Statistical Science
1998, Vol. 13, No. 4, 378–387

A Conversation with C. C. Li

T. Timothy Chen and John Jen Tai

Abstract. Ching Chun Li was born on October 27, 1912, in Tianjin, China. He received his B.S. degree in agronomy from the University of Nanjing, China, in 1936 and a Ph.D. in plant breeding and genetics from Cornell University in 1940. He did postgraduate work in mathematics, mathematical statistics and experimental statistics at the University of Chicago, Columbia University and North Carolina State College, 1940–1941. He is a Fellow of the American Statistical Association (elected 1969), an elected member of the International Statistical Institute, a Fellow of the American Association for the Advancement of Science and an elected member of Academia Sinica (Chinese Academy). He served as President of the American Society of Human Genetics in 1960. His tenure at the University of Pittsburgh began in 1951. He was Professor and Department Chairman, Biostatistics, from 1969 to 1975, and he was promoted to University Professor in 1975. Although he retired in 1983, he has remained active in research.

The following conversation took place in Pittsburgh during the 1998 Spring Meeting of the International Biometric Society, Eastern North American Region, at Professor Li's home.

EDUCATION

Chen: Dr. Li, you have made significant contributions to the interface between genetics and statistics. Could you tell us how you decided to choose these two fields as your profession? Was there a need in China?

Li: As in many other things in life, I had no plan to study genetics *and* statistics as a combination for my career. It happened, gradually and slowly, according to my interest. Was there a need in China? We don't study something because China needs it. Besides, China needs everything. Every other country also needs everything. The "need" should never be a reason to study anything. You follow your own interest.

Tai: You spent four years, from 1937 to 1941, in the United States for your Ph.D. degree and postdoctoral research. Which schools did you attend?

Li: During those four years, I attended four schools: Cornell University (1937–40), University of Chicago (1940, summer), Columbia University (1940–41, postdoctoral) and North Carolina State College, Raleigh (1941, summer). The year at Columbia was to study statistics. I came to know Professors Hotelling and Wald.

Tai: Were there teachers who influenced you a lot during this period?

Li: Two professors played a vital role in my professional life. One was Theodore Dobzhansky of Columbia University and another was Sewall Wright of the University of Chicago. Dobzhansky pioneered in field studies of natural populations of *Drosophila*. Wright was the pioneer in genetic analysis using correlations and path coefficients.

Chen: You not only obtained an advanced degree, but you also met your wife Clara in Chicago and were married in the International House at the campus of the University of Chicago. Incidentally I lived in I-House for two years when I first came to the U.S. in 1967. Could you tell us a little bit about Mrs. Li's family background?

Li: After my summer school at Raleigh, North Carolina, I was ready to go back to China. At that time, we—the nonquota students—were not allowed

T. Timothy Chen is Professor and Head, Biostatistics Section, University of Maryland Greenebaum Cancer Center, Baltimore, Maryland 21201 (*e-mail: tchen001@umaryland.edu*). *John Jen Tai is Professor, Graduate Institute of Epidemiology, College of Public Health, National Taiwan University, Taipei 100, Taiwan. This interview was conducted when TTC was at the National Cancer Institute, Bethesda, Maryland, and JJT was at the Institute of Statistical Science, Academia Siniea, Taipei, Taiwan.*

to seek employment. You either could be a student or go home. On my way to the West Coast, I decided to stay in Chicago for some time, as I still had a few friends there from previous years. Clara and I were both staying at the I-house. She was a graduate of the University of Wisconsin and was working at that time for the United China Relief. When we got married, all her family attended. My old friends at Cornell came to Chicago for our wedding.

CHINA

Tai: After these four years in America, you returned to China. But you got stuck in Hong Kong for a few months due to the Japanese invasion. What happened during that period?

Li: The Japanese invaded Hong Kong and Pearl Harbor almost simultaneously. From the day we got stranded in Hong Kong to the day we walked out of Kowloon it was approximately two to two-and-a-half months (December 1941 to early February 1942). We experienced many, many things during that period. The most important experience was starvation. We learned what that means. On the other hand, we made many friends for mutual help and survival. In order to get to Free China, we had to join an underground organization which would guide us to safety. The first major stop was Huiyang, which was in Free China. Our final stop was Guilin, Guangxi, which was the most beautiful place in China, if not the world. It took us 38 days to get from Kowloon to Guilin, where our first son was born. The details of our stay in Hong Kong and of this trip would fill a fairly thick book.

Chen: After that you taught for eight years, from 1942 to 1950, at various universities in China. What positions did you hold? You were the youngest department head in a major university. What did you accomplish during that period?

Li: In the fall of 1942, I accepted a position at the Agriculture College, National Guangxi University, which was in a suburb named Satang (Sand Place), of Liuzhou. This was my first job and it was in a most primitive place (no running water, no electricity, no medical care, etc.). But it was also the place where I made some lifelong and trusted friends who have affected my life in subsequent years. The other two places I worked were the University of Nanjing (Nanking) (actually in Chengdu, Sichuan), 1943–46, and National Beijing (Peking) University, 1947–50. At the Beijing University, I also served as the Chairman of the Agronomy Department and the Director of its Experimental Stations. The work mainly consisted of teaching, conducting seminars and some research projects at the Experimental Station.

Chen: At that time you published a textbook, *Introduction to Population Genetics* [6], in English, which was revised seven years later to become your famous *Population Genetics* [7], published by the University of Chicago Press. What motivated you to write this book?

Li: I started my writing since I got to Beijing in 1946. The book was based on my lectures in Guangxi and Chengdu as well as in Beijing. The purpose was to introduce population genetics, not only to China, but also to a larger audience everywhere. The timing was poor, very poor indeed. When the National Peking University Press finally got the book ready in about December of 1948, the communist troops were already at the suburbs of the city! During the siege of Beijing, I was not in the city. I was in Liang Sheung, a suburb of Beijing. So, I never saw the book myself. Since the communist troops entered the city of Beijing, the book was never on sale publicly in the bookstores. Fortunately, the American Embassy shipped the book to the U.S. My brother, Jerome Li, reprinted 500 copies of the book. The book reviews written by the American and British geneticists in 1950 were all based on these reprinted copies. The reviews were more flattery than I deserve. It was this book which helped me in finding a job in the U.S. through the efforts of Professor H. J. Muller. I named my son Steven Muller Li.

Tai: You finally left China because of Lysenkoism. Could you first explain what Lysenkoism is, and why Mendelism was rejected in China in the early fifties?

Li: First, there would be no Lysenkoism [13, 14] if we didn't have Stalin. Lysenko was promoted by Stalin personally and openly. Why should Stalin hate Mendelian inheritance? Nobody knows, or nobody would risk a guess. I guess it was Hitler's eugenics in Germany (which was presumably based on genetic theory) that Stalin was really fighting. Thus Lysenkoism denies the existence of genes or any other materials (e.g., chromosomes) that control heredity. It espouses the idea that inheritance is due to environmental effects. Therefore, the inheritance of acquired characteristics became the law of inheritance. Lysenkoites have always ignored evidence from experiments. They never have experimental designs or even simple replications. They think statistics are to serve the capitalists. They even claimed that one species can be converted into another species under the right environmental conditions!!!

Tai: What kind of persecution did you go through?

Li: My counter question to them was the inheritance of blood groups in man and other animals. The

gene theory works very well for the blood groups phenomena. What explanations do Lysenkoites have to account for the inheritance pattern in blood groups? They never had any answer to that question. In 1948 or early 1949, the Chinese Lysenkoites obtained a copy of my *Population Genetics*. Their comments were "the book was absurd." Thus, the book became a liability to me instead of a credit. Subsequently my courses on genetics and statistics were disbanded, and I was isolated and forced to resign the Chairmanship of the Department of Agronomy. They even spread the rumor that I had called the Soviet Union a "red imperialist."

Tai: What lessons can we learn as an individual or society from your experience during that period?

Li: What lessons can we learn from the Lysenko episode? The minimum requirement is the separation of science from politics. This is not so easy as it sounds, especially for the communists. The next best thing to do is to persuade the communists to respect the autonomy of Science. The long–term basic cure is to raise the standard of science education for the general population. But, nothing is easy.

Chen: You spent about one year in Hong Kong after you escaped Communist China. How did you spend your time during that year?

Li: After my family and I left China, we stayed in Hong Kong for 15 months (March 1950 to May 1951). In the first few months, I couldn't do anything. I was like a zombie. The events were like a nightmare. Gradually and patiently, I began to recover. Later on, I bought a copy of Julian Huxley's *Heredity, East and West*: *Lysenko and World Science* [4] and began to translate the book into Chinese. The work was slow. I didn't finish it until after I got to Pittsburgh. Later, the Chinese version was published in Taipei. It did not sell. For some reason, the people of Taiwan do not care what the communists are doing in Mainland China.

PITTSBURGH

Chen: How did you obtain a position at the University of Pittsburgh?

Li: Again, Professor H. J. Muller was instrumental in getting me the position at the University of Pittsburgh. It happens that Dr. Thomas Parran, the former Surgeon General, was establishing a new Graduate School of Public Health at the University of Pittsburgh. Dr. Parran needed a human geneticist in the new school. He wrote to Muller and asked him for recommendations. Muller was very happy, saying I have just the right man for you. He wrote a splendid letter of recommendation for me. I arrived in Pittsburgh in May 1951.

Chen: From 1951 on you stayed at Pittsburgh for 32 years until your retirement in 1983. You were promoted from Research Fellow to University Professor of Biometry and Human Genetics. You were the Department Head for six years and you were elected as the President of the American Society of Human Genetics in 1960. Could you tell us what you did to build up the department, and to expand the Human Genetics Society under your leadership.

Li: You have a good summary of my life in Pittsburgh. I have little to add. If you insist, maybe I could add the following. During the last 30 years, human genetics has just grown and grown, steadily and sometimes by leaps and bounds. Please don't think I have anything to do with it. I am happy that human genetics grows as a science, but its intimate relationship with health problems makes it more visible. The only contribution I made was probably that I popularized population genetics to a certain extent.

Tai: Coming to Pittsburgh you had to switch from plant genetics to human genetics. How did you do it?

Li: There was a short period of readjustment for me when I first arrived at Pittsburgh. The transition period was made less painful by the thoughtfulness of Dr. Antonio Ciocco, the Department Head of Biostatistics at that time. One day, Dr. Ciocco came to my office smiling and with a book in his hand. He said, "Here is a book on epidemiology. You may glance through. This book will take your mind off plant breeding." After a few days, I finished the book and returned it to Ciocco. He said, "What do you think of the book?" My answer, "It is truly a great book on epidemiology; many diseases had been discussed, but not a single word about genetics—its role in diseases." He was visibly moved. He said that it will take a while to introduce genetics to epidemiology. I am happy to report that *Genetic Epidemiology* is now publishing its volume 15 in 1998. The Editors of this journal for the last few years were faculty at our Department of Human Genetics. The moral is "If you live long enough, you will see it happen."

GENETICS AND STATISTICS

Chen: During these 32 years you published more than 80 original papers, 24 reviews and 7 books. One of your earliest papers—that you wrote with Horvitz in 1953 [20] on estimation of the inbreeding coefficient—has an interesting citation pattern. The number of citations has increased in recent years. During the period 1990–94 there were 59 citations.

FIG. 1. *Professor Antonio Ciocco (left) and C. C. Li. Ciocco was Chairman of the Department of Biostatistics, Graduate School of Public Health, University of Pittsburgh for 20 years (1949–1969) and was succeeded by Li.*

What is the major contribution of that paper, and why does it get more citations in recent years?

Li: I didn't know that citations of Li and Horvitz [20] went up in 1990–94. I thought it was a dead paper. The various methods of estimating the inbreeding coefficient F are based on the fact that F has several different meanings. It may be viewed as the extent of the decrease of heterozygosis in the population. This gives us an estimate right away. In the meantime, F may also be viewed as the correlation coefficient of the uniting gametes (that formed the observed population). This gives us a new and different estimate of F and so on. Horvitz and I always thought that ours was an unfinished paper because we did not calculate the variances of those estimates. On the other hand, the calculation of the variance of a determinant is not easy. We prefer to wait for somebody who has higher tools to finish the paper.

Tai: The well-known I, T, O matrices, developed by you and Sacks [22] to describe genes identical by descent between two relatives, have proved to be a very useful technique in modern genetic analysis. Could you tell us how you got the idea?

Li: I obtained this idea from reading Professor William Feller's *An Introduction to Probability Theory and Its Applications* [1]. It was a great book. I learned so much from it. My colleagues were also reading it. In order to break the monotony of reading, we took turns presenting chapters of the book. (Good old days for me.) Feller had the T matrix (see Feller's 1968 edition, page 144). In obtaining T^n, Feller produced a complicated expression while I introduced the matrix O, so that

$$T^2 = \frac{1}{2}T + \frac{1}{2}O.$$

However, the real defect of Feller's treatment was that he did not have the identity matrix I. For instance, Feller asserted that the transition matrix for full sibs is T^2. I knew this is wrong from my genetic knowledge of full-sib pair distributions. I pointed

out that T^2 is the transition matrix for half-sibs, which is correct. Then, what is the transition matrix for full sibs? This is where I made some real original contributions to the transition problem. To make a long story short, I discovered that the full-sib transition matrix involves the identity matrix. Let S be the transition matrix for full sibs. Then

$$S = \frac{1}{4}I + \frac{1}{2}T + \frac{1}{4}O.$$

The correlations between relatives may be read off from the transition matrix directly without calculation.

R. A. Fisher [2] calculated the correlation table for all common human relatives. The most complicated one is the double first cousins. Fisher obtained the correct distribution and thus the correct correlation by the complete tabulation of all possibilities. By my method, the transition matrix for double first cousins is simply

$$S^2 = \left(\frac{1}{4}I + \frac{1}{2}T + \frac{1}{4}O\right)^2 = \frac{1}{16}I + \frac{6}{16}T + \frac{9}{16}O.$$

This expression when converted into joint distributions agrees with that given by Fisher. Of course.

Tai: How did you get to collaborate with Sacks about this paper?

Li: Dr. Sacks was a professor of matrix algebra at the University of Pittsburgh. But he has no contact with genetics. I told my friends that I needed somebody to check the manuscript, such as $ST = TS = T^2$ where $S \neq T$. Is this possible? Dr. Sacks agreed to read and check it. The answer is that it is possible when T is singular (determinant is zero). Dr. Sacks checked the entire manuscript and found everything all right. Amen!

Feller's second edition of the book (1957) was even more comprehensive and better overall. We studied it again and learned more. Feller acknowledged that T^2 is only for half-sibs and cited our paper (wrongly cited as printed in *Biometrika* instead of *Biometrics*). But he never did get the full-sib transition matrix right and did not see where the I-component came from. The lesson: even for a gifted mathematician, it requires a certain amount of genetic knowledge to do genetic problems with Mendelian inheritance.

Tai: You have done much fundamental research in selection and path analysis. Was it because of Sewall Wright's influence? Could you describe your interaction with Wright?

Li: At first, I didn't know the name, still less his work. I learned his name in 1937 when our professor of genetics used the brand-new book by Dobzhansky as a textbook. The book cited S. Wright many, many times. I found a few of his papers; they were different from others! That changed my direction of studying.

Ordinary statistical textbooks don't have path analysis, but they have plenty of covariance, regression coefficients and correlation coefficients. But, when all variables are standardized (without arbitrary physical units such as centimeter, pound etc.) we will find that covariance = regression slope = correlation. Hence, we may regard correlation has a direction (from cause to effect) like regression. Wright's path analysis, in one word, is an analysis in a network of standardized variables. In many cases, some genetic results may be obtained by simply examining a diagram without calculation. Of course, I don't understand all of his diagrams. That, however, did not prevent me from enjoying the cases which I do understand.

Chen: You were invited to write a very long expository paper of 88 pages for *Biometrics* in 1967 entitled "Genetic equilibrium under selection" [9]. How was this invitation proposed?

Li: I apologize for my poor memory in old age. I cannot recall at the moment who (a familiar friend) recommended me to produce a review article on genetic selection for *Biometrics*. I spent almost a year (off and on) to write that article, which consists of 100 numbered short sections (88 pages in print). I understand that there was some discussion among the editors and referees as to whether the article should appear in two installments or in one. The final decision was "in one" for the convenience of the readers. I got many requests for reprints, largely from teachers who taught population genetics and had classes of 10–20 students. Some of them asked me if I could send them 20 copies for the class. I obliged quite a few times.

Tai: In 1968 you did a joint work with Nathan Mantel [21] on developing a simple method for estimation of the segregation ratio. Your method had a significant impact on segregation analysis [25] (i.e., the analysis of the offspring phenotypes from two heterozygous parents). How was this collaboration initiated?

Li: My collaboration with Mantel to develop the method of discarding the singleton recessives to estimate the segregation ratio was no accident. Mantel had a joint appointment at our Department of Biostatistics for a number of years. He was not the only one. There were three or four others who were working at NIH but had a joint appointment in our Department. They came and delivered lectures and advised students. Sometimes, I also attended their lectures, particularly Mantel's. The joint paper, Li and Mantel, was the natural product. I only regret

we did not have enough time to have more joint work.

Chen: You published eight books from 1948 to 1982. Three of them are still getting a large number of citations. Could you tell us the background of each book. Let us begin with your 1964 book *Introduction to Experimental Statistics* [8], then two books in 1975, *First Course in Population Genetics* [11] and *Path Analysis* [12].

Li: All three books grew out of my lectures; I taught these three courses for many years. Lecture notes accumulated fast. To organize them into a book was a neat way to discard some of my old folders. For each book named above, I had a personal satisfaction for reasons unrelated to science or academic achievement. I will try to be brief to explain. The first book, *Experimental Statistics*, grew out of a course in experimental design for agriculture students, but the principles apply to all experiments. This was one of three courses I was teaching at the Peking University College of Agriculture before 1949. After 1949, these courses were abolished largely because of me. The book was published by McGraw-Hill. Soon after its publication, it was translated into Spanish. I was told that the Spanish edition was even more popular than the English edition. Even more unexpectedly, it was translated into Chinese about two years ago. I hope that the Chinese students will find it useful, although the topic has been taboo since 1949.

About the second book, *Population Genetics*. Since Lysenko appeared on the scene, I spent close to 20% of my professional time reading English translations of original work in Russian. I wondered when and how I could turn the situation around. The *First Course in Population Genetics* did it. Four Soviet genetic scholars translated the book into Russian in 1978. The third book, *Path Analysis*, was intended to be a primer for those who want to know what it is and what it is not.

Chen: During the mid-1950s, you were involved in cancer chemotherapy trials as a biostatistician. These early trials provided impetus for the development of the whole area of survival analysis. Could you tell us more about these trials?

Li: In the mid-1950s, there were clinical trials all over the country. The one I got involved in was a group of VA hospitals in Eastern states (Massachusetts to Florida). Intellectually, as well as scientifically, there was no problem in conducting clinical trials. All empirical sciences depend on trials for information and progress. A basic problem, however, did happen. It was almost impossible to convince physicians who had never conducted trials before that the treatments ought to be assigned to patients at random. The physicians thought the idea of randomization was ridiculous, unethical, wasteful etcetera, and no physician would ever do that. They, the physicians, are the ones who decide which patients get what! If you use random numbers, what do you need physicians for? Apparently, they thought that randomization was an invention of C. C. Li and not a universal requirement for all experiments. Finally, the VA system project officer had to say to those physicians, "no randomization, no grant!" I was involved in this project for only about two or three years, after which the responsibility was transferred to Dr. Patno, who had been attending the meetings with me all the time.

GENETIC ISSUES

Tai: Since early 1970s, the rapid development in the field of molecular biology has revolutionized the study of genetics. Do you have any comments about the impact of applying molecular techniques to the study of population genetics and evolution theory? Is it possible that some evolution theories will be modified from the viewpoint of molecular level?

Li: Molecular genetics has indeed developed by leaps and bounds. In fact, some of the pioneers of the 1970s are now obsolete, and the new leaders are emerging. It will be like this in the immediate future, I think, until a plateau is reached. Hence, it is hopeless for me to try to keep up with it. However, I am interested in their findings and their thinking about its evolutionary consequences. Be sure, an evolutionary event is a given past event. The difference is: we were on the phenotype level, and now they are dealing with the molecular mechanism for the phenotype traits. There shouldn't be any contradiction with respect to the evolutionary event. In fact, the molecular mechanism may provide an understanding of the phenotype. There are a few young population geneticists working on molecular evolution. I am proud to say that I know one of them—Professor Wen–Hsiung Li. His book, *Molecular Evolution* (1997) [24], is an instant success. A number of universities have adopted it as a textbook.

Chen: What are the issues for study of a complicated trait like human intelligence? You had a very interesting paper, "A tale of two thermos bottles: properties of a genetic model for human intelligence" [10], which was also translated into French. What was the exact message you want to convey?

Li: Clearly, we cannot go into the controversy of whether IQ is largely affected by environmental factors or by genetic factors here in one paragraph. The chief message I was trying to convey in the Thermos

FIG. 2. *From left: Sewall Wright, Mrs. Clara Li, Aravinda Chakravarti and C. C. Li, at the Pittsburgh Symposium on Human Population Genetics, October 1982. The occasion was to celebrate C.C.'s 70th birthday and retirement.*

Bottles article is that "like father, like son" is not true at all, whether IQ is environmental or genetic. It is the segregation phenomena of the Mendelian inheritance in human populations that we are actually observing. Some social scientists, unlike biologists, are born environmentalists; it is difficult for them to imagine that genetic factors are also in play. This is the group most difficult to reach. I think my article did reach a number of social scientists, because the article was quoted and the diagrams reproduced in the (American) *Education Yearbook*, 1973–74, by Arthur Jensen [5].

This paper of mine, incidentally, also contradicted the Chinese Communist belief that if a father is a hero, the son is a good guy. If father is reactionary, the son is a rascal. These beliefs are obviously not true and can be readily contradicted by observations. Yet, the Chinese Communists hold them to be true and numerous people have been arrested simply because of their fathers's behavior.

Chen: The founders of statistics like Pearson and Fisher were heavily involved in the eugenics movement. Two years ago there was some controversy about the Chinese "eugenics and health protection law." What is your thinking about eugenics?

Li: Francis Galton was far more involved in eugenics than Pearson and Fisher. In fact, Galton had the idea of eugenics even before the rediscovery of Mendel's law in 1900. Hence, the idea of eugenics and the laws of heredity are not necessarily related. Karl Pearson, throughout his life, never believed in Mendelian inheritance. His reason was that Mendelian inheritance yields discrete traits, while most important traits are all continuous. (This argument was false, as Fisher showed in 1918 [2]). The Chinese eugenics movement is something else. As usual, the Chinese Communists switch from one extreme to another without a blink of an eye. I guess human ideas and behaviors are like the Earth being round. Thus, when A goes east and B goes west, they are further and further away from each other, but only for a while. Then they are getting closer and closer together and eventually meet again. Politically, it is almost the same thing. A goes right and B goes left. They are further and further apart for a while, but eventually the far right and far left meet again at one place. Thus, there is no difference between far right (Hitler) and far left (Stalin). In China, the Communists switch from far left (Lysenko) to far right (eugenics) almost naturally. The Chinese Eugenics Program will, no doubt, lead to gross abuse of the patients, regardless of what they say or what the regulations are. Abuse and corruption will prevail. The 18th International Congress of

Genetics will be held in Beijing, August 10–15, 1998. The Local Program Committee (Chinese) somehow is trying to suppress discussion of the Chinese Eugenics Program at the Congress meetings. I don't have the details. I know only that the British Genetic Society will boycott the Beijing Congress, but I suppose that the American Genetics Society will go to Beijing. A scientific subject is not allowed to have a public debate; this kind of thing can only happen in a totalitarian state.

Chen: Genetic Diversity Project encountered resistance from some third-world countries. Recently there were also some debates in China about exodus of Chinese genetic materials [23]. You also wrote a letter to *Science* [3] about this. What is your thinking about this?

Li: It is true that some other third-world countries also have the same kind of problems as the Chinese have now. But, still, I don't think the Chinese arguments are all sound. Take the most popular assertion as an example. The Chinese say that the Chinese DNA are unique and thus are a national treasure and should not go abroad. This sounds very much like nonsense to me. Every country's DNA is unique, as no two countries have exactly the identical history or environment. The second argument of the Chinese government is equally absurd. They say the Chinese population is large and China has many unique diseases. This is a national treasure, I suppose! If so, I think it is also a reason for international research, or at least not a reason for keeping it to yourself. This Chinese "patriotism" reminds me of the patriotism of the Chinese Boxers (1900) who advocated, "Support the Ching Dynasty and Kill the Foreigners". The results were the Allies landing in Taku-port, occupying Tianjin and setting up the Foreign Territories in all major cities of China. We surely can do better without the "patriots."

Our letter to *Science* (December 1997) expressed but a small part of our viewpoint and thinking. Did it have any effect on the Chinese authorities? That we don't know. Perhaps a little. The evidence is: originally the Chinese authorities said they would make public the new regulations by the end of 1997. But, now, it still is in draft form, circulating among Chinese for comments. They apparently decided not to rush the regulations. Dr. Huan-ming Yang, the writer of the draft regulations, wrote me, gave me a copy of the draft regulations and asked for comments and suggestions.

Tai: DNA profiles have been used in forensic investigation. A few years ago there was debate about the proper way of computing matching probabilities due to population heterogeneity. You were involved in a controversy about the correct formulation of the paternity index in parentage testing from 1985 to 1988 [16–19]. Your recent 1996 paper "Population genetics of coincidental DNA matches" [15] won the Gabriel W. Lasker Award as the best paper of the year in *Human Biology*. In this paper you proposed calculating the matching probability unconditionally. Could you first describe the paternity index controversy?

Li: In general, a paternity test should be like a screening test which always increases the probability of paternity among the nonexcluded people. If there are several tests all resulting in nonexclusion, then the probability of paternity would be very high. In fact, the probability of paternity should increase monotonically with the number of genetic tests. The probability of paternity calculated by my method is indeed monotonic. Why did I not use the "paternity index" method? Briefly, the paternity index method could make the paternity probability *decrease* after a nonexclusion! It all depends on the genotype of the accused man and the gene frequencies of the population; none of such factors has any implication on paternity per se. As I have pointed out before, if we continue to have such a situation for six or seven nonexclusions, and the paternity probability decreases for each nonexclusion, then the final paternity probability would be small (near zero) after these six or seven nonexclusions! This is absurd. My method will yield a very high paternity probability after having six or seven nonexclusions. One may argue that the paternity probability may increase or decrease by the paternity index method. Thus, it is unfair to assume as in my example that in all seven genetic tests, the paternity probability has decreased in all cases. Of course, I am not assuming that it happens every time, but it is a distinct mathematical possibility. What would you say when it does happen?

Tai: What is your thinking about the use of DNA profiles in forensic science?

Li: First, let me say I am for using DNA evidence in court; it is far more reliable than so-called eye-witnesses. Different eye-witnesses see different things. This does not imply that some of them are necessarily lying, because they do see different things. We call DNA a witness too. This witness is far, far more reliable. As to the probability of DNA profile matching, the problem is somewhat similar to the paternity problem we discussed above. Namely, they changed the subject in the middle of the process. The calculation of the DNA matching probability will make the point clear. Let us ask the following question Q: What is the probability that the DNA profiles of two random individuals from

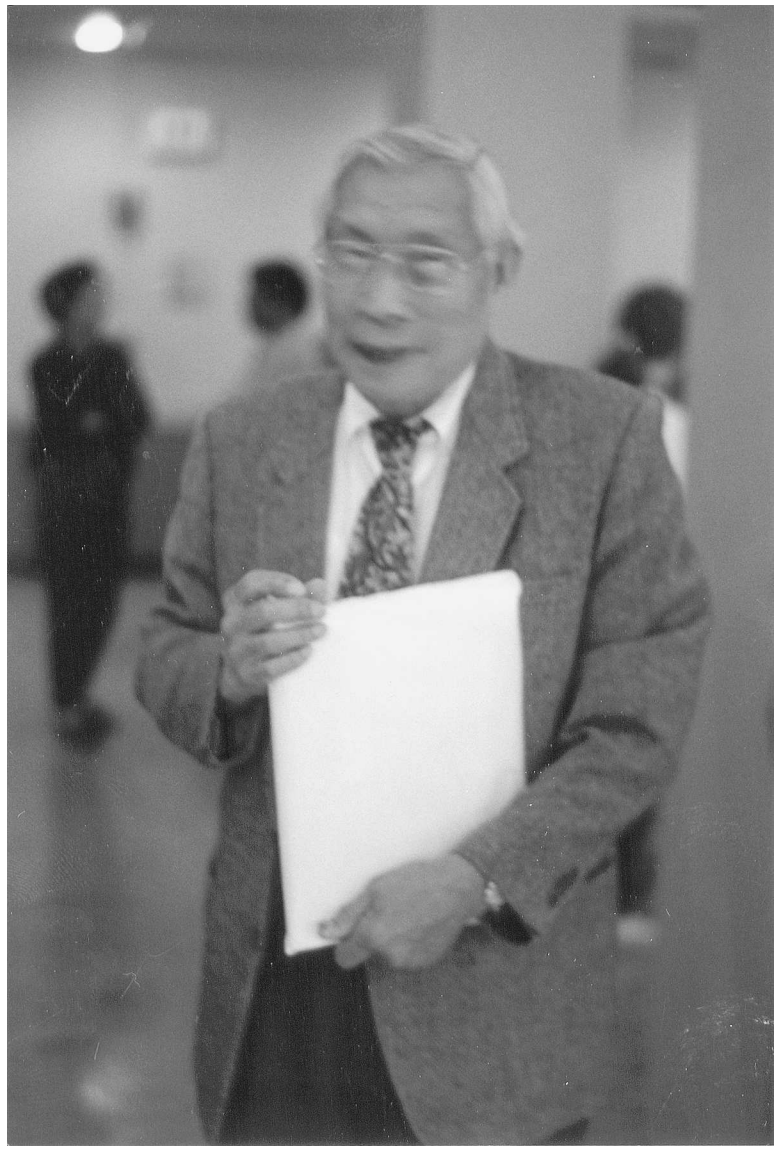

FIG. 3. *C. C. Li at the surprise party for his 85th birthday, October 1997. The folder under his arm is the letter of commendation from Mark A. Nordenberg, Chancellor of the University of Pittsburgh.*

a population will match? The question Q above is simple. We not only should know what it asks, we should also know what it does not ask. The answer (M_0) by my method is the answer to Q and nothing else. The Q mentions no particular genotype of anybody at all. My answer made no mention of any genotype at all. The answer and the question fit, like lock and key. Whether the question Q and its answer M_0 are useful or not is a separate problem.

The method of calculating conditional probabilities of DNA match proceeds like the following. Let the two random individuals be A and B and let their DNA profiles be "A" and "B", respectively. Usually, in practice, the two DNA profiles are not determined simultaneously in a laboratory (starting at the same time and finishing at the same time). Suppose that the "A" profile became known first. Then they say "A" is given, so that the matching probability is that B has the same genotype as A and thus "B" must match "A". So, the conditional probability of match is simply the frequency of "A" in the population. The answer is the frequency of a genotype in the population. This procedure involves several points worth noting: (i) It depends on whether "A" or "B" became known first. The conditional probability of matching is always the frequency of the first known genotype. (ii) The first known genotype, say "A", is not really a "given" condition; it is part of the typing results in the laboratory. It is observed, not given. (Given by whom?) By a "given" condition, we mean the condi-

tion is already there before we do anything. In our problem, "A" was not known; it became known after profiling. It is our finding! I find the "conditional" probability quite arbitrary and meaningless and of no general use. Finally, it is not the answer to the original question Q.

Tai: With one eye blind and the other with cataract, at the age of 86 you still go to your office to do research everyday. You continue to publish important papers, such as your Lasker Award paper. In addition to interest, what really motivates your perseverance?

Li: Simple answer: nothing. I go to my office because there is nothing else better to do.

Chen: Dr. Li, we have been talking for almost three hours now, and Mrs. Li is calling us to go to the dining room to have some ice cream. We really enjoyed our conversation with you and we thank you for describing your life experiences and giving your views on a variety of issues. Your comments tonight will be useful as part of the recorded history of statistics and genetics, and hopefully will prompt more statisticians to become interested in problems of genetics.

Li: Thank you both for your interest.

REFERENCES

[1] FELLER, W. (1950). *An Introduction to Probability Theory and Its Applications*. Wiley, New York.

[2] FISHER, R. A. (1918). The correlation between relatives on the supposition of Mendelian inheritance. *Trans. Roy. Soc. Edinburgh* **52** 399–433.

[3] GUO, S. W., ZHENG, C. J. and LI, C. C. (1997). Gene war of the century? *Science* **278** 1693–1694.

[4] HUXLEY J. (1949). *Heredity, East and West: Lysenko and World Science*. Schuman, New York.

[5] JENSEN, A. (1973). *Education Yearbook*. Longman, New York.

[6] LI, C. C. (1948). *Introduction to Population Genetics*. National Peking Univ. Press.

[7] LI, C. C. (1955). *Population Genetics*. Univ. Chicago Press.

[8] LI, C. C. (1964). *Introduction to Experimental Statistics*. McGraw-Hill, New York.

[9] LI, C. C. (1967). Genetic equilibrium under selection. *Biometrics* **23** 397–484.

[10] LI, C. C. (1970). A tale of two thermos bottles: properties of a genetic model for human intelligence. In *Intelligence: Genetic and Environmental Influences* (R. Cancro, ed.) 162–181. Grune and Stratton, New York.

[11] LI, C. C. (1975). *First Course in Population Genetics*. Boxwood, Pacific Grove, CA.

[12] LI, C. C. (1975). *Path Analysis, A Primer*. Boxwood, Pacific Grove, CA.

[13] LI, C. C. (1987). Lysenkoism in China. *Journal of Heredity* **78** 339–340.

[14] LI, C. C. (1987). To the memory of the fallen Nikolai Invanovich Vavilov (1887–1943). *Journal of Heredity* **78** 343.

[15] LI, C. C. (1996). Population genetics of coincidental DNA matches. *Human Biology* **68** 167–184.

[16] LI, C. C. and CHAKRAVARTI, A. (1983). On the exclusion and paternity probabilities. In *Inclusion Probabilities in Parentage Testing* (R. H. Walker, ed.) 609–622. American Association of Blood Banks. Arlington, VA.

[17] LI, C. C. and CHAKRAVARTI, A. (1985). Basic fallacies in the formulation of the paternity index. *American Journal of Human Genetics* **37** 809–818.

[18] LI, C. C. and CHAKRAVARTI, A. (1986). Some fallacious thinking about the paternity index: a reply to Dr. Jack Valentin's comments. *American Journal of Human Genetics* **38** 586–589.

[19] LI, C. C. and CHAKRAVARTI, A. (1988). An expository review of two methods of calculating the paternity probability. *American Journal of Human Genetics* **43** 197–205.

[20] LI, C. C. and HORVITZ, D. G. (1953). Some methods of estimating the inbreeding coefficient. *American Journal of Human Genetics* **5** 107–117.

[21] LI, C. C. and MANTEL, N. (1968). A simple method of estimating the segregation ratio under complete ascertainment. *American Journal of Human Genetics* **20** 61–81.

[22] LI, C. C. and SACKS, L. (1954). The derivation of joint distribution and correlation between relatives by the use of stochastic matrices. *Biometrics* **10** 347–360.

[23] LI, H. and WANG, J. (1997). Backlash disrupts China exchanges. *Science* **278** 376–377.

[24] LI, W. H. (1997). *Molecular Evolution*. Sinauer Associates, Sunderland, MA.

[25] NICHOLAS, F. W. (1982). Simple segregation analysis: a review of its history and terminology. *Journal of Heredity* **73** 444–450.