APPENDIX II

TAB H

FEDERAL RULE OF CIVIL PROCEDURE 26
DISCLOSURE OF EXPERT TESTIMONY
SCOTT MINNICH, Ph.D.

Case: *Tammy Kitzmiller, et al. v. Dover Area School District and Dover Area School District Board of Directors*

Case No. 04-CV-2688

Expert's Background and Experience:

My background and experience includes extensive training in the molecular genetics of microorganisms. Over the past ten years, my research interests have focused on the regulation of bacterial flagellum biosynthesis and type III protein secretory systems in bacterial pathogens. We are currently funded by the National Institutes of Health for vaccine work against several select agents. Between October 2003 and May of 2005, I served as a WMD subject matter expert with the Iraq Survey Group operating out of Baghdad and Mosul. I have taught extensively in undergraduate, graduate and medical school programs and currently teach a General Microbiology Course for undergraduates and coordinate and lecture in an Infectious Disease course for first year medical students.

Attached to this report as Exhibit A is a copy of my curriculum vitae.

I. The following includes a complete statement of my opinions to be expressed, the reasons and basis underlying them, and the data and other information considered in forming them.

Intelligent design theory is a scientific theory, and it holds that the deep complexity and clearly evident design in organisms is the result of an intelligent agent. Given that even the simplest cells are comprised of nanomachines that currently defy our own intelligent capability to produce, yet have the general features of many machines we have made on a larger scale, intelligent design theory is simply an inference to the best explanation as to the origin of this design. This explanation is in contrast to the generally accepted mechanism of neodarwinism that holds that mutations and natural selection are sufficient to account for the diversity and 'apparent' design recognized as an inherent property of all organisms. Advocates of intelligent design theory base their conclusions on experience and the published scientific evidence. Arrival of this position requires a strong working knowledge of evolutionary principles. Although critical of portions of evolutionary theory, intelligent design advocates are supportive of teaching evolution, but presenting it as any other science should be presented in the classroom. That is to say, what is the evidence, what is the contrary or conflicting evidence, what other models can account for the same set of data?

In the debate within the scientific community regarding evolution, antagonists of intelligent design often quote Theodosius Dobzhansky, "Nothing in Biology makes sense

outside the light of Evolution." [*The American Biology Teacher*, 1973, **35**, pp. 125-129.] In essence, this is saying that one cannot understand biology without an understanding of evolutionary principles. This is simply not the case. Evolution is such a broad discipline that it has, in reality, played only a minor role in experimental science. Unlike the hard sciences of chemistry and physics, Evolution is a historical science and the evolutionary scientist is faced with trying to explain what already has happened. As such this endeavor is unique because, as Ernst Mayer has stated,

> "laws and experiments are inappropriate for the explication of such events and processes. Instead, one constructs a historical narrative, consisting of a tentative reconstruction of the particular scenario that led to tentative reconstruction of the events one is trying to explain" (Ernst Mayr *Darwins Influence on Modern Thought*, Sci. Am. July 2000.)

This being said, it may be surprising to the public, that evolution as a discipline had little impact over the revolutionary progress made in biology over the past 50 years. This is admitted by the prominent evolutionist, Carl Woese from the University of Illinois. In a recent review article titled "A New Biology for a New Century" [Microbiol. Mol. Biol. Rev. (2004) 68:p.173-186], Woese notes:

> "Molecular Biology's success over the last century has come solely from looking at certain ones of the problems biology poses (the gene and the nature of the cell) and looking at them from a purely reductionist point of view. It has produced an astounding harvest. The other problems, evolution and the nature of biological form, molecular biology chose to ignore, either failing outright to recognize them or dismissing them as inconsequential, as historical accidents, fundamentally inexplicable and irrelevant to our understanding of biology. Now this should be cause for pause. Any educated layman knows that evolution is what distinguishes the living world from the inanimate. If one's representation of reality takes evolution to be irrelevant to understanding biology then it is one's representation, not evolution, whose relevance should be questioned!"

This is an interesting quote for multiple reasons. First, if evolution is critical to understanding biology as Dobzhansky claimed, how is it that the greatest period of advancement in biological research ignored evolution? Or that, as Woese admits, this historical period of unprecedented advancement included a group of scientists that considered evolution as "inconsequential"! I agree with Woese, this should be 'cause for pause' but not for the reason he provides. Evolution even now is often the filter by which experiments are explained after their completion, not the driving force behind the experimental design.

Proponents of evolution recognize, as they must, the significant gaps and problems with the theory of evolution. For example, experts in the field acknowledge that we have no phylogenetic history (i.e., inability to historically trace the roots) of a single biochemical pathway or subcellular organelle. This is acknowledged in the

introduction of a recent *Nature* paper attempting to account for the origin of new biological information in cells:

> *"From the outset, Darwin realized that 'organs of extreme perfection and complication' such as the eye posed a difficulty for his theory. Such features are much too complex to appear* de novo, *and he reasoned that they must evolve by incremental transitions through many intermediate states, sometimes undergoing changes in function. There now exists substantial evidence concerning the evolution of complex features that supports Darwin's general model.* ***Nonetheless, it is difficult to provide a complete account of the origin of any complex feature owing to the extinction of intermediate forms, imperfection of the fossil record, and incomplete knowledge of the genetic and developmental mechanisms that produce such features.***" [Lenski *et al.*, The evolutionary origin of complex features. Nature. 2003 May 8;423(6936):139-44.]

Thus, proponents of Darwin's theory of evolution assume that evolution is true, even though we lack the intermediate structures, we lack fossils, and we do not have adequate knowledge of how natural selection can introduce novel genetic information.

The focus of the paper quoted above presumes to show how new information can be generated by organisms via mutation and natural selection. The problem is that the organisms are virtual organisms programmed to respond to selective conditions. Lenski, the author of this paper, has spent years doing long-term chemostat experiments (growth of organisms in continuous culture) with *Escherichia coli* and *Saccharomyces cerevisae*, looking at evolutionary changes out to 20,000 generations. [Lenski et al. Nat Genet. 2004 Apr;36(4):423-6.] The admitted results of these experiments are that it is remarkable how little change does occur. Switching to virtual conditions and showing that virtual organisms can assimilate new "genetic information" in fewer generations than real organisms is backwards, particularly when the real experiments do not provide the desired results.

As the scientific literature demonstrates, there are significant gaps and problems in the theory of evolution that even the most staunch advocates of this theory must and do recognize. In conclusion, I think it is evident from the scientific literature that basic questions in evolution are in contention and that the importance of evolution to understanding biology is by our (that is the scientific community) own admission, conflated.

Evidence for design in nature.

The main scientific contention in this arena is the evidence for design in biological systems. Scientists readily acknowledge the evidence for design in nature; the question, however, centers on whether the design is real design (the product of intelligent causes) or only apparent design (a consequence of natural laws of chemistry and physics coupled with mutation and natural selection).

As a molecular biologist, I have worked extensively on the genetic program of the bacterial flagellum. People working on the bacterial flagellum at various institutions have referred to it as the most efficient machine in the universe. David DeRosier in a published *Cell* paper (the most prestigious biology journal) states that of all molecular machines, the bacterial flagellum most resembles something designed by man. [Cell. 1998 Apr 3;93(1):17-20.] In fact this is an understatement. We do not have sufficient understanding of this molecular machine to build one from scratch. What we do know is that this machine is a true rotary engine some of which can operate at up to 100,000 rpm, it self assembles, is water cooled, is of such small mass that it can counter-rotate in less than a single turn, has remarkable assembly controls and checkpoints programmed into its assembly, and is hard-wired into a signal transduction system that allows bacteria to make decisions based on short-term memory to follow chemical gradients. The components of the motor are referred to as the same components in engineered machines we have constructed: drive shafts, stators, rotors, u-joints propellers, etc. In short, this is a true rotorary engine that is far more complex than anything we can presently engineer. And this is referring to just the machine itself. More complex, is the genetic algorithm, or set of instructions, for producing the machine. We know that the timing and expression patterns for individual genes is highly controlled and that the genes are 'fired' in the order in which the components are assembled. This assembly process is beautifully animated and available on the worldwide web (http://stock.cabm.rutgers.edu/blast/#B).

In addition to the rotary flagellar engine, which is ~40nm in size, there is another rotary engine in cells. In a review article of the smallest rotary engine, the F_1F_0 ATPase, the description of this nanomachine is considered more efficient than a man made machine. In describing the torque generated and the transfer of this energy to ATP synthesis (the cell's energy currency) the authors state:

> "This torque times 2Pi/3 (=120 degrees), ~80pN per nm, is the mechanical work done in one third of a revolution. This work is comparable to the free energy of hydrolysis of one ATP molecule of ~80pN per nm. If one ATP is consumed per 120 degree as one may anticipate from the make of this motor, the efficiency of our F1 is nearly 100%, far superior to a Honda V6". [Kinosita et al. Cell 1998 vol93:21-24]

The efficiency of these engines is truly remarkable. And we do not have a phylogenetic history of a single such machine.

The Department of Energy's Genomes to Life website several years ago stated that the molecular machines in even the simplest of organisms dwarf the engineering feats of the 20th century. Consider that statement. In essence it is saying that unguided and non-forward looking, unintelligent 'chance and necessity' can build machines far superior to intelligent engineers of the last century. In a paper published in *Cell*, Simon Conway Morris has acknowledge that the remarkable convergences seen in life systems seem to imply that nature is somehow "channeled" and if this is the case, teleology (purpose in construction) is back on the table for discussion. [Morris SC. Evolution: bringing molecules into the fold. Cell. 2000 Jan 7;100(1):1-11.]

What is evident from our present golden age of molecular biology is that the complexity and specificity of the cell was not anticipated. As Bruce Alberts, President of the National Academy of Science, has stated in the journal *Cell*, no one anticipated the complexity of the cell's macromolecular molecular machines. [Alberts B. The cell as a collection of protein machines: preparing the next generation of molecular biologists. Cell. 1998 Feb 6;92(3):291-4.] Alberts clearly states that our current view of the cell is vastly different and more complex than the view of the cell when he was a graduate student in the 1960s. Similarly, Richard Losick (Harvard) and Lucy Shapiro (Stanford) make the same observation: "When the authors were graduate students in the 1960s, the bacterial cell was generally viewed as an amorphous vessel housing a homogeneous solution of proteins". The complexity is now described by these authors as:

> "How profoundly our view of the bacterial cell has changed since we first started our lifelong fascination with life's smallest creatures. Who would have imagined that bacteria have proteins that assemble into rings, that cluster at the poles of cells, that localize and delocalize as a function of the cell cycle, or that bounce off the ends of the cell with a periodicity of tens of seconds? Who would have suspected that the origins of replication move to the poles of cells, that the machinery for replicating DNA is stationary, and that it is the chromosome that moves through the chromosome-duplicating factory or that plasmids would jump from the cell center or the cell quarter points following their replication? The pace at which cytology is revealing the unexpected is quickening, and one wonders with anticipation what other delightful surprises await those who use the light microscope to peer inside the bacterial cell." [Losick and Shapiro. 1999. Changing views on the nature of the bacterial cell: from biochemistry to cytology. J Bacteriol. 1999 Jul;181(14):4143-5.]

The point conveyed here is that our view of the cell now is vastly different from when Darwin's theory was first proposed, let alone our view of 40 years ago. The cell is now recognized as being orders of magnitude more complex and sophisticated than Darwin envisaged. It seems reasonable to revisit the question as to whether natural selection is sufficiently up to the task of <u>design engineering</u> this recognized sophistication. What is evident is that this new understanding of the cell will now require a change in our college curricula to carry our understanding to the next level. In the *Cell* paper by Alberts (National Academy President) quoted above, he now advocates the incorporation of **design engineering** into our biology curricula as a means to dissect the interactions of the macromolecular machines now identified in even the simplest of cells. Thus, while our understanding of the complexity of the cell has increased by orders of magnitude, the mechanism to generate this complexity (mutation and natural selection) has remained constant. We will require biologists to be trained in design engineering to understand the workings of the cell, but refuse students to consider the cell may be the product of intelligent engineering. Do we know how natural selection can produce machines that dwarf our own intelligent engineering? To quote Carl Woese in a recent review article,

> *The creation of the enormous amount of and degree of novelty needed to bring forth modern cells is by no means a matter of waving the usual wand of variation and selection. What was there, what proteins were there to vary in the beginning? Did all proteins evolve from one aboriginal protein to begin with? Hardley likely! Evolution's rule, to which there are fortunately a few exceptions, is that you can't get there from here. Our experience with variation and selection in the modern context does not begin to prepare us for understanding what happened when cellular evolution was in its very early, rough-and-tumble phases(s) of spewing forth novelty.* [Woese C. 2004. A new biology for a new century. Microbiol Mol. Biol. Rev. 68:173-186.]

The fact that so much effort goes into explaining away design in nature begs the question. Richard Dawkins, a staunch advocate of evolution, in his book *The Blind Watchmaker* says that until Darwin, one could not be an intellectually fulfilled atheist. [Dawkins R. 1986. The Blind Watchmaker: Why the Evidence of Evolution Reveals a Universe Without Design]. He acknowledges the appearance of design in nature, but argues that it is only apparent design and not real design. The fact of the matter is that the scientific evidence for real design is overwhelming. The 1998 issue of cell devoted to reviewing our present state of knowledge of macromolecular machines includes a short description of the issues content.

> "Like machines invented by humans to deal efficiently with the macroscopic world, protein assemblies contain highly coordinated moving parts. Reviewed in this issue of *Cell* are the protein machines that control replication, transcription, splicing, nucleocytoplasmic transport, protein synthesis, protein assembly, protein degradation and protein translocation—the machines that underlie the workings of all living things". [Anonymous. Cell. 1998. vol. 68. table of contents page].

By our own admission then, the cell is comprised with essential components having the appearance of 'invented' machines, in fact they are even more sophisticated than man-made machines; yet, we will not allow consideration that the origin of these machines arose from some form of intelligence.

Design principles in the laboratory.

During the last half-century, it is probably fair to say that we have gained a greater understanding of biology than the entire history of efforts in the preceding millennia. The vast inroads we have made in our understanding of the cell came by techniques essential to a design engineer, not elements derived from the theory of evolution. In particular, the mainstay technique of modern biology has made use of the concept of irreducible complexity of the cell's subsystems. Irreducible complexity, a term coined by Michael Behe in his scientific argument for intelligent design, essentially states that molecular machines are comprised of a core set of components essential for function of that machine. If that component is removed from the machine, there is a

resulting overall loss of function. If there is no function then there is nothing to select. In biological terms, irreducible complexity implies that mutations in genes encoding pieces of molecular machinery will yield selectable phenotypes based on this loss of function. It is the process of using mutagenesis and devising genetic screens or selections to identify loss of function that has yielded astonishing findings over the last 60 years. Irreducible complexity of molecular machines is the bread and butter of the modern approach to understanding the cell.

Applying this to my own system of studies on the bacterial flagellum, initial inroads to understanding the function of this machine were gained by exposing cells to mutagenic compounds or agents, and then scoring for cells that had attenuated or lost motility (the ability to swim). Individual mutations were mapped to sort out the number of genes involved in building a flagellum and their chromosomal positions determined, the genes cloned and sequenced. Recombinant DNA methodology allowed expression of individual genes to overproduce their encoded proteins and allow the reconstruction of portions of the machine to define their precise roles in overall function. Literally thousands and thousands of man-hours have gone into the dissection of this single molecular machine and the efforts have provided an astounding picture of how it works. The common feature for similar efforts on each cellular machine is that all of the components, or a core subset of movable parts, are essential for function; in short, the systems are irreducibly complex by definition. Review any published list of bacterial flagellar genes and effects of a mutation in each gene, and this becomes immediately apparent. This approach of using mutagenesis to identify genes involved in a defined process, coupled with biochemistry to essentially rebuild the structure to understand how it works, is referred to as reverse engineering. This is much the same technique engineers use when they analyze a machine with which blueprints are lacking. In other words, the idea is that you take things apart and put them back together again while in the process evaluating what each component contributes to the whole. So in summary, it is the processes more akin to design that propelled biology from a mere descriptive science to an experimental science, more so than any contribution from evolution. Most importantly, this concept of irreducible complexity poses a problem for the gradual appearance of such machines. If it is the summation of all the parts that provide function, and the loss of a single component renders the machine useless (much like 'invented' machines we make) then natural selection has nothing upon which to select.

Design criteria have served me well in my own studies and research. As a graduate student faced with designing a rapid method for the detection of *Salmonella* in foods, I was part of a team of scientists that focused on developing a comprehensive set of antibodies against flagella antigens of this organism. When monoclonal antibody methodology came on line (the ability to clone a single antibody producing cell line and thus purify a single specific antibody type), I reasoned that even though the flagella of *Salmonella* made up a diverse family of antigenically distinct proteins, the fact that these proteins all had the same ultimate function and properties suggested that there should be a common antigen that may be detectable by a monoclonal antibody approach. Such an antibody was found specific for *Salmonella* by a colleague working at Ross laboratories. Using this same approach, another colleague isolated another monoclonal antibody cell

line reactive for all Gram negative enteric flagellins. Both of these antibodies have had years of employment in various rapid detection systems for pathogens.

More recently my research focused on looking at the regulation of gene expression in pathogenic organisms as they infect mammalian hosts. Of key interest was the observation that pathogenic *Yersinia* shut off motility at host temperature while inducing virulence genes. This reciprocal regulation by temperature of virulence and motility was first used as a set of convenient phenotypes to acquire mutations in the cellular thermostat. My students and I quickly found out that the regulation was more than coincidence, that the systems were coordinately regulated in an opposing manner — that a single mutation affected regulation of both motility and secretion of anti-host factors. Soon after, a former colleague of mine from Princeton informed me that he had cloned and sequenced a flagellar gene from a nonpathogen (*Caulobacter crescentus*) and found that it carried sequence identity to a *Yersinia* virulence gene. [Sanders LA, Van Way S, Mullin DA. Characterization of the *Caulobacter crescentus flbF* promoter and identification of the inferred FlbF product as a homolog of the LcrD protein from a *Yersinia enterocolitica* virulence plasmid. J Bacteriol. 1992 Feb;174(3):857-66.] Another group at Stanford made a similar observation with three more *Caulobacter* genes. [Zhuang WY, Shapiro L. *Caulobacter* FliQ and FliR membrane proteins, required for flagellar biogenesis and cell division, belong to a family of virulence factor export proteins. J Bacteriol. 1995 Jan;177(2):343-56.] In contemplating the significance of these observations, one of my students and I considered possible models to explain the inverse relationship between synthesis of a flagellum and secretion of virulence proteins. In listing the common features, it became apparent that while we viewed the flagellum as a highly efficient motor for propelling the cell, it was also a highly efficient dedicated protein secretory device, and that the common denominator between the two systems was one of protein secretion. The flagellum might be able to secret virulence proteins. As outlined in a recent paper, this hypothesis made a number of predictions, which the majority have turned out to be true. [***Minnich and Meyer 2004.*** Genetic Analysis of Coordinate Flagellar and Type III Regulatory Circuits in Pathogenic Bacteria, in Design and Nature II, Witt Press.] However, when we presented this new way of looking at the flagellum in presentations and grant applications as we gathered data in the mid 1990s, we were criticized routinely, often with the comment that there was no evolutionary link between these two disparate systems and that such an idea was "whimsical."

As we were developing these ideas, I considered the possibility that our interpretation might lead to an intermediate structure to the bacterial flagellum. This would possibly negate the idea of this system being irreducibly complex. As a result, proponents of evolution now became interested in these findings. However, as additional understanding of what we now call type III protein secretory systems and bacterial flagellum emerged, it appears that the more complex flagellum had preceded the less complicated type III system. And my own studies on the relationship of these systems have convinced me that the question of their co-descent is not from mutation and natural selection, as others have argued. These were published in a recent proceedings and our conclusion from a design inference is stated as follows:

"To counter this argument (irreducible complexity), particularly as it applies to the flagellum, others have used the TTSS. Since the secretory system that forms part of the flagellar mechanism can also function separately, Miller [18, 19] has argued that natural selection could have "co-opted" the functional parts from the TTTS and other earlier simple systems to produce the flagellar motor. And, indeed, the TTSS contains eighteen proteins that are also found in the forty protein bacterial flagellar motor. Miller thus regards the virulence secretory pump of the *Yersinia* Yop system as a Darwinian intermediate, case closed. This argument seems only superficially plausible in light of some of the findings presented in this paper. First, if anything, TTSSs generate more complications than solutions to this question. As shown here, possessing multiple TTSSs causes interference. If not segregated one or both systems are lost.

Additionally, the other thirty proteins in the flagellar motor (that are not present in the TTSS) are unique to the motor and are not found in any other living system. From whence, then, were these protein parts co-opted? Also, even if all the protein parts were somehow available to make a flagellar motor during the evolution of life, the parts would need to be assembled in the correct temporal sequence similar to the way an automobile is assembled in factory. Yet, to choreograph the assembly of the parts of the flagellar motor, present-day bacteria need an elaborate system of genetic instructions as well as many other protein machines to time the expression of those assembly instructions. Arguably, this system is itself irreducibly complex. In any case, the co-option argument tacitly presupposes the need for the very thing it seeks to explain—a functionally interdependent system of proteins. Finally, phylogenetic analyses of the gene sequences [20] suggest that flagellar motor proteins arose first and those of the pump came later. In other words, if anything, the pump evolved from the motor, not the motor from the pump.

Molecular machines display a key signature or hallmark of design, namely, irreducible complexity. In all irreducibly complex systems in which the cause of the system is known by experience or observation, intelligent design or engineering played a role in the origin of the system. Given that neither standard neo-Darwinism, nor co-option has adequately accounted for the origin of these machines, or the appearance of design that they manifest, one might now consider the design hypothesis as the best explanation for the origin of irreducibly complex systems in living organisms. That we have encountered systems that tax our own capacities as design engineers, justifiably lead us to question whether these systems are the product of undirected, un-purposed, chance and necessity. Indeed, in any other context we would immediately recognize such systems as the product of very intelligent engineering. Although some may argue this is a merely an argument from ignorance, we regard it as an inference to the best explanation [21, 22], given what we *know* about the powers of intelligent as opposed to strictly natural or material causes. We know that intelligent designers can and do produce irreducibly complex systems. We find such systems within living organisms. We have good reason to think that these systems defy the creative

> capacity of the selection/mutation mechanism. The real problem may not be determining the best explanation of the origin of the flagellum. Rather it may be amending the methodological strictures that prevent consideration of the most natural and rational conclusion—albeit one with discomfiting philosophical implications."

What is ironic about this debate is that the clear relationship between the flagellum and type III secretory systems was recognized on the basis of reverse engineering (i.e., design principles). Early attempts to draw attention to this fact were negated by evolutionary arguments. When the evidence became overwhelming about the relationship between these seemingly 'disparate' systems, it was immediately claimed as evidence for evolution. This example is illustrative of my experience as a scientist, which has led me to believe that evolution is best seen as postscriptive (the taillights of biology), while design principles (the headlights of biology) tend to drive scientific inquiry and progress. Furthermore, the conclusions in the invited paper above were presented at a scientific conference held in Rhodes, Greece titled "Design and Nature"; a conference dedicated to the emerging field of biomemetics. This field is promoting the cross-fertilization between engineers, architects, and biologists with the increasing recognition that biological systems have solved very complex engineering and structural problems that may be of great value for human design problems. Hence, engineers are looking to Nature for solutions. This underscores the underlying foundation of design in biological systems and the inference that such systems are the product of intelligent cause.

Another example that bears directly on this debate is the routine evidences purported to support evolution. It has been conceded in the public literature that the experiments of Kettlewell (peppered moths) and Haekel's embryos are fraudulent. [Pennisi E. Haeckel's embryos: fraud rediscovered. Science. 1997 Sep 5;277(5331):1435.] Other examples of Darwin's finches and the problems of the fossil record are either ignored or glossed over. But paramount in this group is antibiotic resistance. In his Pulitzer Prize winning account of the Grant's work with Galapagos finches, Jeremy Weiner notes that the demonstration of antibiotic resistance in bacteria was exactly the type of experiment Darwin would have loved, what he predicted. [Jonathan Weiner. *The Beak of the Finch*. Vintage. New York, NY, 1994 p. 258] In the November 2004 issue of *National Geographic*, antibiotic resistance was given as part of the "overwhelming evidence" supporting Darwin's theory. [Quammen, D. Was Darwin Wrong? National Geographic. 206: 2-35.] In fact, antibiotic resistance is an excellent demonstration of the limits and shortcomings of present day teachings of evolution.

The principle of antibiotic resistance is straightforward. One can take an antibiotic sensitive strain of the laboratory strain of *Escherichia coli* and add 100 million to a billion cells on an agar medium containing a lethal concentration of a given antibiotic, such as streptomycin or rifampin. After incubating the plate for 24 to 48 hours, examination will demonstrate 1 to 10 colonies on the Petri plate (each arising from the seeding of a "spontaneous" resistant mutant to the drug). Hence, it demonstrates the principle of mutation and selection and further shows how powerful natural selection is at rooting out very rare genetic events (1 to 10 events in a billion, or a frequency of 1×10^{-9}).

These are true mutations; the cells, if sub-cultured, maintain resistance to the antibiotic through subsequent generations. Students are often asked to speculate on what would happen to this organism over millions of years with numerous small mutagenic steps occurring.

When one examines this from a design perspective, different conclusions can be drawn from the same public evidence. First, one can ask, what is the "fitness" cost for such a mutation? Because the organism in question is haploid and clonal, this can be assessed very easily. One can compare the growth characteristics of the derived spontaneous mutant and its parental strain (the strains are termed isogenic and perfect for assessing the difference(s) due to antibiotic resistance). When this is done, the majority of individual isolates (mutations) can be shown to come with a severe fitness cost, in my own experience it is not uncommon for a doubling of the generation time. Such results are not uncommon as referenced in the literature. [Reynolds MG. 2000. Compensatory evolution in rifampin-resistant *Escherichia coli*. Genetics, Vol. 156, 1471-1481.] While beneficial to the surviving organism exposed to the antibiotic, it has a crippling effect on the cell and makes it much less competitive in the natural environment. The mutations derived from antibiotic resistance generally have a negative effect on the information processing system of the cell. Critics will argue this is true, but if followed in time, the negative effects will be corrected by additional mutations, or what are referred to as compensatory mutations. Thus, if the initial drug resistance mutation slows down growth rate as a result of the mutation, a compensatory mutation can arise that restores full growth potential. In other situations, however, we would simply call these mutations "outside" suppressors, and while they may not have a scoreable phenotype under the original conditions of selection, they can be uncovered if the growth conditions are changed, such as higher or lower temperature or salt concentrations. This is exactly what we have found (unpublished observations). In fact there is a term describing this phenomenon, referred to as 'Mueller's ratchet'—with each turn of the ratchet (mutation) the conditions for adapting to the next change become tighter until the organism cannot respond at all. Hence this 'centerfold' example for describing evolution has nothing to do with the 'complexifying' mutations required to impart new information, which are then required to drive evolution from the simple to the complex. If anything, antibiotic resistance acquisition illustrates the limits of evolution and that acquired mutations eventually lead down a genetic box canyon. It also illustrates another concept of design. The more complicated a machine is, the more difficult it is to modify the machine. Again to quote Carl Woese,

> "Hold classical evolutionary concepts up to the light of reason and modern evidence before weaving an evolutionary tapestry around them. Most of them will turn out to be fluid conjectures that 19th century biologists used to stimulate their thinking but conjectures that have now, with repetition over time, become chiseled in stone: modern concepts of cellular evolution are effectively petrified versions of 19th century speculations." [in, A New Biology for a New Century, cited above.]

In short, the modern day supports of evolutionary theory are rife with problems. While it is repeatedly argued that evolution is essential to our understanding of modern biology, the truth of the matter is very different. Students get a superficial encounter with the evidence and critical analyses of the arguments are discounted or suppressed. The repeated assertion that the theory is one of the most robust in science is more dogmatism than it is science. Even a reputed evolutionist in a paper in *Cell* notes that about the only thing biologists can agree about evolution is that it happened, everything else is in contention. [Conway SC. Evolution: bringing molecules into the fold. Cell. 2000 Jan 7;100(1):1-11]. Evolution cannot explain genotype vs. phenotype, the origin of information or even how life initiated. We find repeated incidents of convergent evolution at the macro and molecular level. The very genetic code, what Francis Crick, the co-discoverer of the shape of DNA, referred to as a "frozen accident," does not appear to have evolved. Yet, it is a true code representing the most efficient information storage system known in the universe. Analysis of this code with the tools of supercomputers now shows us that of all possible codes, assuming ours is arbitrary, the natural code is hands down the best set of amino acid codons optimized to minimize the effects of point mutations. [Hayes, B. 2004. Ode to the Code. American Scientist. 92: (6) Page: 494.] Which is more realistic, to assume that unguided law repeatedly arrives at the best solutions—solutions to problems that we are just now beginning to appreciate—or that the possibility exists that there is a guiding design behind this deep complexity of life? As John Polkinghorn has stated, biologists of this day suffer from the 'triumphal arrogance of 19th century physicists that assumed all of nature could be explained by Newtonian mechanics.' [Polkinghorn, J. 1998. Belief in God in an Age of Science. Yale University Press.]

The history of science is a continuing history of new revolutionary ideas that come and go and come again. For example, the complaint lists Darwin's theory in the same category as the germ theory of disease, tectonic plates, and solar-centrisism. Yet each of these theories went through severe criticism before they were accepted. I have read and am familiar with the text *Of Pandas and People.* This is a good text that critically analyzes various aspects of Darwin's theory. It asks critical questions in terms of the evidence and mechanism required to drive evolution. Such questions are essential for the advancement of science. Making students aware of the controversy in the science community is good for students and it is good for science. Repressing evidence and ideas has the opposite result.

II. My qualifications as an expert witness are included in my curriculum vitae, which is attached to this report as Exhibit A, and in my experience and background outlined in this report.

III. The compensation I will receive for my study, case preparation, and testimony in this matter is $100.00 per hour. All travel expenses will be billed at cost.

IV. I have not testified as an expert at trial or by deposition within the preceding four years.

Signed: _____ Date: 3/31/05

EXHIBIT

tabbies

A

Principal Investigator/Program Director (Last, first, middle): Miller, Samuel I.

BIOGRAPHICAL SKETCH[JG1]

Provide the following information for the key personnel in the order listed for Form Page 2.
Follow the sample format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Minnich, Scott A.	Associate Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
Washington State University; Pullman WA	B.S.	1971-1975	Microbiology and Public Health
University of Idaho; Moscow, ID	M.S.	1975-1978	Microbiology
Iowa State University; Ames, IA	Ph.D.	1978-1981	Microbiology

A. Positions and Honors:

2003 (Oct)-2004(May)Sabbatical Leave: Subject Matter Expert with the Iraq Survey Group, WMD Weapons Inspector, Iraq.

1994-present	Associate Professor	University of Idaho; Moscow, ID
1989-1994	Assistant Professor	University of Idaho; Moscow, ID
1987-1989	Assistant Professor	Tulane University; New Orleans, LA
1984- 1987	Postdoctoral Fellow	Princeton University; Princeton, NJ
1983-1984	Research Director	Animal Health Diagnostics; IGEN, Inc. Rockville, MD
1983-1984	Research Scientist	IGEN, Inc. Rockville; MD
1981-1983	Postdoctoral Fellow	Purdue University; W. Lafayette, IN
1979-1981	Research Assistant	Iowa State University; Ames, IA

B. Selected peer-reviewed publications:

Kapatral V, Campbell JW, Minnich SA, Thomson NR, Matsumura P, Pruss BM. Gene array analysis of Yersinia enterocolitica FlhD and FlhC: regulation of enzymes affecting synthesis and degradation of carbamoylphosphate. Microbiology. 2004 Jul;150:2289-300.

Yoon JW, Minnich SA, Ahn JS, Park YH, Paszczynski A, Hovde CJ. Thermoregulation of the Escherichia coli O157:H7 pO157 ecf operon and lipid A myristoyl transferase activity involves intrinsically curved DNA. Mol Microbiol. 2004 Jan;51(2):419-35.

Steven R. Monday, Scott A. Minnich, and Peter C. H. Feng. A 12-Base-Pair Deletion in the Flagellar Master Control Gene flhC Causes Nonmotility of the Pathogenic German Sorbitol-Fermenting Escherichia coli O157:H$^-$ Strains. J. of Bacteriol.l 2004, Vol. 186 p. 2319-2327, , No. 8

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Young GM, Smith MJ, **Minnich SA**, Miller VL. The *Yersinia enterocolitica* motility master regulatory operon, flhDC, is required for flagellin production, swimming motility, and swarming motility. J Bacteriol 1999 May;181(9):2823-33

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Minnich, S.A., N. Ohta, N. Taylor, and A. Newton. 1988. Role of the 25-, 27-, and 29-kDa flagellins in *Caulobacter crescentus* cell motility: Method for the construction of Deletion and Tn*5* insertion mutants by gene replacement. J. Bacteriol. 170:3953-3960.

Minnich, S.A., Continuation of the Biographical sketch

Mullin, D.A., **S. A. Minnich**, L.S. Chen, and A. Newton. 1987. A set of positively regulated flagellar gene promoters in *Caulobacter crescentus* with sequence homology to *nif* gene promoters of *Klebsiella pneumoniae*. J. Mol. Biology. 195:939-943.

Minnich, S.A., and A. Newton. 1987. Promoter mapping and cell cycle regulation of flagellin gene transcripts in *Caulobacter crescentus*. Pro. Nat. Acad. Sci. U.S.A. 84:1142-1146.

Swaminathan, B., J.A.G. Aleixo, and **S. A. Minnich**. 1985. Enzyme immunoassays for *Salmonella*. Food Technol. 39:83-89.

Swaminathan, B. and **S.A. Minnich**. 1985. Enzyme- immunoassays for the detection of *Salmonella*. In Biotechnology : Applications and Research, eds., P.N. Cheremisinoff and R.P. Ouelette. Technomic Pub. Co.

Aleixo, J. A. G., B. Swaminathan, and **S.A. Minnich**. 1984. *Salmonella* detection in foods and feeds in 27 hr. by enzyme immunoassay. J. Microbiol. Meth. 2:135-145.

Aronson, A. I., W. Beckman, and **S. A. Minnich**. 1984. Regulation of *Bacillus thuringiensis* protoxin production. in *Genetics and Biotechnology of Bacillus*, eds., J. Hoch and E. P. Geiduschek. Academic Press.

Minnich, S.A., and A.I. Aronson. 1984. Regulation of protoxin synthesis in *Bacillus thuringiensis*. J. Bacteriol. 158:447-454.

Held, G.A., L.A. Bulla Jr., J. Hoch, E. Ferrarie, A.I. Aronson, and **S.A. Minnich**. 1982. Cloning and localization of the leptodopteran protoxin gene of *Bacillus thuringiensis* subsp. *kurstaki*. Pro. Nat. Acad. Sci. U.S.A. 79:6065-6069.

Minnich, S.A., P.A. Hartman, and R.C. Heimsch. 1982. Enzyme immunoassay for the detection of salmonellae in foods. Appl. Environ. Microbiol. 43:877-883.

Hartman, P.A., P.S.C. Feng, and **S.A. Minnich**. 1982. Expanding horizons of miniaturized methods in food and water microbiology. in *Rapid Methods and Automation in Microbiology*, ed. R.C. Tilton. ASM Press.

Hartman, P.A., and **S.A. Minnich**. 1981. Automation for rapid identification of salmonellae in foods. J. Food Protect. 44:385-393.

C. Research Support

Novel Strategies for Vaccine Development NIH/RCE 5 years $1.8Million
P.I. Hovde, C, Minnich SA, Bohach G.

Surface protein profiles of Gram negative pathogens, NIH/RCE $185,000
P.I. Minnich, SA and Bohach, G

Regulation of type III secretion in *Yersinia enterocolitica*

P.I.: Minnich, SA

Agency/Type/Period: NIH/BRiN/2002-2004 $45,000

The major goals of this project are to understand the pathogenic *Yersinia* type III protein secretion systems. We have shown that environmental regulation is essential due to cross-recognition of secreted protein substrates. The aims are focused to investigate the regulation of the flagellar type III system.

Temperature regulation of *Yersinia enterocolitica*.

P.I.: Minnich, SA

Agency/Type/Period: USDA/Hatch(CSRS)/2002-2004

The major goals of this project are to study the mechanism by which pathogenic *Yersinia* adapt to the host environment. Our focus is the role of temperature-induced changes in DNA structure and methylation.