Book Reviews

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Genetic, Linguistic and Archaeological Perspectives on Human Diversity in Southeast Asia. Edited by Li Jin, Mark Seielstad, and Chunjie Xiao. River Edge, NJ: World Scientific Publishing Co., 2001. Pp. 172. $58.

Genetic, Linguistic and Archaeological Perspectives on Human Diversity in Southeast Asia is the result of a collaborative effort to stimulate interaction between scientists from different disciplines who share a common interest: the role of Southeast Asia in the history of modern humans. The book furnishes a number of papers summarizing the major lines of research in the region, which were presented at an international conference at the University of Yunnan (China) in June 2000. This volume consists of 11 separate contributions organized into four parts: "Prehistory of Human Populations: Archaeological, Linguistic and Paleontological Perspectives," "The Peopling of Southeast Asia," "The Peopling of East Asia," and "The Peopling of Oceania."

The book begins with a first part, organized into three different chapters, that covers a wide range of nongenetic perspectives on the origins of East and Southeast Asian populations. The first chapter is an excellent and concise tutorial in archaeology and provides a reasonable introductory framework in both the archaeology and linguistics of the region for newcomers to the field. This chapter first discusses the entry of modern humans in Southeast Asia and raises the interesting question of possible cohabitation on mainland Southeast Asia between *Homo erectus* and ancestral hunter-gatherer populations of *Homo sapiens*. Then, it moves to the possibility of an agriculturally driven demic expansion of northern populations, possibly associated with rice cultivation, into Southeast Asia. Paleoclimatical and archaeological evidence points to the Yangzi Valley region as the geographic origin of the crucial transition from hunting/gathering to farming lifestyles. It is interesting that the authors highlight the need for genetic studies in surviving groups of Negrito hunter/gatherers, such as Andaman Islanders. On the basis of craniometry and dental morphology, some authors have noted parallels between this group and sub-Saharan Africans. It is unfortunate that publication of genetic data from this group is still pending. The chapter by William Yang on "Human Diversity and Language Diversity" provides an overview of world linguistic classifications, comments on possible pitfalls of genetic-linguistic comparisons due to the different time-depths of these approaches, and, finally, focuses on the split of the Sino-Tibetan language family. This chapter is a model to be followed of how a very descriptive section, often boring to read, can be clear, comprehensible, and pleasant reading. The last chapter of this section describes the archaeological findings of excavations in two sites (Nong Dor and Khok Pahnom Di), occupied by hunter/gatherer societies, in Central Thailand.

I believe that the lack of a chapter presenting the paleoenvironmental data concerning changing sea levels is unfortunate in the introductory part of the book. It is known that sea levels have fluctuated in the past 100,000 years and that, ~65,000 years ago, sea level was close to 80 m below current sea level (see Bard et al. [1990] Nature 346:456–458). Undoubtedly, referring to these data in the context of the colonization of Australia and the Pacific Islands would have been alluring.

The four contributions in Part II, "The Peopling of Southeast Asia," provide interesting genetic data on populations from mainland Southeast Asia. This part begins with a chapter, entitled "The Case for an African Rather than an Asian Origin of the Human Y-Chromosome YAP Insertion," that approaches a rather controversial issue hotly debated in recent years. The phylogeographic distribution of the YAP element, an *Alu* insertion of the Y-chromosome, together with some associated mutations, was used to postulate a new modern prehistorical migration of modern humans, the "Back to Africa" hypothesis. According to this hypothesis, a recent migration of modern humans would have brought a substantial set of Asian Y-chromosomes to Africa. Underhill and Roseman give a general overview of the current Y-chromosomal phylogeny and also discuss in detail the phylogeography of YAP$^+$ lineages, re-evaluating the geographic origin of the *Alu* insertion. The phylogenetic position of the marker M174, undiscovered at the time of the proposed "Back to Africa" hypothesis, precludes an exact geographic localization of the YAP element and, consequently, weakens considerably the "Back to Africa" scenario. By integrating independent genetic and paleoanthropological data, the authors conclude that an African origin of this mutation is the most parsimonious explanation. Although I basically agree with the authors' conclusions, the geographic origin of the *Alu* insertion and its demographic implications remain an open question until new mutations can geographically root this molecular event. In the contribution of Su et al. on the "Genetic History of Ethnic Populations in Southwestern China," we encounter Y-chromosome and mtDNA data on 13 populations from the Yunnan province that belong to different language families. The authors present a remarkable Y-chromosome analysis of these populations and conclude that their genetic profile is consistent with the postulated three major ancient population lineages that peopled this region at different times. In contrast with the Y-chromosome analysis, the mtDNA data seems somewhat meager to me and lacks sufficient resolution to reach any conclusions. In this context, the paper by Yao et al. (see [2002]

Am J Hum Genet 70:635–651), published in the March issue of the *Journal,* is an excellent example of a well-resolved phylogeographic analysis of Han Chinese mtDNAs. The integration of Yao's Han data with an extended mtDNA data set from the different ethnic groups inhabiting the Yunnan province certainly would have given further insights into the maternal history and peopling of Yunnan.

The chapter by Srikummool et al. explores a fairly appealing issue: tracing sexually asymmetrical events associated with different cultural practices in males and females, such as differing rules of postmarital residence. By analyzing Y-chromosome variation in different Thai populations, the authors observe a higher Y-chromosome diversity within the Karen population, which is predominantly uxorilocal (i.e., the women stay in their birthplace and the men move), than in the neighboring patrilocal populations (where women move into the natal households of their husbands). This is consistent with a higher male gene flow in uxorilocal populations and suggests higher male migration rate. I am concerned, as well as were the authors, by the lack of mtDNA data that could confirm satisfactorily the role of sex-specific migrations in influencing the patterns of genetic variation. I regret that, because of different publication times, the authors do not contrast their data with those of Oota et al. (see [2001] Nat Genet 29:20–21). The latter, through a detailed comparison of Y-chromosome and mtDNA variation, also addresses the question of different migration rates caused by different male-to-female cultural practices in northern Thailand and demonstrates that mtDNA and Y-chromosome variation is correlated with matrilocal versus patrilocal residence. This section finishes with a chapter that presents data on five polymorphic protein-coding loci from 16 ethnic groups living in Malaysia and Southeast Asia. To understand better human migrations to Southeast Asia associated with the development of a farming economy, the author makes an interesting comparison with genetic data obtained from swamp buffalo populations in the region.

In Part III, two contributions discuss the current genetic information concerning the peopling of East Asia. The first chapter is primarily focused on the Chinese Genome Diversity Project and its achievements, such as the National Cell Line Repository. Also, a population study based on 30 autosomal microsatellite markers in 28 Chinese populations belonging to six different language families is presented, and the possible distinction between southern and northern Chinese populations is discussed. The chapter by Su and Jin provides a very detailed Y-chromosome analysis in a large set of East Asian populations and examines their genetic variation in the context of the first arrivals of modern humans to East Asia. In the context of the "Out of Africa" model, the data presented support a recent African origin of East Asian populations. In a more recent time scale, the authors sustain, on the basis of the Y-chromosome diversity, a South Asian origin of East Asians and a subsequent diaspora toward the north. It is to be noted that the authors revisit the contentious discrepancy between genetic and archaeological data observed in Asia. Indeed, allelic genealogies tend to support the "Out of Africa" model. Conversely, archaeological evidence argues in favor of a continuous evolutionary chain to connect *Homo erectus* and *Homo sapiens* in China, lending support to the "Trellis" model, which propounds an independent origin of modern humans in East Asia. Even though one would like to see this section expanded and more critically examined, Su and Jin are to be applauded for their well-written and -summarized discussion about this exciting issue.

The last section of this volume finishes with two contributions that delve into the peopling of Oceania. Although presented in separate chapters, both the two last contributions of the volume discuss and contrast the different models proposed to explain the peopling of the Pacific. The two most-known models are (1) the "Express Train," which posits an intrusive colonization of the Pacific by a rapid eastward migration of farmers from Southern China/Taiwan, and (2) the "Entangled Bank," which views the colonization of the Pacific as a continuous gene flow among the different Pacific populations. Stephen Oppenheimer has proposed a more consensual intermediate scenario, termed "Eden in the East," that defends a parallel expansion of two different sets of competing populations and, interestingly, incorporates paleoenvironmental data. In summary, mtDNA data are mostly consistent with an Asian origin of most Micronesians and Polynesians, as are linguistic and archaeological evidence; however, the expectations of a Taiwanese origin of these populations, as proposed by the "Express Train" model, are not generally observed in the genetic patterns. Conversely, the Y-chromosome patterns seem to suggest substantial male gene flow among Pacific populations, giving little support to the agriculturally driven expansion initiated in southeast China and/or Taiwan. The conclusions of both chapters stress the necessity of further studies to better understand the peopling processes of this region. After the Yunnan conference, several papers have revisited this subject, and the general view is that Micronesian and Polynesian Y-chromosomes appear to have originated from different source populations within Melanesia or Eastern Indonesia. (See, e.g., Kayser et al. [2000] Curr Biol 10:1237–1246; Hurles et al. [2002] Genetics 160:289–303.) However, Kayser et al. found a number of chromosomes among Polynesians that can be traced directly back to mainland Asia. This observation led to the proposal of a new model, termed the "Slow-boat" model, positing that Polynesian ancestors did originate from mainland Asia/Taiwan, but did not move rapidly, as the "Express Train" states, through Melanesia. Rather, they effectively admixed with Melanesians en route to the colonization of the Pacific. It seems, therefore, that a consensus is being achieved and that sex-dependent migrations, unmasked by the analysis of the Y-chromosome and mtDNA, also may have played an important role in the colonization of the Pacific.

The criticisms about absent data in no way detract from a highly interesting book; rather, they highlight the difficulty of presenting an up-to-date description of such a fast-moving field. The volume provides a good snapshot of the state of knowledge of human diversity of Southeast Asian populations. Both geneticists unfamiliar with studies of Southeast Asian populations and archaeologists and linguists seeking a general genetic overview of the region will find very useful information in this book. The book is also a valuable example of a multidisciplinary approach (wedding genetics, archaeology, and linguistics) employed to better evaluate, and possibly distinguish between, the different hypotheses concerning human origins and movements. The authors are to be congratulated for bridging the dysfunctional gap between people from related but methodologically distinct disciplines. The use of population genetics in "Archaeogenetics" or "Anthropological Genetics" is not the sole application of this discipline. Establishing a formal population-genetics framework in molecular epidemiology and disease-predisposition studies is, without doubt, a challenging and highly profitable aspect of what sometimes is perceived as "just dissecting gene pools at a population level." The definition and comparison of present-day patterns of genetic variation not only offer unique insights for a deep study of human evolutionary history but also provide the necessary population-genetic backdrop that constitutes an important prerequisite for understanding the genetics of complex traits.

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RNA Binding Proteins: New Concepts in Gene Regulation. Edited by Kathryn Sandberg and Susan E. Mulroney. Norwell, MA: Kluwer Academic Publishers, 2002. Pp. 308. $165.

The editors compiled this book on the basis of the expanding interest in and understanding of post-transcriptional events that regulate mRNA stability, location, and translation. Their second stated purpose is to provide a book that not only can be used as an outline for teaching graduate students and young investigators but also contains enough information to be useful to the seasoned researcher. Having set this lofty goal, they recruited a group of authors to write chapters that included background information, data analysis, and study questions. The 17 resulting chapters were then grouped into three focus areas: translational control, mRNA metabolism, and hormonal and homeostatic regulation.

The first chapter adheres closely to the stated purpose outlined by the editors and allows anticipation that this pattern would be repeated in the subsequent chapters. That anticipation is quickly shattered, since the style and information provided vary significantly as one proceeds through the chapters. One gets the impression that there was a lack of editing, since there exists considerable redundancy both within and between chapters. If this book is to be a learning guide for the student, there needs to be a glossary or a more complete definition of terms. Some chapters assume an esoteric knowledge of the material presented, making them difficult to follow without a significant amount of background in the area. Unfortunately, there is misinformation in a few of the chapters.

The last chapter, authored by the editors, returns to the purpose of the book and looks much like Chapter I in style. It summarizes the recurring theme in all chapters: that mRNA stability and expression are controlled by linear nucleic acid sequence within the 5′ UTR, the coding region, and the 3′ UTR, as well as by the secondary structure of the molecule. Proteins that specifically bind to these regions are being characterized by standard methods, and most of the authors illustrate or describe these procedures in their chapters about their favorite mRNA. Cells from different tissues handle the mRNAs in a variety of ways, and the response can be affected by external stimuli.

The idea of study questions at the end of each chapter addresses the goal of using the text as a course outline. The problem, again, is the inconsistency of these questions. Some simply ask for regurgitation of information that was presented in the chapter, whereas others are thought provoking and encourage understanding of the experimental design and data interpretation. A course outline could come from the first and last chapters alone.

Initially, I was excited about the potential for this text and the reasons given for its writing. In the end, my reaction was disappointment for its falling far short of the expectation. Chapters were repetitious in describing methods. Part of the problem might be that we are still in the early stages of understanding mRNA synthesis and expression. One area omitted from these chapters was the advancing understanding of how other RNA species help in the regulation of mRNA production and use.

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