Integrating different windows on reality: socio-economic and institutional challenges for culture collections

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Abstract

The task of a comprehensive exploration of microorganisms in medicine, agriculture, industry, basic, applied and environmental sciences is resource extensive. The nature of highly specialised methods and the resulting wealth of data make close collaboration of experts from different fields an essential requirement for their most efficient translation into social benefits. Resulting commercial applications are one driving force in further developments that might generate conflicts between intellectual property rights and the need of accessible, shared databases. Culture collections for microorganisms might act as mediators by defining the regulations for access to data and materials. We will address problems and potentials of sharing information as part of organising broad access to diverse forms of information on microbial commons. It is the main argument of this paper that a focus on genetic information only, by neglecting the importance of combining and sharing facts coming from the behaviour and the environment of living organisms, results in loss of expertise, knowledge and social opportunities both for developed and developing countries, the latter as the reservoir of most of the remaining biodiversity on Earth.

Biographical notes

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1. The socio-economic function of culture collections

Microbial culture collections have grown in response to the societies need to address and solve problems associated with traditional food production, industry, medicine and to develop modern microbial processes. Their general aim is to collect, authenticate, maintain and distribute cultures of microorganisms and associated information for high-technology developments as well as for the day-to-day requirements of general health care, agriculture, food production and teaching (Fig. 1). The current preference given to knowledge generation based on modern, high-technology approaches such as the determination of the genotype[1] – the inheritable information carried in the genetic code of the organism - starts to downgrade the existing knowledge of classically used phenotypic methods that analyse the observable structures and functions of a living organism. The resulting loss of expertise will reduce the possibility to relate modern to classical microbiological knowledge and the genotype to the phenotype[2]. It also hinders the continued use of technically less demanding classical methods in less developed countries. These countries hold most often the largest still existing biodiversity, as the destruction of the natural environment is the least advanced.

Please insert Fig. 1 about here.

It is the goal of microbiological culture collections not only to maintain materials and expertise, but also to enhance the understanding of microorganisms to promote their application. The large numbers of organisms aggregated in culture collections provide an excellent basis for this. To take advantage of these resources, the research focusing on properties of the organisms has to be accompanied by data repositories that facilitate data analysis in order to effectively allow the generation of knowledge.

More than 500 culture collections, storing over one million microbials have been created in more than 60 countries since the establishment of the first collection in Prague, Czech Republic in 1890 (www. wfcc.info; Sly et al., 1990). With the arrival of biotechnology and

the industrial utilisation of living organisms, which evolved through basic research in the 1970's and 1980's, the collections needed to become proficient in industrial relationships as well as remaining expert centres in microbial taxonomy[3], conservation, physiological and biochemical testing for research and educational purposes. Accordingly, collections catalogued and digitised their information, developed databases, coordinated their efforts for the benefit of the users, developed educational programmes to inform the public, promoted themselves as industrial partners, and, with the availability of the Internet, put all this information online for the benefit of international experts and the public. Entering the market economy was only possible with governmental support to add the new skills without loss of traditional expertise.

In 1992 the Convention on Biological Diversity was ratified by 150 nations (http://www.biodiv.org/convention/articles.asp). Following this, culture collections were required to develop new strategies to realise the conservation and sustainable use of biological diversity as well as the fair and equitable sharing of its benefits. Strategic changes that reflect this development must be accompanied by well-defined policies and by adequate funding. Current resources are not sufficient to face the challenge of securing access to materials and data in the best technological and socially most acceptable way. The debate continues as to what is needed, who should provide it and who should finance it. These basic questions must be resolved collectively among the international scientific community and the policy makers to establish a long-term strategy that will ensure continuous, stable and progressive development of culture collections. Scientific and technological progress will continue to change the requirements of the end user and hereby demand new services, which must be developed and implemented simultaneously with the continuation of the traditional tasks of culture collections. To respond to this requirement, culture collections should be the place to conduct research that is unlikely to be carried out elsewhere and that relates to the primary goals of the collections (conservation and taxonomy). The skills for much of this research are embodied in the collection personnel by virtue of their daily tasks. It would be economic insanity not to utilise this resource for the societal benefit.

2. Integrating different windows on reality

Human society is benefiting from our knowledge about microorganisms. This knowledge is constantly increasing with improved technologies. In order to translate this accumulated

knowledge into benefit for all and not just for experts in particular fields, it is important to share this knowledge and to correlate different findings with each other. For example the knowledge of the genetic code of a microorganism is useless without the knowledge of its translation into observable physical properties. Physical properties on the other hand have no meaning if they are not set into context with life. In addition, the physical properties of microorganisms are not a constant but are known to change in response to the environment.

The basic argument of this paper is that neglecting the importance of combining and sharing knowledge coming from these different levels of reality results in loss of expertise, knowledge and social opportunities both for developed and developing countries, the latter as the reservoir of most of the remaining biodiversity on Earth. In this section, we introduce the basic notions – in simple terms – that play a role in the different approaches to living organisms. Going beyond an atomistic and segmented approach to reality is the ultimate *rationale* for the development of appropriate institutional frameworks for sharing of data and resources.

Our world consists of observable objects. Apart from the small fraction of objects visible to the human eye, most of these objects, and also properties of the visible objects, are only detectable with the help of tools. Depending of these tools, we get different impressions of the objects as the tools explore different properties. Each of this property is part of our reality. Although we have to deal with different properties, many of them are not independent of each other. For example, the property of taste of cheese is partly determined by the property of chemical composition of the cheese. In addition, properties may change with time as can easily be imagined on the example of taste and chemical composition of the cheese. Only all properties of an object (including temporal changes) would describe an object completely. However, the task of such a comprehensive description is impossible to complete, as human knowledge and with it the ability to detect more properties is constantly evolving.

Our natural environment is to a large extent determined by organic life forms. Most of them are hidden for the unaided eye. Many of these life forms, referred to as microorganisms, are essential for the existence and the well-being of higher organisms including humans. Examples of the role of microorganisms are the natural recycling of organic material and the participation in food chains or symbiotic relationships like in the digestive system of higher organisms. Even a large proportion of the human body mass consists of microorganisms.

Although we do not perceive microorganisms as single individuals without the help of instruments like a microscope, they exist as individuals, are one of the earliest life forms on earth and determine the fate of our world.

Many microorganisms show similar appearance when observed by microscopy. However, they often differ in their interactions with the environment. In contrast to other larger life forms, which are more easily distinguishable, the characterisation of microorganisms requires the evaluation of as many as possible properties to differentiate between them. Their reliable identification is for example essential to distinguish pathogenic from benign and beneficial microorganisms or to evaluate their suitability in industrial processes (for example cheese production). The sum of observable properties and characteristics of a microorganism is regarded as the phenotype. This phenotype is determined both by the inheritable information carried by the organism or the genotype and the environment. The process of interaction between the molecules that represent the genotype and the environmental factors is complex and only partially understood. Hence the knowledge of the genotype, represented by the genetic code, does not always allow the prediction of the phenotype. For example, the taste of a particular cheese is not only determined by the genetic code of the cheese-producing microorganism but also by its environment (temperature, milk composition, etc.). The phenotype of the microorganism provides the most essential information for understanding an organism's position in the global balance of life and is essential for any potential exploitation. While the genetic material of cells can be decoded, digitised and stored in standardised data formats on large scales, the phenotypic information is highly divers, more difficult to transform into a digital format and standardised data formats need to be developed.

The ability of microorganisms to multiply readily is the basis of their ancient role for the production, conservation and spoilage of food and has made them famous as model organisms in molecular genetics. Their importance in past and future applications leads to large amounts of accumulated information on genotype and phenotype that has to be efficiently managed and utilised in its entirety to gain further benefit from it. However, the attention that is paid to phenotypic data by many approaches of data management is on the decline. This tendency may become critical to our knowledge of microorganisms also due to the loss of expertise. On the other hand, modern analytical techniques allow the generation of highly detailed data that represent the total phenotype better than single biochemical tests.

3. The need to integrate phenotypic and genotypic properties

The recognition of the loss of taxonomic expertise when experienced specialists retire without replacement by well-trained successors and the bias of developing comprehensive classifications for attractive organisms such as mammals and flowering plants, while simultaneously neglecting difficult groups such as microorganisms, has initiated discussions on an exclusively DNA-based taxonomy. It was proposed to use exclusively a DNA sample of an individual as a reference and to generate one or several gene sequences as an identification tag for the species from which the individual was derived (Tautz et al., 2003). While such a system will improve the recognition and classification of organisms for which no other characters can be determined (i.e. non-cultivable organisms), all other organisms would be characterised very incompletely by a tiny portion of their genome while neglecting phenotypic properties (Lipscomb et al., 2003). Although a DNA-based taxonomy is efficient to build an integrative database for all cultivable and non-cultivable organisms, it would disregard all other biological aspects that may contribute to our understanding of the organisms and their interactions. Molecular methods are also excellent tools to reconstruct natural relationships of organisms, however, additional difficulties[4] to the issues mentioned above arise from the continuum of individuals[5]. An unambiguous molecular definition of species would only be possible if the used gene sequences were constant among all members of one species and different from all other species. There is no evidence that most genes meet this criterion and any diagnostic character that would do so would work without the need to be molecular. Therefore, a definition of species from molecular data alone will be as subjective as it would be if based solely on phenotypic similarities. It is the combination of phenotypic and genotypic characters that has the potential to improve the recognition of microbial species effectively.

The circumscription of higher taxonomic groups would be even more difficult or impossible if based on molecular data alone. The current hierarchical system is based on the expertise of generations of taxonomists who decided which phenotypic characters are the most significant and most informative for a higher order grouping (genera, families, ..., kingdoms). These decisions were made according to the best knowledge of individual persons, therefore they are subjective and in some cases even inappropriate (i.e. not following the natural pattern of ancestry). However, one would ignore centenaries of knowledge accumulation if basing taxonomy solely on DNA sequences. Not only science would suffer from neglecting the

phenotype, but more importantly, valorisation of microorganisms for biotechnology would potentially be limited, as differential phenotypic abilities would not be recorded for newly discovered organisms.

We should rather use the possibilities that are offered by genotypic data to carefully correct inappropriate groups than to invent a new system solely based on DNA data. As we currently do not fully understand the interactions of genotype and environment, data on all three parameters (genotype, phenotype, environment) need to be evaluated to describe living organisms in the most appropriate way.

4. Yeast as a model

Let's illustrate the importance of going beyond genetic information through an important and well-known model in the life sciences: the model of yeast. This model shows the importance to combine genotypes – the information encrypted in the genetic code – and phenotypes – the observable characteristics and properties of the organism. Here we focus on the scientific and socio-economic challenge to integrate both. This will set the stage for our discussion of the institutional challenges.

Yeasts are single celled fungi that are fast and easy to grow. Yeasts have been used in the production of food and beverages such as bread and beer since ancient times. The yeast species *Saccharomyces cerevisiae*, also known as bakers yeast, constitutes the best-developed eukaryotic system[6] to model physiological, biochemical and many other processes. Consequently, it was the first eukaryote for which the complete genome[7] was decoded by sequence analysis of the entire genetic code (Goffeau et al., 1996). Complete genome sequences of about 20 yeast species are currently available. These are far fewer than for prokaryotes[8] as the yeast genome is considerably more complex. In contrast to bacteria, yeasts are more similar and in some functions even equivalent to higher organisms like humans. Using comparative approaches and models of interaction between the genome and cell functions allows drawing general conclusions regarding simple biochemical processes.

Yeasts are also essential in many ecological networks such as the recycling of biomass. They are far more specialised than bacteria regarding the nutrient sources that they are able to utilise and regarding the ecological niches they may thrive in, and therefore the associated

environmental data are of greatest significance for the study and application of these microorganisms. This is in particular important for the evaluation of constantly shrinking, partly un-explored ecological systems, in particular in developing countries. The data on the natural environment of yeasts are a primary source of information acquired directly in the process of collecting the organisms. They include information on the geographical location and the substrate from which they were recovered (e.g. flowers, soil, animals, etc). Ideally, a future database would link the organisms of different kingdoms (e.g. bacteria, fungi, plants, animals) that are found in close natural associations, to investigate the significance of possible interactions. The adaptation of many yeasts to well defined ecological niches has led to a large diversity of particular physiological properties, which is currently not fully exploited as only a small fraction of the yeasts are utilised in industrial processes. These few species and very few strains of them are often optimised by genetic engineering for various applications under considerable efforts and costs. The natural potential of yeasts could be used more efficiently if their phenotypic properties would be more accessible than they are currently.

Please insert Fig. 2 about here.

Data management systems should not only facilitate storage, linkage and retrieval of the different data types but also facilitate the effective processing, comparison and analysis of all available data so that conclusions can be drawn that extend the knowledge beyond pure accumulation (Fig. 2). For example, the environmental survey of yeasts in a particular habitat generates data on the presence of particular yeast species. The analysis of the acquired data (description of yeasts by morphology, physiology, genetic and biochemical data, host organisms, geographic distribution) allows then predictions about species that have not been observed but are present in the habitat. The observed yeasts might allow conclusions about their environmental adaptations and functions (Lachance, 2006).

Please insert Table 1 about here. The Table is submitted as a separate file as it contains images.

Yeasts have classically been grouped based on phenotypic properties like colony appearance, cell morphology and physiological properties (Table 1). This system of characters has served well up to the point at which genotypic characters allowed for a more precise distinction of organisms and enabled the reconstruction of natural relationships among them. Based on

contradictions between genotypic and phenotypic classifications, it was recognised that the current phenotypic classification of yeasts is in large parts artificial. This means that it groups organisms of phenotypic homogeneity but genetic heterogeneity, as it takes only that part of an organism's potential into account, which is expressed under the given environmental conditions. The full phenotypic potential may involve additional, yet unrecognised properties. A second problem is caused by the fact that phenotypic properties that might be variable within a group have been used to circumscribe this group. Genetically heterogeneous groups are not predictive of the full phenotypic potential of their members, as would be expected from a hypothetically natural classification. Such a natural classification would facilitate the valorisation of yeasts as it assists the selection of organisms that may possess a desired property. The awareness that (a) some crucial phenotypic properties were missed and (b) that some less characteristic phenotypic properties were overweighed necessitates the constant re-evaluation of the characters currently in use for yeast classification. The evaluation of increasing numbers of properties due to methodological and conceptual improvements was contributing to a continuing increase in the number of recognised yeast species (Fig. 3). The discrepancy between the estimates of recognised and described yeast species in 2005 demonstrates the urgent need for increased resources to deliver formal descriptions of the rapidly increasing number of recognised species. The continued evaluation of existing criteria and the search for new phenotypic and genotypic discriminative criteria is essential for the classification of the increasing numbers of new species in a realistic and meaningful scheme.

Please insert Fig. 3 about here

The utilisation of DNA based molecular methods, namely the use of gene[9] sequences, is highly influential for the integration of new species and the approximation of natural relationships by the classification system. These natural relationships are essential for the development of a classification system that is predictive of the organism's full phenotypic potential. However, as explained before, DNA sequence data also show limitations. The recognition of species and species relationships may require sequences of different genes in different groups of organisms, making the approach of a single, all-purpose gene for identification impossible. It has also been recognised that one or two genes can often not resolve distinct species and therefore several gene sequences need to be determined for a reliable identification. Analyses of whole genome sequences have shown that the reliable

reconstruction of natural relationships in a subgroup of yeasts required a minimum of 20 different gene sequences (Rokas et al., 2003).

The problems encountered with the use of either only classical taxonomic data or only DNA sequence data have lead to the development of polyphasic approaches that utilise all available data from both sources, phenotype and genotype, to generate a consensus classification. In some cases the consensus classification is a compromise containing the minimum of contradictions. It is assumed that with more information the consensus will gain stability. Polyphasic taxonomy has been extensively developed in bacteria as reviewed by Vandamme et al. (1996), who provided descriptions of the involved methods. However, equivalent principles are also applicable to yeasts. The evaluation and inclusion of many sources of information is essential to understand reality in a way that allows the effective valorisation of microorganisms. The generation of phenotypic and genotypic types of data is currently achieved in a targeted way by determining characteristics that are *a priori* assumed to be informative.

The non-targeted search for informative characteristics has become feasible by recently developed methods that are screening the largest accessible parts of geno- and phenotypes. New, rapid methods of instrumental analytical chemistry allow the simultaneous detection of the chemical cell composition, e.g. the proteome[10] and the metabolome[11]. These methods provide an overview of all detectable chemical compounds in the cell. This simultaneous detection of hundreds of chemicals (and therefore potential characters) has the advantage of not having to select a particular compound or group of compounds as a target that is supposed to provide the information. Innovative methods for data analysis have been developed to extract valuable information for the characterisation of microorganisms, their biochemical pathways and for the identification of potentially industrial useful products (Raamsdonk et al., 2001; Himmelreich et al., 2003; Wang et al., 2004).

5. Institutional challenges for culture collections

Information systems will be able to create increasingly realistic models of nature, as more and more diverse and complex information will be fed into them. With this increasing knowledge, we not only face scientific and technical challenges, but have also the chance to achieve a new

quality in utilising microorganisms for the benefit of human society. We would be able to select the best-suited organisms for a particular application. This task can only be achieved if different parts of society (science, economy, politics) work together in order to share costs, rewards and to optimise resources.

The currently stagnating communication between increasingly specialised and therefore partitioned communities (industry, medicine, basic research) has restrictive consequences to the development of comprehensive knowledge. An example from the world of classification and taxonomy is a yeast known as *Pichia pastoris*, used commonly as a expression system for the production of heterologous proteins[12]. Recent biodiversity surveys have resulted in the discovery of similar yeasts, leading to their reclassification including *P. pastoris* in the new genus *Komagataella* (Kurtzman, 2005). It now becomes apparent that many industrially used strains belong not to *Komagataella (Pichia) pastoris*, but in fact to the newly described species *Komagataella phaffii*. Knowledge of the distinct, genotype-based classes within *P. pastoris* might have facilitated the selection of potent phenotypes as production strains. Further characterisation of *K. phaffii* might show subtle differences that have led to its empirical selection for industrial purposes. As biotechnologists and taxonomists have worked independently in this case, the discovery was only made by chance.

On one hand, the integration of many types of different data (genetic, ecological, biological, and chemical) into data and metadata repositories is technically demanding, as these enormous amounts of data require complex processing for digitisation (Table 1) and a high degree of data fusion for effective knowledge generation (Fig. 2). On the other hand, the design of a repository has to be as simple, intuitive and user-friendly as possible to fulfil the social aspect of intellectual accessibility to all involved disciplines. The personnel that is managing and utilising the repository may be specialised in one or some types of data, but can never be an expert for all of them. To utilise all available data in polyphasic analyses (cf section 4 above), the information should be presented in a format that is comprehensible for non-specialists. Software that fulfils the above requirements does presently not exist. This is mainly due to the diversity of data but also to the fact that some characters are difficult to digitise and model (for example colour, odour or shape) without over-simplification of the natural diversity. A large array of specialised software is necessary to manage and analyse the different types of data. To ensure the highest scientific quality of database and analysis

software, the development demands a collaborative and multidisciplinary basis, including experts from the fields where the data originate.

This challenge has both a scientific, economic and an institutional dimension. Comprehensive information systems should integrate traditional data (e.g. morphology, physiology), genotypic data (e.g. DNA sequences), novel phenotypic data (e.g. spectroscopic data) and many other types of information. This information needs to be shared between different disciplines as all can contribute to and gain from more specialised and detailed data that are not commonly available. Information systems will be essential for linking the genome as representative of the potential of an organism with the proteome, as the sum of expressed proteins in response to the environment, and the metabolome that indicates the current status of a cell by the totality of its small molecules, information on ecological factors and pathogenesis. The establishment of such links will not only greatly contribute to our understanding of life but also have implications for the utilisation of microorganisms. The challenge is to share this information between often contradicting interest without compromising on intellectual property rights. This not only applies to commercial entities but also to the protection of national resources. Developing countries are important partners to conserve biodiversity. They often possess very diverse, partly threatened and poorly studied ecological systems. As they do not have the resources to implement the most recent technologies, it is crucial to generate inventories of their patrimony using basic microbiological methods.

Culture collections are situated at the intersection of societal requirements and multiple types of information. They have succeeded at this frontier and will continue to stimulate the establishment of a microbial commons by the way they manage biological, scientific, social and ethical concerns.

Notes

[1] The genotype is the inheritable information carried by all living organisms. This information is used as a set of instructions for building and maintaining an organism. These instructions are encrypted in the genetic code, copied at the time of cell division and passed from one generation to the next. These instructions are intimately involved with all aspects of the life of an organism, controlling everything from the formation of protein macromolecules to the regulation of metabolism.

[2] The phenotype includes anything that is part of the observable structures and functions of a living organism. These are physical parts, the sum of the atoms, molecules, macromolecules, cells, structures, metabolism, energy utilisation, tissues, organs and behaviours.

[3] Taxonomy is used here in its original sense as the science of finding, circumscribing, formally describing and naming organisms. Taxonomic classification follows a hierarchical structure that creates groups of organisms with decreasing similarities in their properties and, more recently, in their natural genealogical relationships. The most similar individuals or strains are grouped in one species and similar species in one genus (Fig. 4). Thus, each strain can be assigned to a species; each species can be assigned to a genus, etc.
Please insert Fig. 4 about here

[4] Another important issue showing the limits of a “genetic approach only” is raised by comparative DNA analysis. These challenges include the difficulties to compare sequences of different lengths, distinguishing orthologs from paralogs and the selection of appropriate genes that are informative for a large range of diverse organisms. Orthologous genes are direct evolutionary counterparts derived from a common ancestor through vertical descent. As a consequence, orthologs often, but not necessarily, assume the same function in different organisms. To compare the same gene from different species, those genes have to be orthologs. Paralogous genes originated from a common ancestor by duplication and then diverged from the ancestral copy by mutation and selection or drift. As a consequence, paralogs often, but not necessarily, assume different functions in an organism (Koonin, 2005).

[5] No clear boundaries of distinct groups (e.g. species) exist. More and more sensitive techniques reveal a continuum of individuals with an increasing number of non-assignable

individuals. Although it is difficult to develop models of such fuzzy groups, a future data management system has to be able to illustrate this reality without the current inevitability to reduce the true multidimensionality.

[6] Eukaryotes are organisms with a higher structural complexity of the cells than the more simple prokaryotes. Eukaryotes are characterized by having many functions segregated into semi-autonomous regions of the cells (organelles). The name of the eukaryotes origins from the most evident organelle, the nucleus (Greek, *eu* = true + *karyon* = nucleus). Eukaryotes include humans, other animals, plants, fungi and a rich variety of microorganisms.

[7] The genome is the whole hereditary information of an organism that is encoded in the deoxyribonucleic acid (DNA) and ribonucleic acid (RNA).

[8] Prokaryotes (Greek, *pro* = before + *karyon* = nucleus) are single celled organisms that lack the characteristic eukaryotic organelles. Neither their genome nor any other of their metabolic functions are restricted to an enclosed area of the cell. Instead everything is openly accessible within the cell. Prokaryotes include viruses, bacteria, and blue-green algae.

[9] A gene constitutes a portion of the genome that encodes a single protein or another molecule of functional relevance. The genome of the yeast *Saccharomyces cerevisiae* contains about 6000 genes.

[10] The proteome is the totality of all proteins in a cell, produced under a given set of environmental conditions. While the genome remains constant (disregarding potential mutations) for the cells of an organism, the proteome varies with the activity and the environment of the cells.

[11] The metabolome is the totality of all small molecules of a cell such as nucleotides, vitamins, and antioxidants. It mediates the information about environmental changes to the genome. While the genome is representative of what might be and the proteome is what is expressed, it is the metabolome that represents the current status of the cell (e.g. nutrition, age, effect of toxins).

[12] Expression systems for heterologous proteins allow the production of proteins that are foreign to the producing cells, which have been programmed by genetic engineering to express them. Such systems consist of the host cells, a DNA construct that contains the gene encoding the desired protein and the appropriate environmental conditions for the expression. Expression systems are used for the large-scale production of high-value proteins such as enzymes, vaccines and various blood factors.

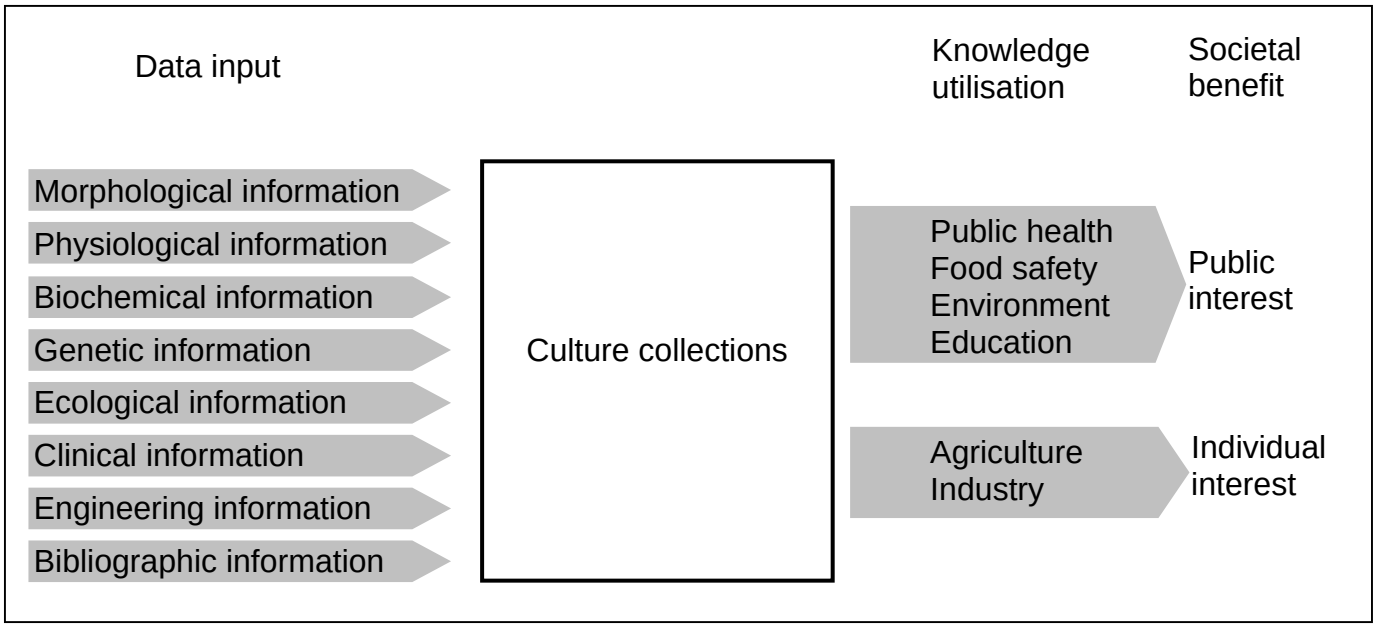


Fig. 1: Information types generated and sectors of knowledge utilised by culture collections.

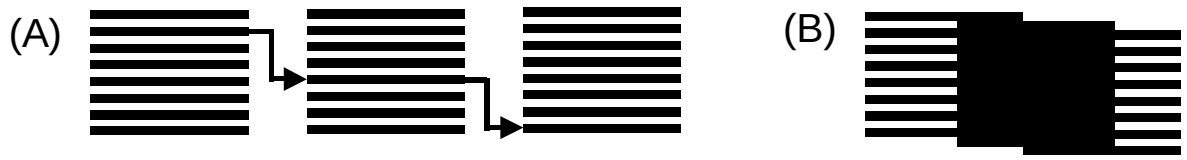
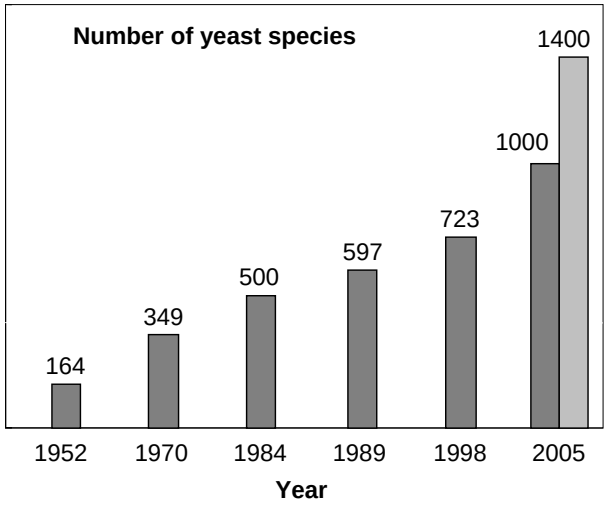


Fig. 2: Not just the storage, linkage and retrieval (A), but the processing, comparison and analysis of data (B) is needed, effectively fusing data to new knowledge.

Fig. 3 Quantitative development of taxonomically described yeast species (dard bars) and recognised yeast species (light bar). The numbers for the year 2005 are based on estimations of leading yeast taxonomists (pers. Comm. Lachance), the others taken from Lodder, 1970; Kreger-vanRij, 1984; Barnet et al., 1990; Kurtzmann & Fell, 1998.



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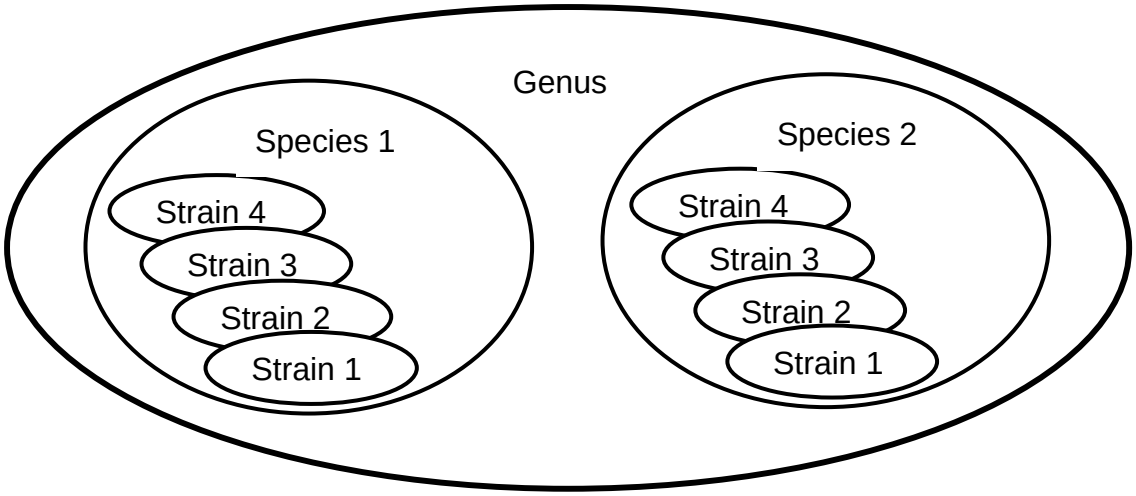
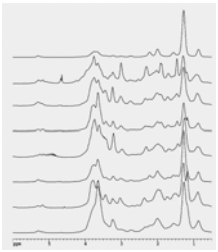
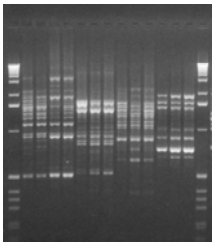
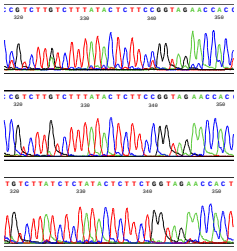


Fig. 4: Hierarchy of individuals (strains) and the two lowest principal taxonomic ranks (species and genus) to group them.

Data type:	Phenotypic information		Genotypic information	
Data format:	Non-digitised	Digitised	Non-digitised	Digitised
Examples:	Culture appearance (Colour, odour, surface structure, texture) Shape and structure of colonies and cells (morphology) Mating behaviour Expression of growth inhibitors (mycocins) Isoenzyme profiles	Growth tests on various nutrient sources (physiology) Characterisation of cellular compounds (proteins, fatty acids, polysaccharides, etc.) and biochemical pathways by instrumental analytical chemistry (e.g. MS, HPLC, IR, NMR*)	Microsatellite primed polymerase chain reaction (MS-PCR) Randomly Amplified Polymorphic DNA analysis (RAPD) Restriction Fragment Length Analysis (RFLP) Hybridisation of total or partial genomic DNA Secondary structures of RNA	DNA sequences Amplified Fragment Length Analysis (AFLP)
				
	Cell morphology	NMR spectra	MS-PCR	DNA sequence data

* MS: Mass Spectrometry is an analytical tool used for measuring the molecular weight of molecules and their fragments.
HPLC: High Pressure Liquid Chromatography can be used to separate compounds that are dissolved in solution.
IR: Infrared spectroscopy is using the absorption of infrared light by substances to examine molecular structures.
NMR: Nuclear Magnetic Resonance spectroscopy is using different energetic states of molecules in a magnetic field to determine their molecular structure.

Table 1: Phenotypic and genotypic properties commonly recorded for yeasts.

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