Preface

The early 1980s marked the beginning of a new era in animal genetics – an era to which most of us can directly relate. Riding on the excitement surrounding the availability of recombinant DNA technology and the development of the human gene map, animal geneticists around the world started taking subtle but decisive steps toward the development of gene maps in domesticated animals. Identification of syntenic and linkage groups in cattle, pig and horse were among the early key developments that provided stimulus and laid the foundations for future gene maps. Almost 20 years have passed since these initial steps were taken. During this period **animal genomics** has evolved in an unprecedented manner and is progressing in the true spirit of a “revolution” – the “genomics revolution”.

Organized genome analysis projects in cattle and pigs were initiated during the late 1980s. Since then, the number of domesticated species being analyzed has tremendously expanded. Today, genome programs are in place for almost all important domesticated animals. The objectives are simple and perhaps age-old: to improve production, reproduction, disease resistance, diagnostics and health care. However, the tools to reach these goals and the expected outcome have changed. Exciting, yet unbelievable, is the fact that for some species like chicken, cattle and dog, whole genome sequencing is either in progress

or is close to finishing. For others like pig, cat etc., blue prints for sequencing are in place. Five years ago, all this was unimaginable. No doubt, these are exciting times in animal genomics.

In the fall of 2001, the editorial board meeting of *Cytogenetic and Genome Research* discussed possibilities of several new issues of the journal that could focus on emerging areas in genome research. I was thrilled that **animal genomics** was recognized as one of the rapidly evolving research areas. However, I was not so thrilled (let me be honest!) when the burden of all this fell on my shoulders – not because this was a challenging task, but because there are stalwarts who could do it better. With no escape, I have simply acted as a junction-point to channel your research and thoughts.

The joy for me in preparing this volume has been the incredible and relentless enthusiasm from the contributors, remarkable turn-around time by the reviewers and constant encouragement from Michael Schmid, the chief editor. Together, we all have a wonderful tribute to **20 years of animal genome research**.

Enjoy reading it!

Bhanu Chowdhary
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