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“Genomic Impact of Eukaryotic Transposable Elements”, Pacific Grove, California February 6 –10, 2009

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This Special Issue of *Gene* – Evolutionary Genomics – is dedicated to the Symposium “Genomic Impact of Eukaryotic Transposable Elements”, which took place in Pacific Grove, California between February 6 and 10, 2009.

The international conference, devoted to genomic impact of transposable elements (TEs), was organized by the Genetic Information Research Institute and was accompanied by an informal workshop centered on emerging problems associated with classification and analysis of repetitive DNA. The 2009 Asilomar conference was a continuation of the 2006 meeting, which was initiated by the National Library of Medicine, a long-term supporter of Repbase. The format of both conferences was substantially shaped by the co-organizers of the 2006 conference and by the Repbase Scientific Advisory Board.

Over 140 scientists from around the world attended the conference, including several members of the National Academy of Sciences and of the National Academy Medicine. The historical perspective underlying the conference was highlighted by the presence of Roy Britten, who together with Eric Davidson envisioned the role of repetitive DNA in the evolution of gene regulation in the sixties. After decades of downplaying the importance of repetitive DNA, this seminal idea continues to inspire generations of researchers as illustrated by core presentations on cutting-edge research, many of which covered evolution of gene regulation and its relationship to TEs and repetitive DNA. The major issue that emerged during the workshop session was the need for standardized and efficient computer tools for classification of TEs. This issue is partially addressed in the current conference volume.

The non-coding DNA represents the largest fraction of eukaryotic genomes and its scientific exploration is only beginning. As the amounts of the eukaryotic sequence data continue to explode, a wide range of research expertise is needed to organize and interpret this “genomic dark matter” which includes a large fraction of repetitive DNA derived from TEs. Therefore, the major goal of the Asilomar conference series is to bring together experts on TEs with researchers representing different biological specialties, particularly those related to genome studies, and forge research collaborations. The interactions among participants were facilitated by the informal conference atmosphere and discussions lasting until late evening hours in front of over 60 posters as well as in the adjacent main conference hall and the courtyard. Judging from the post-conference feedback many fruitful collaborations were established.

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The short duration of the conference and the unpredictable February weather did not permit for many outdoor activities. Nevertheless, the conference participants enjoyed an evening visit to the Monterey Aquarium accompanied by a special dinner.

I would like to thank all the conference participants for their contributions to a successful meeting and all authors for their submissions to the special issue of *Gene*, as well as the reviewers, editors, and journal staff for their extraordinary effort to make this issue appear in a timely manner.