



As we conclude the preparation of this special issue of *Genetics and Molecular Biology* it seems appropriate, first of all, to recall the comments of our colleague Andy Simpson who said when referring to genome sequencing: *Sequencing networks (...) generally foster a collaborative spirit* (*Nature Rev Genetics* 2:979-983, 2001). In fact, the present enterprise started as a nationwide network of 25 research laboratories, the Brazilian Genome Consortium (BRGENE), established to sequence the genome of *Chromobacterium violaceum*. This initial effort induced the organization of regional networks, such as the Southern Brazil (Genesul) subsequently set up to study pathogenic and non-pathogenic strains of *Mycoplasma hyopneumoniae*. Now, we have come full circle back to a national network undertaking the studies presented here.

This is also an appropriate moment to point out that this work is a demonstration that we have reached a critical mass able to push forward the field of bioinformatics and computational biology in our country.

The coverage presented here, far from being exhaustive, is limited to selected important aspects of *Mycoplasma* physiopathology, which reflect the particular interests of the individual groups. The data generated by the sequencing effort are being explored in functional studies aiming at a better understanding of *M. hyopneumoniae* and *M. synoviae* biologies, to facilitate the development of new strategies for pathogen detection and prophylaxis. Without doubt, one can find here a truly collaborative spirit.

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This work is dedicated to the memory of our colleague Laurimar Fiorentin from CNPSA-Embrapa.

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