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More than anything, the article points to a real need for the community to adopt a set of evaluation arguments to methodologically track consistency, completeness and ontology assessment in the context of known methodologies for evaluating ontologies.

Mark Miller & Rami Rifaieh

San Diego Supercomputer Center, University of California, San Diego, La Jolla, California 92093-0505, USA.

e-mail: mmiller@sdsu.edu

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#### Larisa Soldatova and Ross King respond:

We are pleased that our commentary has stimulated debate about the current and future role of ontologies in biology. Our article contained a factual and constructive analysis of the problems in MO. Some of our analysis requires a wider discussion, such as prospective ways of improving and developing ontologies. Other problems could be fixed immediately, such as the names and definitions of classes.

We agree with most of the points made by Musen *et al.* In particular, we agree that “Much of the most influential ontology work in biomedicine has been stimulated by the pressing needs of bench biologists themselves in managing burgeoning quantities of data. As a consequence, many of the ontologies developed thus far are somewhat unprincipled in comparison to what we now know can be achieved.” This summarizes our main criticism of MO and other bio-ontologies. We also strongly support the creation by the US National Institutes of Health of the National Center for Biomedical Ontology. Musen *et al.* do, however, misunderstand our proposal for dealing with the problems of ontology use in biology.

Figure 2 in our article clearly shows that our proposal is to create an intermediate ontology of experiments, which will abstract out the key concepts in scientific experiments. This ontology will link down to subject specific experimental ontologies, such as those in the omics, and up to SUMO. Building ontologies as an extension of an upper ontology enhances formalization and axiomatization for logical inference, data mining and knowledge discovery.

We agree less with the points in the letter of Stoeckert *et al.* We are particularly unhappy with the statement: “It is therefore ironic, and of notable concern, that the authors of this commentary have never communicated their analysis, or suggestions for improvements to any of the extended family of MO developers, that includes ontologists in an advisory capacity”. We spoke to, and voiced our concern, with several of the authors of the Stoeckert *et al.* letter. We greatly appreciate their and others’ work in the bio-ontologies community in organizing biological knowledge. They are undoubtedly pioneers in the application of ontologies to science. We doubly appreciate this because in Aberystwyth, we run the informatics for the UK National Metabolomics Center for Plants and Microbiology, which makes us well aware of the practical difficulties in dealing with modern ‘omics’ data.

Dealing with the specifics of their letter, we first note that Stoeckert *et al.* do not actually refute any of our original points, and their letter confirms our belief that the designers of MO are hypnotized by the needs of today, rather than planning for the needs of tomorrow. We contend that MO is still relatively small and it is not too late to redesign its structure.

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problems in bio-ontologies, not only those in MO. The most important of these problems is a lack of standards for bio-ontology design. In this regard, we see the value of the OntoClean methodology, but on its own it does not provide the required standards.

Concerning our preference for the use of trees rather than directed acyclic graphs in ontologies (point no. 9), the argument for this is as follows. Consider two classes  $A1$  with a set of instances  $\{a1\}$ , and  $A2$  with instances  $\{a2\}$ , with intrinsic properties  $IPA1$  and  $IPA2$ , respectively. And consider the class  $B$  that is a subclass of both classes  $A1$  and  $A2$ . Then, by the definition (see our commentary), the class  $B$  is populated by instances from both classes  $A1$  and  $A2$ ; and all instances of  $B$  ( $\{b\}$ ) inherit the properties  $IPA1$  &  $IPA2$ . For each individual instance of  $B$ : or  $\cdot$ . Therefore either  $a1_j$  has  $IPA1$  &  $IPA2$  or  $a2_k$  has  $IPA1$  &  $IPA2$ . This means that either  $a1_j$  can be classified as  $A2$  or  $a2_k$  can be classified as  $A1$ . The result is that an instance, in the same classification system, can be classified into two distinguishable classes, which clearly can cause errors in logical inference.

Finally, given the number of problems in MO (which Miller & Rifaieh accept) we do not consider it to be “completely unwarranted” to call for a complete redesign of MO’s structure while preserving its undoubtedly useful parts. All software engineers are aware of occasions when it is necessary to apply lessons learned in an initial version to a clean new design.

It is time for a new generation of bio-ontologies, which should serve not only as controlled terminologies for humans, but also allow computer programs to automate scientific investigations.

## European GMO labeling thresholds impractical and unscientific

### To the editor:

In the next few months, the European Union (EU) will witness a burst of novel authorizations for genetically modified (GM) plants. In this context, a huge effort is underway in the laboratories of the European Commission (EC), of the Member States, of third countries and of private companies, to elaborate, assess and validate the necessary sampling strategies and molecular analytical procedures required to implement European

regulatory requirements<sup>1</sup> for labeling food and feed products containing ingredients from GM organisms (GMOs). It is now three years since the legislation was first introduced, yet enormous technical and scientific challenges remain in reducing regulations to practice.

The EC first introduced labeling thresholds for the accidental unavoidable presence of GM ingredients because of the technical and practical impossibility of ensuring their

absolute absence in food or feed<sup>2-4</sup>. The latest regulation fixes the labeling threshold as follows: "... foods containing material which contains, consists of or is produced from GMOs in a proportion no higher than 0.9% of the food ingredients considered individually or food consisting of a single ingredient, provided that this presence is adventitious or technically unavoidable"<sup>4</sup>. The term GMO is defined by article 2(2) of Directive 2001/18/EC<sup>5</sup> as follows: "'GMO' means an organism, with the exception of human beings, in which the genetic material has been altered in a way that does not occur naturally by mating and/or natural recombination." Finally, ingredient is defined by the article 4(a) of the Directive 2000/13/EC as "... any substance, including additives, used in the manufacture or preparation of a foodstuff and still present in the finished product, even if in altered form"<sup>6</sup>. From the practical point of view, in the field of GM plants, the ingredient is the part of the organism directly employed or further transformed to be used as food or feed (e.g., maize kernels or soybean beans).

The first question facing a scientist attempting to develop an assay to implement the GMO regulations is: what does "0.9% of the food ingredients" mean in terms of genes? Or, put another way, how to translate the gross generic definition of "ingredient" into something making sense at the molecular level?

Currently, the method of choice for transgenic sequence detection is real-time PCR. In this approach, PCR is used to amplify a GM line-specific marker sequence and the results are quantified with respect to the amplified level of an endogenous sequence specific for the whole ingredient, termed a reference gene or 'normalizer.' The normalizer is usually a gene or a sequence marker within a gene that is species specific, well conserved and present at the same copy number among different lines of the same species.

In practice, certified reference materials (CRMs) are mandated in the European regulations for use in calibrating GMO quantification systems<sup>7-10</sup>. CRMs are prepared from certified seeds of the GM inbred line and of the non-GM parental variety used for the transformation are homogenized and grinded to powder. Subsequently, the resulting GM and non-GM flours are blended on a gravimetric weight/weight basis following strict certified procedures. Different concentration levels are prepared to obtain the so-called CRM series. Genomic DNA can be extracted from these

materials to be used as a calibrator in real-time PCR.

Defining the relative GMO content in a product on the basis of the weight/weight ratio of raw materials (ingredients) should imply the assumption that a conserved direct proportionality is found between the weight of the ingredient and the total number of genes or genomes contained in it. Unfortunately, such proportionality doesn't exist in reality<sup>7,8,10</sup>. As a consequence, the true molecular dosage of GM sequences can vary in an analyzed ingredient sample (or in a CRM) with respect to the nominal GM content defined as stipulated by current regulations. This ingredient versus gene dosage ratio has four main sources of variation.

First, no data are available on whether different lines of the same plant species exhibit a conserved ratio between the weight of what is considered an ingredient and the number of genomes contained in it<sup>8</sup>. Even when considering the same line, it is conceivable that factors influencing plant growth like zonal and/or weather conditions could cause a significant drifting of this ratio among different batches. In addition, the generalized little availability of certified GMO material and of its parental organism material makes it difficult to investigate this possible source of variability<sup>9</sup>. As an example, the certification document<sup>10</sup> for the Monsanto's (St. Louis, MO, USA) Roundup-Ready soybean reference material series 410-S issued by the Institute for Reference Materials and Measurements (IRMM; Geel, Belgium) of the Joint Research Center clearly states "... the ratio GMO-DNA/non-GMO-DNA reference materials may significantly deviate from the certified powder mass ratio values." Moreover, the same document also notes "one has to be careful to draw quantitative conclusions from measurements of unknown samples as DNA and/or protein based GM quantification may depend on varieties." The same two statements are repeated in other GMO-CRM certification documents (<http://www.erm-crm.org>).

Second, it is well known that some species of cultivated plants, like maize (*Zea mays*), show significant intraspecies variation in nuclear DNA content. In maize, several sources of variability have been described, such as the location from which lines originate, environmental factors, growth parameters and yield parameters<sup>11-14</sup>. As a consequence, it is not possible to establish one single defined DNA C-value for all maize lines. Laurie & Bennett<sup>15</sup> estimate that the C-value of DNA from different maize lines ranges from about 2.364 Mb (2.45 pg) to

about 3.233 Mb (3.35 pg). This high genetic plasticity of plant genomes doesn't represent a real problem if real-time PCR is used for the analysis and as long as the copy number of employed reference genes (normalizers) remains constant among the different lines. On the other hand, it becomes necessary to check the reference gene copy number in all lines employed in agriculture.

Third, if we consider diploid organisms, both the genetic modification and the species-specific reference marker could be found in homozygosis or in heterozygosis. As a consequence, the ratio between the genetic modification and the normalizer could be 1:1, 1:2 or 2:1. Usually, GM lines are self-pollinated to obtain homozygous lines (inbred lines) for the novel trait<sup>8</sup>. On the other hand, in common agricultural practice, inbred lines are crossed with specific selected non-GM lines to obtain hybrids. What's more, different hybrids of the same GM event are often raised for the use in different geographic/climatic situations. As a result, the ratio between the GM-specific marker and the species-specific reference gene could vary significantly from lot to lot.

Finally, the ploidy of the tissue that the ingredient is derived from could vary from the usual diploid asset of organisms. Several cultivated hybrid plants are tetraploid or polyploid<sup>8</sup>. In addition, the endosperm of seeds, composed mostly of starch-containing cells, is a triploid tissue arising from the fusion of a sperm nucleus with two polar nuclei of the egg cell. In some seeds, for example in maize, the endosperm persists as a storage tissue and is used to nourish the germinating seedling<sup>16</sup>. These facts, along with what is described in the previous point enhances the degrees of variability of the ratio between the GM trait and the species-specific normalizer.

If one strictly follows the definition of "GMO ingredient" as stipulated by current European regulations, there is no difference between, for example, an inbred diploid line being homozygous for the genetic modification, a diploid line being heterozygous for the modification and a tetraploid line with only one modification per genome: they are formally all full GM ingredients (that is, 100% GMOs). On the other hand, from an analytical point of view, a homozygous diploid, heterozygous diploid and tetraploid line with only one modification exhibit 100%, 50% and 25% GMO content, respectively. This situation is worsened if we consider a marketed product ingredient resulting from the randomized mixture of different lots and lines of the same species depicting different genomic assets in terms

of zygosity, ploidy and C-value. In this case, it is impossible to determine each component's specific contribution and molecular analytical tools will necessarily over- or underestimate the nominal GM component of the product ingredient. *De facto*, the quantification of the GM content in a sample provides us with neither the true molecular dosage of the modification(s) (e.g., the number of modified haploid genomes versus the total number of haploid genomes) nor the content defined on the basis of European regulations; instead, it gives us a relative gene dosage determined with respect to the employed CRM.

Taken together, these problems create an unclear environment in which the regulations are unenforceable using the molecular analytical tools available. Every analytical result could potentially be invalidated by means of scientific data demonstrating that the CRMs used are not representative for the samples under analysis. The EU legislators continue to fudge; the current regulation 1829/2003 (ref. 4) uses the same imprecise 1% threshold as its predecessor 49/2000 (ref. 2). And the EC's most recent recommendation (2004/787/2000)<sup>17</sup> only partly solves the problem by defining the percentage of GM DNA as "the percentage of GM-DNA copy numbers in relation to target taxon specific DNA copy numbers calculated in terms of haploid genomes."

Three years after the current EC regulation<sup>4</sup> was issued, all the operative structures described within it (that is, the European Food Safety Agency and the Community Reference Laboratory) are now fully active. Yet, only two novel authorizations were granted in 2004 (*Bt11* sweet corn and NK603 maize). All the other 25 GM plants, which are listed as authorized in the Community Register of GM Food and Feed ([http://europa.eu.int/comm/food/dyna/gm\\_register/index\\_en.cfm](http://europa.eu.int/comm/food/dyna/gm_register/index_en.cfm)), were placed on the market in the EC before the entry into force of the current regulation.

European legislations must move quickly to amend the current regulation so that rules provide an exact and scientifically acceptable definition of GMO content that can be adopted in testing. It is not a question of moving the regulatory goal posts; the current legislation doesn't even tell us where to put the goal posts.

Florian Weighardt

via Milano 1095, 21027 Ispra (VA), Italy.  
e-mail: [florian.weighardt@poste.it](mailto:florian.weighardt@poste.it)

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## ATCC not involved in negotiations with India

### To the editor:

The American Type Culture Collection (ATCC) would like to clarify statements in an news article by K.S. Jayaraman published in the September issue of *Nature Biotechnology* (23, 1031, 2005) entitled "Materials exchange deal meager boost to India's biotech." The article describes mid-June discussions between a delegation of US Department of Commerce officials, led by acting deputy secretary David Sampson, and a delegation from India led by science minister Kapil Sibal.

The article suggests the two groups reached agreement on a proposal to govern the transfer of biological material from the United States to India. The proposal seems to mention ATCC specifically: "Under the plan," the article states, "India's Department of Biotechnology would procure biological materials from the American Type Tissue [sic] Collection (ATCC) and warrant against their misuse or subsequent acquisition by bioterrorists, with safeguards and export controls similar to those around nuclear technology."

ATCC would like to notify the scientific community that no ATCC representative was invited to attend the Department of Commerce's meeting with the India

delegation and ATCC is not aware of any specific agreement made by the US Federal Government with India or any other country for obtaining biological materials from ATCC. Aside from the fact that an agreement was apparently made without

ATCC's involvement, firmly established policies at ATCC block any type of exclusive relationships with individual countries. Furthermore, for decades, and continuing today, Indian scientists registered with our organization have been welcome to order products from ATCC for their research.

The article also mentions that Indian scientists have experienced "problems working with" ATCC.

Our records indicate that all orders from registered scientists in India have been successfully filled. ATCC is glad to provide its high-quality research materials to Indian scientists. All of ATCC's rules, shipping policies or pricing schemes are applied to all countries equally. In no way does ATCC restrict access to its collection for registered scientists in India or another country.

### Jesus Soriano

ATCC Vice President for Licensing, Contracts and Compliance, American Type Culture Collection, Contracts, Compliance and Licensing, 10801 University Blvd., Manassas, Virginia 20110, USA. e-mail: [jsoriano@atcc.org](mailto:jsoriano@atcc.org)



## Erratum: Biotech entrepreneur, educate thyself!

Emily Waltz

*Bioentrepreneur*, published online 15 December 2005, corrected 27 March 2006; doi:10.1038/bioent896

In the online version of this article (paragraph 4), Chad Walton is incorrectly said to have graduated from a dual-degree program. The text should read, "...Chad Walton, who received a master of biomedical technology (MBT) from the University of Calgary..." The program with the eight students he is referring to is the MBT program, not the dual-degree program. The MBT program does, however, have a business component. The error has been corrected in the HTML version of the article.

## Erratum: European GMO labeling thresholds impractical and unscientific

Florian Weighardt

*Nat. Biotechnol.* **24**, 23–25 (2006), corrected 27 March 2006

In the print version of this article and the version published online, several inaccuracies were introduced into the text through editorial modifications. On page 23, column 2, rows 3–4, the text: "It is now more than three years since the legislation was first introduced..." should have read "...more than five years..." On page 24, column 1, rows 35–37: "Currently, the method of choice for transgenic sequence detection is real-time PCR." should have read "...for transgenic sequence quantification..." Page 24, column 1, rows 51–55: "CRMs are prepared from certified seeds of the GM inbred line and of the non-GM parental variety used for the transformation are homogenized and grinded to powder." should have read, "For the GM inbred line and the non-GM parental variety used for the transformation, CRMs are prepared from certified seeds, homogenized and grinded to powder." On page 25, column 1, rows 22–25: "The EU legislators continue to fudge; the current regulation 1829/2003 (ref. 4) uses the same imprecise 1% threshold as its predecessor 49/2000 (ref. 2). And the EC's most recent recommendation (2004/787/2000)<sup>17</sup> only partly..." should have read "...uses the same imprecise threshold definition as its predecessor 49/2000, which introduced a 1% threshold<sup>2</sup>. And the EC's most recent recommendation (2004/787/EC) only partly..." The errors have been corrected in the PDF version of the article.

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## Erratum: Biogenerics at the crossroads

Carole S Ben-Maimon & Rob Garnick

*Nat. Biotechnol.* **24**, 268 (2006), corrected 27 March 2006

In the print version of this article and the version originally published online, Carole Ben-Maimon was incorrectly listed as president and CEO of Barr Pharmaceuticals. She is, in fact, president and COO of Duramed Research, a subsidiary of Barr Pharmaceuticals. Her email address was also incorrect; her correct email address is cbenmaimon@barrlabs.com. The error has been corrected in the PDF version of the article.

Finally, the conclusion that MGED should be rebuilt from scratch seems completely unwarranted. The authors could better have served the community by suggesting a more realistic methodology for improving and cleaning the MGED ontology.

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In practice, certified reference materials (CRMs) are mandated in the European regulations for use in calibrating GMO quantification systems<sup>7-10</sup>. For the GM inbred line and the non-GM parental variety used for the transformation, CRMs are prepared from certified seeds, homogenized and grinded to powder. Subsequently, the resulting GM and non-GM flours are blended on a gravimetric weight/weight basis following strict certified procedures. Different concentration levels are prepared to obtain the so-called CRM series. Genomic DNA can be extracted from these materials to be used as a calibrator in real-time PCR.

Defining the relative GMO content in a product on the basis of the weight/weight ratio of raw materials (ingredients) should imply the assumption that a conserved direct proportionality is found between the weight of the ingredient and the total number of genes or genomes contained in it. Unfortunately, such proportionality doesn't exist in reality<sup>7,8,10</sup>. As a consequence, the true molecular dosage of GM sequences can vary in an analyzed ingredient sample (or in a CRM) with respect to the nominal GM content defined as stipulated by current regulations. This ingredient versus gene dosage ratio has four main sources of variation.

First, no data are available on whether different lines of the same plant species exhibit a conserved ratio between the weight of what is considered an ingredient and the number of genomes contained in it<sup>8</sup>. Even when considering the same line, it is conceivable that factors influencing plant growth like zonal and/or weather conditions could cause a significant drifting of this ratio among different batches. In addition, the generalized little availability of certified GMO material and of its parental organism material makes it difficult to investigate this possible source of variability<sup>9</sup>. As an example, the certification document<sup>10</sup> for the Monsanto's (St. Louis, MO, USA) Roundup-Ready soybean reference material series 410-S issued by the Institute for Reference Materials and Measurements (IRMM; Geel, Belgium) of the Joint Research Center clearly states "... the ratio GMO-DNA/non-GMO-DNA reference materials may significantly deviate from the certified powder mass ratio values." Moreover, the same document also notes "one has to be careful to draw quantitative conclusions from measurements of unknown samples as DNA and/or protein based GM quantification may depend on varieties." The same two statements are repeated in other GMO-CRM certification documents (<http://www.erm-crm.org>).

Second, it is well known that some species of cultivated plants, like maize (*Zea mays*), show significant intraspecies variation in nuclear DNA content. In maize, several sources of variability have been described, such as the location from which lines originate, environmental factors, growth parameters and yield parameters<sup>11-14</sup>. As a consequence, it is not possible to establish one single defined DNA C-value for all maize lines. Laurie & Bennett<sup>15</sup> estimate that the C-value of DNA from different maize lines ranges from about 2.364 Mb (2.45 pg) to about 3.233 Mb (3.35 pg). This high genetic

plasticity of plant genomes doesn't represent a real problem if real-time PCR is used for the analysis and as long as the copy number of employed reference genes (normalizers) remains constant among the different lines. On the other hand, it becomes necessary to check the reference gene copy number in all lines employed in agriculture.

Third, if we consider diploid organisms, both the genetic modification and the species-specific reference marker could be found in homozygosity or in heterozygosity. As a consequence, the ratio between the genetic modification and the normalizer could be 1:1, 1:2 or 2:1. Usually, GM lines are self-pollinated to obtain homozygous lines (inbred lines) for the novel trait<sup>8</sup>. On the other hand, in common agricultural practice, inbred lines are crossed with specific selected non-GM lines to obtain hybrids. What's more, different hybrids of the same GM event are often raised for the use in different geographic/climatic situations. As a result, the ratio between the GM-specific marker and the species-specific reference gene could vary significantly from lot to lot.

Finally, the ploidy of the tissue that the ingredient is derived from could vary from the usual diploid asset of organisms. Several cultivated hybrid plants are tetraploid or polyploid<sup>8</sup>. In addition, the endosperm of seeds, composed mostly of starch-containing cells, is a triploid tissue arising from the fusion of a sperm nucleus with two polar nuclei of the egg cell. In some seeds, for example in maize, the endosperm persists as a storage tissue and is used to nourish the germinating seedling<sup>16</sup>. These facts, along with what is described in the previous point enhances the degrees of variability of the ratio between the GM trait and the species-specific normalizer.

If one strictly follows the definition of "GMO ingredient" as stipulated by current European regulations, there is no difference between, for example, an inbred diploid line being homozygous for the genetic modification, a diploid line being heterozygous for the modification and a tetraploid line with only one modification per genome: they are formally all full GM ingredients (that is, 100% GMOs). On the other hand, from an analytical point of view, a homozygous diploid, heterozygous diploid and tetraploid line with only one modification exhibit 100%, 50% and 25% GMO content, respectively. This situation is worsened if we consider a marketed product ingredient resulting from the randomized mixture of different lots and lines of the same species depicting different genomic assets in terms of zygosity, ploidy and C-value. In this case, it

is impossible to determine each component's specific contribution and molecular analytical tools will necessarily over- or underestimate the nominal GM component of the product ingredient. *De facto*, the quantification of the GM content in a sample provides us with neither the true molecular dosage of the modification(s) (e.g., the number of modified haploid genomes versus the total number of haploid genomes) nor the content defined on the basis of European regulations; instead, it gives us a relative gene dosage determined with respect to the employed CRM.

Taken together, these problems create an unclear environment in which the regulations are unenforceable using the molecular analytical tools available. Every analytical result could potentially be invalidated by means of scientific data demonstrating that the CRMs used are not representative for the samples under analysis. The EU legislators continue to fudge; the current regulation 1829/2003 (ref. 4) uses the same imprecise threshold definition as its predecessor 49/2000, which introduced a 1% threshold. And the EC's most recent recommendation (2004/787/EC)<sup>17</sup> only partly solves the problem by defining the percentage of GM DNA as "the percentage of GM-DNA copy numbers in relation to target taxon specific DNA copy numbers calculated in terms of haploid genomes."

Three years after the current EC regulation<sup>4</sup> was issued, all the operative structures described within it (that is, the European Food Safety Agency and the Community Reference Laboratory) are now fully active. Yet, only two novel authorizations were granted in 2004 (*Bt11* sweet corn and NK603 maize). All the other 25 GM plants, which are listed as authorized in the Community Register of GM Food and Feed ([http://europa.eu.int/comm/food/dyna/gm\\_register/index\\_en.cfm](http://europa.eu.int/comm/food/dyna/gm_register/index_en.cfm)), were placed on the market in the EC before the entry into force of the current regulation.

European legislations must move quickly to amend the current regulation so that rules provide an exact and scientifically acceptable definition of GMO content that can be adopted in testing. It is not a question of moving the regulatory goal posts; the current legislation doesn't even tell us where to put the goal posts.

Florian Weighardt

via Milano 1095, 21027 Ispra (VA), Italy.  
e-mail: [florian.weighardt@poste.it](mailto:florian.weighardt@poste.it)

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## ATCC not involved in negotiations with India

### To the editor:

The American Type Culture Collection (ATCC) would like to clarify statements in a news article by K.S. Jayaraman published in the September issue of *Nature Biotechnology* (23, 1031, 2005) entitled "Materials exchange deal meager boost to India's biotech." The article describes mid-June discussions between a delegation of US Department of Commerce officials, led by acting deputy secretary David Sampson, and a delegation from India led by science minister Kapil Sibal.

The article suggests the two groups reached agreement on a proposal to govern the transfer of biological material from the United States to India. The proposal seems to mention ATCC specifically: "Under the plan," the article states, "India's Department of Biotechnology would procure biological materials from the American Type Tissue [sic] Collection (ATCC) and warrant against their misuse or subsequent acquisition by bioterrorists, with safeguards and export controls similar to those around nuclear technology."

ATCC would like to notify the scientific community that no ATCC representative was invited to attend the Department of Commerce's meeting with the India delegation and ATCC is not aware of any

specific agreement made by the US Federal Government with India or any other country for obtaining biological materials from ATCC. Aside from the fact that an agreement was apparently made without ATCC's involvement, firmly established policies at ATCC block any type of exclusive relationships with individual countries.

Furthermore, for decades, and continuing today, Indian scientists registered with our organization have been welcome to order products from ATCC for their research.

The article also mentions that Indian scientists have experienced "problems working with" ATCC. Our records indicate that all orders from registered scientists in India have been successfully filled.

ATCC is glad to provide its high-quality research materials to Indian scientists. All of ATCC's rules, shipping policies or pricing schemes are applied to all countries equally. In no way does ATCC restrict access to its collection for registered scientists in India or another country.

Jesus Soriano

ATCC Vice President for Licensing, Contracts and Compliance, American Type Culture Collection, Contracts, Compliance and Licensing, 10801 University Blvd., Manassas, Virginia 20110, USA. e-mail: [jsoriano@atcc.org](mailto:jsoriano@atcc.org)

