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2000 ASHG PRESIDENTIAL ADDRESS
On Discovery, Genomes, The Society, and Society*

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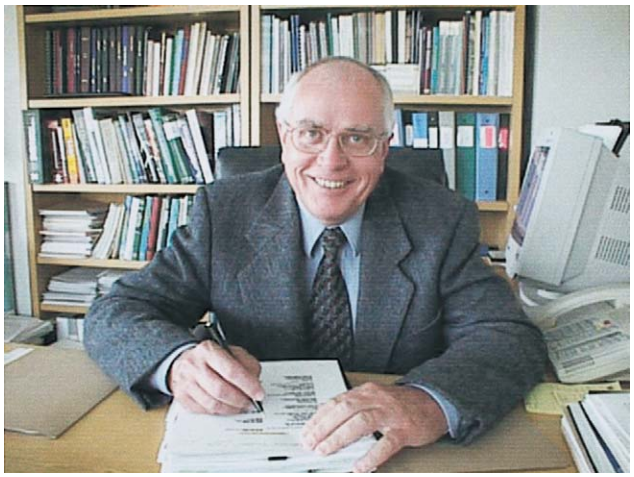

Ronald G. Worton

Dedicated to the memory of Roy Schmickel

Fellow geneticists, old friends and new, I am truly honored to be your President in this first year of the new millennium, and a year that marks the 50th annual meeting of the American Society of Human Genetics. A presidential address to the Society is a difficult task. Some of your past presidents have reflected on topics that were important at the time; others have reviewed a decade of achievement or made predictions about the coming decade. Those who have served in a year that marks a Society anniversary have used the occasion to reflect on the Society and its role. None, however, have had the daunting task of standing before the Society on the 50th anniversary of the annual meeting, in the first year of a new decade, a new century, and a new millennium, in a year that might well be called "The Year of Our Genome."

What I want to do today is to look back over the last century and touch on some of the highlights, then spend a few minutes on the biggest event of the century—the Human Genome Project. I will then look at the future of human genetics and will end with some thoughts on the role of the Society in the new millennium. These thoughts will reflect discussions held at a retreat of the ASHG Board of Directors in the spring of 2000.

Looking Back

In reflecting on the past, one thing struck me, and that is the enormous amount of knowledge that has been forthcoming in a time frame that is miniscule in comparison with the time of human existence, or even compared with the span of the last millennium. Indeed, the principle of inheritance did not even emerge until the start of the 20th century, and it was not until 1915 that the architecture of the genetic material was first described. If we date the definitive elucidation of the physical basis of heredity to Morgan's 1926 *Theory of the Gene,* it tells us that, for the first 925 years of the last millennium, the world was ignorant of this fundamental principle.

The second quarter of the century was not great for human genetics. Quoting Dunn in his 1961 presidential address (Dunn 1962), "progress in human genetics seemed to have been impeded less by a lack of means than by a lack of clear scientific goal, and this at a time when the major problems of genetics were taking a clear form." While studies of fruit flies were revealing the principles of gene transmission, conservation, and evolution, "most observations on human heredity were not oriented in any clear way toward such problems. Matters of greater moment seemed to be the inheritance of 'insanity' and 'feeblemindedness' and other vaguely defined mental ills … pursued for immediate social ends."

As human genetics emerged from the eugenics period, the role of genes in disease was poorly understood, as revealed by H. J. Muller in his 1950 presidential address (Muller 1950). Quoting an editorial in the *Journal of the American Medical Association,* he noted that "until recently the prevailing view has been that mutation as

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a direct cause of disease is extremely rare and of little practical significance. Since observational data are limited to relatively few generations and since human crossbreeding experiments may not be performed, we shall never be able to demonstrate with certainty that a hereditary human disease arises from mutation." This was 1947, not the Middle Ages.

The third quarter of the 20th century began a true golden age of genetics. Following the discovery of DNA as the genetic material in 1948 and the description of its structure in 1953, rapid progress ensued to determine the genetic code and the intermediate role of RNA in the process of manufacturing protein. The rapid gains were all achieved in simple organisms, including phage and bacteria—the age of human molecular genetics still two decades away.

For human genetics, the third quarter of the century was the time when biochemical genetics, clinical genetics, and cytogenetics began to flourish. Building on the work of the pioneers who studied blood groups and clotting factors, new technologies such as chromatography and gel electrophoresis launched the discipline of biochemical genetics. Victor McKusick, in his 1975 presidential address, identifies 1959 as the origin of both clinical genetics and cytogenetics (McKusick 1975). The discovery in 1960 of an extra chromosome 21 in Down syndrome will stand as one of the landmark discoveries of all time, and it was the driving force behind the later development of prenatal diagnosis for genetic disorders.

The discovery of the sex-chromosome anomalies XXX, XXY, and XYY presented a special problem for researchers who wished to determine the true phenotype without biasing the family's treatment of the affected individual. The controversy over newborn screening programs to identify and study such individuals was politically intense and became the subject of John Hamerton's presidential address in 1976 (Hamerton 1976).

The last quarter of the century can truly be called the era of human molecular genetics—beginning with recombinant DNA technology that had surfaced at Stanford in 1976 and then gone underground, both figuratively and literally, for 2 years to assess the safety of recombinant molecules. Early landmarks included Y. W. Kan's demonstration that a polymorphism in the β-globin gene could be used to predict sickle cell disease in utero (Kan et al. 1976) and the 1980 paper by Ray White, David Botstein, and colleagues outlining how RFLPs could be used as genetic markers to track and map disease genes in families (Botstein et al. 1980).

Many of the early discoveries in human molecular genetics were reported at meetings of the ASHG, making this an exciting time to be a member of the Society. I will always remember the 1984 meeting in Toronto (then my home) when Jane Gitschier, then a postdoctoral fellow at Genentech, reported the cloning of the factor VIII gene and stunned the audience with the enormity of the effort and the sheer size of the gene—180 kb. Of course, to someone who has now spent more than a decade working with the 2,500-kb dystrophin gene, 180 kb seems downright civilized.

Prior to 1985, it was not possible to predict the impact that new technology would have on the cloning of human-disease genes by positional cloning. One of the first was the Duchenne muscular dystrophy gene (the *DMD* gene), cloned by isolating DNA from band p21 of the X chromosome. I had the good fortune to be intimately involved in the identification of the *DMD* gene (Ray et al. 1985) and, along the way, made lasting friendships with my three erstwhile competitors and sometime collaborators: Lou Kunkel, Kay Davies, and Ed Southern.

While speaking about the *DMD* gene–cloning effort, I want to acknowledge three colleagues who were critical to the gene cloning and to my own career development. The first is Christine Verellen, a friend and colleague from Belgium, who demonstrated that an X:21 translocation in a young Belgian girl with muscular dystrophy caused the disease by breaking through the gene and inactivating the normal X chromosome (Verellen-Dumoulin et al. 1984). This young girl's DNA became the substrate of our gene-cloning effort. The second is Peter Ray, a molecular biologist who joined the cloning project shortly after it started and became a valuable collaborator and friend for the next 12 years. The third is Roy Schmickel, former head of the Department of Human Genetics here at the University of Pennsylvania, who provided critical DNA probes and assisted us in cloning the X:21 translocation junction. His tragic accidental death robbed the human genetics community and the city of Philadelphia of a great scientific leader. This address is dedicated to his memory.

I couldn't leave the 1980s without saying a few words about cystic fibrosis (CF). In 1983, a young member of our faculty consulted me about using RFLPs to map the CF gene. My advice was to forget it, as I perceived it as a high-risk project and a potential drag on his career. Little did I know then that Lap-Chee Tsui would map the gene within 2 years and clone it 4 years later. Cloning the CF gene by Lap-Chee's laboratory in collaboration with the groups of Jack Riordan and Francis Collins was a true landmark. The set of three papers in *Science* (Kerem et al. 1989; Riordan et al. 1989; Rommens et al. 1989), which should be on the required reading list of every graduate student in human genetics, laid it all out, demonstrated that it was possible, and opened the floodgates for a decade of positional cloning.

This thumbnail sketch brings us to 1989, the date most often attributed to the start of the Human Genome Project. The driving force was the realization that the only way to identify genes involved in complex disease

was to develop a catalogue of all the human genes, a map of their chromosomal location, and a sequence of their nucleotides, to allow prediction of their function.

The Human Genome Project

Those who entered the field of human genetics after 1990 might think that the Human Genome Project (HGP) was widely supported in the scientific community. In fact, it was launched with considerable controversy. Many scientists feared that it would drain precious resources from "legitimate" science and that the emphasis on "human" in the HGP was misguided. Others thought it simply could not be done. Indeed, I recall a Cold Spring Harbor meeting in 1986 at which Wally Gilbert filled the whiteboard with calculations and estimates of the number of people, sequencing machines, and dollars required to do the job. One of the skeptics pacing at the edge of the room was Jim Watson, who 3 years later became the first director of the U.S. component of the genome project.

Much of the opposition to the HGP was defused by two facts. First, in most countries, the HGP was launched with an infusion of new money for science, eliminating the argument that it took resources from hypothesis-driven research. Second, scientists realized the importance of sequencing bacteria, yeast, the nematode, and the fruit fly as a preliminary to the human genome. This had the effect of stimulating science across a broad spectrum of biology and allowed many new players to enter the mainstream of genome science.

I would like to emphasize the international character of the HGP, because there is a tendency in this country to think of the U.S. component as "The Genome Project." Certainly the United States has been and continues to be a major driving force, and, in the early years, the dozen or so genome centers geared to producing chromosome-by-chromosome physical maps produced many of the cosmids, YACS, and BACS that became the substrate for the public sequencing project. But it was scientists at Généthon in France who demonstrated that YAC maps could be constructed for the whole genome, instead of the more time-consuming chromosome-by-chromosome approach (Cohen et al. 1993). They also added hundreds of polymorphic markers to the genetic map, thereby anchoring the genetic map on the growing physical map (Weissenbach et al. 1992). One has to give enormous credit to Daniel Cohen and Jean Weissenbach for these pioneering efforts.

In Britain, the Medical Research Council and the Wellcome Trust created the Sanger Center just outside Cambridge. With Washington University in St. Louis, they sequenced the genome of *Caenorhabditis elegans,* the first multicellular organism to be sequenced, and their concerted approach was a quantum leap ahead of the "cottage industry" that had developed earlier to sequence the yeast, *Saccharomyces cerevisceae*. I give full credit to John Sulston and Bob Waterston for this pioneering effort that set the stage for the human genome–sequencing effort. In fact, as these two groups completed the *C. elegans* genome in 1998, they were already shifting sequencing teams onto the human genome, and other labs from the United States, France, Germany, Japan, and even China joined the effort. At that time, most predicted 5 years to completion of the human sequence, bringing the project to fruition in 2003.

This prediction did not take into account the impatience and energy of Craig Venter, nor the resources of Celera. The international "public project" had barely settled in to its 5-year grind when Celera announced that they had assembled the money, the machines, and the people to do the job in less than a third of the time, projecting completion before the end of 2000. To prove their point, they joined forces with key scientists working on the *Drosophila* sequence and, in the space of a few months, finished the sequence and initiated a 2-week retreat to begin the process of identifying all the genes and describing their functions (Adams et al. 2000).

The essential difference between the government-funded "public project" and Celera's "private project" was that the former was built on the premise that the human genome had to be divided into "bite-sized" chunks, all mapped to specific chromosomes and ordered along the chromosome before sequencing could begin. Celera, on the other hand, sequenced random fragments from the whole genome and let the computers do the assembly into chromosomes, relying heavily, however, on the data freely available from the "public project" to provide the anchor points for proper assembly.

While the media have portrayed these as competing efforts and have essentially declared Celera the winner, I think it important to point out that this was not, by any stretch, a competition played on a level playing field. Since the public project put all its data into a public database as soon as it was generated and Celera did not, it was a very one-sided affair.

Perhaps this is the point at which to commend the pioneers of the public project for making the sequence publicly available. Not everyone in the project agreed with this philosophy, and I suspect that it would not have been possible without the insistence of the leaders, including Sulston and Waterston, Francis Collins on behalf of the NIH, and Michael Morgan on behalf of the Wellcome Trust.

Whatever else one says about the "public" versus "private" project, one has to admit that completing the sequence 3 years ahead of schedule is a good thing. If the Celera data are released to the public in the new year, as they have suggested, it will add greatly to the total information on the human genome. If the data are

available only with a restrictive material transfer agreement, they will be far less useful than the information from the public project.

So here we are in the year 2000, a draft sequence essentially in hand and the world waiting to begin the exploitation phase. Huge questions loom before us, and the prospect of predicting what will unfold in the next decade, the next century, and the next millennium is quite daunting.

Looking Ahead

The main difficulty in predicting the future is that predictions are based on linear projections of current knowledge, current technologies, and current thinking. But the most important aspects of the future are largely dependent on knowledge that we don't yet have, technologies that have not yet been invented, and concepts that haven't yet developed. For this reason I do not plan to spend a lot of time on predicting the future. I am confident that the future will be exciting, that it will have a huge impact on the practice of medicine, and that it will challenge us all in ways we have not yet thought about. However, there are a few things we can say about the near future, based on straight-line projections of current knowledge.

For example, it would not be too big a stretch to suggest that the greatest applications of genetics in the next decade will involve molecular pharming—the use of genetically modified plants and animals as vehicles for producing valuable proteins. It is also quite clear that pharmacogenomics is an area that will mature quickly and that, within a few years, every useful polymorphism in the genome will be identified and placed on a gene chip. A genome screen will identify for each person what will be the most efficacious drug with the fewest side effects, and medicine will become tailored to the individual rather than the population. I would also suggest that, in human biology, the golden age of DNA is drawing to a close. DNA will have given us the all-important catalogue, but the next big steps in understanding human biology belong to the chemists, biochemists, cell biologists, and physiologists. Proteomics will take over from genomics at the forefront of research in human biology.

Over the next quarter century, human genetics will continue to have a role in defining disease genes. The easy part, identifying genes for single-gene disorders, is essentially over. Sorting out the genes that are involved in the common complex diseases is altogether a different matter and will take considerable time to realize because of the complexity of gene-environment interaction. In time, however, we will develop a detailed catalogue of which genes contribute to which diseases, and to what degree. How valuable this information will be for the average person remains to be seen. And to what extent individuals will alter their behavior on the basis of a gene screen is a matter for considerable debate.

One area where I predict intense public interest is in selection of children. Pre-implantation diagnosis for single-gene diseases is now feasible, involving in vitro fertilization with removal of a single cell from the eight-cell embryo, for genetic testing. With new gene-chip technologies, one can imagine that it will be possible to examine each embryo for several hundred genetic characteristics. This would allow parents to select children with a particular combination of genetic assets and risks while rejecting others with fewer assets or greater risks. Since people are generally more concerned about the attributes of their children than they are about themselves, it is not unreasonable to suggest that couples with the necessary knowledge and resources will seek to optimize their chances for having children with superior attributes.

When we do get to the point where we understand many of the genes involved in complex disorders, using the information properly will require an enormous amount of public education. And the public has a huge appetite for it. Hardly a day goes by without a news item about a gene for something or other—heart disease, baldness, bad behavior, good behavior, sexual preference, weight control, and even aging. Yet my experience is that very often the articles themselves are filled with misconceptions, and the expectations are totally unrealistic. Often the headline itself is totally misleading. And some are both misleading and astonishing. One wonders sometimes whether the problem lies in the quality of the information provided to the media or in the capacity of the media to adequately interpret the information. But one thing is certain, and that is the need for all of us to be more involved in providing accurate information and to be more ready to assist in the interpretation of genetic information.

Role of the ASHG in the Public Dialogue

As President of the ASHG over the last 10 months, I have been given the opportunity to deal with issues that are at once sensitive, important, challenging, and disturbing. In each case, the Society has either been called upon to respond with a public statement, to endorse someone else's statement, or to provide input to a government document. The issues have been varied, and many of them have been far removed from my area of expertise. As a Canadian, I have found it a special challenge to deal with a system of government that is foreign to me, and I have therefore relied heavily on my Board colleagues, especially the past and future Presidents.

I want to illustrate the ASHG public dialogue with three examples. The first, and by far the most significant, was the death of Jesse Gelsinger, the 18-year-old Ari-

zona man who lost his life in a gene-therapy experiment in September 1999. This sent shock waves throughout the scientific community and raised new questions about the prospects for gene therapy. The astonishment to our community was that the experimental therapy was being carried out by a group led by Jim Wilson, then one of the country's most respected researchers, in a highly respected academic program right here in Philadelphia. The ramifications of this unexpected death were profound. During the first few months of my presidency, investigations by the FDA began to reveal a number of problems with the trial, and calls began to grow for more oversight of gene therapy. The scrutiny spread to all gene-therapy trials and revealed that many investigators and sponsors have either failed to report serious adverse events to the RAC or have requested that such reports be shielded from the public view. According to an NIH audit of adenoviral protocols following Mr. Gelsinger's death, only 5% of observed serious adverse events, including deaths, were ever reported to the NIH.

This raised a question for the Society—what, if anything, should we be doing? The Society has a keen interest in gene therapy, its scientific basis, and its translation into clinical practice. ASHG members are frequently called upon to provide advice to families presented with the opportunity to participate in experimental gene therapy. On this basis, the ASHG Board considered it appropriate to develop a statement on gene therapy. Our statement, published earlier this year, makes several points. One is the need for more-rigorous research, referring specifically to unrealistic expectations, attributed in some cases to overzealous pronouncements by gene-therapy enthusiasts. Another was that clinical trials should be undertaken only after solid evidence of both safety and efficacy in appropriate animal models. We argued that the greatest responsibility for patient safety lies with the investigators themselves, who more than anyone should know the potential risks and benefits of the proposed trial. We concluded by suggesting a "litmus test" for ASHG members faced with advising families on participation in experimental procedures: "… if you or your family were in this circumstance, would you enroll yourself or your loved one in this trial?" We concluded that only in the case of an affirmative answer to this question would it be appropriate to seek patients for enrollment or to support a family's decision to enter a clinical trial.

One of the areas in which we failed to take a strong stand was on the issue of conflict of interest, for those who are engaged in clinical trials and also have a financial interest in the sponsoring company. Our position was that as long as the conflict of interest is declared and as long as institutional policies are followed, this is sufficient. Others, however, have taken a stronger stance. Rodney Howell, President of the American College of Medical Geneticists, in an article published in a Miami newspaper, unequivocally stated that such conflict of interest was unacceptable. Similarly, the American Society of Gene Therapy issued a public statement with the same hard stance on such conflict. Partly as a result of these strong statements, my own view is rapidly changing. I have come to the conclusion that active participation in a clinical trial, either as a referring physician, as a clinical researcher, or as part of the scientific team, when one has a financial stake in the outcome, is a conflict that should not be allowed under any circumstance. I wish now that we had put this into our published statement.

The second important issue was the invitation to respond to revised guidelines being considered by the U.S. Patent and Trademark Office in relation to the patenting of genes. In our March 22, 2000, response, we endorsed some of the changes designed to "raise the bar" on criteria needed to obtain a patent, and we went a step further. Referring to our earlier 1991 published statement on patenting, we argued that patentability should be based on demonstrated function and utility, not on a theoretical function derived from comparative sequence analysis. Our message was consistent with the March 14, 2000, statement by President Clinton and British Prime Minister Tony Blair, which stated that "to realize the full promise of research, raw fundamental data on the human genome, including the human DNA sequence and its variations, should be made freely available to scientists everywhere." This triggered the biggest-ever decline in the value of biotechnology stocks. How their statement could cause such precipitous reaction is beyond my comprehension, and it points to an astonishingly unsophisticated knowledge base among biotech investors.

The third issue that we faced and that I want to share with you is the halting of all human-subject research at Virginia Commonwealth University (VCU) by the Federal Office for Protection from Research Risks. The case that triggered this action involved the father of a research participant, who complained to federal officials about a VCU genetics study asking his daughter questions about her family history that he considered an invasion of his own privacy. He argued strenuously that, for his daughter to provide family information on a questionnaire, the informed consent of every family member for whom information was disclosed was required. On the face of it, this seems to be a logical stance for him to take, although in practical terms it is not hard to see how this could hamper genetics research. This troubled genetics researchers because inquiring about the family history from a third party has always been an integral part of human genetics research. Indeed, the procedure for collecting family history data at VCU that was the subject of the original complaint

has subsequently been rereviewed and approved by a second independent institutional review board (IRB).

While the ASHG had no opportunity or reason to intervene in this decision, we did think that it was important to inform the Society membership through a "membership alert" prepared by our past president, Uta Francke. The alert warned that, if all members of a family had to be considered as research subjects, subject to informed consent, then it would be "enormously cumbersome and prohibitive, and will seriously impede medical research." Uta also conceded, however, that the father has a point, and that it is incumbent upon genetics researchers to consider seriously whether family members about whom they collect family history should be categorized as human subjects, subject to informed consent.

The Public Trust

Following the alert, I had the opportunity to communicate in several e-mail exchanges with the man who lodged the original complaint. His outrage was an eye-opener for me, and it soon became clear that it was based not only on his daughter's disclosure of information that he considered to be intensely personal, but also on his perceptions of IRBs that failed to protect the public's interest. As he pointed out to me, one only has to read the *Washington Post* to come away with a view that research, especially in genetics, is out of control and inconsistent with the value system of most Americans. Whether or not this is a valid view is immaterial; it is the perception of the truth as portrayed in the public press that dictates public opinion. As I am not a regular reader of the *Washington Post*, he offered to send me a file with downloaded information from the their Web site. Again, it was an eye-opener. Here are a few of the headlines he encountered in his everyday reading.

GENE THERAPY RUN AMOK (January 29, 2000)
A LOT OF RULES, TOO MANY EXCEPTIONS (January 30, 2000)
OUR FLIMSY SURVEILLANCE OF SCIENCE (January 31, 2000)
GENE TEST ERRORS WENT UNREPORTED (February 11, 2000)
PROTECTION OF PATIENTS IN RESEARCH IS FAULTED (April 13, 2000)
PATIENT'S DEATH IN GENE TEST NOT REPORTED (May 3, 2000)
CAN SCIENCE BE SUPERVISED? (editorial, June 6, 2000)

Is it any wonder that he is enraged and ready to do battle with a system that seems to have failed him, certainly failed Jesse Gelsinger, and apparently failed many others? If the litany of charges contained in the articles under these headlines are all true, then we have a very large problem indeed. If only some of the charges are true, it is still a huge problem, as the perception of wrongdoing is a problem for all of us. I do not believe for a moment, however, that the problem is only one of perception.

What we do about it is the subject of my final few moments.

The Future of the ASHG

Every ASHG President wants to be remembered for something and to leave the Society in a little better shape than he or she found it. On assuming my new title in January of 2000, I was concerned about the role of the Society and how well it performed in its chosen role. Two things were clear—we have a very good *Journal* that gets better each year, and we have a very good annual meeting that most people in the Society attend regularly. Both make money for the Society. Furthermore, we have a great office staff in Washington, we are financially stable, and people like the membership directory. What more could we ask?

Consulting the last two Presidents, I heard from Uta and Art that we are missing something. We serve our members well, but we are not visible enough. We have only a small "presence" in Washington, and no presence whatsoever anywhere else in the United States. When opportunities arise for input on important issues in Washington (and, I might add, in Ottawa), we are not always at the top of the list of organizations to be consulted. The National Human Genome Research Institute, for example, seemed to have far more visibility and influence than our Society, yet it is the Society that represents the majority of researchers in human genetics in North America.

But is this bad? Should we be presenting ourselves more actively? Should we be proactive in addressing the issues that are out in the public domain? To address these questions, we decided in October 1999 that it was time for a Board retreat—2 days away from our labs, offices, and clinics, to review the Society, its strengths and weaknesses, and its purpose. We enlisted the help of Brook Rolter, as facilitator, and met for 2 days on May 5 and 6, just prior to the annual spring Board meeting on May 7, 2000. From all accounts, the time invested was worthwhile, and I believe we have set the Society on a new course.

In essence, we decided that the Society could not afford to confine its main activities to the *Journal* and the annual meeting. We decided that we needed to adopt a mandate that includes lobbying, public education, and advocacy. This is not new to the Society, and we have for years had committees that dealt with education and with social issues. We have also provided support for congressional fellows who spend a year in Washington

learning the inner workings of government. Despite these measures, the Board's concern was that the Society itself worked in a largely reactive mode and that it needed to become proactive. Furthemore, I was concerned that the President is expected to function as the "keeper of the light" for the Society, yet I already had a full-time job and often felt like an absentee lighthouse keeper—running to head off impending disaster at every turn in the weather.

Given this, the Board took two very important decisions at its retreat and formalized these decisions at the Board meeting the following day. The first is to hire a full-time professional geneticist as Executive Vice President (EVP) of the Society. This person will be a well-respected geneticist who will have credibility with the members of the Society, with government, and with the public. The EVP will report to the Board through the elected President and will not have any substantial administrative duties, as these will still be the responsibility of the Executive Director. We have already circulated notice of this position via e-mail, and the position will be advertised shortly in the *Journal*.

The second decision was to hire a part-time Web Editor to guide the further development of our Web site and to make it a professional arm of the Society, much like the *Journal*. The Board views the Web Editor as being similar to the *Journal* Editor. The appointment will be for an extended period of time and will be remunerated by the Society in proportion to the time commitment. The Web Editor will work from his or her academic home base and will be able to hire a full-time Web Master to develop and maintain the site.

Although this will be costly, the Board is convinced that we cannot afford *not* to make this important transition. We are entering into a period when genetics will dominate the field of medicine and health care and when the media will be filled with information about developments in genetics. As Senator Edward Kennedy once said, "The public will immerse itself in the affairs of science. Whether or not it does so constructively will depend on the willingness of scientists to welcome public participation." The Board has, I believe, taken the necessary steps to ensure that your Society will be at this exciting forefront, able and willing to partake in and occasionally lead the public discourse on the future of molecular medicine.

Thank you, and enjoy the rest of the meeting.

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