



Canales, barreras y opciones para el uso de microorganismos en la industria alimentaria



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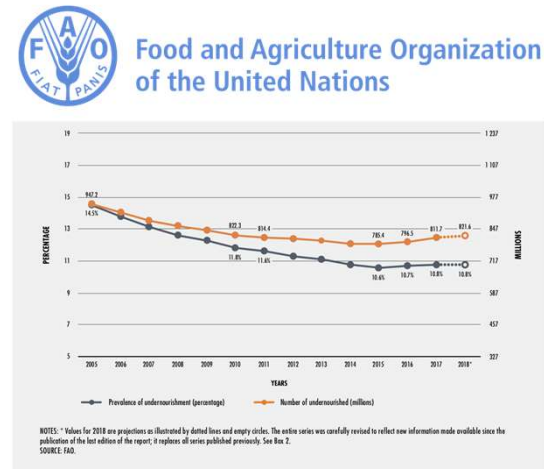
- Los problemas de la alimentación
- Soluciones desde la Microbiología
- Ejemplos y limitaciones
- El futuro

Canales, barreras y opciones para el uso de microorganismos en la industria alimentaria



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El principal problema se llama hambre

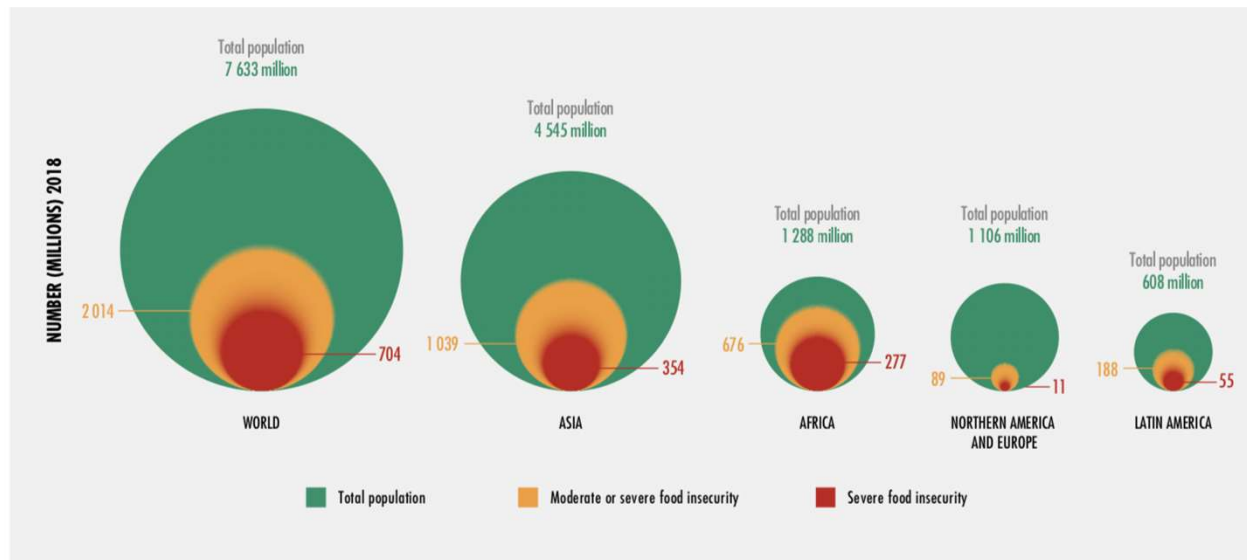


- A pesar de un crecimiento económico mundial sin precedentes, 1100 millones de personas viven en la pobreza extrema y más de 820 millones pasan hambre crónica
- La agricultura moderna se ha mostrado eficaz a la hora de contener la hambruna, pero lo hecho no es suficiente; de forma preocupante los datos de FAO correspondientes al año 2016 muestran que tras diez años de disminución de esta cifra, en ese año había aumentado 10 millones con respecto al año anterior
- Lo indecendente es que producimos la suficiente cantidad de alimentos para satisfacer la ingesta de todos los habitantes del planeta

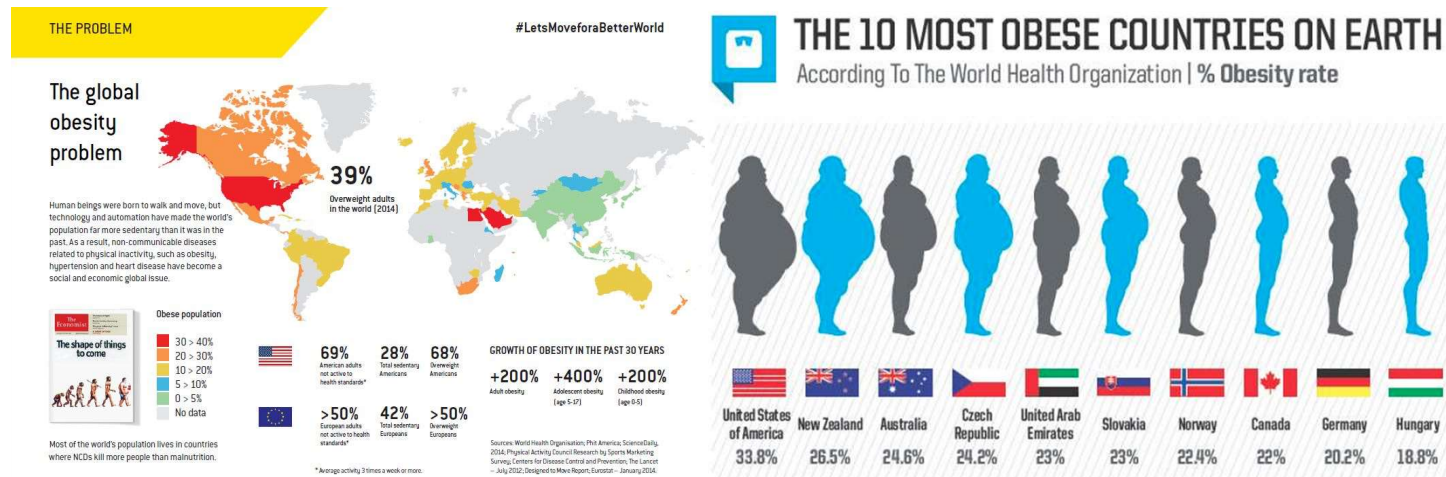
No está uniformemente distribuido



Food and Agriculture Organization
of the United Nations



La pandemia de la obesidad



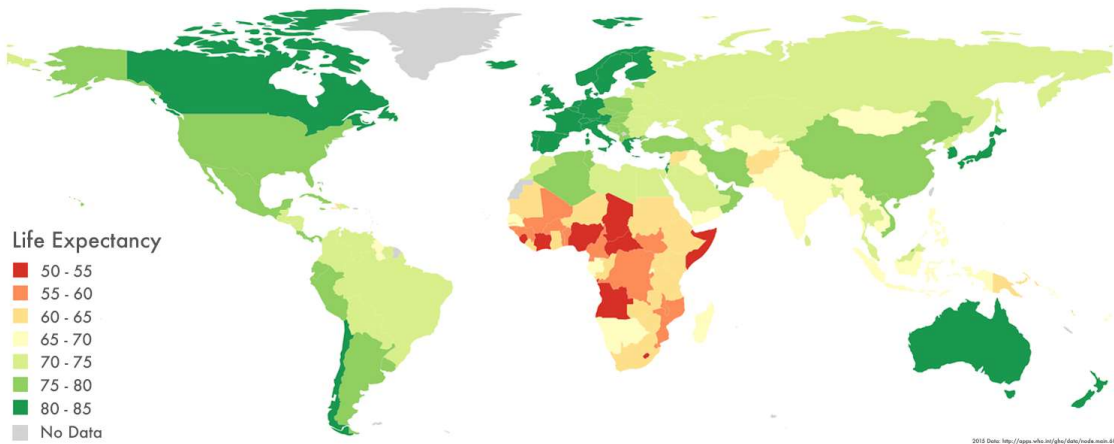
- Desde el año 1975, según datos de OMS la obesidad se ha triplicado en el mundo; se calcula que hay más de 1900 millones de adultos con sobrepeso, de los cuales más de 650 millones son obesos
- En casi todos los países del planeta hay más muertes por obesidad y sobrepeso que por hambre
- Es un problema de dietas inadecuadas y hábitos de vida poco saludables; también intervienen factores genéticos
- Es particularmente preocupante la obesidad infantil ; en ella el papel de las nuevas tecnologías y del ejemplo en casa es crucial (modelo Amsterdam)

La obesidad en España



- España ocupa la posición 62 en el ranking de países obesos del planeta
- En la UE ocupamos la cuarta posición en obesidad infantil
- Hay diferencias entre comunidades autónomas: la comunidad más obesa es Asturias y la menos Baleares
- El problema es nuestra evolución preocupante durante los últimos años; en un estudio reciente, científicos del Hospital del Mar concluyen que en el 2030 el 80% de los varones españoles y el 55% de las mujeres tendrán sobrepeso o serán obesos
- Este problema epidemiológico costará al sistema de seguridad social unos 3 billones de gasto
- Hay que cambiar radicalmente dietas y estilos de vida

La inversion de la pirámide poblacional



- Hace cien años la esperanza de vida de una española era de 42 años y la de un español de 39; hoy, cuatro generaciones más tarde, es de 85,6 y 80,1 años, respectivamente
- Actualmente el 18.5% de la población española tiene más de 64 años y los octogenarios representan el 5.8% de la misma
- España es el quinto país del planeta en expectativa de vida, después de Japón, Suiza, Singapur y Australia
- En la década de los ochenta Japón, en base a datos previos de esta índole, desarrolló la estrategia FOSHU y fue el comienzo de la alimentación funcional

Alimentación para seniors



- En la década de los ochenta Japón, en base a datos previos de esta índole, desarrolló la estrategia FOSHU que fue el comienzo de la alimentación funcional
- Cada vez hay más intereses en desarrollar productos a la carta (propiedades organolépticas, texturales y nutricionales) para este colectivo social
- Es un problema multifactorial donde también intervienen condicionante sociales (ancianos que viven solos)

Parejas e infertilidad



- En sólo una generación, las parejas españolas han aumentado diez años la edad a la que deciden tener su primer hijo
- Dependiendo de la comunidad autónoma la tasa de infertilidad está entre el 15 y el 17% (800.000 parejas)
- El tabaco, el sobrepeso y la contaminación ambiental son las causas fundamentales
- El 3% de los bebés que nacen en España lo hacen por técnicas de fecundación *in vitro*
- Cada día tenemos más datos que indican que al menos parcialmente la fertilidad puede incrementarse con dietas y aportaciones nutricionales adecuadas

Efectos colaterales de la tardanza en ser padres



- Muchas parejas sustituyen la falta de un bebé con un animal de compañía
- En muchos casos es el paso previo a tener un hijo (“período de entrenamiento”)
- En nuestro país, según Nielsen el 40% de los hogares tienen un animal de compañía frente a sólo un 11% con niños entre 0 y 6 años
- El consumo de alimentos para mascotas ha subido en nuestro país un 6% en los últimos tres años

El cambio climático



La huella hídrica



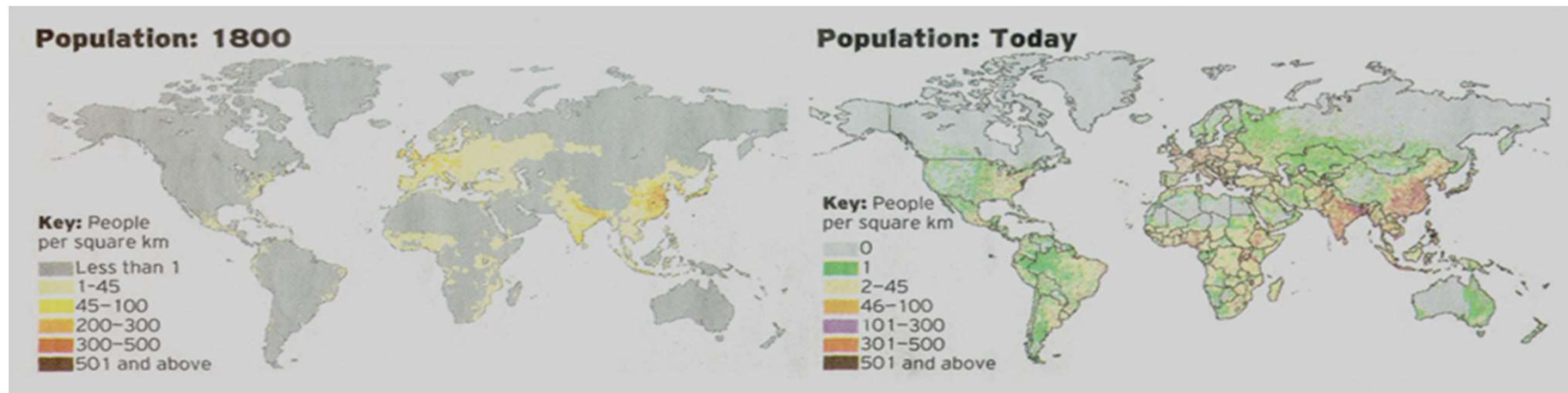
- La agricultura consume el 87% del total del agua utilizada a nivel mundial: en Asia representa el 86% de la extracción de agua anual total, frente al 49% en el Norte y Centro América y el 38% en Europa
- De los cuatro cereales más cultivados, el arroz es el mayor consumidor de agua (5.000 l de agua para producir 1 kg de arroz)
- La huella hídrica alimentaria es brutal: para obtener 1 kg de carne de vacuno se precisan 15.000 litros de agua, 4000 para 1 kg de pollo, 8.000 para 1 kg de café y más de 100.000 para 1 kg de vainilla
- Más de 900 millones de personas no tienen acceso al agua potable y muere cada 20 segundos una persona por mal uso de agua potable (más que por guerras, atentados o violencia general)

Resíduos y desperdicio de la comida



- Dependiendo del país se pierde entre la mitad y un tercio de lo producido
- En los países pobres las causas principales son problemas de almacenamiento de la materia prima (ratas, parásitos, hongos), existencia de una mínima infraestructura de transporte y refrigeración y unos puestos de venta con problemas sanitarios o de refrigeración y el mal empaquetamiento
- En los países ricos son los altos estándares de calidad, las temperaturas de almacenamiento inadecuadas en el punto de venta, la falta de planificación y la fecha de caducidad sobrepasada
- A todo esto hay que sumar en los países ricos la compra o la preparación de comidas excesivas

El cambio demográfico



- La población del planeta aumenta día a día; en el año 1800 poblaban el planeta 880 millones de personas y hoy ya somos 7000 millones
- Sólo había seis ciudades con más de 1 millón de habitantes (Berlín, Londres, Nueva York, París, Pekín y Tokio); hoy hay más de 450
- Actualmente, la mitad de la superficie del planeta está ocupada por ciudades o terrenos agrícolas; hemos desplazado los sitios de producción de los de consumo
- Durante los próximos 30 años se perderá la décima parte de terreno agrícola por erosión, salinidad y cambio climático

Y además, las nuevas tendencias de consumo



Orgánico

Vegano

No-GMO

Exótico

Km 0 (local)

Libre de alérgenos

Bienestar animal



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Las bacterias en nuestro entorno



- Las bacterias son ubicuas; hay bacterias en los sitios más inhóspitos: en los lagos helados de la Antártida, en los geiseres del Parque Nacional de Yellowstone o en el desierto de Atacama
- Se calcula que en 1 gramo de tierra hay 10 millones de bacterias y en un mililitro de agua de un río 1 millón
- Son los seres vivos más numerosos en el planeta; se calcula que en la Tierra hay del orden de 5×10^{30} bacterias (5 quintillones = 5 billones de trillones)

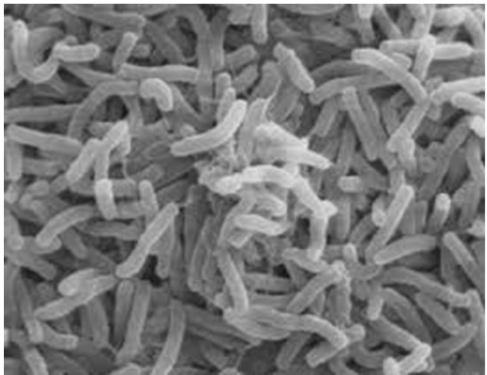
Ratio bacteria/personas



7×10^9 personas



5×10^{30} bacterias



Más de un trillón de bacterias por cada persona en el planeta

¿Qué sabemos de ellas?

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Species Numbers in Bacteria

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Abstract

A modified biological species definition (BSD), i.e., that bacteria exchange genes within a species, but not usually between species, is shown to apply to bacteria. The formal definition of bacterial species, which is more conservative than the modified BSD, is framed in terms of DNA hybridization. From this I estimate there are a million species of bacteria in 30 grams of rich forest topsoil and propose that there will be at least a billion species worldwide.

Bacteria are a major component of the cellular life on Earth and are found everywhere from the top of mountains in Antarctica to the deep-sea vents. They are found in the deep subsoil, the open ocean and all over every surface of you. The refrain for undergraduates is that only about 10 percent of the cells moving with you are eukaryotic, the rest bacterial symbionts. But because bacterial cells are so much smaller than eukaryotic cells, they make up only about 10 percent of your weight. (So, tomorrow, when you step on the scale you can subtract 10 percent off the scale weight because it is not really yours.)

Of the three great branches of cellular life, two are bacterial: the Eubacteria and the Archaea. The third branch is the Eukaryotes of which plants, animals, and fungi make up three kingdoms. The Eubacteria are divided into 40 kingdoms and the Archaea are divided into two kingdoms. The question I will try to answer in this paper is how many species of bacteria might there be. Before we can estimate the number of species of bacteria there may be in the world, we have to determine whether bacterial species are real entities and how they can be defined.

Bacterial Species

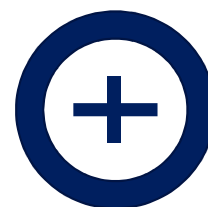
Bacteria are different from eukaryotes in an essential characteristic of life history. Bacteria are haploid and always reproduce asexually by fission. They have other mechanisms for sex, the transfer of genes between lineages, such as transformation, transduction, and conjugation.

The effects of sex in bacteria are different than in animals. In bacteria only a small fraction of the genome is transferred, unlike animals, where 50% of the offspring genome is transferred from the male during sex. Sex in bacteria can be between clones of the same species, closely related species, or distantly related species, whereas in animals sex is almost always limited to members of the same species. During sex in bacteria, pieces of genes or whole genes are transferred and replace the alleles present by homologous recombination, rather than form heterozygotes of the female and male alleles as in animals. Also, in bacteria, new genes can be added to the genome by non-homologous recombination.

The distinction between sexual and asexual as is made in plants and animals does not make sense for bacteria. The amount of sex, or lateral gene transfer between lineages, in bacteria can vary from very little to a lot. *Borrelia burgdorferi*, the causative agent of Lyme disease,

- Las bacterias se pueden domesticar cultivándolas en placas de cultivo en el laboratorio; cuando las logramos crecer las clasificamos y las estudiamos
- En general se considera que sólo crecen en las placas de cultivo el 10% de las bacterias que se cuantifican microscópicamente
- Hay más de 30.000 especies bacterianas clasificadas hasta la fecha, pero seguro que hay muchísimas más sin clasificar; algunos autores hablan de un millón de especies bacterianas en el planeta
- En resumen: conocemos sólo una parte muy limitada del mundo bacteriano

Su papel en la alimentación



Todo cambió en febrero del 2001



- El 15 de febrero del 2001 se publicaba en la revista Nature el primer borrador del genoma humano obtenido por el “International Human Genome Project”; un día más tarde, la revista Science publicaba un segundo borrador obtenido por la compañía norteamericana Celera Genomics
- Estas dos publicaciones abrieron la puerta a la necesidad de secuenciar miles de genomas; para ello había que mejorar las técnicas de secuenciación genómica y secuenciar más genomas con menos coste y en menos tiempo

Secuenciación genómica masiva



La carrera genómica



2001

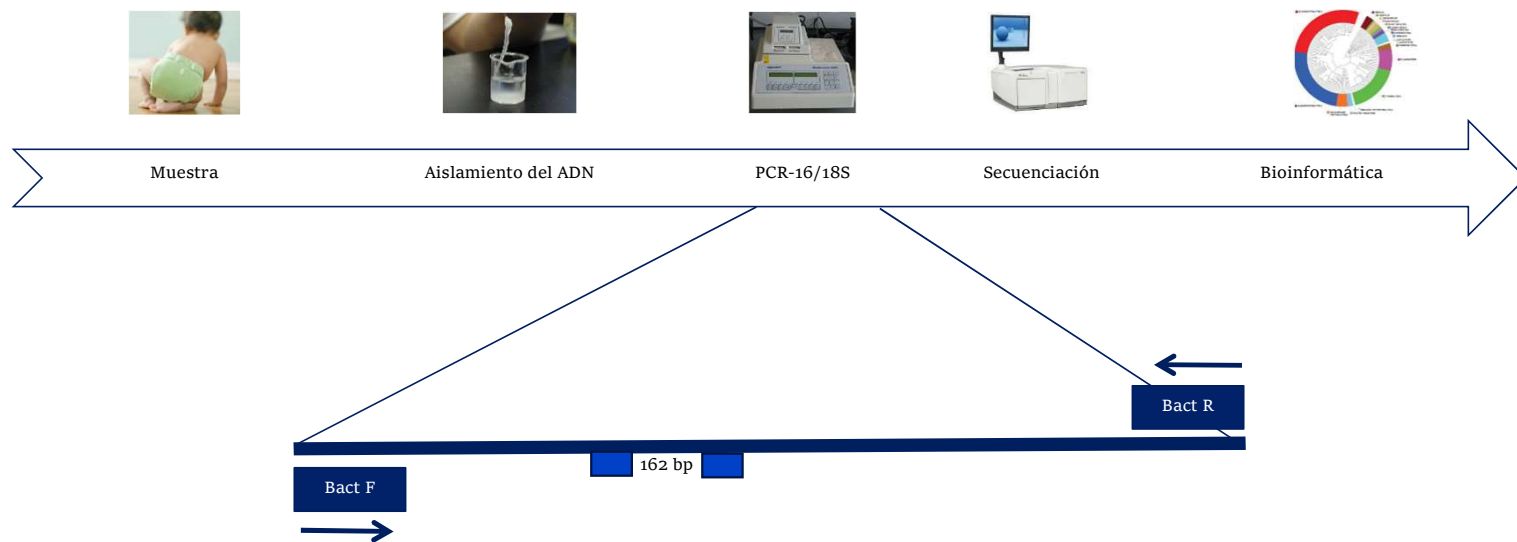
10 años
3000 millones \$
3000 científicos



2020

3 semanas
6000 €
1 técnico FP

Estudiando ecosistemas microbianos



Descifrando microbiomas



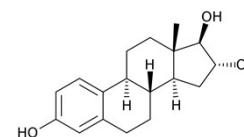
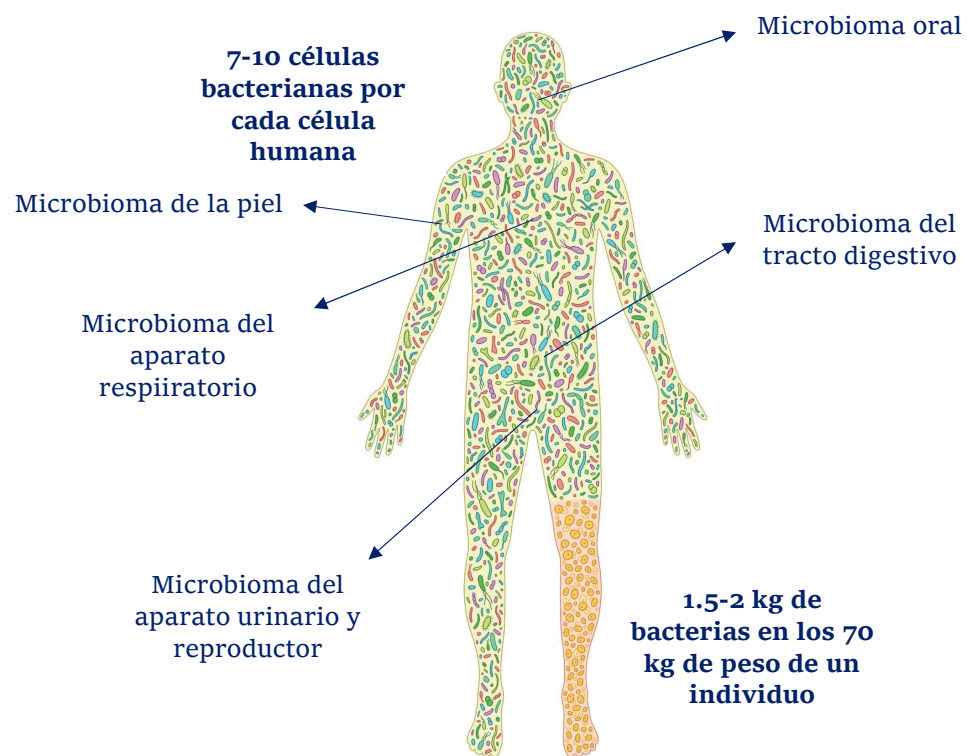
3-4
20-30

Dominio
Reino
Phylum
Clase
Orden
Familia
Género
Especie



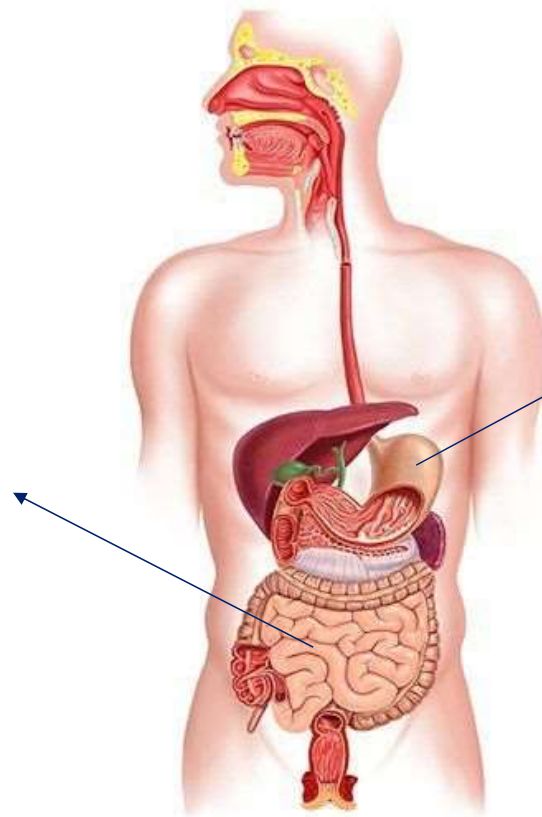
8-10
>1000

Nuestro cuerpo está lleno de bacterias



El papel central del microbioma digestivo

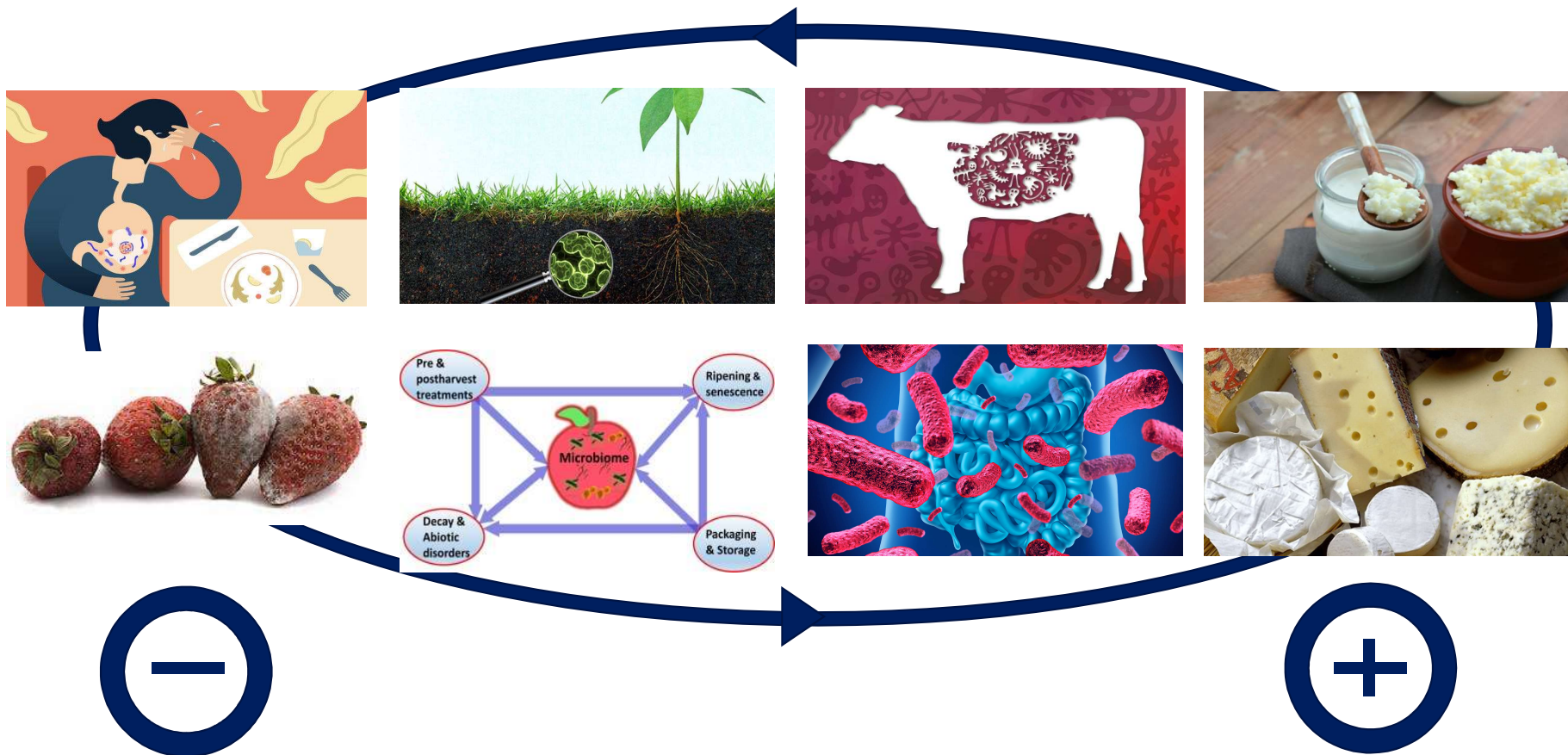
- Representa el 75% del microbioma humano
- Su complejidad es muy grande (más de 1000 especies bacterianas distintas)
- No hay dos microbiomas intestinales iguales
- Tiene un papel biológico fundamental: extrae energía de lo que comemos, produce metabolitos que protegen nuestro epitelio intestinal y activa nuestro sistema inmune



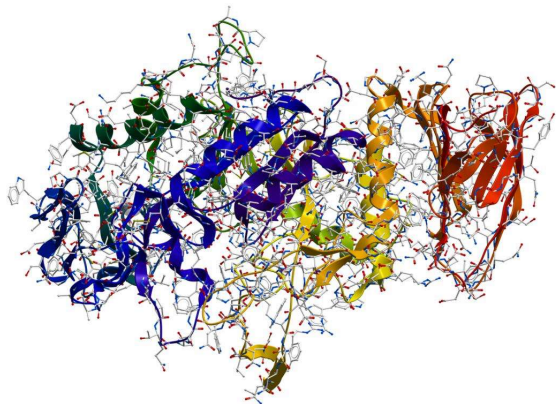
Clostridium
Lactobacillus
Streptococcus
Veillonella

Dieta
Antiácidos
H. pylori

Microorganismos y alimentación



Ingredientes alimentarios microbianos



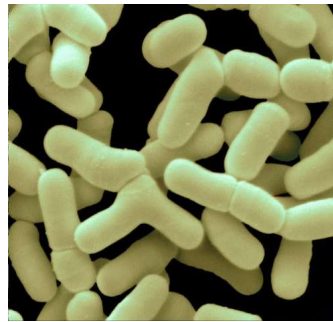
- Ácidos grasos insaturados
- Ácidos orgánicos
- Aromas
- Aminoácidos
- Bacteriocinas
- Carotenoides
- Enzimas
- Flavonoides
- Oligosacáridos
- Polisacáridos
- Polioles
- Terpenoides
- Vitaminas
- Xilitol



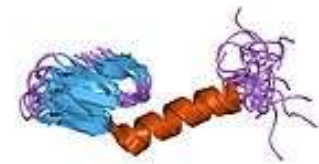
El uso de los microorganismos en la industria agroalimentaria



**Consortio
microbiano**

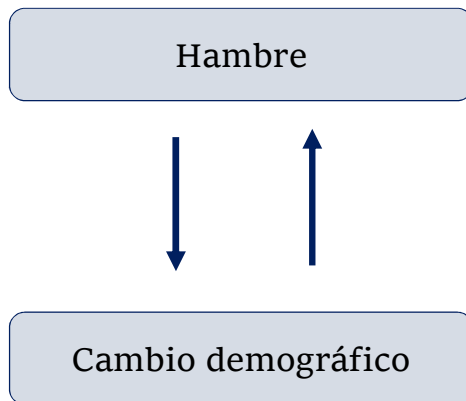


**Microorganismo
(starter,
probiótico)**



**Metabolito
microbiano**

¿Puede ayudar la microbiología?

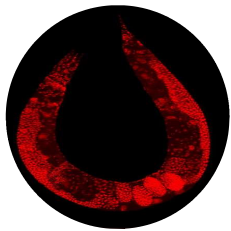


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- Soluciones desde la Microbiología
- ***Ejemplos y limitaciones***
- El futuro

Obesidad



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Probióticos para la fertilidad

Probiotic administration improves sperm quality in asthenozoospermic human donors

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RESEARCH ARTICLE

Abstract

The objective of this study is to analyse the effect of the ingestion of two selected antioxidant probiotics strains (*Lactobacillus rhamnosus* CECT8361 and *Bifidobacterium longum* CECT7347) on sperm quality parameters in asthenozoospermic males after three and six weeks of administration. Nine asthenozoospermic men without any medical treatment under similar diet conditions participated in the study. The quality of individual sperm samples was evaluated before (previous to ingestion), during (after 3 and 6 weeks of ingestion) and after probiotic administration (3 and 6 weeks after finishing the treatment). Sperm motility was evaluated by computer-assisted sperm analysis system, DNA fragmentation by sperm chromatin structure assay, cell viability by flow cytometry and measurement of intracellular H₂O₂ (reactive oxygen species; ROS) by flow cytometry using dichloro-dihydro-fluorescein diacetate. Sperm motility was drastically improved after the treatment (approximately 6 fold change), DNA fragmentation was statistically reduced after probiotic administration from (approximately 1.2 fold change) and intracellular H₂O₂ level was decreased (approximately 3.5 fold change). Cell viability was not affected by the treatment. The significant improvement in sperm motility and the decrease in DNA fragmentation reported in this study provide preliminary evidence that probiotics could be administrated to improve motility and decrease DNA fragmentation and ROS levels in asthenozoospermic human males.

Keywords: *Lactobacillus rhamnosus*, *Bifidobacterium longum*, sperm motility, DNA fragmentation, ROS

1. Introduction

Nowadays, 15% of couples are affected by infertility (Hull *et al.*, 1985). It has been suggested that 40% of these events are caused by the male factor (Fleming *et al.*, 1995). World Health Organization (WHO) establishes different subtypes of sperm abnormalities: asthenozoospermia, oligozoospermia, teratozoospermia or their combinations (WHO, 2010). Asthenozoospermia pathology is defined by reduced motility or absent sperm motility in the fresh ejaculate. It is known that 1 of 5,000 men is affected by absolute asthenozoospermia (Eliasson *et al.*, 1977) and this condition involves a poor fertility prognosis. Male gamete motility is critical for spermatozoa migration in the female reproductive tract, for penetration of the oocyte, and for processes involved in fertilisation (Ortega *et al.*, 2011).

Consequently, the likelihood of natural reproduction and sperm motility are strongly correlated (Beauchamp *et al.*, 1984).

Since the introduction of the intracytoplasmic sperm injection (ICSI) the low fertilisation prognosis of these patients has improved drastically with successful gestations and live births after injection of immotile cells (Ortega *et al.*, 2011). However, new fields should be explored to try to improve sperm motility and facilitate assisted reproductive technologies (ARTs) in clinical centres or natural pregnancies.

Probiotics are defined as 'live microorganisms, which when administered in adequate amounts, confer a health benefit on the host' (FAO/WHO, 2002). The intestinal microbiome



Report of Major Impact

ajog.org

Evidence that the endometrial microbiota has an effect on implantation success or failure



Inmaculada Moreno, PhD¹; Francisco M. Codoñer, PhD¹; Felipe Vilella, PhD¹; Diana Valbuena, MD, PhD¹; Juan F. Martínez-Blanch, PhD; Jorge Jiménez-Almazán, PhD; Roberto Alonso; Pilar Alami, MD, PhD; Jose Remohi, MD, PhD; Antonio Pellicer, MD, PhD; Daniel Ramon, PhD²; Carlos Simon, MD, PhD²

BACKGROUND: Bacterial cells in the human body account for 1–3% of total body weight and are at least equal in number to human cells. Recent research has focused on understanding how the different bacterial communities in the body (eg, gut, respiratory, skin, and vaginal microbiomes) predispose to health and disease. The microbiota of the reproductive tract has been inferred from the vaginal bacterial communities, and the uterus has been classically considered a sterile cavity. However, while the vaginal microbiota has been investigated in depth, there is a paucity of consistent data regarding the existence of an endometrial microbiota and its possible impact in reproductive function.

OBJECTIVE: This study sought to test the existence of an endometrial microbiota that differs from that in the vagina, assess its hormonal regulation, and analyze the impact of the endometrial microbial community on reproductive outcome in infertile patients undergoing in vitro fertilization.

STUDY DESIGN: To identify the existence of an endometrial microbiota, paired samples of endometrial fluid and vaginal aspirates were obtained simultaneously from 13 fertile women in preovulatory and receptive phases within the same menstrual cycle (total samples analyzed n = 52). To investigate the hormonal regulation of the endometrial microbiota during the acquisition of endometrial receptivity, endometrial fluid was collected at preovulatory and receptive phases within the same cycle from 22 fertile women (n = 44). Finally, the reproductive impact of an altered endometrial microbiota in endometrial fluid was assessed by implantation, ongoing pregnancy, and live birth rates in 35 infertile patients undergoing in vitro fertilization (total samples n = 41) with a receptive endometrium diagnosed using the endometrial receptivity array. Genomic DNA was obtained either from endometrial fluid or vaginal aspirate and sequenced by 454 pyrosequencing of the V3–V5 region of

the 16S ribosomal RNA (rRNA) gene; the resulting sequences were taxonomically assigned using QIIME. Data analysis was performed using R packages. The χ^2 test, Student's t-test, and analysis of variance were used for statistical analyses.

RESULTS: When bacterial communities from paired endometrial fluid and vaginal aspirate samples within the same subjects were interrogated, different bacterial communities were detected between the uterine cavity and the vagina of some subjects. Based on its composition, the microbiota in the endometrial fluid, comprising up to 191 operational taxonomic units, was defined as a *Lactobacillus*-dominated microbiota (>90% *Lactobacillus* spp.) or a non-*Lactobacillus*-dominated microbiota (<90% *Lactobacillus* spp. with >10% of other bacteria). Although the endometrial microbiota was not hormonally regulated during the acquisition of endometrial receptivity, the presence of a non-*Lactobacillus*-dominated microbiota in a receptive endometrium was associated with significant decreases in implantation (60.7% vs 23.1% ($P = .02$), pregnancy (70.6% vs 33.3% ($P = .03$), ongoing pregnancy (58.8% vs 13.3% ($P = .02$), and live birth (58.8% vs 6.7% ($P = .002$)) rates.

CONCLUSION: Our results demonstrate the existence of an endometrial microbiota that is highly stable during the acquisition of endometrial receptivity. However, pathological modification of its profile is associated with poor reproductive outcomes for in vitro fertilization patients. This finding adds a novel microbiological dimension to the reproductive process.

Key words: assisted reproductive techniques, bacterial pathogens, embryo implantation, endometrial microbiota, endometrial receptivity array

Introduction

Bacteria present in the urogenital tract make up 9% of the total human microbiota,^{1,2} and most of them are not easily culturable. The vaginal microbiota was first identified in 2002 by molecular methods used to detect nonculturable bacteria.^{3–5} A normal vaginal microbiota is defined by the presence of bacterial species (spp.) of the *Lactobacillus* genus that are commonly associated with a

healthy genitourinary status. The vaginal microbiota typically changes throughout the menstrual cycle, depending on factors such as vaginal hygiene, sexual activity, use of intimate products, and underwear composition; greater microbiota stability is associated with the estradiol peak at ovulation and progesterone rise in the midluteal phase.⁶ However, alterations in the vaginal microbiota can lead to several pathologies. For example, bacterial vaginosis (BV) is a vaginal syndrome produced by the overgrowth of anaerobic bacteria such as *Anaerobium vaginæ*, *Gardnerella vaginalis*, *Mobiluncus curtisi*, and *Mycoplasma hominis* to the detriment of *Lactobacillus* spp.^{3,6}

Further, the vaginal microbiota has been shown to be different in

pregnant and nonpregnant women in terms of stability and composition,⁷ demonstrating that the vaginal microbiota could have implications for reproductive⁸ and obstetrical⁹ processes. BV has been associated with obstetric complications including early and late miscarriage rates^{10,11} and preterm birth.¹² Interestingly, a microbiological culture of the tip of the transfer catheter in patients undergoing in vitro fertilization (IVF) revealed that the presence of bacterial species in the uterine cavity at the time of embryo transfer negatively affects implantation and pregnancy rates. Indeed, *Enterobacteriaceae* spp., *Streptococcus* spp., *Staphylococcus* spp., *Escherichia coli*, and Gram-negative bacteria have been associated with decreased

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Use of Lactic Acid Bacteria to Reduce Methane Production in Ruminants, a Critical Review

Natasha Doyle^{1,2}, Philliswa Mbandiwa^{2,3}, William J. Kelly^{2,4}, Graeme Attwood¹, Yang Li⁴, R. Paul Ross^{2,5}, Catherine Stanton^{1,6} and Sinead Leahy^{2*}

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Enteric fermentation in ruminants is the single largest anthropogenic source of agricultural methane and has a significant role in global warming. Consequently, innovative solutions to reduce methane emissions from livestock farming are required to ensure future sustainable food production. One possible approach is the use of lactic acid bacteria (LAB), Gram positive bacteria that produce lactic acid as a major end product of carbohydrate fermentation. LAB are natural inhabitants of the intestinal tract of mammals and are among the most important groups of microorganisms used in food fermentations. LAB can be readily isolated from ruminant animals and are currently used on-farm as direct-fed microbials (DFMs) and as silage inoculants. While it has been proposed that LAB can be used to reduce methane production in ruminant livestock, so far research has been limited, and convincing animal data to support the concept are lacking. This review has critically evaluated the current literature and provided a comprehensive analysis and summary of the potential use and mechanisms of LAB as a methane mitigation strategy. It is clear that although there are some promising results, more research is needed to identify whether the use of LAB can be an effective methane mitigation option for ruminant livestock.

Keywords: lactic acid bacteria, methane, methanogens, bacteriocins, direct-fed microbials, silage inoculants, mitigation

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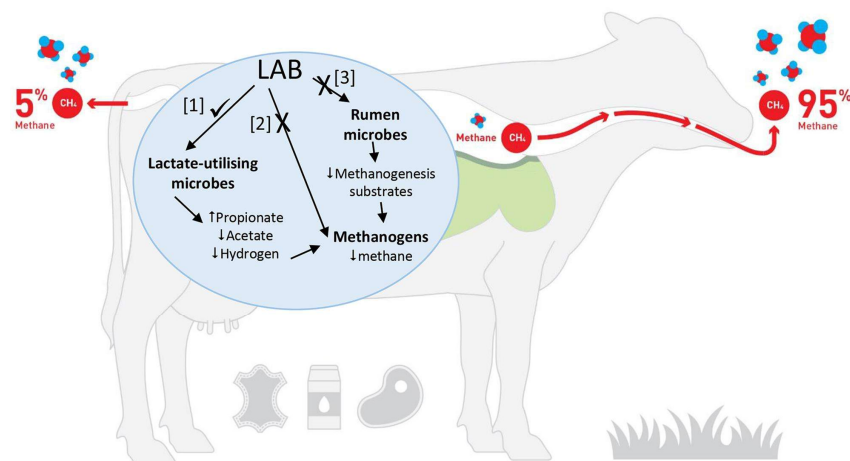
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INTRODUCTION

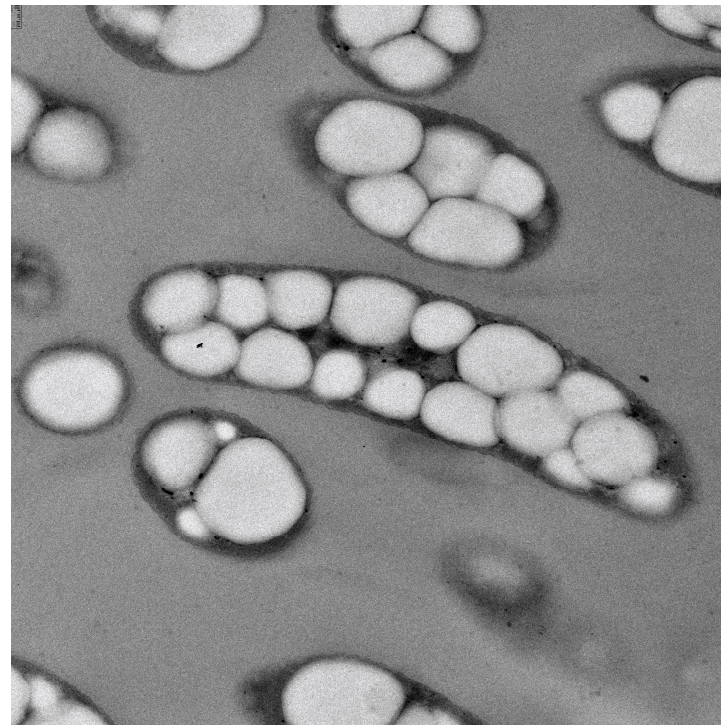
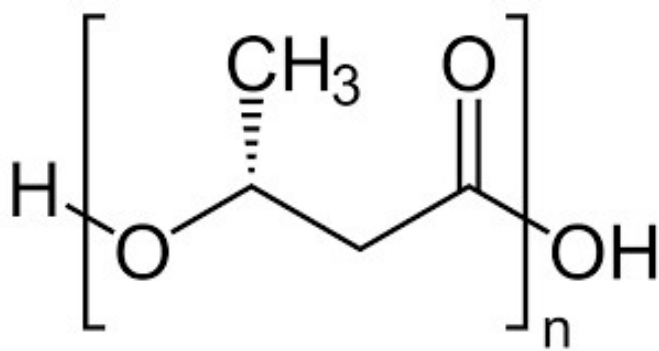
While ruminant animals play an important role in sustainable agricultural systems (Eisler et al., 2014) they are also an important source of greenhouse gas (GHG) emissions (Reisinger and Clark, 2018). Regardless of the ruminant species, the largest source of GHG emissions from ruminant production is methane (CH₄), with more than 90 percent of emissions originating from enteric fermentation (Opio et al., 2013). Enteric fermentation is a digestive process by which a community of microbes present in the forestomach of ruminants (the reticulo-rumen) break down plant material into nutrients that can be used by the animal for the production of high-value proteins that include milk, meat and leather products. Hydrogen (H₂) and methyl-containing compounds generated as fermentation end products of this process are used by different groups of rumen methanogenic archaea to form CH₄, which is belched and exhaled from the lungs via respiration from the animal and released to the atmosphere. In the coming decades, livestock farmers will face



La huella hídrica



Residuos: la bioeconomía



Y las modas



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Probiotic yeast *Kluyveromyces marxianus* CIDCA 8154 shows anti-inflammatory and anti-oxidative stress properties in *in vivo* models

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RESEARCH ARTICLE

Abstract

Inflammatory bowel diseases (IBDs) are complex affections with increasing incidence worldwide. Multiple factors are involved in the development and maintenance of the symptoms including enhanced oxidative stress in intestinal mucosa. The conventional therapeutic approaches for IBDs are based on the use anti-inflammatory drugs with important collateral effects and partial efficacy. In the present work we tested the anti-inflammatory capacity of *Kluyveromyces marxianus* CIDCA 8154 in different models. *In vitro*, we showed that the pretreatment of epithelial cells with the yeast reduce the levels of intracellular reactive oxygen species. Furthermore, in a murine model of trinitro benzene sulfonic acid-induced colitis, yeast-treated animals showed a reduced histopathological score ($P < 0.05$) and lower levels of circulating interleukin 6 ($P < 0.05$). The capacity to modulate oxidative stress *in vivo* was assessed using a *Caenorhabditis elegans* model. The yeast was able to protect the nematodes from oxidative stress by modulating the SKN-1 transcription factor through the DAF-2 pathway. These results indicate that *K. marxianus* CIDCA 8154 could control the intestinal inflammation and cellular oxidative stress. Deciphering the mechanisms of action of different probiotics might be useful for the rational formulation of polymicrobial products containing microorganisms targeting different anti-inflammatory pathways.

Keywords: innate immunity, probiotic yeast, inflammatory bowel disease.

1. Introduction

Inflammatory bowel diseases (IBDs), mainly represented by ulcerative colitis (UC) and Crohn's disease (CD), are chronic debilitating conditions that are difficult to treat. In the last few decades, they have an increased global incidence, especially in developing countries (Molodecky *et al.*, 2012). IBDs are complex and multifactorial affections; it was demonstrated that diet, age, genetic background, ethnicity, and clinical history of infections among others influence in the incidence and morbidity of the disease (Cabrè and Domènech, 2012; Kaser *et al.*, 2010). It is a widely held view that in IBDs and in CD in particular, the mucosal immune system inappropriately reacts against the normal commensal microbiota (Alfa *et al.*, 2002) and some associations have been reported, for example it was shown that Crohn's disease patients are frequently colonised

by adherent-invasive *Escherichia coli* (Chassaing and Darfeuille-Michaud, 2011). Some symbiotic bacterial species have been shown to prevent intestinal inflammatory host responses, but the physiologic intestinal microbiota also contains microorganisms that have been shown to induce inflammation under particular conditions (Antonopoulos *et al.*, 2009; Asquith and Powrie, 2010; Atarashi *et al.*, 2011). It has been shown that IBDs are linked with oxidative stress in the gut epithelia, which may be involved in the development of ulcerative colitis-associated carcinogenesis. This process is contributed by DNA damage induced by reactive oxygen species (ROS) and reactive nitrogen species (RNS) (Lih-Brody *et al.*, 1996; Roessner *et al.*, 2008; Seril, 2003) that are generated in the intestinal mucosa and released as proinflammatory mediators. These species can damage the intestinal barrier and expose the mucosal immune system to luminal content, which enhances the immune system

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Canales, barreras y opciones para el uso de microorganismos en la industria alimentaria



- Los problemas de la alimentación
- Soluciones desde la Microbiología
- Ejemplos y limitaciones
- ***El futuro***

Conocer la biodiversidad microbiana



Bacteria from acidic to strongly alkaline insect midguts: Potential sources of extreme cellulolytic enzymes

Cristina Vilanova^a, Guillem Marco^a, Laura Domínguez-Escribà^a, Salvador Genovés^b, Vicente Sentandreu^a, Esther Bataller^b, Daniel Ramón^b, Manuel Porcar^{a,c,*}

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ABSTRACT

Bacterial isolates from the European Corn Borer (ECB) *Ostrinia nubilalis* and the coleopteran Colorado Potato Beetle (CPB) *Leptinotarsa decemlineata* midguts were identified and characterized. Twenty-four colonies, selected on solid media with cellulose as the sole carbon source and pH values ranging from 5 to 12, were identified through 16S sequencing as members of the genera *Acetivibrio*, *Corynebacterium*, *Klebsiella*, *Microbacterium*, *Mycobacterium* and *Sphingobacterium*. A complete enzymatic characterization revealed widespread – albeit moderate – cellulase properties in all but one isolate and high xylanase activity in the four CPB isolates. Different enzymatic patterns in terms of optimal pH, substrate use and degradation times were observed, and several isolates were selected as promising cellulase producers at extreme (pH 12) conditions. Implications of the results for the biotechnology industry are discussed.

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1. Introduction

Cellulose, hemicellulose and pectin are the major structural components of the primary plant cell wall [1,2]. Cellulose is a biopolymer of multiple β -1,4-linked units of D-glucose and forms organized structures called microfibrils. These microfibrils are cross-linked by hemicelluloses, which are short chains of variable sugar monomers such as xylose and, to a lesser extent, mannose or arabinose [3]. The resulting network is embedded in a matrix of pectins, complex polysaccharides containing α -1,4-linked units of D-galacturonic

acid or other sugars like rhamnose [4,5]. Consequently, a range of enzymatic properties are required for the proper degradation of such a complex and organized structure. Cellulases are a class of hydrolases that perform several enzymatic activities, namely endo- β -1,4-glucanase (also known as endoglucanase or carboxymethyl cellulase (CMCase)) and exo- β -1,4-glucanase (exoglucanase) [6]. This set of enzymes is able to break the microfibril structure down into small, linear chains of glucoses. Nevertheless, to enable a complete degradation of cellulose to monosaccharides, xylanases are also needed to convert hemicellulose into

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SCIENTIFIC REPORTS

OPEN A highly diverse, desert-like microbial biocenosis on solar panels in a Mediterranean city

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Pedro Dorado-Morales^{1,2,*}, Cristina Vilanova^{1,2,3,4}, Juli Peretó^{1,2,3,4}, Francisco M. Codoñer⁴, Daniel Ramón⁴ & Manuel Porcar^{1,2,4}

Microorganisms colonize a wide range of natural and artificial environments although there are hardly any data on the microbial ecology of one of the most widespread man-made extreme structures: solar panels. Here we show that solar panels in a Mediterranean city (Valencia, Spain) harbor a highly diverse microbial community with more than 500 different species per panel, most of which belong to drought-, heat- and radiation-adapted bacterial genera, and sun-irradiation adapted epiphytic fungi. The taxonomic and functional profiles of this microbial community and the characterization of selected culturable bacteria reveal the existence of a diverse mesophilic microbial community on the panels' surface. This biocenosis proved to be more similar to the ones inhabiting deserts than to any human or urban microbial ecosystem. This unique microbial community shows different day/night proteomic profiles; it is dominated by reddish pigment- and sphingolipid-producers, and is adapted to withstand circadian cycles of high temperatures, desiccation and solar radiation.

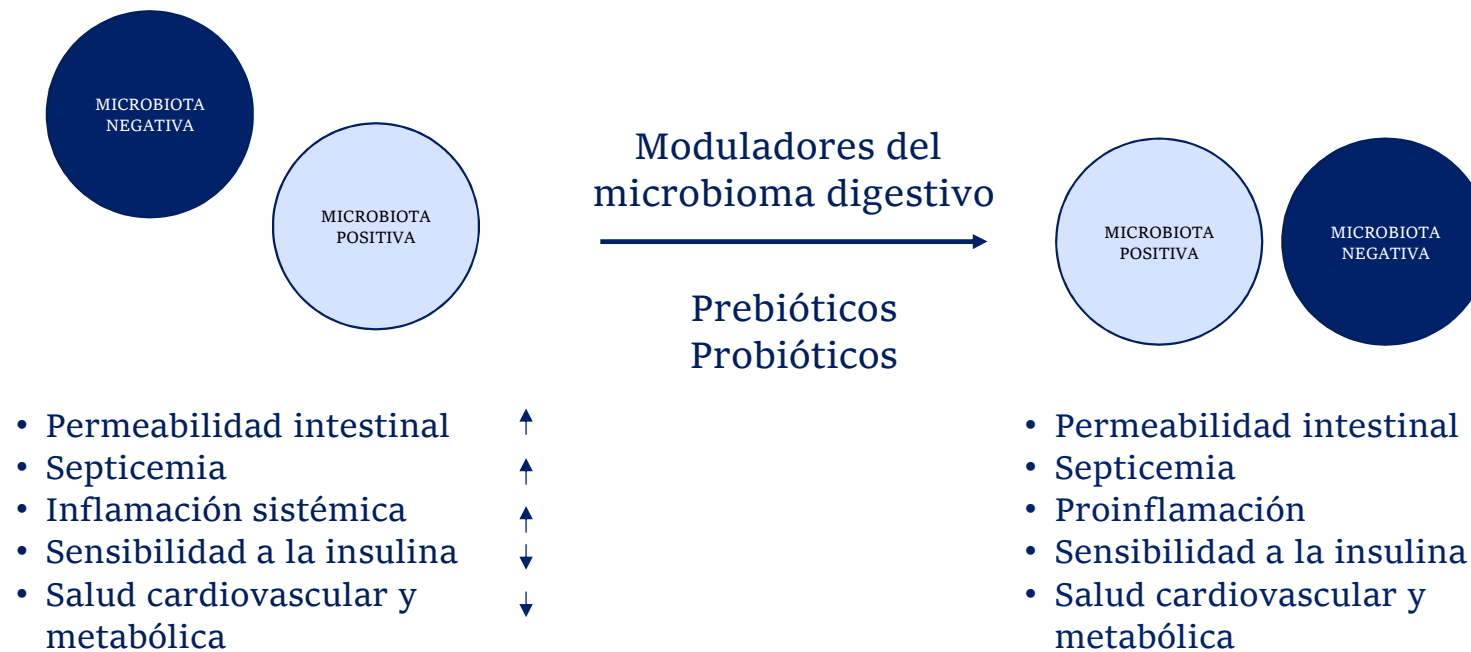
Today, photovoltaic panels cover around 4000 square kilometers, and are forecasted to be the world's main electricity source by 2050 (<http://www.epia.org>). Solar panels are unique biotopes characterized by a smooth flat glass or glass-like surface, minimum water retention capacity and maximum sunlight exposure, all of which determine circadian and annual peaks of irradiation, desiccation and heat. Extreme natural habitats such as thermal vents, mountain plateaus or hyper arid deserts are known to host microbial biocenoses adapted to those particular selection pressures^{1–3}; and artificial or humanized environments, such as industrial reactors⁴, radioactive waste⁵ or oil spills⁶ are also colonizable by specialized microorganisms. Among artificial environments, indoor biomes constitute around 0.5% of the ice-free land area, a surface comparable to the subtropical coniferous forest⁷. Geography and building type, among other factors, structure indoor microbes, which are inoculated by human skin and outdoor air⁸ and even by indoor plants⁹. One of the recently studied indoor habitats is the subway. A recent study of the aerosol microbial communities of the New York City subway platforms¹⁰ revealed that such communities were a mixture of soil, environmental water, and human skin commensal bacteria. In a similar work in the Hong Kong subway networks¹¹, researchers found that each subway line harbored a different phylogenetic community, depending on architectural characteristics, nearby (outdoor) microbiomes, as well as connectedness with other lines.

Most of the so-called built environment studies have so far focused in the indoor biomes but less attention has been paid to artificial, outdoor environments. A recent example of those is an ambitious city-scale metagenomics screening on the bacterial diversity of New York (including both indoor and outdoor biomes), which found a very high diversity of microorganisms—roughly 1700 bacterial taxa—half of which did not match any known organism¹². However, many artificial outdoor environments remains unexplored to date.

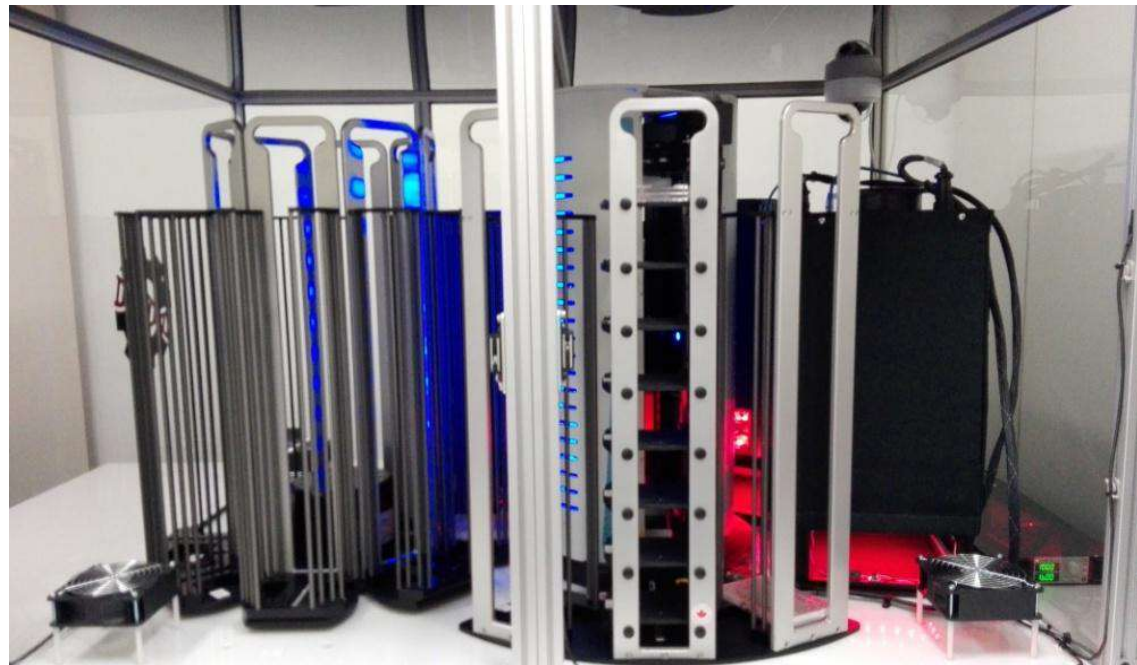
In the present work, we aimed at studying solar panels, an outdoor artificial environment whose role as biotope had not previously been reported. The goal of our study was to identify possible microbial communities thriving in the harsh conditions of the panels' surfaces, and to determine to which extent this highly irradiated

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Ingeniería del microbioma digestivo



Escrutinio de alto rendimiento



Big data genómica: ¿quién tiene más datos?

MIT Technology Review



Biotechnology / DNA Testing

China's BGI says it can sequence a genome for just \$100

Super-cheap DNA sequencing could boost cancer screening, prenatal tests, and research into population genetics.

by Antonio Regalado

Feb 26, 2020

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