, leading to different complex formations (heterodimers/tetramers) with *S100A8* and varied functions in inflammation and disease.¹⁵⁷



LABORATORY MEASUREMENT

Calprotectin is a useful biomarker of inflammation in biological fluids such as meconium, feces, serum, plasma, and other body fluids.^{158,159} As a large protein complex, it does not readily move across anatomical boundaries. Immunoassay-based techniques, such as enzyme-linked immunosorbent assays (ELISA), chemiluminescent immunoassays, or fluorescence immunoassays, are used most frequently to measure the *S100A8/S100A9* heterodimer.¹⁶⁰ These assays show high sensitivity and specificity.¹⁶⁰ Fecal calprotectin concentrations are useful for estimating intestinal inflammation because the protein is fairly stable in stool.¹⁶¹ Sample handling, extraction methods, and biological variability can influence results and need standardization. Measured calprotectin levels correlate with neutrophil activity and inflammatory burden, and are useful for confirming the presence of an inflammatory response, monitoring the change in severity, and response to treatment.¹⁶²

CLINICAL IMPORTANCE

Neonates typically have higher serum concentrations ($0.79 \pm 0.33 \mu\text{g/mL}$) and fecal levels of calprotectin ($0.34 \pm 0.68 \text{ mg/gm}$ stool) than those seen in adults; in adults, serum/stool levels of calprotectin are considered important as these rise with acute or chronic inflammation, infection, autoimmune disease, or malignancy.^{163–166} Neonatal gut macrophages show a hyper-inflammatory profile and produce calprotectin (unpublished data).¹⁶⁷ Serum/fecal calprotectin levels are physiologically high in the immediate postnatal period, possibly due to immune activation, gut colonization, and perinatal adaptations.¹⁶⁸ Levels gradually decrease with age and stabilize as the immune system undergoes maturation.^{168,169}

Neonates typically show high intestinal calprotectin levels.¹⁶⁵ Neonatal sepsis, necrotizing enterocolitis (NEC), hypoxic stress, and/or infection are associated with higher serum/fecal calprotectin levels, but interpretation can be challenging because of higher and variable baseline levels during this period.^{170,171} Clinical confounders such as neutropenia and/or hyperglycemia can alter calprotectin expression.^{172–175} Serial fecal calprotectin levels can help monitor the severity of illness in sepsis, NEC, postoperative ileus, in the postoperative period after surgery for congenital heart defects, and in some intestinal infections.^{56,176–178} In infants with Hirschsprung disease, fecal calprotectin can help assess clostridial infections and resulting gut inflammation.^{179,180} It may allow tracking of microbial activity/overgrowth, dysmotility, or evolving complications. A gradual decline may reflect improving gut function.¹⁵⁸ Inter-individual variability linked to the type of feedings (breast milk vs formula), mode of delivery, antibiotic use, and intestinal microbiota composition may limit its value.^{56,181}

In one study of NEC, serum calprotectin levels rose from $0.79 \pm 0.33 \mu\text{g/mL}$ in controls to $28.7 \pm 1.85 \mu\text{g/mL}$ in stage II and $38.2 \pm 9.67 \mu\text{g/L}$ in stage III NEC.¹⁶⁴ In another, serum calprotectin levels were recorded as $72.6 \pm 10.6 \text{ mg/dL}$ in controls and $241.1 \pm 57.5 \text{ mg/dL}$ in NEC.¹⁶³ A compact review of a few studies showed elevated serum/stool calprotectin levels in NEC.¹⁸² A meta-analysis of 10 studies with 568 patients with NEC showed a pooled sensitivity, specificity, diagnostic odds ratio (DOR), and area under the curve (AUC) of 0.86 [95% confidence interval (CI): 0.80–0.91], 0.79 (95% CI: 0.75–0.83), 34.78 (95% CI: 15.30–79.07), and 0.92, respectively.¹⁸³ The pooled sensitivity, specificity, DOR, and AUC of subgroup analysis were 0.85 (95% CI: 0.79–0.90), 0.89 (95%

CI: 0.85–0.92), 41.03 (95% CI: 16.87–99.78), and 0.92 for nine studies using ELISA; 0.85 (95% CI: 0.79–0.90), 0.89 (95% CI: 0.85–0.92), 42.08 (95% CI: 18.44–96.04), and 0.93 for six prospective studies; 0.91 (95% CI: 0.82–0.97), 0.93 (95% CI: 0.88–0.96), 69.51 (95% CI: 17.67–273.40), and 0.95 for four studies of preterm infants; and 0.86 (95% CI: 0.77–0.92), 0.94 (95% CI: 0.90–0.97), 53.23 (95% CI: 15.68–180.73), and 0.94 five studies that defined NEC as stage II or above.

Elevated fecal calprotectin can be identified in neonatal diarrhea, where it can help assess the severity of gut mucosal inflammation.¹⁸⁴ Such measures are sensitive but not specific. Elevated fecal calprotectin in an infant with diarrhea may also be the result of food protein-induced enterocolitis, cow's milk protein allergy, or bacterial enteritis.¹⁰¹ Altered fecal calprotectin levels can support diagnosis, help assess disease severity, and response to treatment, but these should be interpreted alongside other clinical/laboratory findings.

Serum calprotectin levels in neonates have been studied as a potential biomarker for the detection of early sepsis, but diagnostic accuracy varies.¹⁸⁵ Some studies have found it less valuable than procalcitonin and C-reactive protein, whereas others show promising sensitivity and specificity for sepsis/NEC if specific cut-off values (such as $>1.7 \mu\text{g/mL}$ or 1.2 ng/mL) are used.^{178,186,187} There may be a need to monitor inter-assay consistency and assay kit performance.¹⁸⁸

Serial fecal calprotectin levels can help monitor the severity of illness in neonatal sepsis, NEC, neonatal postoperative ileus, and some intestinal infections.^{56,176–178} In infants with Hirschsprung disease, fecal calprotectin can help calibrate clostridial involvement and intestinal inflammation.¹⁷⁹ Monitoring changes in calprotectin over time can help assess changes in the severity of inflammation, microbial activity/overgrowth, dysmotility, or evolving complications, whereas a gradual decline may reflect improving gut function.¹⁵⁸ Unfortunately, the diagnostic value of calprotectin levels may be limited due to the wide inter-individual variability, type of feedings (breast milk vs formula), mode of delivery, antibiotic use, and intestinal microbiota composition.^{56,181}

In infants with enterostomies, fecal calprotectin levels again require cautious interpretation as levels are often elevated independent of overt pathology.¹² Exposure of the intestinal mucosa to altered luminal flow, surgical inflammation, and changes in microbial composition can all increase calprotectin release from neutrophils and epithelial cells.¹⁸⁹ Consequently, absolute cutoff values are poorly defined; it is more useful as a longitudinal marker.¹⁹⁰ Rising levels may help identify inflammation, as in enterocolitis/infection, or in mucosal recovery prior to stoma closure.¹⁵⁸ Declining levels may indicate adaptation and healing.¹⁵⁸

CONCLUSION

Calprotectin has been found of clinical value as a reliable, circulating biomarker of inflammation in the newborn. Elevated plasma levels reflect neutrophil-driven inflammation, making it particularly useful for detecting active disease, predicting relapses, and evaluating treatment effectiveness, thereby improving patient management. Fecal calprotectin is particularly useful in differentiating inflammatory from functional bowel disorders to inform responses to therapy. It is interesting to speculate on the therapeutic value of a multifunctional molecule of this nature. However, its biology suggests that the variability in its production and its low specificity are likely to limit its probable worth as a

synthetic therapy. Perhaps a focus on calprotectin's long-evolved powers to scavenge nutrients offers opportunities to manage invasive, resistant bacteria on the neonatal unit.

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Clinical Imaging: Point-of-care Ultrasound for Endotracheal Tube Localization in Neonates: Why It Matters

Monika Kaushal¹, Kalyan C Balla²

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ABSTRACT

Endotracheal tube (ETT) malposition is a frequently encountered difficulty in the management of critically ill infants in the neonatal intensive care units (NICUs). Chest radiography (CXR) still remains the gold standard for confirmation of correct positioning of the ETT, but it is limited by temporal delays, radiation exposure, and workflow inefficiencies. Point-of-care ultrasound (POCUS) offers a rapid, radiation-free, and reliable alternative for confirming the position of the ETT at the bedside. This review summarizes the clinical rationale, scanning technique, available evidence, and practical strategies for using POCUS for ETT localization in neonates.

Keywords: B-mode, Clinical rationale, Depth, Double trachea sign, Dynamic range, Endotracheal tube, Evidence, Focal zone, Frame rate, Gain, Hockey-stick probe, Infants, Linear high-frequency probe, Linear small-footprint or hockey-stick probe, Malposition, Microlinear probe, Newborn, Partial ossification, POCUS, Radiation exposure, Regression formula, Scanning, Sonography, Standardized protocols, Suprasternal notch, Tip-to-arch distance, Workflow inefficiencies.

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KEY POINTS

- Endotracheal tube (ETT) malposition is a frequently encountered difficulty in the management of critically ill infants in the neonatal intensive care units (NICUs).
- Point-of-care ultrasound (POCUS) offers a rapid, radiation-free, and reliable way for confirming ETT position at the bedside.
- In this article, we have summarized available information on the use of ultrasonography for ETT localization in neonates, including the scanning technique(s), supporting evidence, and practical strategies that we have found useful in the NICU.

INTRODUCTION

Accurate placement of the ETT is critical for effective ventilation and prevention of complications in neonates. Despite careful technique, malposition remains common, with studies reporting ETT misplacement rates up to 30% and umbilical venous catheter (UVC) malposition rates as high as 40% when confirmed radiographically.^{1,2}

Chest radiography (CXR) continues to serve as the conventional gold standard for ETT verification; however, it introduces delays, exposes infants to ionizing radiation, and may disrupt workflow during critical stabilization. In contrast, POCUS enables real-time confirmation of ETT position within minutes at the bedside, facilitating prompt correction and minimizing the risk of hypoventilation, atelectasis, or lung injury. This article reviews the rationale, technical aspects, and implementation of POCUS for ETT localization in neonatal intensive care practice.

Clinical Importance of ETT Position

Malposition of the ETT can have serious consequences. A high ETT position risks accidental extubation and CO₂ retention, while a low-lying tube can cause unilateral ventilation, atelectasis, or barotrauma.³ Furthermore, ETT depth may change dynamically with head and neck movement—flexion or extension can shift the

¹Department of Neonatology, Emirates Specialty Hospital, Dubai Healthcare City, Dubai, United Arab Emirates

²Department of Neonatology, Emirates Hospital, Jumeirah, Dubai, United Arab Emirates

Corresponding Author: Monika Kaushal, Department of Neonatology, Emirates Specialty Hospital, Dubai Healthcare City, Dubai, United Arab Emirates, Phone: +971 503761828, e-mail: monikakaushal022@gmail.com

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tip position by up to 2 cm.⁴ Relying solely on delayed radiographic confirmation may prolong periods of hypoxia or ineffective ventilation. Early bedside confirmation using ultrasound, therefore, provides a clinically significant advantage in preventing avoidable morbidity (Fig. 1).

Our ETT-POCUS Algorithm

Clinical Technique for Placement and Monitoring

- Intubate and maintain a neutral head position.
- Place probe horizontally over suprasternal notch (marker right).
- Confirm single tracheal structure and absence of the double trachea sign.
- Rotate the probe perpendicular to identify the aortic arch and ETT tip.
- Measure tip-to-arch distance.
- Adjust ETT by 1–2 mm and re-scan.
- Document measurements.
- Obtain CXR if discrepancy or policy requires.

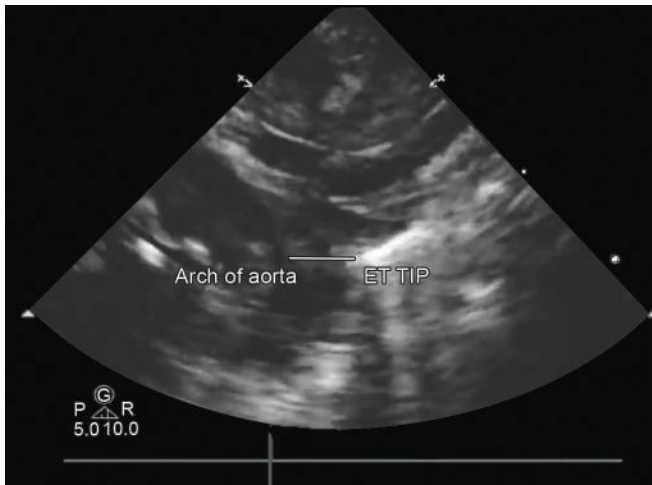


Fig. 1: Sonography shows a hyperlucent ETT in the trachea. A distance of 5–10 mm (marked) between the tip of the ETT and the aortic arch is consistent with optimal placement of the tube

Probe Selection by Gestational Age

Gestational group	Recommended probe	Frequency range	Rationale
Term and late preterm (>34 weeks)	Linear high-frequency probe	8–12 MHz	Optimal penetration and detail of trachea/ETT tip
Preterm (28–32 weeks)	Linear small-footprint or hockey-stick probe	10–15 MHz	Better surface contact, improved near-field resolution
ELBW (<28 weeks)	Microlinear or hockey-stick probe	12–18 MHz	Excellent resolution for superficial structures

ELBW, extreme low birth weight

Machine Settings

- Mode: B-mode
- Depth: 1.5–3 cm
- Focal zone: At the tracheal level
- Gain: Moderate to low
- Dynamic range: 50–70 dB
- Frame rate: >30 fps

Optimal Tip-to-arch Distances

Infant group	Ideal tip-to-arch distance (mm)	Reference
Term (>1,500 gm)	6–9	Şahin et al., 2024 ⁵
VLBW (<1,500 gm)	5–8	Singh et al., 2019 ⁶
ELBW (<1,000 gm)	≈7–9 (Regression formula)	Levkovitz et al., 2023 ⁷

Evidence Supporting ETT-POCUS

Recent studies have validated ultrasound-based measurements against radiography. Levkovitz et al. demonstrated a strong

correlation ($r = 0.83$) between ultrasound-measured ETT-AA distance and radiographic tip position.⁷ Şahin et al. reported 92% concordance between ultrasound-confirmed ETT positions and CXR-confirmed placement at tracheal levels T1–T3.⁵ Meta-analyses further support high specificity and workflow efficiency with POCUS compared to traditional CXR.^{8,9}

Pitfalls and Pearls

- Poor visualization in ELBW infants: Use higher-frequency probes (10–15 MHz).
- Partial ossification: Slightly reduces the acoustic window but remains interpretable.
- Gentle probe pressure: Prevents tracheal compression or vagal response.
- Anatomic variations: Confirm in multiple planes.
- Short tracheal length: Even minor tube adjustments can cause malposition.
- Head movement: Stabilize during and after scanning.
- Reintubation: Always reconfirm ETT location.

Influence of Polymers Used to Prepare ETTs on Ultrasound Visibility

Neonatal ETTs are commonly made of polyvinyl chloride (PVC) or silicone-based soft-flex materials. In our experience, PVC tubes show higher echogenicity and clearer visualization than those composed of silicone (soft-flex tubes); the acoustic properties of the latter are closer to those of human soft tissues.^{6,10–12}

Implementation in NICU Practice

Successful integration of ETT-POCUS requires structured training, workflow checklists, image archiving for quality assurance, and policy updates to designate ultrasound as a first-line verification tool. Early adopter NICUs report improved efficiency, reduced repeat CXRs, and greater clinician confidence.

CONCLUSION

Point-of-care ultrasound provides a rapid, accurate, and radiation-free method for confirming ETT position in neonates. Currently available evidence supports its reliability and shows a strong correlation with radiographic confirmation. Standardized protocols and regular competency assessments can help establish POCUS as the preferred first-line tool for airway verification in NICUs.

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Radiology Case Reports: Midgut Malrotation without Volvulus

Anil G Rao

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ABSTRACT

Intestinal malrotation is a congenital condition in which the intestines become fixed in an abnormal position during fetal development and do not rotate further. This condition presents most frequently during infancy with symptoms such as bilious vomiting and abdominal distension, although some individuals may remain asymptomatic or develop chronic abdominal pain, nausea, or vomiting later in childhood or adolescence. The diagnosis is typically made using imaging studies, and treatment usually involves surgical correction to prevent serious complications. The pathophysiology of malrotation is not well known; there is an error in embryologic development of the midgut between weeks 5–10 of gestation, when the intestine normally herniates, undergoes a 270-degree counterclockwise rotation, and then returns to the abdominal cavity. Mutations or altered expression of genes involved in laterality and gut morphogenesis, such as *forkhead box F1 (FOXF1)*, paired-like homeodomain 2 (*PITX2*), and components of the nodal growth differentiation factor (NODAL) signaling pathway, have been implicated. Here, we present plain and contrast-enhanced radiological images from an infant who presented with signs of intestinal obstruction. The management of intestinal malrotation primarily involves supportive management and surgical intervention to prevent life-threatening complications such as midgut volvulus. The standard treatment is the Ladd procedure, which includes detorsion of the bowel if volvulus is present, division of obstructing Ladd bands, widening of the mesenteric base to reduce the risk of future twisting, and repositioning of the intestines in a nonrotated configuration.

Keywords: Asplenia, Case report, Copy number variants, Development, *Forkhead box F1*, Intestinal herniation, Intestinal rotation, Intestine, Ladd band, Ladd procedure, Meckel's diverticulum.

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KEY POINTS

- Midgut malrotation is a congenital condition in which the intestines become fixed in an abnormal position during fetal development and do not rotate further.
- The pathophysiology of malrotation is not well known. There is an error in embryologic development of the midgut between weeks 5–10 of gestation.
- Mutations or altered expression of genes involved in laterality and gut morphogenesis, such as *forkhead box F1 (FOXF1)*, paired-like homeodomain 2 (*PITX2*), and components of the nodal growth differentiation factor (NODAL) signaling pathway, have been implicated, particularly in patients with heterotaxy or other congenital anomalies.
- Management of intestinal malrotation primarily involves supportive management and surgical intervention to prevent life-threatening complications such as midgut volvulus. The standard treatment is the Ladd procedure, which includes detorsion of the bowel if volvulus is present and division of the obstructing Ladd bands.

Intestinal malrotation is a congenital condition in which the intestines become fixed in an abnormal position during fetal development and do not rotate further.¹ Consequently, the bowel is seen abnormally positioned in the abdomen and may be inadequately anchored, increasing the risk of intestinal obstruction or twisting of the bowel, known as volvulus.² This condition presents most frequently during infancy with symptoms such as bilious vomiting and abdominal distension, although some individuals may remain asymptomatic or develop chronic abdominal pain, nausea, or vomiting later in childhood or adolescence. Diagnosis is typically

Department of Pediatric Radiology, Advocate Children's Hospital, Chicago, Illinois, United States of America

Corresponding Author: Anil G Rao, Department of Pediatric Radiology, Advocate Children's Hospital, Chicago, Illinois, United States of America, Phone: +8477238236, e-mail: radresearch2000@gmail.com

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made using imaging studies, and treatment usually involves surgical correction to prevent serious complications.

CASE DESCRIPTION

Here, we present plain and contrast-enhanced radiological images from a 1-week-old male infant who presented with bilious vomiting for which an upper gastrointestinal (UGI) series study was done (Figs 1 to 5). The findings were consistent with a midgut malrotation without volvulus:

Figure 1: Frontal supine abdomen radiograph showing a gas-distended stomach without bowel obstruction.

Figures 2 and 3: Fluoroscopic image in the right lateral decubitus position (Fig. 2) and supine frontal view (Fig. 3) following

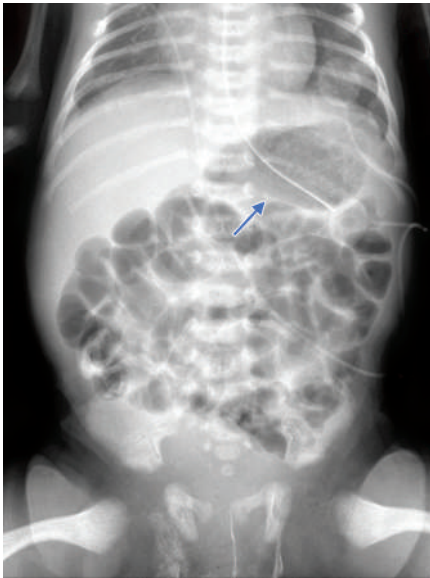


Fig. 1: Scout supine frontal abdomen radiograph showing a distended stomach (arrow) with a nonspecific nonobstructive bowel gas pattern

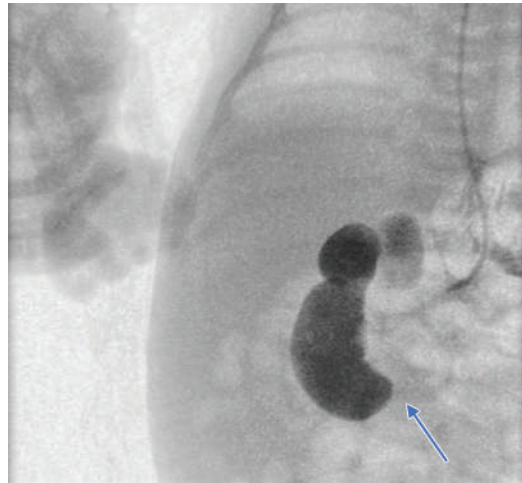


Fig. 3: Supine frontal fluoroscopic image showing dilated duodenum with tapering in its proximal third portion (arrow)

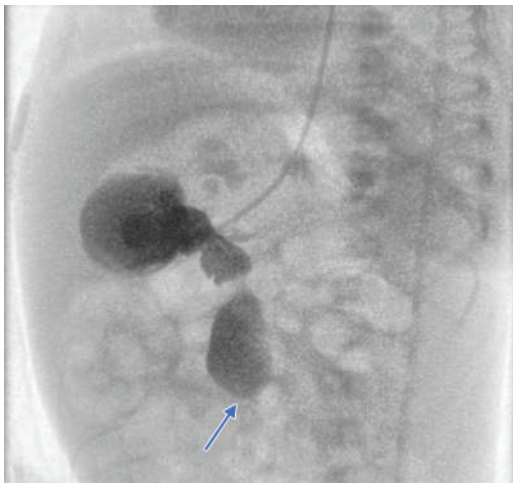


Fig. 2: Right lateral decubitus fluoroscopic image of abdomen after water-soluble contrast injection into the stomach showing dilated second portion of the duodenum (arrow)

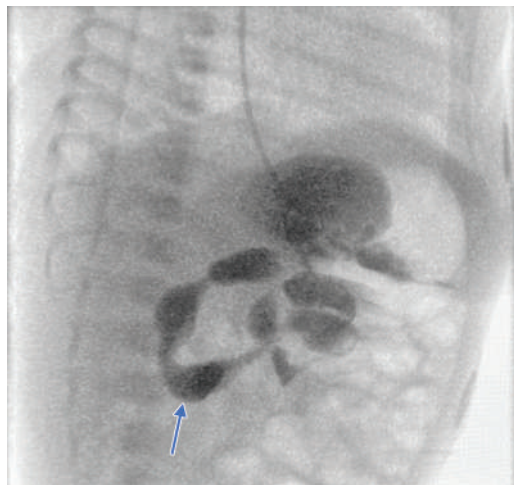


Fig. 4: Left lateral decubitus fluoroscopic image showing the appearance of the retroperitoneal course of the duodenum (arrow) with contrast flowing into proximal jejunum, excluding complete obstruction

water soluble contrast injection into the stomach through the nasogastric tube, showing dilated stomach and dilated first and second portions of the duodenum with narrowing at the proximal third portion of the duodenum. The second portion also has a retroperitoneal course.

Figures 4 and 5: Fluoroscopic right lateral decubitus and supine frontal views showing progression of contrast to the distal portions of the duodenum and proximal jejunum with the focal transition/stenosis in the proximal third portion. This was reported as duodenal obstruction/stenosis, and the duodenojejunal junction was felt to be normal on this study.

At surgery, duodenal obstruction at this site was seen due to Ladd's bands, and the patient also had midgut malrotation. Ladd's procedure was performed, and the patient was discharged following an uneventful postsurgical recovery. This case highlights

that an UGI series study is not 100% sensitive or specific for the diagnosis of midgut malrotation and midgut volvulus, even though it is done as the first line of imaging evaluation for these entities. False positive and false negative results can therefore happen.

The pathophysiology of malrotation is not well known. There is an error in embryologic development of the midgut between weeks 5–10 of gestation, when the intestine normally herniates, rotates 270 degrees counterclockwise around the superior mesenteric artery, and then returns to the abdominal cavity.³ In malrotation, this rotational process is incomplete or abnormal, leading to improper positioning of the duodenum and cecum and inadequate fixation of the mesentery.⁴ The resulting narrow mesenteric base predisposes the bowel to twisting (midgut volvulus), while abnormal peritoneal bands (Ladd bands) may form and compress the duodenum, causing obstruction.¹

Malrotation is usually sporadic, though familial cases and associations with genetic syndromes suggest a heritable



Fig. 5: Supine frontal fluoroscopic image of the abdomen showing a transition in the lumen of the duodenum in its proximal third portion (arrowhead), indicating obstruction and appearance of normal position of the duodenojejunal junction (arrow) to the left of the spine and almost at the same level or in retrospect, at a lower level than the first portion of the duodenum. This can be seen when the stomach is distended

component.⁵ The genetic pathogenesis of intestinal malrotation is not fully understood. There are anatomic disruptions in embryonic left–right patterning, midgut rotation, and mesenteric fixation during early development.^{5,6} Mutations or altered expression of genes involved in laterality and gut morphogenesis, such as *FOXF1*, paired-like homeodomain 2, and components of the NODAL signaling pathway, have been implicated, particularly in patients with heterotaxy or other congenital anomalies.^{6–9} Copy number variants have also been noted.¹⁰ These genetic disturbances can possibly interfere with normal midgut rotation around the superior mesenteric artery, leading to abnormal intestinal positioning and fixation that might increase the risk of obstruction and volvulus.⁶

Intestinal malrotation is frequently associated with other congenital anomalies, particularly those involving abnormal embryologic development and left–right axis formation. It commonly occurs in association with congenital diaphragmatic hernia, abdominal wall defects such as omphalocele and gastroschisis, and cardiac anomalies, especially in patients with heterotaxy syndromes.^{11–15} Malrotation may also be seen alongside intestinal atresias, Meckel's diverticulum, and anomalies of the spleen, including asplenia or polysplenia.^{16–18} These associated conditions reflect a broader disturbance in embryonic development and often influence the timing of diagnosis, clinical presentation, and overall management of intestinal malrotation.¹

Management of intestinal malrotation primarily involves supportive management and surgical intervention to prevent life-threatening complications such as midgut volvulus.^{4,19} The standard treatment is the Ladd procedure, which includes detorsion of the bowel if volvulus is present, division of obstructing Ladd bands, widening of the mesenteric base to reduce the risk of future twisting, and repositioning of the intestines in a nonrotated configuration; an appendectomy is often performed to avoid diagnostic confusion later.^{20–22} Surgery is recommended even in many asymptomatic patients due to the unpredictable risk of volvulus.²³

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