A Scientist Dreams, Ambitions and Realities

Khidir W. Hilu

Abstract The path towards my professional field started in a circuitous way. By the time I decided against dental school, botany was the only option left for me to pursue on the decisive college admission day. To top it off, I landed in my current specialty of plant systematics because I failed the class in my final exam as a college junior. I took that failure as a challenge and made a successful career out of it. Since then and by choice, my research has been focusing on plant biodiversity, tackling it at different taxonomic levels from species to kingdom. Understanding the dynamics of biodiversity and its synergistic interactions with the surroundings is a fundamental effort to reveal historic life events and bring attention to potential future ones including extinction threats. The field interacts with progress in science and technology, and thus, advances come in peaks and valleys, reflecting magnitudes of innovations and stagnations. Initial assessment of biodiversity patterns was egotistically based on plants' usefulness to humans, culminating in artificial classifications. Next peaks epitomize creative use of many thoughtfully selected traits, and introductions of chemical, developmental and microscopic ones. We transitioned towards comprehensive classifications. However, the work was untestable, lacking components we treasure in science: the empirical approach, and the scientific method. Yet, we thought we knew the "true" system(s) of plant classification until the era of biotechnology and bioinformatics arrived late in the twentieth century, turning our field upside down. The outcome was shocking but by no means disappointing. This latest revolutionary peak emerged with unparalleled excitement, presenting golden but rather challenging opportunities. Pioneering this in my lab became one of my career highlights. I did not, and you should not, be left behind by shying away from being in the forefront of progress. In fact, aim to lead it.

K. W. Hilu (✉)
Department of Biological Sciences; Inter-department of Genetics, Bioinformatics and Computational Biology, Virginia Polytechnic Institute and State University (Virginia Tech), 1275 Falcon Ridge Rd, Blacksburg, VA 24060, USA
e-mail: hilukw@vt.edu

D. Breviario and J. A. Tuszynski (eds.), *Life in Science*,
https://doi.org/10.1007/978-3-031-23717-1_6

1 Motivations: How I Developed an Interest in Science

I grew up in and around Baghdad, Iraq, with an illiterate mother and a father who only finished fifth grade. Science was nowhere in the picture. However, they both strongly promoted education and invested the little money they earned in our education. Their wishes and investments were highly rewarded. My parents' honest effort and motivation ignited in me the desire and will to achieve. The hard work and focus started early in my life. Fortunately, I loved school, learning excited me and exams were mere welcome challenges. So, the road started quite smoothly with the home support and the innate energy and desire. Well, until graduating high school and the crucial decisions on colleges and career choices were eminent.

Ironically, botany, plant systematics and biodiversity were never on my mind, and were rather foreign to me. I did not receive advice from teachers, mentors, or my parents. Wavering about careers, I tried, without success, admission to the police academy because my father was a policeman. I applied to become a commercial pilot because I enjoyed traveling, but neither did this work out for the naïve me. So, attending college was my next option, one that luckily was supported by my family despite their low income. I applied to dental school and was accepted on the spot, but then changed my mind because I did not like the looks of blood. Next, I considered liberal education, but changed my mind considering the narrow job market. After this wavering, the college of science sounded attractive. By this time there was only one department left with a vacancy, that was Botany. Luck and a little bit of thinking for the 16-year-old boy established the foundation of my career in botany. These experiences never left me and the lack of direction I experienced built in me the strong desire to mentor students and young Ph.Ds, which I will elaborate on later.

So, what landed me in plant systematics and evolution? As a freshman, I excelled in math and the math professor of my class, who was the department head, singled me out and asked if I would want to transfer to his department at the end of my freshman year, adding "you do not belong to botany"! My reply was a yes with excitement for math. Unfortunately, or rather fortunately, he left the country before the end of the year, and I remained in botany. In my junior year, I was required to take the undergraduate plant taxonomy course. It was interesting but did not turn on enough excitement to pursue it as a career. That is until the final exam when I was unable to identify the ornamental plant, crape myrtle (*Lagerstroemia indica*), an error that ironically accounted for more than half of the course grade. So, I failed my first plant taxonomy course, which was a heart breaker because I had never failed a course before. But we had the two summer months to study and retake the exam. I did not pity myself but instead took this first career failure as a challenge. My decision was to collect, key out and learn the names of as many plants that I could access in Baghdad. Passing the test was then easy. Interestingly, I relished the summer experience that brought me in intimate contact with the plant world and exposed me to the fascinating complexity of plants and their interaction with the environment. It was the turning point in my career, and my life as well. It taught me a valuable lesson that I carried along with me to this day. In fact, I have five crape myrtles planted in our garden as a daily reminder!

Soon after that, an opportunity knocked on my door. Our Plant Taxonomy teaching assistant was about to go overseas for his doctorate. Noticing my interest and experience in plants, he recommended me as a replacement (Teaching Assistants are full time jobs offered to students that excel in the department). Being the top graduate in my class qualified me for the position. I worked on my master's degree in plant taxonomy while teaching the course until I was offered a scholarship to pursue my doctorate. I received admission in my top choice schools, Cambridge University, England, and the University of Illinois in the United States. Surprising to people then and now, I chose the latter because I was told that you will have to take a large number of courses in the American system, a situation that appealed to me due to my love of learning and knowledge. I worked under the advisership of J.M.J deWet and Jack Harlan in the Crop Evolution Lab, both are highly renowned scientists. Finding a university job in the United States for an immigrant like me was an evident challenge. After a temporary teaching position and two postdoctoral positions, I was offered a tenure-track position at Virginia Tech in 1982 where I taught and started my research career until retirement in 2019.

2 Work Done: My Personal Scientific Approach

In 4 years as a tenure-track faculty, you have one chance to show the department your national and international scholarly status and the unquestionable success as a researcher and a teacher. One of the colleagues in the department advised me early that the department relies on three factors for promotion: research, research, and research. I listened to his advice but decided that educating young scientists via serious teaching and advising should not be overlooked. My approach to research was to (1) incorporate the most recent advances in the field, (2) take on major projects and (3) do not always follow the ongoing currents but challenge the establishments and be innovative and a leader. It was an ambitious strategy for a young scientist but a good aim even if I accomplished part of my goals. I basically searched for potentially rewarding major challenges. It was the era when bioinformatics was in its infancy and computing was done via *punch cards*, a very primitive but effective modern means then. I capitalized on this approach and became a member of the new field of Numerical Taxonomy. This field allowed me to tackle my first large-scope study: the classification of the entire grass family Poaceae, the 5th largest family of flowering plants and ecologically and economically most important one. I started this major undertaking a year after my graduation and included a graduate student. As a temporary teacher and then a full-time postdoc, I had to find the time during these two years to do the work, which I did happily. The hefty paper was completed and published the year I started my permanent job at Virginia Tech. That pioneering work and subsequent studies raised me to prominence in the field of grass systematics at an early stage of my career.

Life is full of patterns if we consciously look for them. Throughout my career as graduate student and professional scientist I searched for patterns and was thrilled with what I encountered. One delightful observation started when I was a graduate student at the University of Illinois. I always loved libraries and literature search, and the University has some of the best in the nation, so I spent considerable time in them. This was immensely rewarding in broadening my knowledge beyond plant taxonomy. It led me to one particularly fascinating finding that turned into a major achievement. Often plant taxonomists and geneticists cross, for various purposes, plants of distinctly different features and recover progeny with characters that have simple Mendelian distribution of 3:1 or 9:3:3:1. What shocked me is that researchers overlooked the enormous evolutionary meaning of such patterns. Prominent changes of major features in flower, fruit and habit which were then construed as the result of numerous cumulative mutations appeared to be controlled by one or a few major mutations. I was tremendously excited by this discovery since it goes against Darwin's gradual evolution and in concert with Stephen Gould's theory of punctuated equilibrium. When that major contribution to science (Hilu 1983) appeared, some colleagues were excited while others were skeptical. One of the skeptical scientists was the late G. Ledyard Stebbins, one of the founders of the Synthetic Theory of Evolution, who was awarded the American National Medal of Science. He was my academic "grandfather" as my two major professors were his graduate students. I invited him once to present talks at our university. He was extremely upset that I challenged their theorem of gradual evolution, but he settled with the advice that I conduct further research on the subject. Professor Stebbins became one of my mentors. Later work shows substantial support to my findings, and I was told that my publication has become a classic paper in genetics.

For the next leap in my research, I decided to take a calculated risk. New research start emerging in systematic biology and evolution where bioinformatics (computer technology and software programing) is combined with molecular biology (gene and genome mutations), another novel and powerful field. The two in concert revolutionized our field. In fact, they turned our latest understanding of plant phylogeny (genealogy) upside down. They handed us a shockingly new picture of the plant tree of life, guiding us towards a radical restructuring of plant classification. What we thought we knew and understood suddenly appeared inaccurate. However, during the excitement we initially let our guard down by relying on one gene. Realizing the pitfall, the field exploded, and a variety of genes and genomes of varied evolutionary modes were employed and critically evaluated. Trees of life were reconstructed and timescale were estimated. But questions remain regarding intrinsic biases in the molecules used. It is crucial to be mindful that these findings are mere testable hypotheses. Future technological innovations may alter our understanding of biodiversity. I hope that we will not repeat the mistake made when we assumed that we knew it all! Science evolves as biodiversity does.

This is an exciting era shedding new lights and laying out new perspectives. I, among many of us, was taken away by its power of resolution and the immensity of discoveries it offers. So, it fits the criteria I put forth for my career, innovative approaches. However, implementing this innovative approach in my research program was a risky enterprise since molecular biology is outside my expertise for one thing, and I had a limited time to demonstrate the required level of publications for my tenure. Venturing into a new field will delay the required publications. But the temptation and desire were overwhelming. For advice and assurance, I went to our department head to discuss the issue. As a molecular biologist, he understood the power of the field and its potential prospects, so he gave me the green light to start my training and build a lab with some financial support from the department. That initiative was one of the pillars of my career. I ended up publishing the first paper on the molecular systematics of the family Poaceae.

At the start, most colleagues were using the chloroplast photosynthetic gene *rbcL* to discern phylogenetic relationships among plants. That is because of abundance of sequences in gene banks due to its importance in photosynthesis, ease of sequencing, and reliable alignments (matching) of the sequences even among distantly related species as it mutates at a relatively low rate. Other slowly mutating genes were added for the reconstruction of flowering plants phylogeny. Shockingly, those genes individually did not result in identical phylogenetic tree. So, and rightly, combining sequences from different genes became the favored approach. However, the dogma of using slowly evolving (mutating) genes dominated the field. The argument was low mutation rate produces more phylogenetic signal and low amount of misleading noise. In contrast, rapidly evolving genes were considered to provide more noise than reliable signal and should be avoided in studying deeper level plant evolution. I questioned this theorem and decided to evaluate it. That was the time when I made a move that elevated my lab and career yet to another level and positively altered the field. The department at that point has already granted me tenure and promotion, so my job was secure. I decided to join a highly respected molecular biology lab at the Australian CSIRO institute in Canberra to gain experience in molecular biology and DNA sequencing. So, with a job security and knowledge, I made my move. After extensive search, I found a rapidly evolving chloroplast gene called *matK* that had been used a couple of times in molecular phylogenetics of closely related species. With a modest data set of sequences of this single gene, I constructed a phylogeny and compared it with what was available. To my delight, the structure of the tree based on *matK* alone was as good as those based on data from combining larger numbers of sequences derived from several slowly evolving genes. This finding clearly showed that there is an overwhelming power in the rapidly evolving *matK* gene, i.e., it possesses plethora of phylogenetic signal and was not impended by noise as others assumed. What was left is to convince the botanical community of these astounding results. I published several convincing papers from my lab that critically analyzed the *matK* in grasses and beyond.

I strongly believe in collaborations among labs. I always thought that in collaborations, one plus one could add up to 10! So, I invited a group of bright graduate students from the University of Bonn, Germany, to join my lab on the *matK*/rapidly evolving genes concept. They, as well as their advisor, were excited. We gathered immense amounts of data and analyzed them in several creative bioinformatic ways, and the outcome provided an overwhelming support for the approach. Then I invited several plant systematics from various countries to contribute their data on *matK* and co-author a major paper on flowering plant systematics based solely on *matK*. The paper was a significant contribution to the field and has been very highly cited (Hilu et al. 2003). In fact, since the publication of that paper in 1983, the GenBank showed a significant surge in number of *matK* sequences deposited and the gene became a molecular choice in plant systematics rivaling the *rbcL* gene.

The other issue that faced me as a young scientist in this pursuit is how much challenge can I handle by expanding beyond the group of plants I am comfortable with, the grass family. Moving into flowering plants meant working on the largest and most dominant group of plants on earth. I started my doctoral degree working on the origin and evolution of an African/Indian crop plant called finger millet. The ensuing expansion months after my graduation to the systematics of grasses, the fifth largest flowering plant family, was a major undertaking for me at that time of my career. To demonstrate the efficacy of *matK* in plant systematics at deeper historic levels required the expansion to the immense group of flowering plants and even to seed plants by including groups like conifers and cycads. One must be comfortable, confident, and competent to be successful in such a move. There were already several labs to deal with in the United States, Europe and beyond that were well established in the field. So, as a young scientist one must be realistic about what I handle and how much one can give to such an enormous step. After critical thinking and evaluations of my academic and personal situation, I decided to proceed. Considerable amounts and time and effort were spent in the preparation process. My approach was to collaborate rather than to compete if possible. It was a fruitful approach at the start and throughout my career. After publishing the paper on flowering plants as a whole, I tackled various subgroups in detail. The collaborative approach also resulted in the very rewarding joint project on the assembly of the Tree of Life (AToL) project. Our team represents the leading labs and scientists from the United States and overseas and focused on flowering plants with about $3 million grant from the U.S. National Science Foundation. It was a gratifying project in terms of discoveries, major publications, and graduate and undergraduate student education. This collaborative project and others exposed our lab members over the years to legends in the field and established lasting cordial relationships. Although collaborations are not always free of some shortcomings, I still strongly recommend to young scientists such interactions.

Despite the hard work, the pressure of expanding the research program and the balance required between research-teaching and mentoring, the road was full of excitement and rewards. After the success of the flowering plants projects, I decided to venture into land plants. I proposed a collaborative study with two colleagues from the Mexico National University and the University of Bonn to contrast phylogenetic trees based on rapidly evolving *matK* genes and other slowly evolving genes. We placed the trees in a time frame using fossil records to show emergence dates of various plant groups. The study again showed that *matK* sequence data alone was as effective as sequence data from the other genes combined. The latest scientific move was to combine data and effort with colleagues working on fungi to learn about the co-evolution and diversifications of these two vital parts of biodiversity since they moved to land over 700 years ago. The outcome was quite significant and was published in the journal Nature Communications (Lutzoni et al. 2018).

Equipped with scientific tools and knowing that there is complementary expertise from colleagues around you, one can be creative and think outside-the-box. My latest joyful scientific voyage was a study of the evolution of allergenicity in the peanut crop using the crop and numerous wild species in its genus. Using peanuts allergen genes sequencing generated in my lab by graduate and undergraduate students, I collaborated with a biochemist colleague and his graduate student to assess the evolution of allergenicity in the peanut genus. The colleagues generated three-dimensional models of the allergen proteins and we mapped their evolution on the phylogenetic tree of the genus. We supplemented these results with immunoblotting using sera from peanut allergy patients to estimate allergenicity. The study pointed out the molecular changes that intensified allergenicity in peanuts and circumscribed the regions that could be modified to reduce or even eliminate allergenicity (Hilu et al. 2019). It also provided information on wild species that can be used in human therapy.

I retired in 2020 but am still active in scientific writing. Scientific activities and endeavors in many of us never cease but continue and evolve.

3 Science Today and Tomorrow

My field of research does not create breakthroughs in technology but has been actively and continuously taking advantage of them whenever they emerge. This feature has kept the field on the move, advancing it to new heights in refinement and resolution of the patterns of plant classification and evolutionary relationships. Early scientists in our field were critical thinkers. They did not shy away from highlighting pitfalls, eliminating them, and building upon what then was regarded adequate. Artificial systems such as classifying plants based on their edible usefulness to humans was replaced by yet another artificial system based on medicinal applications. Then, they correctly thought that features from the plants reproductive parts are more reliable. Unfortunately, Linnaeus who spearheaded these efforts chose one character for initial classification, generating yet another artificial system. Increasing the number of features used in classification from both reproductive and vegetative parts is an example of building upon what existed and moving us to a more natural classification system. Simple mathematical evaluation of the data increased objectivity in classification, a welcome progress. Charles Darwin's introduction of the theory of evolution helped to move the assessment of patterns of biodiversity from a snapshot picture (phenetic) to an evolutionary system (phylogenetic). Finally, the usage of molecular characters from the genomes and the analyses of these large data sets with varied kinds of software using computers and supercomputers is brought us to where we are now.

One of the major differences between the current status of the field and previous periods is that we can assess patterns of biodiversity with the scientific methods. Our approaches and outcomes can be critically evaluated statistically. The sophistication of these approaches continues to reach new heights. Different means are available to reconstruct the tree of life and above all to test and evaluate their accuracy. We have made outstanding strides to elevate the field to new heights. With this level of sophistication in the field, it is often advisable and profitable to collaborate with other scientists to bring together the skills of experts in molecular work, computer science, morphology etc. to achieve the most reliable and sophisticated results. It also increases chances to obtain the needed funding to finance the research. Another notable achievement is that our field is actively interacting with other fields like ecology, agronomy, forestry, medicine, paleontology, etc., providing ways and means by which our efforts can be utilized.

What I have presented is just the overall picture of where our field stands currently. The future is difficult to predict but new layers of sophistication will definitely emerge, driven by technological advances and creativity. We should keep in mind that future directions are determined largely by preferences in funding policies. I believe the status of the world with pandemics impacting human health, geopolitics severing localized or global economics, acute climatic changes that impact agriculture and food supplies, and uneven population growth will continue to provide new grounds for research in science and technology. It is gratifying to see how our field has been useful in dealing with the ongoing COVID-19 pandemic. Phylogenetics was implemented in tracing the patterns of emergence of mutational variants, the geographic area of their origin, routes of distribution, and the rates at which mutations emerge. These tools are also of notable value for refining computer models that focus on the expansions of existing pandemics and the predication of future ones. Bringing such information together helps global health organizations to plan for containment, designing new drugs based on mutation patterns to combat the virus and preparations for future events.

Extreme climatic change is also another major issue facing humanity. Global warming, droughts and desertification, floodings, and pollution, among others, are playing a large role in rates of extinction and loss of biodiversity. Phylogenetics could be very useful in discerning the distribution patterns of organismal extinction. For instance, phylogenetic and systematic studies can point out which group of organisms are more vulnerable for extinction and the geographic regions that are suffering the most from species losses. Such information will help us prioritize groups in need of preservation. Evolutionary history of lineages will reveal the differential rates of extinctions in lineages and which one(s) have suffered reduction in their species number and highlights the ones that are on the way to elimination. A good number of plants and animals have potentials for providing valuable drug products or have potential for domestication as food crops, rendering the focus on them and their phylogenetically related species a priority. Some of these plants are closely related to our crops and thus may have valuable genetic components that can improve the crops.

Relevant to my field, I see expansion in collaboration between computer scientists and engineers, software developers, and systematists/phylogeneticists. The latter group of scientists have been moving towards handling large number of species and using information from whole genomes. These are mega-scale datasets and will require an immense amounts of computing power, speed and storage. Software developers are instrumental in the success and expansion of this arena since creative computer program will be required to speed up the processing of these data with the appropriate type of analyses required. A large number of iterations will need to be implemented in order to converge on statistically reliable pictures of patterns of biodiversity. For the field to succeed and advance, funding for educational institutions is a must since they tend to be non-commercial enterprises. So, novelty and sophistication in grant proposals with compelling reasons highlighting the uniqueness and urgency for doing the study are crucial for funding success. Availability of state-of-the-art computer hardware is essential for processing such studies. Computational time can be accessed from local or national supercomputers, but funds to establish such computers is again a major issue. I was involved in a grant proposal focusing on the establishment of a new supercomputer at my university, Virginia Tech, which we nicknamed the HokieSpeed Supercomputer. To support the need for such a supercomputer, we needed to gather letters from leading scientists in my field indicating the urgent need for such a supercomputer and the strong desire of the scientists to use it in their research. We succeeded in obtaining funding and the HokieSpeed supercomputer served our purpose and those of other colleagues. However, speedy advancement in computer science and engineering required the establishment of more advanced versions. So, progress in the ways to study biodiversity and the advancement in computer hardware and software go hand in hand, pushing each other to new levels. Such association exist in many other academic and industrial fields, and it represents the future directions.

I would like at the end of this section to remind us to look back at the status of the field of systematic biology and evolution hundreds of years ago, where we were then and where we are now, and the potential new directions it may be taking. The strides made are immense and speak loudly of human ingenuity, scientists' endeavors, and the innate desires to explore and succeed.

4 Advice to the New Generation of Scientists

Experience is a treasure that, if we learn from it, can enhance our chances of success regardless of our professions. Experiences could arise from personal achievements or mistakes committed via choices made unintentionally or consciously. They could also come from learning about other's fortunate and/or misfortunate actions. They are resources that we can freely dip in when made available. I would like to share the endeavors of my long academic road from the immature decisions I had to make while applying to undergraduate school to where I am now, an accomplished scientist with over 120 publications and 49 h-factor. I believe that young scientists can benefit from my experiences. I will divide this section into subsections:

Mentoring: It was a blend of luck and some sensible thoughts that anchored me at the start of a road and led me to where I am now. However, I wish I had a mentor at the very start that would have helped me make educated decisions and saved me from potential unfavorable or disastrous choices. Seeking a mentor in your career at all points is quite desirable. Do not look at it as a weakness but as a strength of character. I was fortunate to have one while working on my master's degree and three since the start of my doctoral years. I owe them a lot. Both, the lack of mentors early in my career and the presence of astute ones afterwards motivated me to do a great deal of mentoring as a faculty and researcher. I do not regret the time spent on it. I made concerted effort to encourage students from their freshman college year on (as well as some high school students) to join my lab. We have shortages in the number of women in science as well as students from diverse backgrounds so my lab was quite supportive of minorities and women in science. I believe joining a research lab provides young people with (1) research experience, (2) enhance their focus and career directions, (3) a place where they can associate with serious graduate students, lab technicians and postdoctoral fellows, and (4) a professor that can give them an invaluable, solid letter of recommendation that speaks of their talent from concrete personal interactions not just observation from attending a class (Fig. 1).

I offered undergraduates a choice of the lab projects that suited their interests, paired them up with a graduate student/postdoc involved in that project and acted as the ultimate mentor. We had the tradition of conducting a weekly journal club. Lab members, regardless of their academic status took turns selecting a scientific article and lead the discussion each week. At the end of the meeting each member presents a statement regarding the successes and failures they encountered in their research during that week. This was carried out in an informal and friendly atmosphere which encouraged comments and suggestions from other members. Graduate students took this as a teaching opportunity and the undergraduates used it as a

Fig. 1 Diversity in my lab

learning and confidence-building chance. Although I spend a fair amount of time writing papers and grant proposals to support the research, I took the time daily to informally interact with the students discussing their progress. This nurturing was quite rewarding for the graduate and undergraduate students. Their success and the letters they send me after graduation speak highly of the time they spent in my lab. They considered it as their best academic experience and that they could have not been where they are had it not for that experience. This is my reward knowing that I made a difference in young people's lives.

Mentoring on an international scope: Some of us are fortunate to be working at institutions where state-of-the-art-technology is available in terms of lab equipment and supplies, computer hardware and software and technical assistance, as well as funding to support our research. But there are places in the world that are not so fortunate. I made a concerted effort to invite, mentor and support international scientists from those institutions. I helped Egerton University, Kenya, establish one of the first basic molecular biology labs to study genetic diversity of their native crop finger millet and trained their scientists in my lab and at their institution. Similar efforts were made for helping one of the laboratories in Morocco. I mentored and trained colleagues from Senegal, and doctoral students from Egypt, Jordan, Iraq, Indonesia, and South Africa. I sought funds from national and international organizations as well as from our university to support such efforts. In these efforts, we establish a foundation that hopefully will expand and start impacting others.

Mentoring while teaching: Although class teaching is often regarded as an effort to present information and knowledge to students, I tried to use it as a mean of mentoring too. The classroom is a place where you can interact with a large number of young people. To make use of this golden opportunity, I arrive as early and leave as late as I am allowed for the room. I walk around and take turns visiting with the students, asking them about their majors, their career interest, the preparations they have made for it. I offered advice about how they increase their chances of success. Proposing labs that can accept them to do research was welcomed; many students did not know that such thing existed. I highlight the future trends in the field and underscore the importance of some of the trends. As a young faculty, you will find this also an opportunity to recruit some excellent students to help you in your research program while they advance their own education and career. I welcome students who want further information to meet me in my office when I have the time or have them meet with graduate students. We do not always have the time to go the extra mile but if we do, it can make a difference.

Scientific Meetings: Attending scientific meetings are foundation builders of knowledge and careers. My doctorate major advisor did not like attending them, so I traveled with other faculty. I shadowed them to be introduced to the leaders in the field and ventured on my own to meet people and attend talks. My questions went beyond their research to their professional experiences. I listened carefully and learned. It did not bother or discourage me if some were in a rush to move on to another activity or if they did not remember me the next time I talked to them. Such effort could pay dividends when the people you met are on committees that decide your grant proposal or maybe even a job you applied to after graduation. I attended a lot of presentations and paid attention not only to the scientific component but also to the method of presentation and the handling of questions. Attending was a notable excitement for me and the whole experience was enriching and rewarding. As a faculty, I strongly encouraged my graduate and undergraduate students to attend scientific meetings and helped them to cover the expenses whenever I could. At first, they needed my assistance in introducing them to my colleagues but then I noticed confidence building in them manifested by their independence. They started connecting names on publications they read with people they met and interacted with, deepening their interest. I encouraged them to contribute presentations or posters in meetings and worked very closely with them on the material to be presented, the proper organization and the effective way to present a talk. They were required to present it at least once in front of the lab team prior to the meeting. It is easier to start their presentations in a department seminar, followed by smaller regional meetings then moving to national and international meeting. This way you minimize the shock and pressure of starting at the top of the pyramid.

Scientific publications: Requiring graduate students to write at least one chapter of their dissertation as a scientific paper and submit it for publication prior to graduation is quite important. In fact, I required them to write each chapter first in the form of a paper ready for publication and then format it to fit the university dissertation requirements. This approach has multiple benefits. The students take advantage of the faculty experience in publication writing, which is an intricate undertaking. I recall the disappointment when my major advisor returned the first draft of one of my dissertation chapters when I formatted it into a publication version. It had more red pen corrections than the black ink. I thought I had written an excellent manuscript, so the revision was painful, but the experience was invaluable. So, I learned that talking to the students about the positive aspects of the revision first before handing them the revisions help built confidence and increased the quality of the second draft. Another benefit for writing up and submitting your dissertation chapters during your graduate program is that we normally become quite involved with the high demands of the new job regardless if it is academic or commercial enterprise. In academia, these involvements include establishing a new lab, preparations for teaching new courses, writing grant proposal to support your research, and the time-consuming departmental and university committees. One more advantage to publishing your work at the graduate stage, is the edge you secure in your job applications and grant applications. It will have a notable impact on the committee members when they notice your success at this early stage of your career.

Be very critical of what you publish in terms of accuracy and quality. It is not the number of publications alone that count but the impact of them on the scientific community that matters. I strongly emphasize accuracy in what you publish. Check and check and double check your experiments, scrutinize your data, and repeat the experiments. Should you obtain surprisingly good results, double check the work before you jump to publish it. Erroneous published results could damage the reputation of your lab and strongly impact your credibility. Have a colleague or two read your manuscripts before submitting them for publication. You can return the favor by reading their manuscripts to make the benefits mutual.

Creativity and foresight: In our field for instance, you see someone publishing a scientific paper on the systematics of a plant group and it impresses you. So, you follow the same theme in terms of the overall approach. This work will be lacking creativity. You will likely publish this research, but its impact will not be as effective as if you added creativity and ingenuity. Creativity will elevate the quality of your research and the status of your lab. Be very thoughtful about the questions you are addressing and methodological approaches that can address these questions more effectively. For example, see if geographic approach, genetic focus, or biochemical properties, etc. or combinations of them would fit your project. Be versed in a variety of techniques and tools and do not shy away from learning the old and the new and applying them separately and in combination in your research. Try to visit labs that are known for their expertise in some technologies to learn the techniques and explore possible collaboration if you see it fit or needed.

Part of our job as scientists is to observe, think, explore, and experiment. It is a wonderful profession. Patterns in life exist around us, and those of us who are acute observers and critical thinkers will spot them and start evaluating their biological meaning. Darwin is one example and his observation led to revolutionizing the field of biology. The list of creative thinkers is very long for such biologists, and you can be added to that list. Be an observant scientist and a critical thinker and do not take things at face value. One of my faults is that when I found one group of grasses to be very different in certain class of proteins, I just reported the finding. A colleague followed that report by creating a new subfamily of grasses for that grass group after reading my findings and observing other unique patterns for the group. However, in another case I used critical thinking when I observed in the literature numerous cases where genetic inheritance of traits was noted without realizing the significant patterns they display. Detecting the pattern led me to propose the single gene mutations as major factors in plant evolution and that gradual evolution is not the only means by which plant evolve as the majority of scientists believed. It explains, for instance, why we can find major differences among species in a single genus that are expected to separate or diagnose different genera or families. My proposal of using the *matK* gene and the rapidly evolving genomic regions to effectively resolve evolutionary and systematic patterns in plants also went against the grain of current thought. It was a major fight to assert this concept. But the outcome was all worth it and quite rewarding to me and to my field of science.

If you have a concept you believe in and possess at hand *substantial evidence* to stand on, come out and propose it with all the support you have gathered. That is how we move science forward and avoid stagnation. And, that is how you raise your standing to be an effective leader in your field.

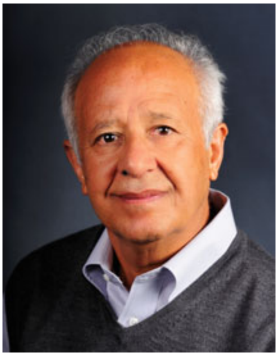
References

Hilu KW (1983) The role of single-gene mutations in the evolution of flowering plants. Evol Biol 16:97–128

Hilu KW, Borsch T, Müller K, Soltis DE, Soltis PS, Savolainen V, Chase MW, Powell M, Alice LA, Evans R, Sauquet H, Neinhuis C, Slotta TA, Rohwer JG, Campbell CS, Chatrou L (2003) Angiosperm phylogeny based on *matK* sequence information. Am J Bot 90:1758–1776

Hilu KW, Friend S, Vallanadu V, Brown AM, Hollingsworth LR IV, Bevan DR (2019) Molecular evolution of allergenic genes in the peanuts genus *Arachis*: Structural and functional implications. PLoS 1 14(11):e0222440. https://doi.org/10.1371/journal.pone.0222440

Lutzoni F, Nowak MD, Alfaro ME, Reeb V, Miadlikowska J, Krug M, Arnold AE, Lewis L, Swofford D, Hibbett D, Hilu K, James TY, Quandt D, Magallón S (2018) Contemporaneous radiations of fungi and plants linked to symbiosis. Nat Commun 9(5451)



Khidir W. Hilu Born 1946 in Baghdad, Iraq. Received BS and MS degrees of Botany in 1966 and 1971, respectively, from the University of Baghdad. Awarded doctoral degree in 1976 from the University of Illinois, U.S.A. Joined Virginia Tech in 1982, became a full professor and remained until retirement in 2017. Supervised and mentored 24 graduate students, ~70 bachelor degree students, and 9 postdoctoral fellows, both US and international. Received numerous teaching and research awards. Research emphasized land plant systematics/evolution with focus on gene choices in phylogenetics, crop genetic resources and biodiversity, and gene evolution using a variety of tools including molecular and bioinformatic methods. Organized national and international symposia and involved in international research collaborations, including Fulbright, FAO and USAID. Professor Emeritus.