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Dear Search Committee,

In the twelve years I've been a professor at University of Chicago, I don't believe we've had any finer student in evolutionary biology than Zhenglong Gu. This is a very tall statement because our University has three graduate programs in evolutionary biology, each of which is among the most competitive in the country to gain admittance. Zhenglong was a student in the Department of Ecology and Evolution, and I served as a member of his Ph.D. thesis committee. His office was down the hall from mine, and so we often discussed his research and other more general issues in evolutionary biology. He also served as a teaching assistant in my course, Fundamentals of Molecular Evolution. So, I am very well acquainted with Zhenglong's work and ability.

Zhenglong was an undergraduate at Peking University, the most prestigious University in China. Our Department makes every effort to accept as many of the most talented foreign students as we can financially afford. There is strong interest in evolutionary biology among Chinese students, and because this field is relatively weak in China, many of the best apply to our graduate programs. Zhenglong is one among several remarkable Chinese students we have had in our program. Zhenglong is unusually outgoing and talkative, and his command of the English language is fabulous. He is very well trained in biology, mathematics and computer science, and this combination of training made him especially well suited as a student of Dr. Wen-Hsiung Li.

Zhenglong entered Dr. Li's lab just as he was making a transition into whole-genome analysis. Through a combination of just plain hard work (Zhenglong once explained to me that he was willing to work harder than anyone else in Wen-Hsiung's lab to ensure good productivity and success), native intelligence, and background training, Zhenglong was perhaps the most valuable and productive student of Wen-Hsiung's, and he produced the most important papers to come out of his lab in the past five years. This alone speaks volumes about Zhenglong's ability, since Wen-Hsiung attracts top talent, and he has a very large lab (of approximately 20 graduate students and postdocs).

Zhengong's research centers on the evolution of genome structure, and in particular the evolution of gene duplication. The availability of genome sequences, genome-wide gene expression microarray data, and systematic genetic analysis of gene knockouts, has

allowed him to analyze gene duplication in entirely novel ways, and through careful analyses he has made some beautiful and important discoveries. I will refrain from describing these discoveries and explaining their significance, as I'm sure this will be done by Dr. Li in his recommendation letter. Rather, I'd like to describe the importance of his research in more general terms. Evolutionary biology has always had two competing research traditions, one operating on a macroevolutionary scale and one operating on a microevolutionary scale. In many instances, these two research traditions have ignored one another, and when they have come in contact, they often clashed. This is also true at the molecular level where, for example, systematists and population geneticists have studied the very same genes to entirely different ends, and often ignore one another's findings. Similarly, whereas the bread and butter of molecular evolution is the description and analysis of multi-gene family evolution, there are also a small number of population geneticists whose interest is the evolutionary dynamics governing the gene duplication process and the origin of novel gene form and function. Can there be any common ground?

Whole genome analysis, I would like to argue, has until very recently belonged entirely in the macroevolutionary (comparative analysis) camp. Part of the reason, to be sure, is that many of us who are firmly planted in the population genetics tradition have failed to realize that genome data can speak to issues related to understanding forces governing microevolutionary processes. I for one always thought that compositional features of genomes, things like base composition, the arrangement of genes along chromosomes, the distribution of introns and their lengths, etc., could best be understood as historical artifacts, as vestiges of ancient events. This view, I now realize, is entirely incorrect, and Zhenglong has had a large part in pointing out flaws in my thinking on this subject. I now recognize that genome data, in its many forms and guises, provides exquisitely detailed information about forces governing the evolutionary process. One simply needs to know what questions to ask, and how to ask them using genomic data.

Perhaps it should come as no surprise that a young scientist, Zhenglong in particular, is breaking down the barriers between the two research traditions. Of all the people in Wen-Hsiung's lab, he is the one who is most interested in formulating questions about evolutionary process using genome data. His creative analyses of yeast microarray data and null mutation phenotypes serve as wonderful examples of how one can translate large-scale genome data to answer questions about evolutionary process.

Zhenglong, and only a few others, are establishing this new standard for evolutionary research. Prerequisites include thorough training in population genetics, molecular evolution and functional molecular genetics, and equally good training in mathematics, statistics, computer science, and computational biology. More recently, as a postdoc, he has gained experimental skills, choosing to work on wild and domesticated strains of yeast. Here he has also made interesting and novel discoveries about recent evolutionary pressures in the domesticated strains, again combining whole genome analysis to address questions about microevolutionary dynamics.

I don't know of anyone at this early stage in career development who has acquired such a broad skill set, and who has put it to use as productively as Zhenglong. It is for this that I confidently recommend him to you.

Sincerely yours,

A handwritten signature in black ink, appearing to read 'MK' followed by a stylized flourish.

Martin Kreitman
Professor