

## WHOLE-GENOME DUPLICATIONS IN SOUTH AMERICAN DESERT RODENTS (OCTODONTIDAE)

MILTON H. GALLARDO<sup>1</sup>, G. KAUSEL<sup>2</sup>, A. JIMÉNEZ<sup>2</sup>, C. BACQUET<sup>2</sup>, C. GONZÁLEZ<sup>2</sup>, J. FIGUEROA<sup>2</sup>, N. KÖHLER<sup>2</sup>, R. OJEDA<sup>3</sup>

<sup>1</sup>Instituto de Ecología y Evolución, Universidad Austral de Chile, Casilla 567, Valdivia, Chile

<sup>2</sup>Instituto de Bioquímica, Universidad Austral de Chile, Casilla 567, Valdivia, Chile

<sup>3</sup>IADIZA-CRICYT, Casilla de Correo 507, 5500 Mendoza, Argentina

The discovery of tetraploidy in the red viscacha rat, *Tympanoctomys barrerae* ( $4n=102$ ) has emphasized the evolutionary role of genome duplication in mammals. The tetraploid status of this species is corroborated here by in situ PCR and Southern blot analysis of a single-copy gene. The species meiotic configuration strongly suggests a hybrid derivation. To investigate the origin of *T. barrerae* further, the recently described *Pipanacoctomys aureus* was studied.

This 92-chromosome species also has a duplicated genome size, redundant gene copy number and diploid-like meiotic pairing, consistent with an event of allotetraploidization. Phylogenetic analysis of mitochondrial sequences indicates sister-group relationships between these two tetraploid rodents. The new karyotypic data and the phylogenetic relationships suggest the participation of the ancestral lineages of *Octomys mimax* in the genesis of *P. aureus*. The high overall DNA similarity and shared band homology revealed by genomic Southern hybridization as well as matching chromosome numbers between *O. mimax* and the descendant tetraploid species support the notion of introgressive hybridization between these taxa.