

# The 50th Anniversary Meeting of the Society for the Study of Evolution and the Annual Meeting of the Society for the Study of Evolution and the Society of Systematic Biologists

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A total of 648 contributions were divided between posters, symposia and oral presentations at this conjoint meeting of the two societies which covered a very large number of fields from population genetics to the relationship of evolution to present day conservation problems. The oral presentations were divided into 76 sessions whose titles ranged from Molecular Evolution to Geographic Variation and Hybrid Zones. The interest in Molecular Systematics was emphasized by the fact that 16 different sessions were devoted to this subject. Unlike many meetings only the title of the papers/posters are given in the program and there are no accompanying abstracts. This is perhaps a good thing as they cannot be quoted in any publication, as is often the case with abstracts of other meetings, and contributors are thus encouraged to publish their presentations as papers if they want them to be cited by other workers. The subject matter of the sessions was also extremely broad and there were papers on very many different groups of both animals and plants. In one session on Molecular Systematics, for example, there were contributions on annelid worms and growth hormone introns in Salmonid fish. This emphasized how similar technology is being used today for many taxonomically different animal and plant groups.

A highlight of the meeting was the lecture commemorating the 50th Anniversary of the Society for the Study of Evolution (SSE) which was given by one of its founder members, the world famous systematists and evolutionary biologist, Prof. Ernest Mayer. The title of his lecture was "Evolutionary Biology as a Discrete Biological Discipline" and Professor Myer must have broken many records in this lecture especially since he is now over 90 years old and is extremely lucid, as was evident by his replies to the questions.

In general it was possible to divide most of the contributions into those that dealt with the analyti-

cal methods used to determine the phylogeny and the relationships of organisms and those related to the evolution and classification of fossil and living organisms. Within these areas there was much discussion of the use of morphological and molecular characters. It was emphasized by many speakers that morphological characters would continue to be the prime method for identification for most groups since it is physically impossible to apply molecular techniques to all living matter. Thus morphology will continue to be the backbone of identification for the very large numbers of specimens that are collected and identified in the majority of the ecological studies presently being performed around the world. Participants presented both morphological and molecular studies on many different living organisms and numerous speakers drew attention to the danger of producing phylogenetic trees using molecular characters which may represent only a very small part of the whole genome or an insufficient number of the taxa.

Questions on taxonomic methodology were addressed by many speakers including Joe Felsenstein (University of Washington) who discussed comparative methods allowing for individual error. An important contribution was made by Gavin Naylor (Harvard University) which emphasized that a good classification based on molecular data does not necessarily depend on analyzing a vast number of base pairs but on choosing sequences whose function is known. He gave examples of this using actual sequence data and showed that in fact using very large numbers of base pairs distorted the correct classification. For example cytochrome sequence data is useful for determining differences at the species or subspecies level but does not produce reliable phylogenetic classifications because of its high mutation rate. This principle applies equally to morphological and molecular characters.

There were few papers on viruses and parasites

and they were presented as part of two separate mini-symposia devoted to Virus Evolution and the Phylogeny and Evolution of Disease Agents and their Vectors. There were eight half hour papers in the latter symposium and only one, by N.J. Besansky on the *Anopheles gambiae* complex, dealt with vector evolution and speciation. The other presentations in this session were on immuno-deficiency viruses, arboviruses, *Leishmania* and malarial parasites.

The SSE 50th Anniversary Awards and American Genetics Association Wilhelmine Key Lecture entitled "Sexual Selection: A Driver of Genetic Change in Hawaiian *Drosophila*" was given by Hampton Carson who based his talk on his own extensive studies. It highlighted how geographical isolation and ecological pressures over differ-

ent time scales relate to the number of species.

The meeting was closed by Alan Templeton who gave the presidential address of the SSE entitled "Genetic Architecture: Getting to the Heart of the Matter".

The general direction of the meeting emphasized that workers in very many groups are now converging within the work area of systematics and evolution. In some cases specialists in taxonomic methodology are using raw data to test theoretical assumptions while in others specialists in different groups are using more accepted methods to resolve problems of relationships between different taxa and the effect of ecological barriers. It is quite amazing that specialists from so many different fields are now being linked by phylogeny and taxonomy.