From *Streptococcus lactis* to *Lactococcus lactis*: A qualitative and quantitative analysis of the scope of research undertaken around a microbial concept

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ABSTRACT

The lactic acid bacterium *Lactococcus lactis*, formerly named *Streptococcus lactis*, has been known and used for many years, even before its re-affiliation in 1985. The number of published papers featuring one of the two names, either in the title or in the key words, currently stands at more than 2,900. From 1945 to 2014, a bibliometric analysis of the evolution of this bacterium allowed us to identify three phases we have called 1, the “exploratory period” (or the “US period” if we refer to the origin of the labs most frequently involved in the publications), 2, the “explanatory period” (dominated by French and Dutch labs) and 3, the “enlargement period” (or the “Asian period”). We noticed in particular that the evolution of research on this bacterium did not depend on its affiliation but rather on the accessibility to powerful tools and information. Trends and competition between labs were certainly driving forces in the knowledge acquired on *Lactococcus lactis*. We can expect to see more research on this bacterial concept, expanding to new fields, with the arrival of new labs in countries such as China and India. Without the investment of these new actors, would the concept stagnate and regress in the future?

Keywords: Bibliometry, *Lactococcus lactis*, *Streptococcus lactis*

INTRODUCTION

In 1985, Schleifer *et al.*[1] proposed to reclassify the former genus *Streptococcus* (*lactis*) from the N group of the Lancefield classification to the new genus *Lactococcus*. His proposal was especially based on nucleic acid hybridizations and immunological relationships. Since then, this affiliation has not been reassessed. The genus *Lactococcus* encompasses, at the present time, 9 species and the *Lactococcus lactis* species 4 subspecies (http://www.bacterio.net/lactococcus.html).

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This gram-positive, nonmotile, catalase negative bacterium belongs to the lactic acid bacteria group, which includes 11 other genera. Its homofermentative metabolism leads solely to the production of L-lactic acid. In appropriate conditions-mild temperatures, high Aw, rather neutral pH, it can quickly decrease the pH and the redox potential of its culture medium. Such attributes are particularly appreciated in the making of fermented dairy products.[2]

During the last 20 years, research teams have methodically deciphered the functioning of this microorganism. But new research fields were concomitantly explored: Medical use, genetic engineering, the use of the bacteria in other food matrixes than dairy products. Strangely, if 41 reviews were published on specific purposes in relation with *L. lactis* – vaccines, live vectors, cell factories, delivery vehicles of antigens, among others – none of them chose to summarize the state of the art on this microorganism. This can perhaps be explained by the tremendous number of documents produced on this subject: 2535 at the end of 2014!

One way of synthesizing a great deal of articles is based on the bibliometric investigation. Bibliometry can be defined as the quantitative analysis of the books, reviews, and articles on a given subject. This method has been used for different goals, including qualitative and quantitative evaluation of scientific performance, collaboration in research, improvement of research strengths, and so on.[3-5] Bibliometric studies have been successfully applied on different topics, as diverse as agroecology,[6] tuberculosis,[7] or nanotechnologies.[8]

In this article, we propose to apply the bibliometric approach to study the evolution of research on *Streptococcus lactis* and later *L. lactis*, from the Second World War until today.

MATERIALS AND METHODS

A bibliometric analysis supposes the building of a scientific corpus on the themes to be studied. The references were extracted from the SCOPUS data base using the following research equation: (title [“bacterial species”] and keyword [“bacterial species”]). In the case of this article, the bacterial species which were tested were: *L. lactis*, *S. lactis*, *Streptococcus faecalis*, *Streptococcus faecium*, *Enterococcus faecalis*, and *S. faecium*. We specifically focused on titles and keywords because of the relevance of the controlled vocabulary. Indeed, widening the scope of our equations to include abstracts would have generated too much noise, leading to results impossible to synthesize. Indeed in the case of *L. lactis*, the narrowing of the analysis solely to the titles and keywords compared with abstracts led to the diminution of the references obtained from more than 6400–2412.

No date limits were firstly set so as to be as exhaustive as possible. The terms are referring to these bacteria, “*Lactococcus lactis*” or “*Streptococcus lactis*” for instance, can be considered as universal. As a consequence, no syntax problems were observed. The final stabilized corpus led to the results displayed in Table 1. The majority of the references obtained referred to scientific articles, reviews, and conference proceedings.

Table 1: Number of articles and reviews obtained after bibliometric analysis on the four different themes: *S. lactis, L. lactis, S. faecalis* and *S. faecium, E. faecalis* and *E. faecium.* The corpus was collected on the basis of a study of titles and keywords

Bacterial species	Period	Number of references collected
S. lactis	1950-2000	395
L. lactis	1985-2014	2535
S. faecium + *S. faecalis*	1970-2010	805
E. faecium + *E. faecalis*	1984-2010	2901

S. lactis=*Streptococcus lactis*, *L. lactis*=*Lactococcus lactis*, *S. faecium*=*Streptococcus faecium*, *S. faecalis*=*Streptococcus faecalis*, *E. faecium*=*Enterococcus faecium*, *E. faecalis*=*Enterococcus faecalis*

Thereafter, two types of analysis were performed on the respective corpus:

- “Statistical” analyzes were carried out on groups of data which were extracted using different methodologies and a script written in the Perl language. This allowed us to divide the data in line with the indicators to be studied: Date, country, and most famous researchers in the field. The latter information was not retained in the present document: Frequently, these researchers have now retired. We chose a Perl script which allowed us to split up the data by date and by titles and keywords and their appearance frequency in the data base. This procedure was all the more interesting as it allowed us to follow the general evolution of the theme via the extraction of the word occurrences (i.e., in our case, the bacterial species) inside the corpus. By following this approach, we tried to put forward the possible emergence of a new concept. In particular, we decided to cross keywords and titles, because the words used in these two sets of data belonged to a strongly controlled vocabulary used for document indexation in the SCOPUS base
- In parallel, the files containing all the references were carefully studied. For each article, the following information was available: The authors, the title, the affiliation, the abstract, the index keyword, the document type, and the source (SCOPUS in all the cases). The display from year to year of the keywords and their appearance frequency proved to be unusable. We were specifically interested in the crossing of the keywords so as to distinguish emerging concepts. This led us to build double- or triple-edged tables from year to year. In the end, we decided in this article, to only explain some typical years. Displaying all the information would have been tedious and probably unusable.

RESULTS

Streptococcus lactis

We started the study of the *S. lactis* corpus just after the Second World War until 2000. The number of publications from year to year appears in Figure 1. Interestingly, we can divide the figures into three main parts: Before 1964, from 1964 to 1980, and after 1980.

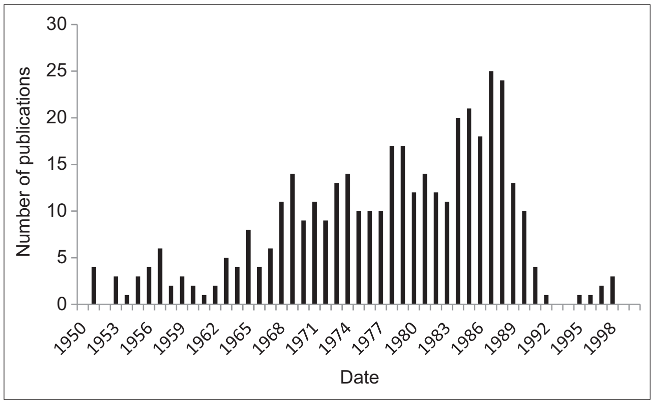

Figure 1: Evolution of the number of articles published on subjects involving the bacterium *Streptococcus lactis*, over the period 1950–2000

From the beginning to around 1964, the number of publications per year was approximately 5. If we consider more specifically the subjects which were studied during this period, by crossing the titles and the keywords, we mainly observe the research works dedicated to the metabolism of *S. lactis*. Subjects are aiming to understand the nitrogen and carbon metabolism and metabolism in general accounted for 47% of the publications. The lactase enzyme was particularly studied. The other subjects covered the following themes: Bacterial growth (19%), medical aspects (5.5%), phage resistance (8%), cell characterization (11%), nisin production (5.5%), and miscellaneous (4%). Strangely, the number of works dealing specifically with milk and dairy products was very small (1 publication). No reference dealt with cheeses.

The second period lasted from around 1964 to 1988 with an increasing production of + 0.6 articles/year ($r^2 = 0.65$). More than 300 articles were published which included the name *S. lactis* in the title (most of them) and in the keywords. It is never easy to classify a pool of articles. Frequently, a paper can fall into two or more classes. We decided that the major theme indicated in the title would determine how we classified an article. For instance, when the term "nisin" was noted, the document was automatically placed in the "nisin" category whatever the other notions developed in the body of the article. This procedure was possible on the *S. lactis* corpus because of the specificity of the research carried out over this period and the low number of articles gathered. It was not, however, appropriate for the *L. lactis* corpus. Interestingly, we can observe that the period was dominated by one major research theme, the study of the metabolism of *S. lactis*. This subject was mainly dedicated to deciphering the functioning of the cell: Energy metabolism (proton ion force, ATPases), carbon metabolism (study of specific enzymes, galactosidases, enzymes from the EMP pathway), nitrogen metabolism (with a specific focus on proteinases), and other functions inside the cell. At that time, researchers tried to purify enzymes in order to study their individual aptitudes. Another main theme of the period was devoted to the study of nisin production (41 articles) and antimicrobial substances (2 articles). This research theme was mainly studied before 1980. Thereafter, it was more or less abandoned.

From 1980 to 2000, the last period, molecular biology tools were progressively introduced (gene transfers, cloning) to better understand the expression of each metabolism or each individual enzyme. The introduction of molecular tools allowed the enlargement of research fields on this bacterium and consequently to new subjects. During the 1980–1988 period, plasmids were particularly studied in relation to the metabolism (especially carbon metabolism) and specific aptitudes (resistance to antibiotics and phages for instance). The infection of *S. lactis* by phages or the research of prophages by the induction led to a regular production of scientific articles. The other subjects which were considered focused on the following themes: Bacterial growth, interactions with other bacteria (*Bacillus* for instance), yeasts and molds, and survival in harsh conditions. Only five articles proposed culture mediums for the specific isolation of *S. lactis* and a further five documents explored medical-related themes. It is important to note that during the whole period, the citrate metabolism – a major capability involved in the development of the buttery and nutty aroma inside dairy products – was merely cited 3 times.

After 1988, 35 articles were published with the name *S. lactis*. This corresponded to the progressive replacement of the genus *Streptococcus* (*lactis*) by the new genus *Lactococcus* (*lactis*). The main themes which emerged during the eighties were prolonged: Molecular cloning, enzyme purification, phage and plasmid study, nisin. It is noteworthy, however, that two "new" subjects seemed to become more and more important: The medical use of *S. lactis* and the study of the citrate metabolism.

Concerning the origin of the research works, we can observe that 46% of the articles produced came from the USA [Figure 2]. The remaining articles were produced equally by the laboratories in the USSR, New Zealand, France and the UK (10–13%) and to a lesser extent, Japan and India.

Lactococcus lactis

The scientific production

The evolution of the number of publications including the term "*Lactococcus lactis*" is presented in Figure 3. We started the study in 1985, the date of the proposal of Schleifer *et al.*[1] to reclassify *S. lactis* as *L. lactis* and we stopped our analysis at the end of 2014. If we compare the evolution of the number of publications by crossing Figures 1 and 3, we can notice a continual increase in the number of articles published per year. The shift from *S. lactis* to *L. lactis* did not change the research policy of the laboratories working on this microorganism. In 1988, 24 articles were published with the name "*St lactis*." By 1991, this number of articles, now with the "*Lc lactis*" name, leapt to 61, more than doubling previous annual output, to stabilize around 80 articles/year. At the end of 1998, the scientific production increased again to reach a mean of 113 ± 14 articles/year. A peak was reached in 2006 and 2009, with 136 articles edited on this subject! In the meantime, from 1985 to 1998, the total number of keywords per year changed from 34 to 750. This indicates that researchers explored new fields in relation, directly or indirectly, with *L. lactis*.

From a qualitative point of view, how can we characterize such an evolution? The mean production on *S. lactis* and *L. lactis* were, respectively, equal to 8 ± 7 and 93 ± 34 articles/year whatever the period considered. Crossing the keyword analysis with the terms cited in the title allowed some tendencies to emerge. If we analyze the period from 1985 to 1998, 703 articles were published on a subject directly or indirectly linked with *L. lactis*. It is interesting to note that over this period, the great majority of research works just concerned the subspecies *lactis*, and occasionally, *L. lactis* subsp. *cremoris*. The biovariant diacetylactis was frequently cited revealing the increasing interest among the scientific community in the citrate metabolism.

Many remarks can be made from the careful analysis of these 703 articles:

- The period was characterized by the increasing utilization of the molecular tools which are still currently used: Cloning (in particular exogenous genes from other microorganisms: Chitinase, superoxide dismutase, lux A/B gene, etc.), use of mutants, sequencing of relevant genes, gene transfer. The technics which were progressively used or tested include electroporation, sodium dodecyl sulfate polyacrylamide gel electrophoresis, polymerase chain reaction, mutation induction, and use of RNA probes and RMN
- The second characteristic of this period related to the preceding remarks concerns the methodology used. For instance, although the nitrogen and the carbon metabolisms were still studied (19.4% and 8.6% of the articles. respectively), researchers began to adopt a genetic approach to these metabolisms (one paper out of four on the subjects). The themes covered the expression of specific genes or their inactivation, the characterization of IS sequences, transposons, and promoters. Generally speaking, all subjects taken together, more than 35% of the articles referred to a genetic approach
- The "traditional" themes, already pointed out for *S. lactis*, were still being studied: Phages (12.8%), plasmids (11.6%), nisin metabolism (11.8%) with the help of the molecular tools indicated above. Concerning the study of bacteriocins, the research works aimed at the expression and the regulation of

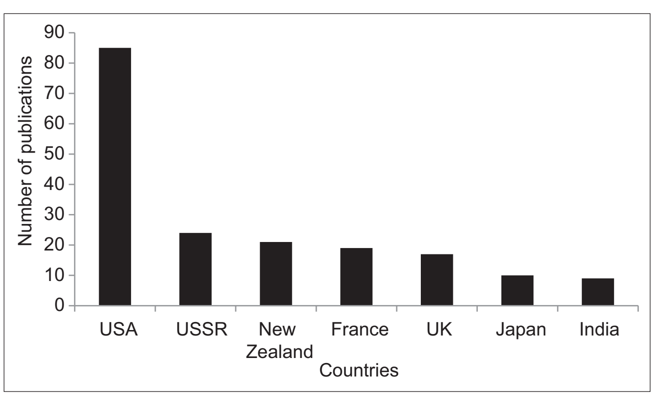

Figure 2: Distribution of the articles published on subjects involving the bacterium *Streptococcus lactis* over the period 1950–2000, according to the origin of the research teams

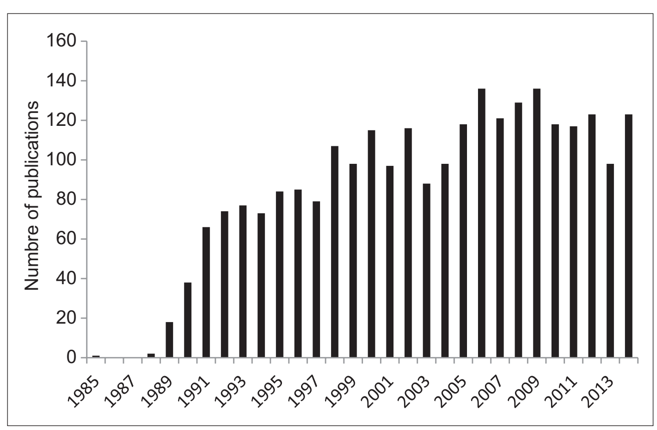

Figure 3: Evolution of the number of articles published on subjects involving the bacterium *Lactococcus lactis*, over the period 1985–2014

the nisin gene and its effect on other microorganisms, and some other antimicrobial substances: Lacoccin A and lacticin 481. The nitrogen metabolism covered the following subjects: Study of extra- and intra-cellular proteinases, peptidases, oligopeptide transport, etc

- If we look at the "new" research themes, the most prevailing were: The citrate metabolism (expression, regulation, enzymes, plasmids involved), the stress metabolism (more specifically the expression of heat-shock proteins followed by cold-shock proteins and rarely, osmotic, starvation, and UV stress), and some "medical" aspects (antigen and interleukin expression, link with digestive microflora, gene transfer)
- Concerning the other subjects which were (seldom) treated, one can cite some articles on the exopolysaccharide metabolism on embedded cells in alginate gel and on autolysis.

After 1998, two major trends were concomitantly observed. The number of articles increased, as indicated above, as well as the number of keywords – from 882 in 1999 to 1618 in 2012 (1344 in 2014). Even if a part of these keywords has no direct connection to the research theme (for instance, government, USA), this reflects a significant broadening of the fields studied. Over the period 1998–2014, we adopted a different approach since it is difficult to study such a corpus year per year (1938 articles!). We decided to specifically focus on the presentation of the years 2000, 2004, 2008, 2012, and 2014. And when some differences were noticed between two dates, we looked at the intermediate years. We opted to emphasize what really changed from period to the period instead of collecting all the themes developed during 1-year.

The examination of the year 2000 showed that some traditional themes were still being studied: Bacteriocins (not only nisin), the carbon, nitrogen, and citrate metabolisms. The reasons invoked to justify these works all cited the need to improve knowledge. The study of stress conditions on the behavior of *L. lactis* was enlarged to other fields (not only the effect of heat and cold): Acid, Aw, osmotic, metals, oxidative (9.2% of the articles). The cloning of exogenous aptitudes was also continued (17.6%), especially for medical purposes. Interestingly, several articles referred to *L. cremoris*. Phages were less studied. In 2004, the situation did not change greatly even if in the meantime, the complete genome of *L. lactis* IL1403 had been sequenced.[9] The study of the metabolism was favored (but not the nitrogen metabolism) and also the incidence of stress and cloning to introduce new aptitudes (50% of the published articles). Phages and plasmids were no longer studied; this is representative of a strong trend which continues at the present time. Among the new themes that emerged, one can cite ecological matters (other food matrixes than dairy products such as sausages, human milk, beer; growth conditions; co-cultures: Collectively these topics account for 6.3% of the articles published). Topics also referred to the tendency of technological engineering of strains to overproduce vitamins or nisin for instance (7.4%). Medical concerns were still being addressed (immune effect, the pathogenic behavior of *L. lactis*; 6.3%). It seems as if researchers had the possibility to explore new fields on the basis of the knowledge acquired before. The other keywords which appeared rather new compared with 2000, were: Proteome (3 articles), adhesion, sequencing, and other uses.

If we compare 2008 with 2004, three major observations can be made:

- No "real" new fields were explored. However, if "traditional" fields represented 55% of the articles published – genetic, bacteriocins, metabolisms… – the tendency to enlarge to other matrixes and ecosystems continued. Some articles on less frequent materials such as fish, vegetables, or water can also be cited
- Approximately one article out of four dealt with a medical objective (human health) – the use of transformed *Lactococcus* strains as vaccines for instance. This is quite different to 2004 (6.3% of the papers published). We refer to articles which indicated a medical objective specifically in the title or even the summary
- The number of articles which referred specifically to terms ending in "omic" was not as numerous as expected: Transcriptomic (12), proteomic (7), genomic (1).

Concerning the recent years (we studied 2012 and 2014 in detail), the tendencies observed in 2008 seemed to have strengthened. The themes aimed at medical and also veterinary purposes largely prevailed (between 23% and 30% of the documents published). Some of the keywords which were noted referred to allergenic responses, interleukin, and bio drug production, anticoagulant peptides, etc. Bacteriocins were still studied as well as the lactococcal metabolism (15–18%). In this latter case, we observed that the authors have started to focus on other metabolic functions such as transporters, minerals, and lipolytic enzymes. If molecular tools (cloning in particular) and genetic approaches were still frequently used, we also noticed an enlargement of the research fields in different directions and to other matrixes than those already cited (other fishes, yam, starch, ethnic food, and dairy products for instance). But we can also cite articles dealing with fermentation, growth, technological uses, ecological matters, microbial interactions (other than bacteriocins) along with "older themes" such as EPS or citrate metabolism (around 20%). Although this shift toward these new topics started in 2008, it seems to have deepened from year to year.

Origin of the Research Teams Involved in the Publications

If we refer to Figure 4, we can notice that the main contributors to the knowledge of *L. lactis* come from France, The Netherlands and the USA. But, this figure hides three facts:

- Firstly, for the analysis, we only kept the first affiliation mentioned in the databases. If this choice is not problematic for the years between 1991 and 2004–2006, we slowly observed thereafter the implication of an increasing number of research teams in many articles, especially from The Netherlands and France. As a consequence, the first affiliation can appear reductive in many cases
- Secondly, article production is not constant. If we look at Figure 5, we can notice a shift in recent times between western and Asian countries. Today (2014), Chinese and Indian labs are the most important contributors (20% and 11%, respectively), followed by Malaysia (5%) and other Asian countries (Pakistan, Vietnam, Korea, and Japan). If French researchers still published 9 articles in 2014, the production of Dutch workers slowly decreased on this theme (12 articles in 2008, only 6 in 2014). This trend is even more significant if we refer to the USA
- Thirdly, the number of countries involved in these research topics doubled from 1991 to 2014 (from 16 to 33). It means that regardless of who the main countries are, many research teams have been working on *L. lactis* throughout the world. This observation has probably to be crossed with the enlargement of the research fields.

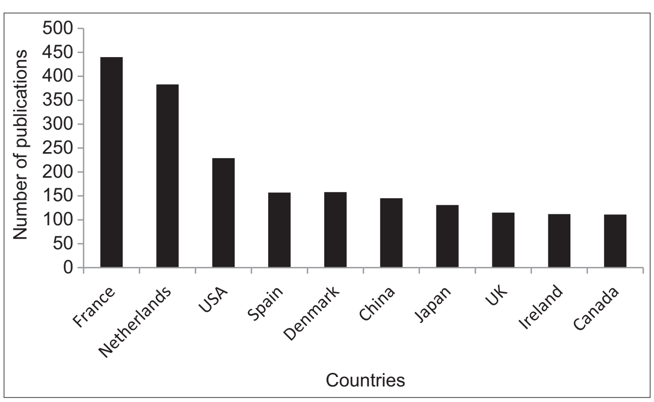

Figure 4: Distribution of the articles published on subjects involving the bacterium *Lactococcus lactis* over the period 1988–2014, according to the origin of the research teams

DISCUSSION

The bibliometric tool has been widely used for many years. This way of exploring the publications produced on a given topic has been applied to the evaluation of scientific performance,[4] the study of the trends in specifics themes or the extent of collaboration among researchers.[3] This technic has also been criticized by some authors concerning some ways in which it has been used.[10] In recent years, Vergidis *et al*.[5] applied bibliometric analysis to the research in microbiology. This allowed the authors to identify nine different world regions according to their quantitative production over the period 1995–2003. In our article, we have proposed to apply the bibliometric approach to the dynamic evolution of the knowledge collected on a specific bacterium, *S. lactis*, and *L. lactis* after its taxonomic re-affiliation. To our knowledge, such work has never been conducted in this specific scientific field.

The methodology we followed was based on the exploration of the SCOPUS database, followed by the specific

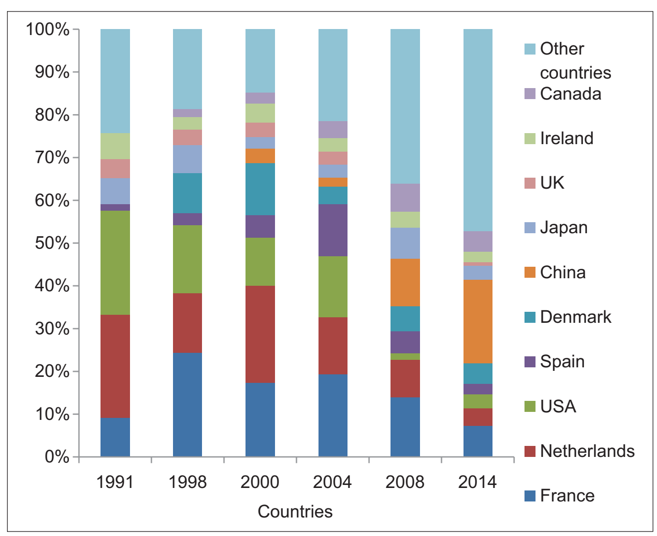

Figure 5: Evolution of the articles published on subjects involving the bacterium *Lactococcus lactis* over the period 1988–2014, among the main contributors

examination of each individual article. This is probably the main limitation to our work. Other works published on similar subjects chose the PubMed database[7] (Falagas *et al*., 2006[11]) which is perhaps more exhaustive. Indeed, we observed that some articles (at that time, no more than five) were not present in the SCOPUS base. As these documents were found fortuitously, we have no idea of the real number of articles which have not been included in the database. But if we consider the number of citations obtained on "*Lactococcus lactis*" (2535), it is difficult to imagine that the missing number of articles would fundamentally change our observations. And it has not been ascertained that PubMed is completely exhaustive.

The examination of the whole set of articles, including the reading of the abstracts, requires a tremendous amount of work. And such an approach may appear debatable if we consider the existence of some technics developed for the bibliometric methodology. We can cite for instance the EXIT approach proposed by Roche *et al*.[12] for the study of the molecular biology corpus. If we are aware of the limits of the approach we followed (in particular, the choice of the sub-themes identified to group the articles), it allowed us to acquire a good knowledge of the subject and to establish an overview of the corpus and the main trends. On a research topic such as *Escherichia coli* generating thousands of references, our methodology would be unusable.

The evolution of the research on *S. lactis* and then *L. lactis* from 1950 to 2014 allowed us to identify three major periods, which corresponded with three different ways of thinking. Interestingly, these periods did not seem to be influenced by the shift from *S. lactis* to *L. lactis*, even if the evolution observed was probably an indirect cause of this shift. We will return to this point later. The first period covering the 30–40 first years corresponded to what we have called the "exploratory period." Researchers tried to decipher the *S. lactis* metabolism, especially by studying the enzymes. This approach was characteristic of this period if we refer to other sciences.[13] Another subject which was particularly studied referred to the nisin action. This subject and in general, bacteriocins was studied over the whole period from 1950 until now. This is probably explained by the increasing concern of governments toward food poisoning bacteria. In Europe, it led concomitantly to the development, at the end of the nineties, of the Qualified Presumption of Safety concept to identify harmless microbes. It is not excessive to call this period the "US period," since nearly 50% of the publications came from research teams in the USA.

The second period started at the beginning of the 80s and lasted until 2008–2010. We have called it the "explanatory period," dominated overall by Dutch and French laboratories. We observed a sort of competition between the two countries on similar subjects, which was certainly at the root of the dynamic of publications and discoveries observed over this period. This period also corresponded with a progressive change in the way of managing research works, especially in France.[14] In a changing economic context, researchers and their industrial partners had to change their way of innovating; this led to exploring new ways of working as well as new research challenges. The development of molecular tools (1965–1980)[13] and their rapid automation allowed researchers to explore the functioning of the *L. lactis* metabolism, from the gene to its expression. With Morange,[15] we can assume that the fad for these new tools was also an explanation for the rapid deciphering of this functioning. An illustrative example of this assertion is the complete sequencing of the genome of the strain *L. lactis* IL1403 by Bolotin *et al.* in 2001.[9] The major metabolic functions (carbon, nitrogen, citrate, EPS, nisin production, etc.) were decrypted, but also some specific features, such as stress behavior, phage resistance, etc., This period was dominated by one of the two main scientific paradigms, reductionism,[16] that is the decoding of the cell at the gene level to rebuild the global metabolism.

The third period started slowly, as early as around 2004, and partially overlapped with the explanatory period. This is what we have named the "enlargement period" that is, the extension of the use of *L. lactis* to other fields: Medical and veterinary topics, other food matrixes, less studied (or completely neglected) metabolic functions. This period which is currently in progress was boosted by contributions made by new research teams from other countries. We also refer to it as the "Asian period," as it is more and more dominated by China (medical use of *L. lactis*) and to a lesser extent India and South Asia. This shift away from the west toward the east explains the new stimulation observed on the subject. It is difficult to explain the decrease of the influence of traditional countries. However, we can propose at least one explanation. The reduction of governmental subsidies obliged many labs to find new sources of grants. If companies financed some works, results were confidential and as a consequence were not published. A study of patents over the same period would be probably interesting to confirm this hypothesis.

From the consideration of the period 1945–2014, some major conclusions can be drawn. First, the transition between *S. lactis* and *L. lactis* went virtually unnoticed, in any case without any effect on the scientific themes studied. It means that the re-affiliation was considered by researchers as a "simple" change of name without any significant effect on their way of approaching this microorganism. In a sense, we can consider that the reality of this bacterium does not depend on its taxonomic name. Or, to express it differently, that according to a school of thought called realism (as opposed to nominalism) the name itself has no meaning, and, therefore, the bacterium possesses an ontological reality whatever the label of affiliation. If the name is independent of the bacterium to which it refers, we can wonder why researchers seemed to be so reluctant to its change. In the case of *L. lactis*, after the re-affiliation proposal in 1985, two articles were published with the new name in 1988 (none in 1986 and 1987) while in the meantime, 88 articles were produced with the name *S. lactis*. After 1989, the shift seemed to be definitively accepted. To explain this delay, we conducted an analysis of the change between *S. faecalis* and *S. faecium* and *E. faecalis* and *E. faecium* [Figure 6]. The re-affiliation from *Streptococcus* to *Enterococcus* was proposed by Schleifer and Kilpper-Bälz in 1984.[17] But as observed for *L. lactis*, a 2–3 years delay was necessary before observing the shift in research papers from the former to the new genus. Could it be a general feature of researcher behavior? It is not our objective to decipher here how researchers behave. Many works are available on this subject (for instance, Politi, 1999 or Chamak, 2004[18,19]). But we can propose two possible explanations: Firstly, the reluctance of researchers to innovation as a consequence of their implication in a common scientific paradigm.[16] They are cautious to any change so long as it has not been carefully checked by the scientific community, thereby necessitating a period of transition. Secondly, the diffusion of scientific publications via web sites is a legacy of the nineties and after. Before then, we can assume that information was distributed less quickly. This observation allows us to think that the last 20 years of the 20th century impacted research at a technical and an informational level. This can be considered a small revolution.

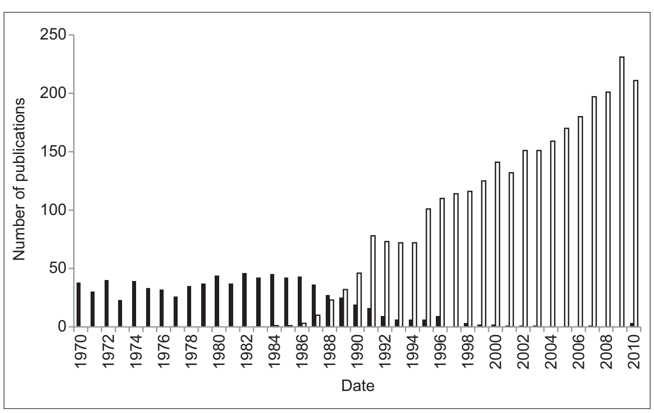

Figure 6: Evolution of the number of articles published on subjects involving the bacterium *Streptoccocus faecalis* and *Streptoccocus faecium* (plain bars) and *Enterococcus faecalis* and *Enterococcus faecium* (empty bars), over the period 1970–2010

CONCLUSION

The bibliometric approach is a very useful tool to analyze any scientific field even one as specialized as the subject of this article. We showed that if the evolution of the bacterial *L. lactis* did not depend on its re-affiliation, it was certainly strongly affected by the current scientific paradigm and by the global evolution of science: Development of tools, information diffusion. In 2015, we can wonder whether the research on *L. lactis* has reached maturity or not. Is there any risk of stagnation? Can we imagine new research prospects for this bacterium on the basis of the current conceptual equipment acquired? Indeed, the environmental use of *L. lactis* has never been considered or rarely. Would this perhaps represent a possible extension in our way of thinking? In our opinion, the technical race which has been observed between laboratories (the fashion motivation according to Morange, 1991)[15] led to the abandonment of some interesting research paths. They are being re-explored by the new countries working on this microorganism. We can, therefore, suppose that research on *L. lactis* will still go on, at a constant level, although perhaps on less recognized themes. As a development of this article, it would be interesting to study the patents published over the same period with the keywords *Lactococcus* and *Streptococcus*. This would show the influence of private grants in the financing of research works. And it would probably partly explain the changes observed.

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