

THE SCIENCE OF BREAST MILK

Exploring Breast Milk Nutrients
and Microbiomics



母乳研究前沿

探秘母乳的营养成分和微生物组

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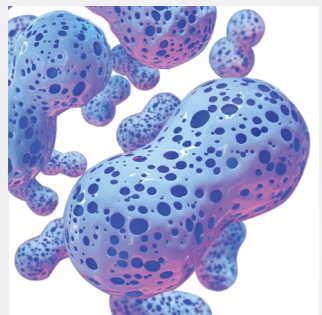
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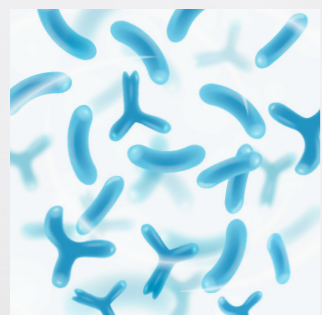
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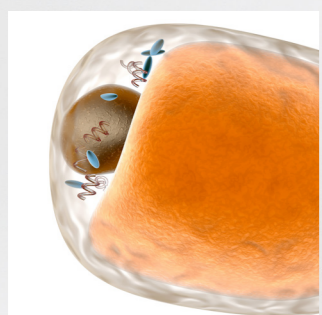
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Cover image: An illustration of chains of amino acids, the building blocks of proteins.
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Unravelling the power of breast milk

Breast milk is considered to be the ideal natural food for infants. It's a rich source of nutrition crucial for a baby's growth and development. Scientists have long been working to unravel the composition of breast milk, while also exploring the impact of the nutrients on the development of infants' neurological, digestive and immune systems.

Breast milk contains a multitude of complex proteins. Lactoferrin is one such protein, found to be central to a baby's brain development, which points to a feeding regime that may protect preterm infants against brain impairment.

Breast milk also provides crucial nutrients to infants and babies in a form that is easily digestible and absorbable. Researchers are studying amino acids — building blocks of proteins — while measuring the composition of these in breast milk and how easily they can be digested.

The unique bioactive components in breast milk may work together to promote a healthy gut microecology in infants. Researchers are looking into the interactions

between the microbiome, the environment and the gut in preterm infants. They are also studying how the infant microbiome metabolizes essential ingredients in breast milk, which could potentially indicate interventions to tackle gut abnormalities in newborns.

The unique composition of breast milk can also facilitate early immune development. Researchers are exploring the immune components in breast milk, which is important to gain insights into the maturation of intestinal barriers and immune systems in infants.

To pool the wealth of information about breast milk, researchers have developed an open, collaborative database. As the database grows, it might help further reveal the links between different breast milk components and their impact on infant health.

The following pages feature outlines of some significant findings about breast milk, made by researchers globally, and the impact of these on infant health. ■

发现母乳的价值

母乳被认为是婴儿最佳的天然食物，富含全面均衡的营养成分，对婴儿的生长发育至关重要。科学家一直在研究母乳的组成，并探索这些营养成分对婴儿早期神经、消化、吸收、免疫系统等方面的多重功能。

母乳中富含多种结构的蛋白质，其中乳铁蛋白被发现对婴儿的大脑发育十分关键，提示一种可以预防早产儿脑损伤的喂养模式。

母乳还以最易消化吸收的形式为婴幼儿提供营养。研究人员正在研究蛋白质的基本成分氨基酸，深入解构母乳中氨基酸的组成及其易消化程度。

母乳中独特的生物活性成分可共同促进婴儿健康的肠道微生态。研究人员正在探索早

产儿体内微生物组与环境、肠道的相互作用，以及婴儿微生物组如何代谢母乳中的关键成分，从而提出针对新生儿肠道问题的潜在干预手段。

母乳的独特成分构成还能满足婴幼儿早期的免疫发育需求。研究人员正在探索母乳成分的免疫功能，这对于深入认识婴儿肠道屏障和免疫功能成熟至关重要。

为了将母乳信息集中起来，研究人员开发了一个公开的协作型数据库。通过数据库的不断扩大，为进一步还原母乳成分之间的内在联系、揭示对婴儿健康的影响提供支持。

接下来的内容汇集了全球研究人员关于母乳的重要发现，以及这些发现对于婴儿健康的重要意义。■

Milk protein increases brain volume in premature babies

Lactoferrin may improve brain development in infants born very premature.

More than one in ten babies worldwide are born prematurely, classified as three weeks or more before the typical 40 week conclusion of a pregnancy. Preterm births put infants at risk of infection, inflammation, and oxidative stress, causing potential brain injury or neurodevelopmental impairments. Those born before 32 weeks, face even greater challenges.

A study¹ led by paediatrician, Mandy Belfort, from Brigham and Women's Hospital and Harvard Medical School, in Boston, United States, has found infants exposed to higher amounts of the protein lactoferrin in breast milk have larger brain volumes. The finding suggests that lactoferrin may protect the brains of very preterm infants. The study was published in *Pediatric Research* in 2024.

Previously, diet-based interventions have shown promise in promoting brain development and lowering the risk of adverse neurodevelopmental outcomes for premature babies. One potential

They emphasize the importance of supporting breast feeding of very preterm babies.

neuroprotective agent is lactoferrin, which is found in milk and has anti-inflammatory and antioxidant properties. But, research into its effects on neurodevelopment is limited.

The Belfort study measured lactoferrin in milk samples from the mothers of 36 very preterm infants as a way to assess their exposure to lactoferrin during their hospital stay. The team collected milk samples 14 and 28 days after the infants' birth. Lactoferrin levels were then used to divide the infants into two groups — low exposure (0.06-0.13 mg/mL) and high exposure (0.22-0.35 mg/mL).

At the point at which a preterm infant would have reached full term, they underwent quantitative magnetic resonance imaging (MRI) scans to measure their total and regional brain volumes.

The babies with higher lactoferrin exposure had significantly larger brains. They also had larger volumes of cortical grey matter — the part of the brain responsible for higher-order functions such as sensory processing; and deep grey matter — the area responsible for tasks such as information processing.

When the researchers adjusted for variables such as gestational age at birth, total protein intake, sex, and 'weight z-score' (a measure of how much weight differs from the average), the association between lactoferrin exposure and brain volumes remained strong.

The findings highlight lactoferrin's

potential neuroprotective effects. The researchers emphasize the importance of supporting breast feeding of very preterm babies, and call for further investigations into the role of the components of maternal milk in protecting the brain of these vulnerable infants. ■

Reference

1. Atayde, A. M. P. et al. *Pediatr. Res* (2024).



Science Photo Library - PASEKAV Brand X Pictures/Getty



A protein called lactoferrin has been linked to improved brain development in preterm infants.

一种名为乳铁蛋白的蛋白质被发现或能促进早产儿大脑发育。

母乳蛋白使早产儿的脑容量更大

乳铁蛋白或能促进极早产儿的大脑发育。

全世界每十个婴儿中就有一个以上是早产儿，即比正常胎龄 40 周提前至少 3 周出生的婴儿。早产儿面临感染、炎症和氧化应激的风险，有可能造成脑损伤或神经发育障碍。出生时不足 32 周的极早产儿面临更大的风险。

美国波士顿布列根妇女医院和哈佛医学院的儿科专家 Mandy Belfort 领导的一项研究【1】发现，摄入含高乳铁蛋白的母乳的婴儿脑容量更大。团队指出，该发现表明乳铁蛋白或能保护极早产儿的大脑。该研究 2024 年发表在《*Pediatric Research*》上。

此前研究显示，饮食干预有助于促进早产儿的大脑发育，降低神经发育不良的风险。乳铁蛋白是母乳中一种潜在的神经保护剂，具有抗炎和抗氧化的特性。但有关乳铁蛋白对极早产儿神经发育影响的研究十分有限。

该研究检测了 36 名极早产儿母亲母乳样本中的乳铁蛋白含量，以此评估这些婴儿在住院期间的乳铁蛋白暴露水平。团队在婴儿出生后 14 天和 28 天采集了母乳样本，并根据母乳乳铁蛋白含量将婴儿分为两组：低暴露组（0.06-0.13 mg/mL）和高暴露组（0.22-0.35 mg/mL）。

当这些早产儿足月时，研究人员再通过定量磁共振成像（MRI）扫描测量它们总脑容量和局部脑容量。乳铁蛋白暴露水平高的婴儿脑容量明显更大，而且大脑灰质（负责感官处理等高级功能的脑区）和深部灰质（负责信息处理等任务的脑区）的体积都更大。

当团队对婴儿出生时胎龄、蛋白质总摄入量、性别和“体重 Z-评分”（显示婴儿体重偏离平均值的水平）等变量进行校正后，乳铁蛋白暴露量与脑容量的关联依然显著。

团队认为，这些发现凸显了乳铁蛋白对早产儿具有潜在的神经保护作用。他们强调，对极早产儿的母亲提供母乳喂养支持非常重要，他们还呼吁进一步研究母乳成分对于保护脆弱早产儿大脑发育的作用。■

他们强调了支持极早产儿母乳喂养的重要性。

Understanding milk's amino acid profile

To understand infants' dietary demands, an accurate assessment of the amino acid composition and digestibility of breast milk is needed.

Amino acids are building blocks of proteins, and essential for an infant's healthy development and growth. They are also needed to synthesize neurotransmitters that are central to neurological development, support the growth of immune cells that fight infections, and contribute to metabolism, providing energy.

Knowing the amino acid composition of the milk, and how easily they can be digested by babies is critical to understanding infants' dietary needs. But most studies provide only a rough estimate of the amino acid composition of milk, and don't investigate how easily they are digested.

Now, a study by biologist, Suzanne Hodgkinson, at Massey University, in Palmerston North, New Zealand, has measured the amino acid composition of human milk from Chinese women, and amino acid digestibility¹. The study was published in the *Journal of Nutrition* in 2023.

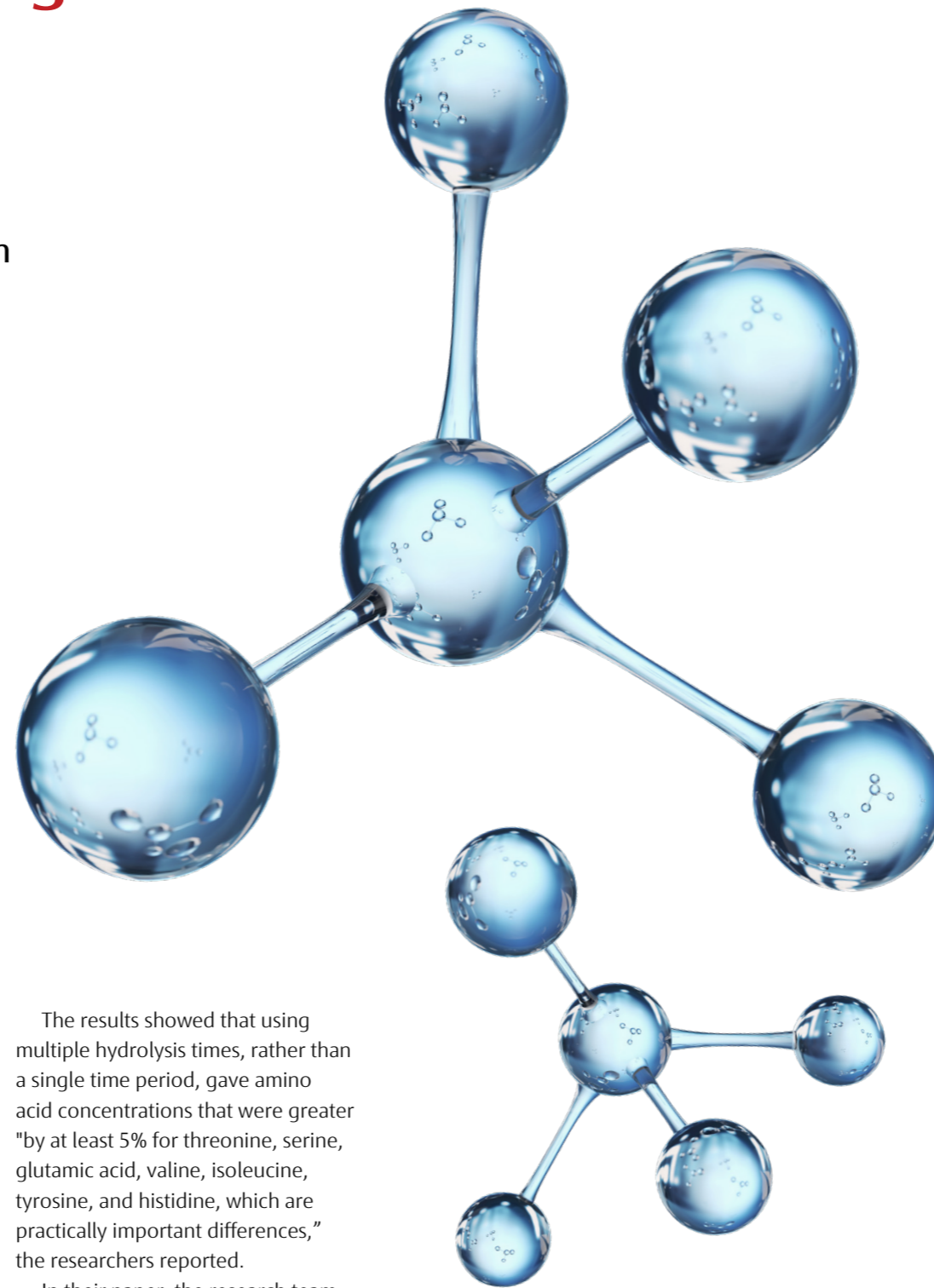
After obtaining milk samples from 75 Chinese women in their 10th to 14th week of lactation, Hodgkinson and her colleagues took a two-step

approach to assessing the milk's amino acid profile. First, they used hydrolysis, a chemical process that breaks down proteins to release their constituent amino acids.

Most previous studies on human milk use a single hydrolysis time period, but Hodgkinson's team employed multiple time periods. This is more accurate because amino acid containing compounds may be broken down at different rates. High-performance liquid chromatography was used to measure the amount of each amino acid in the samples.

In a second step, the team measured the uptake of amino acids from the ileum — the final part of the small intestine — of three-week old piglets, which have digestive systems similar to three-month old human infants. This measurement is important because not all ingested amino acids are absorbed by the gut. The Hodgkinson team fed the human milk samples to six piglets. Eight hours later they collected the contents from each piglet's ileum, and once again measured the amino acid profile.

The comprehensive analysis not only accurately estimated the amino acid composition of milk, it also identified which amino acids may be effectively absorbed by infants. This included analysis of amino acids that cannot be synthesized by the body in sufficient quantities.



The results showed that using multiple hydrolysis times, rather than a single time period, gave amino acid concentrations that were greater "by at least 5% for threonine, serine, glutamic acid, valine, isoleucine, tyrosine, and histidine, which are practically important differences," the researchers reported.

In their paper, the research team compared their comprehensive profile of milk from Chinese mothers with similar analyses from populations of mothers in New Zealand and France. ■

Reference

1. Hodgkinson, S. M. et al. *J. Nutri.* 153(12) 3439-3447 (2023).

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Breast milk is a source of molecules such as amino acids, the building blocks of protein.

母乳是制造蛋白质所必需的氨基酸等分子的来源。

揭示母乳的独特氨基酸谱

要了解婴儿的饮食需求,就要准确评估母乳的氨基酸组成及其消化率。

氨基酸是蛋白质的基本组成成分,对婴儿的健康发育和成长起到了关键作用。氨基酸还能合成神经系统发育所需的神经递质,支持免疫细胞的生长以抵抗感染,并促进新陈代谢,提供能量。

了解不同人群母乳的氨基酸组成及其在婴儿体内的易消化性,对于把握不同群体婴儿的饮食需求至关重要。然而,大多数研究只是大致评估了母乳中的氨基酸组成,并未研究它们的易消化程度。

最近,新西兰梅西大学的生物学家 Suzanne Hodgkinson 领导的一项研究分析了中国女性母乳的氨基酸组成和氨基酸消化率【1】。该研究 2023 年发表在《*Journal of Nutrition*》上。

团队收集了 75 名在哺乳期第 10 至第 14 周的中国女性的母乳样本,并采用两步法全面分析了母乳的氨基酸谱。他们第一步先使用了水解法,这种化学过程能分解蛋白质并释放其中的氨基酸。

之前大部分关于母乳的研究都使用单一的水解时间段,而该团队采用了多个时间段。这种方法更准确,因

为含有氨基酸的化合物会以不同的速率被分解。接着他们采用高效液相色谱法测定了母乳样品中每种氨基酸的含量。

第二步,团队测量了三周大的仔猪的回肠(小肠的最后一段)对氨基酸的吸收情况,这些仔猪的消化系统与三个月大的人类婴儿相似。这些测量非常重要,因为并非所有摄入的氨基酸都能被肠道吸收。团队给六头仔猪喂食了人母乳样本,在八小时后采集了每头仔猪回肠内的消化物,并再次分析了氨基酸谱。

这一全面分析不仅旨在准确评估中国女性母乳的氨基酸组成,还确定了哪些氨基酸可被婴儿有效吸收,包括半胱氨酸这类对营养至关重要的氨基酸。

团队指出,相较于单一时间段的水解,采用多个水解时间段可以得到更高的氨基酸浓度。“对于苏氨酸、丝氨酸、谷氨酸、缬氨酸、异亮氨酸、酪氨酸和组氨酸来说,至少提高了 5%,这是很有实际意义的差异。”

团队还在论文中将他们得到的中国女性母乳谱与新西兰和法国女性的类似分析进行了比较。■

Knowing the amino acid composition of the milk is critical.

了解母乳中的氨基酸组成至关重要。

Gut microbiota and premature baby health

Life-threatening intestinal problems in preterm infants may be rooted in changes in the gut microbiome.

Infants that are born very premature — at least eight weeks earlier than a normal pregnancy of roughly 40 weeks — risk life-threatening conditions such as necrotizing enterocolitis (NEC), an inflammation of the intestine, and late-onset sepsis (LOS), a bloodstream infection. Evidence is building that the baby's gut microbiome — a diverse community of microorganisms in the intestines — is central to these disorders.

Now, neonatologist, David Healy from University College Cork in Ireland, and colleagues have reviewed research into the interactions between the microbiome and the gut in preterm infants and animals. Their findings are published in *Nature Microbiology*¹.

Healy and his colleagues looked into how gut microbiota changes in healthy newborns. Immediately after birth, the gut is dominated by bacteria that thrive in oxygen-rich environments. In the first few days, these consume oxygen, causing its levels in the gut to plummet. This creates an environment conducive for strict anaerobes — organisms that need an oxygen-free environment — eventually leading to the establishment of adult gut microbiota.

Studies have found that, compared to infants born at term, the intestines of premature infants are more permeable; have fewer Paneth cells, which play a role in protection from infection; and an incomplete layer of intestinal mucous. The review reports

that these conditions could increase the chances of harmful bacteria moving across the gut to cause NEC or LOS.

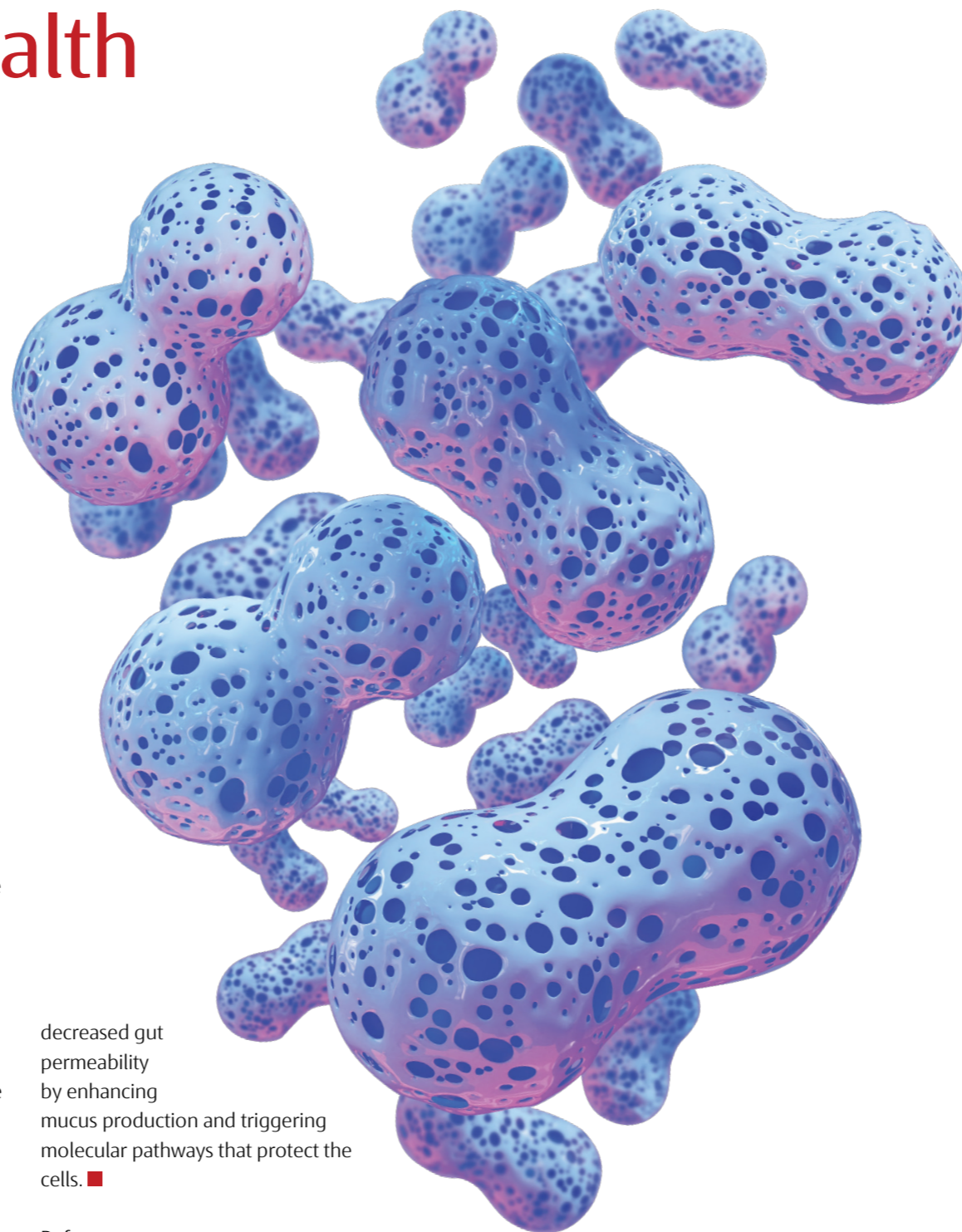
Research also indicates that an increase in diversity and dominance of strict anaerobes within the gut microbiome is linked to fewer complications related to prematurity. For example, NEC occurs in the guts of preterm infants where strict anaerobes failed to dominate.

Several factors may affect the microbiota composition, including whether the infant was delivered vaginally, and whether they were breast fed. However, hospital care has the biggest impact. Neonatal intensive care units are sites of diverse bacterial communities, which along with treatment such as antibiotics, alter how the gut is colonized.

The authors concluded that interactions between the colonizing microbiome and the very preterm intestine may play a greater role in the health and wellbeing of premature infants than is currently appreciated.

Animals studies hint that changes to microbiota might help tackle gut abnormalities in newborns.

In newborn mice, for example, increased intake of certain species of the bacteria *Bifidobacterium* stabilises proteins that help form junctions between cells, reducing the leakiness of the gut epithelium. Meanwhile, in mice with intestinal inflammation, the bacterium *Lactobacillus rhamnosus*



decreased gut permeability by enhancing mucus production and triggering molecular pathways that protect the cells. ■

Reference

1. Healy, D. B. *et al. Nature Microbiology* 7, 22-33 (2022).

Premature infants have intestines that are more permeable.

FOTOGRIIN/Shutterstock



Intake of certain species of the bacteria *Lactobacillus* (shown in an artist's impression) decrease gut permeability in mice with intestinal inflammation.

摄入特定种类的乳杆菌（如图所示）会降低患有肠炎的小鼠的肠道渗透性。

肠道菌群与早产儿健康

早产儿面临的危及生命的肠道问题可能源于肠道微生物组的变化。

正常约 40 周胎龄提前至少 8 周出生的婴儿属于极早产儿。极早产儿面临的生命危险包括坏死性小肠结肠炎（NEC）等肠道炎症，以及迟发型败血症（LOS）等血液感染。越来越多的证据显示，婴儿的肠道微生物组——肠内多样化的微生物群落——对这些疾病至关重要。

爱尔兰科克大学的新生儿专家 David Healy 及其团队回顾了关于早产儿和动物体内微生物组与肠道相互作用的研究。他们的综述发表在《自然-微生物学》（*Nature Microbiology*）【1】上。

Healy 及其团队研究了健康新生儿肠道菌群的变化。研究显示，新生儿刚出生时，肠道内占主导的是在富氧环境下生长的细菌。在最初的几天里，这些细菌会消耗氧气，导致肠道中的氧水平骤降，从而为严格厌氧菌（需要无氧环境的生物）创造了有利的环境，最终促进成年肠道菌群的形成。

多项研究发现，与足月出生的婴儿相比，早产儿肠道的渗透性更高，潘氏细胞（一种能防感染的上皮细胞）较少，且肠粘膜层不完整。该综述发现，这些状况可能会增加有害细菌穿过肠道上皮导致坏死性小肠结肠炎或

迟发型败血症的风险。

研究还表明，肠道微生物组的多样性增加以及严格厌氧菌占主导地位与早产儿并发症的减少有关。例如，坏死性小肠结肠炎只发生在严格厌氧菌未能占主导的早产儿肠道中。

多种因素可能影响肠道菌群的组成，包括婴儿是否是阴道分娩，以及是否接受母乳喂养。但研究团队发现医院护理的影响最大。新生儿重症监护室是各种细菌群落的聚集地，这些细菌群落加上抗生素等疗法，改变了肠道菌群的定植方式。

作者总结道，定植的微生物组与极早产儿肠道间的相互作用，对早产儿健康福祉的决定作用可能比当前认为的更大。

动物研究表明，肠道菌群的变化可能有助于解决新生儿肠道异常的问题。

举例来说，在新生小鼠体内，增加某类双歧杆菌（*Bifidobacterium*）的摄入有助于稳定形成细胞间连接的蛋白质，减少肠上皮的渗透。同时，在患有肠炎的小鼠体内发现，鼠李糖乳杆菌（*Lactobacillus rhamnosus*）能通过增加粘液的产生和触发保护细胞的分子通路，降低肠道的渗透性。■

早产儿肠道的渗透性更高。

Revealing how babies digest breast milk

Establishing how the infant microbiome breaks down human milk oligosaccharide could lead to personalized interventions for preterm infants.

A study based in the United States has unravelled the mystery of how human breast milk is metabolized by the gut¹.

The gut microbiome is central to growth, development and maintaining human health. An ecosystem of incredible diversity, it teems with trillions of bacteria, fungi and other microorganisms, that do everything from converting food to energy and protecting us from pathogens.

Every microbiome is unique, affected by a range of factors including DNA and diet. The microbiome of infants in particular changes rapidly, and has been shown to affect long-term health.

Now, a team of researchers from the University of California, Berkeley in the US has developed a method to determine how interactions in infant microbiomes influence the growth of *Bifidobacterium breve*, a known 'good bacteria' found in infant microbiomes and a common food supplement, and how different infant microbiomes metabolize human milk oligosaccharides (HMOs), an essential component of human breast milk.

The team cultivated three microbiomes in the lab, established from faecal samples taken from two full-term and one pre-term infants, called FT1, FT2 and PT1, respectively.

They then introduced a common HMO called 2'-fucosyllactose (2'FL), made up of the sugars galactose, fucose and glucose, to the model microbiomes.

They found the three microbiomes had significantly different responses to 2'FL: FT1 had a drastic increase in *B. breve*, FT2 had a moderate increase, whereas no effect was observed in PT1. To rule out this being due to the microbiomes having different strains of *B. breve*, they ran a genetic analysis and determined that the strains of *B. breve* in each microbiome were highly similar and that none of them could metabolize 2'FL on their own.

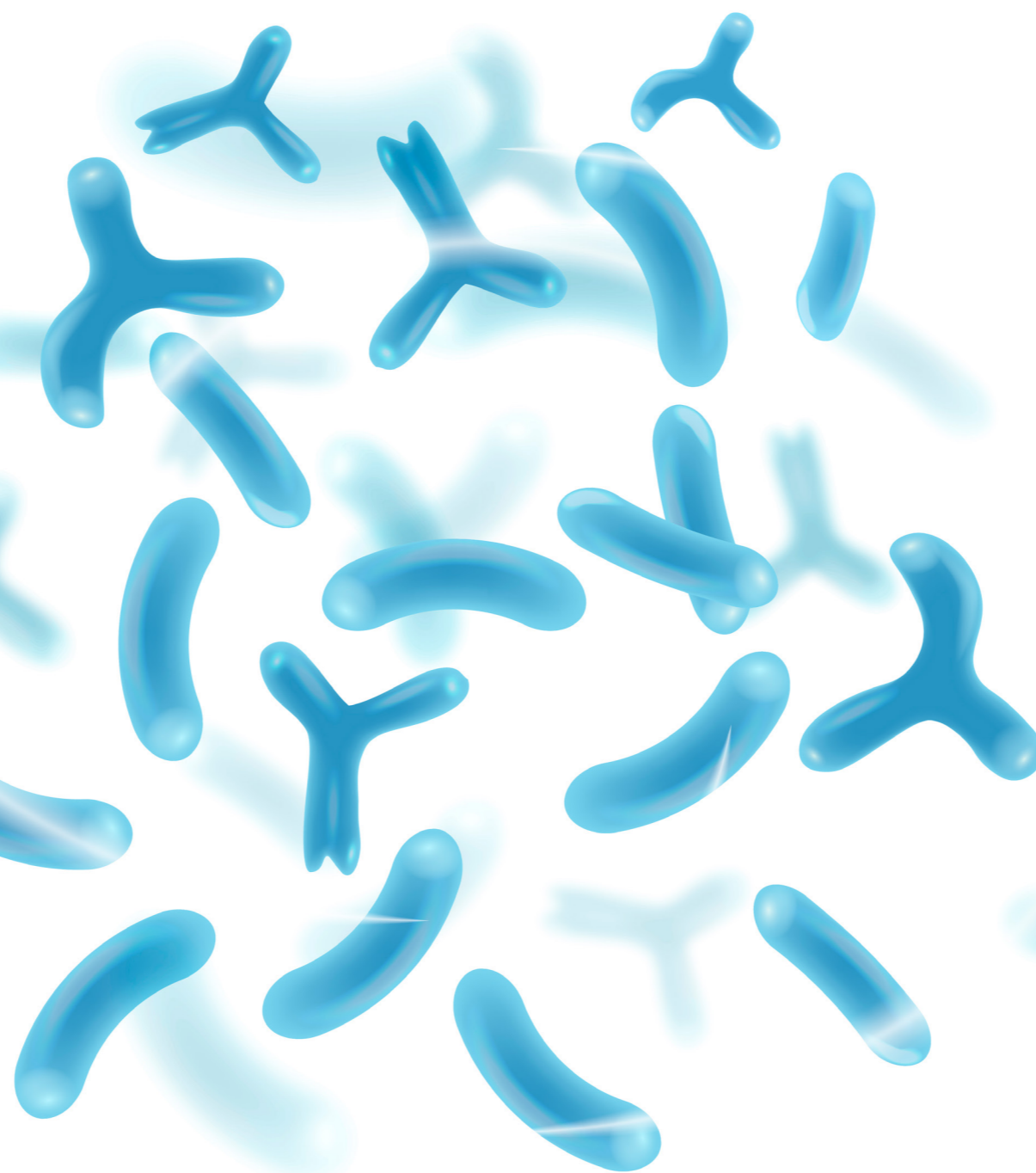
This led them to look at the other species present in the microbiomes that might make this interaction work. They used co-culture experiments to find that the bacteria, *Ruminococcus gnavus*, broke down 2'FL, allowing *B. breve* to use the resulting D-lactose for growth.

To further confirm this, they added *R. gnavus* to the preterm microbiome grown in 2'FL, and the microbiome shifted to become *B. breve* dominated. This allowed them to reshape the preterm infant microbiome into something similar to a full-term infant microbiome.

According to the researchers, this work demonstrates the potential of personalized microbiome interventions, and the models developed could be extended to investigate the interactions between other species in the microbiome. ■

Reference

1. Lou, Y. C. et al., *Nat. Commun.* 14, 7417 (2023).



The microbiome of infants changes particularly rapidly.

Uprate/Shutterstock



An illustration of microorganisms in the gut, which help infants digest breast milk.

肠道微生物图示。肠道微生物能够帮助婴儿消化母乳。

解开母乳消化之谜

探明婴儿微生物组如何分解母乳低聚糖，可为早产儿提供个性化的干预措施。

美国的一项研究揭开了人类母乳如何被肠道代谢的神秘面纱【1】。

肠道微生物组在生长、发育以及维持人体健康方面发挥着关键作用。作为一个多样性异常丰富的生态系统，它含有无数细菌、真菌和其他微生物，它的功能更是无所不包，例如将食物转化为能量，以及帮助我们抵御病原体的侵害。

每个微生物组都有其独特性，受到遗传、饮食等多种因素的影响。婴儿体内微生物组的变化速度尤其快，而且会影响长期健康。

现在，美国加州大学伯克利分校的团队提出了一种方法，可以确定婴儿微生物组内的相互作用如何影响短双歧杆菌（*Bifidobacterium breve*）的生长，以及不同的婴儿微生物组如何代谢母乳中的一种重要成分——母乳低聚糖（HMOs）。短双歧杆菌是婴儿微生物组内的一种“有益菌”，也是一种常见的食品补充剂。

该团队在实验室用两个足月婴儿和一个早产婴儿的粪便样本培养了三个微生物组，分别命名为FT1、FT2和PT1。

他们向这些模型微生物组中添加了2'-岩藻糖基乳糖（2'FL）这

一常见的母乳低聚糖——2'FL由半乳糖、岩藻糖和葡萄糖构成。

研究发现，这三个微生物组对2'FL的响应截然不同：在FT1中，短双歧杆菌数量激增；在FT2中，短双歧杆菌数量适度增加；而在PT1中未观察到任何变化。为了排除这是因为这些微生物组含有不同的短双歧杆菌菌株，团队进行了基因分析，确定了每个微生物组的短双歧杆菌菌株都高度相似，而且都不能单独代谢2'FL。

团队随后决定研究这些微生物组中可能驱使这种相互作用的其他物种。他们通过共培养实验发现，活泼瘤胃球菌（*Ruminococcus gnavus*）能分解2'FL，让短双歧杆菌利用由此产生的D-乳糖生长。

为进一步证实这一点，他们将活泼瘤胃球菌添加到在2'FL中培养的早产儿微生物组中，结果微生物组转变为以短双歧杆菌为主。这使他们能够将这个早产儿微生物组重建为类似于足月婴儿的微生物组。

团队指出，此项工作不仅证明了微生物组个性化干预的巨大潜力，而且所构建的模型也可用于研究微生物组内其他物种间的交互作用。■

婴儿体内微生物组的变化速度尤其快。

A periodic table of breast milk

A publicly available database may help unravel the biochemical components of breast milk.

An international team developed an open, collaborative database to pool our collective knowledge about breast milk.

Human breast milk comprises a range of components, from nutrients such as carbohydrates, lipids, proteins, vitamins and minerals, through to bioactive components including hormones, cytokines, growth factors, antimicrobial substances, cells and more¹.

Adding further complexity, breast milk dynamism depends on the mother, infant and other environmental factors, and varies with time. A big data system would make it easier for researchers to analyse the interplay between these factors and the biochemistry of the milk itself².

Now, a team of researchers from Hungary and the United States have developed a bespoke database called MilkyBase to corral disparate publication records and to collate a wealth of information not only about the biochemical components of breast milk, but also the various conditions under which the samples were measured.

By combining manual entry and machine learning, the team were able to collect approximately 10,000 entries from existing publications. They provide information about the biochemical make up of human breast milk under different conditions of the mother such as diet and the gestational age.

Microsoft's Excel programme was chosen as the initial home of the database, due to accessibility. But the researchers note that as it grows, MilkyBase will be transitioned to SQL, a standard language used to access and organize databases, with an MS Excel interface being preserved for researchers to input their initial information prior to data curation.

As the database grows, the researchers aim to use it to extract patterns about breast milk components and to eventually draw useful data-informed insights. The database designers demonstrated this possibility in a subsequent case study on the dynamics of the protein content in human breast milk².

The team hopes that MilkyBase will provide a resource for researchers to add to, eventually leading to knowledge sharing. Further, the team hopes ultimately researchers could create a 'periodic table' of other food types as a 'pool for collective knowledge'. ■

References

1. Pacza, T. *et al.*, *Sci. Data* **9**, 557 (2022).
2. Martins, M. L. *et al.*, *Innov Food Sci Emerg Technol* **82**, 103167 (2022).

The researchers aim to use it to shed light on breast milk components.

脂肪细胞图示。母乳由多种成分组成，例如脂肪酸。在健康婴儿体内，它们会积聚在脂肪细胞中。

Spectral-Design/Shutterstock; phive2015/Stock/Getty

母乳 “元素周期表”

一个公开数据库有望揭示母乳的生物化学成分信息。

国际研究团队开发了一个专门汇集母乳相关知识的开放协作数据库。

母乳由多种成分组成，既有碳水化合物、脂质、蛋白质、维生素和矿物质等营养物质，也有激素、细胞因子、生长因子、抗菌物质、细胞等生物活性物质【1】。

不仅如此，母乳还会根据母婴和其他环境因素呈现动态化，并会随时间变化。一个大数据库系统将协助研究人员分析这些因素的相互作用以及母乳本身的生物化学特性【2】。

来自匈牙利和美国的一个研究团队开发了名为 MilkyBase 的定制数据库，用于整理不同的公开出版文献，集中了有关母乳生化成分和样本检测条件的大量信息。

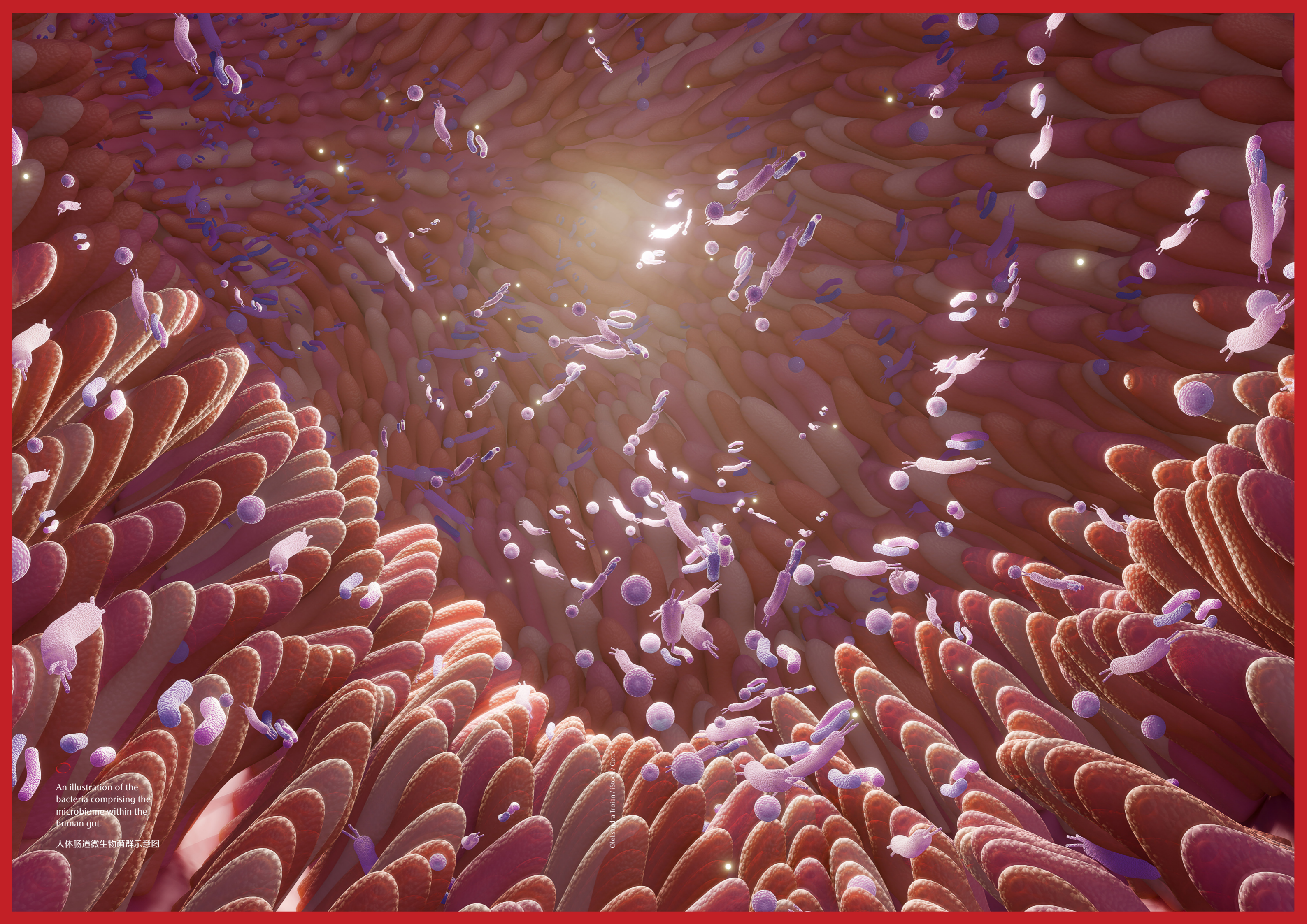
研究团队将人工录入和机器学习技术相结合，从现有出版物中搜集了约 1 万条记录。这些记录揭示了母乳在母亲不同条件下（如饮食和孕周）的生化成分信息。

为保证数据库的及性，团队一开始选择了微软 Excel 作为数据库的初始平台。但团队表示，随着数据库的扩大，MilkyBase 将过渡到 SQL，这是一种用于访问和整理数据库的标准语言，而微软 Excel 界面也将保留，以便研究人员在数据整理前输入初始信息。

随着数据库的扩大，团队期望用它提炼出母乳成分的模式，并最终获得基于数据的重要发现。为证明这一数据库的潜力，设计团队随后开展了关于人类母乳蛋白质含量动态变化的案例研究【2】。

该团队希望 MilkyBase 能成为研究人员贡献和共享知识的资源库。团队还希望研究人员能创建其他类型食物的“元素周期表”，作为“集体知识库”。■

研究人员希望利用它来揭示母乳成分。



An illustration of the bacteria comprising the microbiome within the human gut.

人体肠道微生物菌群示意图

Oleksandra Trohan / iStock / Getty