Heredity (2012) 108, 4–16

www.nature.com/hdy

Heredity

REVIEW

Chromosomal evolution in Rodentia

SA Romanenko, PL Perelman, VA Trifonov and AS Graphodatsky

Rodentia is the most species-rich mammalian order and includes several important laboratory model species. The amount of new information on karyotypic and phylogenetic relations within and among rodent taxa is rapidly increasing, but a synthesis of these data is currently lacking. Here, we have integrated information drawn from conventional banding studies, recent comparative painting investigations and molecular phylogenetic reconstructions of different rodent taxa. This permitted a revision of several ancestral karyotypic reconstructions, and a more accurate depiction of rodent chromosomal evolution.
Heredity (2012) **108,** 4–16; doi:10.1038/hdy.2011.110; published online 16 November 2011

Keywords: rodentia; rodents; comparative cytogenetics; chromosomal evolution

INTRODUCTION

Rodents have a cosmopolitan distribution with range extensions often associated with human movement. After their divergence from a common ancestor with Lagomorpha ~65 My ago, rodents have undergone an impressive radiation leading to the high number of species observed today (Huchon *et al*., 2002; Benton and Donoghue, 2007). Rodents currently represent the most abundant mammalian order—they comprise about 42% of all living mammals, and include 2277 defined species (Carleton and Musser, 2005). Some rodents are used extensively in biomedical research and this has stimulated interest in the study of this group.

Modern taxonomy recognizes 5 suborders (Anomaluromorpha, Castorimorpha, Hystricomorpha, Myomorpha and Sciuromorpha) and 33 families. Sciuromorpha (including sciurids, mountain beaver and dormice), Myomorpha (muroids, jerboas and jumping mice) and Hystricomorpha (gundis, porcupines and caviamorphs) have all received good support as monophyletic taxa based on morphological and molecular data analysis. The evidence for the recognition of Castorimorpha and Anomaluromorpha is less persuasive. The degree of karyotype scrutiny varies within suborders but support nonetheless exists for the division of Rodentia into five subordinal groups.

KARYOTYPIC FEATURES OF RODENTS

Karyotypes of rodents were initially investigated by conventional cytogenetics that provided information on chromosome number and morphology. Interesting observations included the extreme variability of diploid chromosome number (from 2n=10 to 2n=102) and the presence of B-chromosomes in some species (Supplement Data 1). Moreover, before the development of chromosome banding, Matthey (1972) studied numerous rodent groups and described various cases of chromosomal polymorphisms and unusual sex chromosome systems. He led much of the thinking on the occurrence of unequal rates of chromosome evolution in different rodent groups, the existence of ancestral karyotypes, and the direction of karyotypic evolution.

These ideas were subsequently supported to a large extent by comparative G-, Q-, R-banding studies that revealed chromosomes/chromosomal regions with similar banding pattern that led authors to assume homology by descent. These data also showed high levels of chromosomal conservation in certain taxa. For instance, the sciurids were proposed to have conserved karyotypes similar to the hypothesized ancestral karyotype of Rodentia (Petit *et al*., 1984; Viegas-Péquignot *et al*., 1986). The karyotypes of castorimorph and anomaluromorph rodents were also considered conserved (Ward *et al*., 1991). In contrast, there was evidence to suggest that the karyotypes of myomorphs are highly reorganized (Graphodatsky, 1989). Additionally, significant heterochromatic variation (Patton and Sherwood, 1982; Graphodatsky, 1989; Svartman *et al*., 2005 among others) was noted, as were fascinating sex determining systems (for example, Fredga, 1983) and the frequent presence B-chromosomes (Trifonov *et al*., 2002).

NEW INSIGHTS INTO KARYOTYPIC EVOLUTION IN DIFFERENT RODENT CLADES

Cross-species chromosome painting is currently the method of choice for comparative cytogenetic studies in rodents. Labeled whole chromosome probes are used to highlight the regions of homology by fluorescent *in situ* hybridization. The first successful chromosome painting was reported by Scherthan *et al*. However, only a few human probes were localized on mouse chromosomes and it is likely that the highly rearranged nature of the mouse genome contributed to the limited success in chromosome painting between mouse and human (Ferguson-Smith *et al*., 1998). More detailed comparison between human and mouse were facilitated by the availability of whole genome sequences for both species (Guigo *et al*., 2003). The first genome-wide comparison between two rodent genomes (*Mus musculus* and *Rattus norvegicus*) by comparative chromosome painting was made in 1999 resulting in the almost simultaneous publication of papers by Grutzner *et al*. (1999), Guilly *et al*. (1999) and Stanyon *et al*. (1999). Since then, over 100 rodent genomes from all major taxa have been analyzed resulting in the availability of comparative chromosomal maps and a more detailed analysis of karyotypic evolution in several of the major taxonomic groups (Table 1, Supplement Data 2).

Institute of Molecular and Cellular Biology, SB RAS, Novosibirsk, Russia
Correspondence: Dr SA Romanenko, Institute of Molecular and Cellular Biology, SB RAS, Lavrentjev Avenue, 10, Novosibirsk 630090, Russia.
E-mail: rosa@mcb.nsc.ru
Received 31 May 2011; revised 6 October 2011; accepted 7 October 2011; published online 16 November 2011

Table 1 Chromosome painting of Rodentia

Suborder	*Family/ subfamily*	*Species*	*Set of painting probes*	*Number of autosomal conserved segments revealed. Comments*	*Reference*
Sciuromorpha	Gliridae	*Eliomys melanurus*	*Homo sapiens*	45	Sannier *et al.*, 2011
		Eliomys munbyanus	*Homo sapiens*	Paints HSA 2, 5, 6, 14, 15, 18 were hybridized	Sannier *et al.*, 2011
		Eliomys quercinus	*Homo sapiens*	Paints HSA 1, 2, 4, 12, 15, 20, 22 were hybridized	Sannier *et al.*, 2011
	Sciuridae	*Menetes berdmorei*	*Homo sapiens*	⩾34	Richard *et al.*, 2003
		Sciurus carolinensis	*Homo sapiens*	38	Stanyon *et al.*, 2003; Li *et al.*, 2004
		Petaurista albiventer	*Homo sapiens*	36	Li *et al.*, 2004
		Tamias sibiricus	*Homo sapiens*	35	Li *et al.*, 2004
		Callosciurus erythraerus	*Sciurus carolinensis*	21	Li *et al.*, 2004
		Petaurista albiventer	*Sciurus carolinensis*	21	Li *et al.*, 2004
		Tamias sibiricus	*Sciurus carolinensis*	21	Li *et al.*, 2004
		Marmota himalayana	*Sciurus carolinensis*	21	Li *et al.*, 2006a
		Xerus cf. rythropus	*Sciurus carolinensis*	19	Li *et al.*, 2006a
		Marmota himalayana	*Homo sapiens*	35	Li *et al.*, 2006a
		Xerus cf. rythropus	*Homo sapiens*	35	Li *et al.*, 2006a
		Tamias sibiricus	*Homo sapiens*	36	Romanenko *et al.*, 2010
		Marmota baibacina	*Tamias sibiricus*	21	Beklemisheva *et al.*, 2011
		Marmota kastschenkovii	*Tamias sibiricus*	21	Beklemisheva *et al.*, 2011
		Spermophilus erythrogenys	*Tamias sibiricus*	23	Beklemisheva *et al.*, 2011
		Spermophilus major	*Tamias sibiricus*	23	Beklemisheva *et al.*, 2011
		Spermophilus suslicus	*Tamias sibiricus*	23	Beklemisheva *et al.*, 2011
		Spermophilus undulatus	*Tamias sibiricus*	23	Beklemisheva *et al.*, 2011
		Sciurus vulgaris	*Tamias sibiricus*	20	Beklemisheva *et al.*, 2011
		Tamias sibiricus	*Homo sapiens*	36	Beklemisheva *et al.*, 2011
		Tamias sibiricus	*Castor fiber*	40	Beklemisheva *et al.*, 2011
Castorimorpha		*Castor fiber*	*Homo sapiens*	43	Graphodatsky *et al.*, 2008
		Castor fiber	*Homo sapiens*	44	Beklemisheva *et al.*, 2011
		Castor fiber	*Tamias sibiricus*	42	Beklemisheva *et al.*, 2011
Anomaluromorpha		*Pedetes capensis*	*Homo sapiens*	46	Graphodatsky *et al.*, 2008
Hystricomorpha	Caviidae	*Cavia porcellus*	*Homo sapiens*	⩾71	Our unpublished data
		Cavia tschudii	*Cavia porcellus*	30	Our unpublished data
		Cavia tschudii	*Homo sapiens*	⩾71	Our unpublished data
	Bathyergidae	*Cryptomys (Fukomys) mechowi*	*Heterocephalus glaber*	43	Deuve *et al.*, 2006
		Heliophobius argenteocinereus	*Heterocephalus glaber*	45	Deuve *et al.*, 2008
		Bathyergus janetta	*Heterocephalus glaber*	43	Deuve *et al.*, 2008
		Bathyergus siullus	*Heterocephalus glaber*	43	Deuve *et al.*, 2008
		Georychus capensis	*Heterocephalus glaber*	43	Deuve *et al.*, 2008
		Fukomys damarensis	*Heterocephalus glaber*	47	Deuve *et al.*, 2008
		Fukomys darlingi	*Heterocephalus glaber*	45	Deuve *et al.*, 2008
	Octodontidae	*Tympanoctomys barrerae*	*Octodon degus*	Some paints gave satisfactorily results of hybridization only	Svartman *et al.*, 2005
	Thryonomyidae	*Thryonomys swinderianus*	*Heterocephalus glaber*	33	Deuve *et al.*, 2008
Myomorpha	Dipodidae	*Sicista betulina*	*Homo sapiens*	62	Graphodatsky *et al.*, 2008
	Muridae: Murinae	*Mus musculus*	*Homo sapiens*	Only chromosome-specific probes 16, 17 and X were used	Scherthan *et al.*, 1994
		Rattus norvegicus	*Mus musculus*	Only six chromosome-specific probes were used	Scalzi and Hozier, 1998
		Mus musculus	*Rattus norvegicus*	Only 10 chromosome-specific probes were used	Guilly *et al.*, 1999
		Rattus norvegicus	*Mus musculus*	37	Guilly *et al.*, 1999
		Rattus norvegicus	*Mus musculus*	31	Grutzner *et al.*, 1999
		Rattus norvegicus	*Mus musculus*	35	Stanyon *et al.*, 1999
		Mus musculus	*Rattus norvegicus*	35	Stanyon *et al.*, 1999
		Mus musculus	*Cricetulus griseus*	38	Yang *et al.*, 2000
		Rattus norvegicus	*Mus musculus*	48	Helou *et al.*, 2001

Table 1 (Continued)

Suborder	*Family/ subfamily*	*Species*	*Set of painting probes*	*Number of autosomal conserved segments revealed. Comments*	*Reference*
		Rattus norvegicus	*Mus musculus*	64 (combined Zoo-FISH, FISH and RH data)	Nilsson *et al.*, 2001
		Rattus rattus rattus	*Mus musculus*	36	Cavagna *et al.*, 2002
		Rattus rattus rattus	*Rattus norvegicus*	20	Cavagna *et al.*, 2002
		Rattus rattus frugivorous	*Mus musculus*	37	Cavagna *et al.*, 2002
		Rattus rattus frugivorous	*Rattus norvegicus*	20	Cavagna *et al.*, 2002
		Mus platythrix	*Mus musculus*	26	Matsubara *et al.*, 2003
		Rhabdomys pumilio	*Mus musculus*	39	Rambau and Robinson, 2003
		Apodemus sylvaticus	*Mus musculus*	37	Stanyon *et al.*, 2004
		Mus musculus	*Apodemus sylvaticus*	There was no data about the number of autosomal conserved segments revealed	Stanyon *et al.*, 2004
		Apodemus agrarius	*Mus musculus*	36	Matsubara *et al.*, 2004
		Apodemus argenteus	*Mus musculus*	36	Matsubara *et al.*, 2004
		Apodemus gurkha	*Mus musculus*	36	Matsubara *et al.*, 2004
		Apodemus peninsulae	*Mus musculus*	36	Matsubara *et al.*, 2004
		Apodemus semotus	*Mus musculus*	36	Matsubara *et al.*, 2004
		Apodemus speciosus	*Mus musculus*	37	Matsubara *et al.*, 2004
		Apodemus sylvaticus	*Mus musculus*	37	Matsubara *et al.*, 2004
		Mus musculus	*Mesocricetus auratus*	43	Romanenko *et al.*, 2006
		Nannomys minutoides	*Mus musculus*	26	Veyrunes *et al.*, 2006
		Mus musculus	*Nannomys minutoides*	25	Veyrunes *et al.*, 2006
		Coelomys pahari	*Nannomys minutoides*	29	Veyrunes *et al.*, 2006
		Coelomys pahari	*Mus musculus*	34	Veyrunes *et al.*, 2006
		Nannomys mattheyi	*Mus musculus*	26	Veyrunes *et al.*, 2006
		Tokudaia tokunoshimensis	*Mus musculus*	32	Nakamura *et al.*, 2007
		Tokudaia osimensis	*Mus musculus*	33	Nakamura *et al.*, 2007
		Micromys minutus	*Mus musculus*	49	Nakamura *et al.*, 2007
		Millardia meltada	*Mus musculus*	37	Nakamura *et al.*, 2007
		Mus musculus	*Peromyscus maniculatus*	38	Mlynarski *et al.*, 2008
		Apodemus peninsulae	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
		Rattus norvegicus	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
		Rattus norvegicus	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
		Maxomys surifer	*Rattus norvegicus*	25	Badenhorst *et al.*, 2011
		Rattus exulans	*Rattus norvegicus*	20	Badenhorst *et al.*, 2011
		Rattus exulans	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
		Rattus tanezumi	*Rattus norvegicus*	20	Badenhorst *et al.*, 2011
		Rattus tanezumi	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
		Rattus losea	*Rattus norvegicus*	20	Badenhorst *et al.*, 2011
		Rattus losea	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
		Bandicota savilei	*Rattus norvegicus*	21	Badenhorst *et al.*, 2011
		Bandicota savilei	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
		Berylmys berdmorei	*Rattus norvegicus*	20	Badenhorst *et al.*, 2011
		Berylmys berdmorei	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
		Berylmys bowersi	*Rattus norvegicus*	20	Badenhorst *et al.*, 2011
		Berylmys bowersi	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
		Leopoldamys edwardsi	*Rattus norvegicus*	20	Badenhorst *et al.*, 2011
		Leopoldamys edwardsi	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
		Niviventer fuvescens	*Rattus norvegicus*	22	Badenhorst *et al.*, 2011
		Niviventer fuvescens	*Maxomys surifer*	25	Badenhorst *et al.*, 2011
	Muridae: Deomyinae	*Acomys dimidiatus*	*Mus musculus*	39	Nakamura *et al.*, 2007
	Muridae: Otomyinae	*Otomys irroratus*	*Mus musculus*	42	Engelbrecht *et al.*, 2006
	Calomyscidae: Calomyscinae	*Calomyscus* sp.	*Mesocricetus auratus*	36	Romanenko *et al.*, 2007a

Table 1 (Continued)

Suborder	*Family/ subfamily*	*Species*	*Set of painting probes*	*Number of autosomal conserved segments revealed. Comments*	*Reference*
	Cricetidae: Cricetinae	*Allocricetulus eversmanni*	*Mesocricetus auratus*	26	Romanenko *et al.*, 2007a
		Cricetulus griseus	*Mus musculus*	47	Yang *et al.*, 2000
		Cricetulus griseus	*Mesocricetus auratus*	25	Romanenko *et al.*, 2006
		Mesocricetus auratus	*Cricetulus griseus*	23	Romanenko *et al.*, 2006
		Mesocricetus auratus	*Mus musculus*	43	Romanenko *et al.*, 2006
		Cricetulus barabensis	*Mesocricetus auratus*	25	Romanenko *et al.*, 2007a
		Cricetulus longicaudatus	*Mesocricetus auratus*	25	Romanenko *et al.*, 2007a
		Cricetulus migratorius	*Mesocricetus auratus*	25	Romanenko *et al.*, 2007a
		Cticetus cricetus	*Mesocricetus auratus*	25	Romanenko *et al.*, 2007a
		Mesocricetus brandtii	*Mesocricetus auratus*	23	Romanenko *et al.*, 2007a
		Mesocricetus raddei	*Mesocricetus auratus*	21	Romanenko *et al.*, 2007a
		Phodopus campbelli	*Mesocricetus auratus*	34	Romanenko *et al.*, 2007a
		Phodopus roborowskii	*Mesocricetus auratus*	35	Romanenko *et al.*, 2007a
		Phodopus sungorus	*Mesocricetus auratus*	34	Romanenko *et al.*, 2007a
		Tscherskia triton	*Mesocricetus auratus*	30	Romanenko *et al.*, 2007a
		Mesocricetus auratus	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
		Cricetulus griseus	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
		Tscherskia triton	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
	Cricetidae: Neotominae	*Peromyscus maniculatus*	*Mus musculus*	Only chromosome-specific probes 3, 7 and 9 were used	Dawson *et al.*, 1999
		Peromyscus maniculatus	*Mus musculus*	39	Mlynarski *et al.*, 2008
		Peromyscus eremicus	*Mesocricetus auratus*	31	Romanenko *et al.*, 2007a
	Cricetidae: Arvicolinae	*Eothenomys militus*	*Eothenomys proditor*	27	Li *et al.*, 2006b
		Microtus clarkei	*Eothenomys proditor*	27	Li *et al.*, 2006b
		Microtus oeconomus	*Microtus agrestis*	29	Sitnikova *et al.*, 2007
		Microtus oeconomus	*Mesocricetus auratus*	40	Sitnikova *et al.*, 2007
		Ellobius lutestens	*Microtus agrestis*	34	Romanenko *et al.*, 2007b
		Ellobius lutestens	*Mesocricetus auratus*	44	Romanenko *et al.*, 2007b
		Ellobius talpinus	*Microtus agrestis*	35	Romanenko *et al.*, 2007b
		Ellobius talpinus	*Mesocricetus auratus*	43	Romanenko *et al.*, 2007b
		Ellobius tancrei	*Microtus agrestis*	35	Unpublished data
		Microtus oeconomus	*Microtus agrestis*	27	Sitnikova *et al.*, 2007
		Microtus oeconomus	*Mus musculus*	47	Sitnikova *et al.*, 2007
		Dicrostonyx torquatus	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
		Ellobius talpinus	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
		Microtus oeconomus	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
		Microtus rossiaemeridionalis	*Mus musculus*	Microdissected chromosome-specific probes 3, 6, 18, 19 were used	Trifonov *et al.*, 2010
		Microtus arvalis 'arvalis'	*Microtus agrestis*	28	Lemskaya *et al.*, 2010
		Microtus daghestanicus	*Microtus agrestis*	28	Lemskaya *et al.*, 2010
		Microtus dogramacii	*Microtus agrestis*	28	Lemskaya *et al.*, 2010
		Microtus gregalis	*Microtus agrestis*	29	Lemskaya *et al.*, 2010
		Microtus guentheri guentheri	*Microtus agrestis*	28	Lemskaya *et al.*, 2010
		Microtus maximowiczii	*Microtus agrestis*	30	Lemskaya *et al.*, 2010

Table 1 (Continued)

Suborder	*Family/ subfamily*	*Species*	*Set of painting probes*	*Number of autosomal conserved segments revealed. Comments*	*Reference*
		Microtus rossiaemeridionalis	*Microtus agrestis*	29	Lemskaya *et al.*, 2010
		Microtus socialis	*Microtus agrestis*	32	Lemskaya *et al.*, 2010
	Cricetidae: Sigmodontinae	*Akodon cursor*	*Mus musculus*	⩾31	Hass *et al.*, 2008
		Akodon cursor	*Akodon paranaensis*	31	Ventura *et al.*, 2009
		Akodon cursor	*Akodon* sp. *n.*	10	Ventura *et al.*, 2009
		Akodon montensis	*Mus musculus*	⩾26	Hass *et al.*, 2008
		Akodon montensis	*Akodon paranaensis*	21	Ventura *et al.*, 2009
		Akodon montensis	*Akodon cursor*	11	Ventura *et al.*, 2009
		Akodon montensis	*Akodon* sp. *n.*	11	Ventura *et al.*, 2009
		Akodon paranaensis	*Mus musculus*	⩾28	Hass *et al.*, 2008
		Akodon serrensis	*Mus musculus*	⩾24	Hass *et al.*, 2008
		Akodon sp. *n.*	*Akodon paranaensis*	24	Ventura *et al.*, 2009
		Akodon sp. *n.*	*Akodon cursor*	16	Ventura *et al.*, 2009
		Necromys lasiurus	*Mus musculus*	27	Hass *et al.*, 2011
		Oligoryzomys avescens	*Mus musculus*	⩾26	Hass *et al.*, 2008
		Sigmodon arizonae	*Sigmodon hispidus*	29	Swier *et al.*, 2009
		Sigmodon fulviventer	*Sigmodon hispidus*	29	Swier *et al.*, 2009
		Sigmodon hirsutus	*Sigmodon hispidus*	29	Swier *et al.*, 2009
		Sigmodon leucotis	*Sigmodon hispidus*	29	Swier *et al.*, 2009
		Sigmodon mascotensis	*Sigmodon hispidus*	29	Swier *et al.*, 2009
		Sigmodon ochrognathus	*Sigmodon hispidus*	29	Swier *et al.*, 2009
		Sigmodon peruanus	*Sigmodon hispidus*	29	Swier *et al.*, 2009
		Sigmodon toltecus	*Sigmodon hispidus*	29	Swier *et al.*, 2009
		Thaptomys nigrita	*Mus musculus*	30	Hass *et al.*, 2011

Sciuromorpha

The suborder Sciuromorpha is well supported as a monophyletic taxon by both morphological and molecular data (Murphy *et al.*, 2001; Waddell *et al.*, 2001; Churakov *et al.*, 2010) and is subdivided into three families—Aplodontiidae, Sciuridae and Gliridae.

Comparative chromosome painting subsequently allowed a more precise comparison of sciuromorph genomes and currently 17 species (of 307) have been examined by this technique (Table 1), mostly belonging to Sciuridae. Three species of Gliridae have also been studied. These investigations relied predominantly on human (*Homo sapiens*, HSA) paints, although two sciuromorph-specific sets of painting probes were developed from the flow-sorted chromosomes of *Sciurus carolinensis* and *Tamias sibiricus* and used in comparative painting experiments (Li *et al.*, 2004; Beklemisheva *et al.*, 2011).

Studies of ground squirrels confirmed the general tendency for sciurid genome conservation and these data permitted a revision of the putative sciurid karyotype (Richard *et al.*, 2003). The HSA 1/8 and HSA 2/17 associations previously found in sciuromorphs (and considered to represent the sciurid ancestral condition) are absent in the Eurasian ground squirrels—sousliks and woodchucks—while HSA 10/13 and HSA 8/4/8/12/22 are disrupted in four *Spermophilus* species. Some ground squirrels (*Xerus*, *Menetes*) and the flying squirrel (*Petaurista*) have highly conserved karyotypes that are probably very similar to the ancestral squirrel karyotype and do not differ significantly from that of Rodentia (Richard *et al.*, 2003; Stanyon *et al.*, 2003; Li *et al.*, 2004, 2006a; Beklemisheva *et al.*, 2011). In contrast to the general conservation of syntenic groups, most sciurid genomes are characterized by variation in the size and distribution of heterochromatin; additionally, multiple centromeric shifts have been reported in some species (Beklemisheva *et al.*, 2011). Importantly, however, because of the slow rate of karyotype change and some convergence of characters, cytogenetic evidence failed to resolve close associations within Sciuridae.

The availability of comparative banding and painting data led to suggestions of a putative ancestral karyotype for Sciuridae (Richard *et al.*, 2003; Li *et al.*, 2004; Beklemisheva *et al.*, 2011). The consensus is that this comprised 38 elements corresponding to the following human chromosomes and/or segmental associations: HSA 9/11, 1/10p, 3/21, 16q/19q, 7/16p, 20/15/14, 1pq/8q, 10q/13, 2q/17, 7/22qprox/12qdist, 8p/4q/8p/12pq/22qdiss, 3/19p (Supplement Data 3) (Li *et al.*, 2004, 2006a; Beklemisheva *et al.*, 2011). The karyotypes of Gliridae are also relatively conserved. Comparison of three *Eliomys* species made by fluorescence *in situ* hybridization (FISH) using human probes and RBG-banding (R-bands by BrdU using Giemsa) revealed the retention of several eutherian ancestral syntenies in their genomes (Sannier *et al.*, 2011). As karyotypes of other glirids have not yet been studied, and because the different *Eliomys* karyotypes are conserved, one might consider the *E. melanurus* syntenies to reflect the chromosomal signatures for glirids in general. Importantly, however, representatives of Aplodontiidae, as well as other glirid genera, have not been included in comparative FISH experiments, and it is possible that these data could shed additional light on the composition of an ancestral karyotype for Sciuromorpha.

Anomaluromorpha

The monophyly of anomaluromorphs was recently confirmed by DNA sequences (Montgelard *et al.*, 2008; Blanga-Kanfi *et al.*, 2009). Nine extant species are currently recognized in the suborder. The taxon is

poorly studied at a chromosomal level (the diploid chromosome number is known for only one species). There are no descriptions or comparisons of banded chromosomes between representatives of this group. The karyotype of only one species—*Pedetes capensis*—has been investigated using human painting probes (Graphodatsky *et al*., 2008). Surprisingly, some characteristic human chromosomal associations were not detected in *P. capensis*, that is, the HSA 7/16, and 16/19 as well as core glires HSA 1/10, 9/11 (Supplement Data 3). As the basal position of Sciuromorpha is well supported by different phylogenies (Murphy *et al*., 2001; Huchon *et al*., 2002; Adkins *et al*., 2003; Debry, 2003; Blanga-Kanfi *et al*., 2009; Churakov *et al*., 2010), fissions of the ancestral chromosomal signatures (or break points in close proximity to these regions) suggest considerable reorganization of the *P. capensis* genome, and possibly in the genomes of all anomalurids.

Castorimorpha

The Castorimorpha has traditionally been included in the sciuromorpha-like rodent group because of similar morphological traits (see Carleton and Musser (2005) and references therein). The latest molecular data suggest, however, that these species should be considered a separate taxon independent from Sciuromorpha (Blanga-Kanfi *et al*., 2009; Horn *et al*., 2011). According to current taxonomy, Castorimorpha includes beavers, pocket and kangaroo mice, pocket gophers—some 102 species in all.

Karyotypes of only two species have been described using banding techniques—*Castor fiber* and *C. canadensis* (Genest *et al*., 1979; Atlas of mammalian chromosomes, 2006). *Castor fiber* is the only species investigated by comparative chromosome painting (Beklemisheva *et al*., 2011). Characteristic placental associations such as HSA 7/16, 14/15, 16/19 (as well as some regarded as core to Glires, that is, HSA 1/10, 9/11) were not detected in the beaver genome supporting their placement (and that of the whole suborder) into a distinct clade (Supplement Data 3) (Graphodatsky *et al*., 2008).

Hystricomorpha

The representatives of this suborder are poorly studied by comparative cytogenetics. Although some species were described using banding techniques (see Atlas of Mammalian Chromosomes, 2006) there are only three recent publications involving hystricomorph species in chromosome painting studies.

Seven Bathyergidae and one species of Thryonomyidae were compared using naked mole rat probes (Deuve *et al*., 2006, 2008). The investigators' defined autosome–gonosome translocations, fusions and fissions as the major trends of karyotypic evolution in both families. Unfortunately, the lack of a link to human chromosomes does not permit conclusions on possible human associations specific to Bathyergidae and Thryonomyidae. The complexity of chromosomal evolution within Cavia and allies was initially reported by Viegas-Péquignot *et al.* (1986). Reciprocal chromosome painting between human and Guinea pig (*Cavia porcellus*) subsequently localized human paining probes to hystricomorph chromosomes (unpublished data). Only three adjacent chromosomal syntenies, signatures common to most placentals, are retained in the *C. porcellus* genome: HSA 3/21 and HSA 12/22 (twice). HSA 4/8/4 was also identified, but reciprocal painting showed that it was formed by different segments of human chromosomes 4 and 8 to those in other rodents. The fact that the placental signatures HSA 4/8p, 7/16, 14/15, and glirid signatures HSA 1/10, 3/19, 7/16, 8p/4/8p, 9/11, 14/15, 16/19, are absent in *Cavia*, indicates that its genome has undergone significant reorganization through fusions and fissions (Supplement Data 3) confirming that the Hystricomorpha represent yet another rodent suborder with unusually high rates of genome evolution. Interestingly, comparative chromosome painting demonstrated that the karyotypes of two Guinea pigs—*C. porcellus* and *C. tschudii*—are identical (unpublished data) suggesting that additional painting data are needed to establish, which associations are characteristic for suborder.

Myomorpha

Nearly one-third of all rodent species belong to the suborder Myomorpha making this taxon particularly appealing for evolutionary studies. The majority of studied species belong to two large families within Muroidea—the Cricetidae and Muridae. Only few representatives of other families have been included in comparative cytogenetic investigations. Nonetheless, comparative cytogenetic data show that high karyotypic reshuffling is characteristic for Myomorpha (for example, Stanyon *et al*., 1999) but that the elevated rate of chromosomal change was not accompanied by a rapid evolution of morphological features. Generally, the group has been reasonably well investigated by conventional cytogenetics, while 71 species have been investigated by comparative chromosome painting. With one exception (*Sicista betulina*), all studied species belong to the superfamily Muroidea.

It is important to note that the 'catastrophic' reorganization of myomorph genomes (characterized by a significant change of the whole genome, including the formation of a new linkage groups characteristic only for the given taxon, see Graphodatsky, 1989) made their study by the direct hybridization to human painting probes problematic. Consequently, a variety of myomorph probes was developed in order to compare karyotypes within the group (Table 1). However, in spite of these resources, in most instances laboratory mouse paining probes were used to make comparisons among the Myomorpha because these are commercially available. This led to their use as a common reference for the various species. In comparison to the most other muroids, however, mouse chromosomes are highly rearranged and this has detracted to some extent from their use in comparative studies in preference to those derived from species with conserved genomes (largely because of the difficulties in the interpretation of hybridization results).

Cricetidae

The family comprises 681 species grouped in 6 subfamilies. Representatives of four subfamilies have been included in comparative chromosome painting experiments (Table 1) but a reconstruction of the karyotypic relationships within Cricetidae has not been attempted.

Cricetinae

The subfamily contains 19 species from 7 genera. The first data obtained using comparative chromosome painting with golden hamster (*Mesocricetus auratus,* MAU) painting probes (Romanenko *et al*., 2006, 2007b) revealed that the karyotypes of some closely related species differed greatly. Chromosome painting data are currently available for 14 species of 6 hamster genera including *M. auratus* and *Cricetulus griseus* (Yang *et al*., 2000). Comparative painting and banding within the group permitted the analysis of chromosomal evolution and karyotype relationships within the subfamily resulting in findings that are in broad agreement with molecular data (Neumann *et al*., 2006). It was determined that *Mesocricetus, Tscherskia, Phodopus* and *Cricetus* represent a monophyletic clade (Neumann *et al*., 2006; Romanenko *et al*., 2007b). Moreover, different chromosomal rearrangements are characteristic for different lineages. For example, the derivation of *Phodopus* karyotypes necessitates the complex fission and fusion of ancestral chromosomes. Robertsonian

fusions, and appearance of additional heterochromatin blocks, characterized the karyotype evolution of *Mesocricetus*, while inversions are important in shaping the chromosomes of *Allocricetulus, Cricetulus* and *Cricetus*.

In the case of the greater long-tailed hamster, *Tscherskia,* comparative chromosome painting data provided important characters for the separate status of the genus. *Tscherskia triton* was long considered part of *Cricetus* because of morphological similarities. Conventional banding analysis has shown several partial chromosomal homologies between *T. triton* and other *Cricetus* species (Radjabli, 1975). However, painting showed extensive intra- and extra-chromosomal rearrangement in *T. triton* strongly supporting a separate position for the genus within Palaearctic hamsters (Romanenko *et al*., 2007b). This conclusion was subsequently confirmed by molecular data (Lebedev *et al.,* personal communication).

On the basis of the defined signatures, we propose an Ancestral Cricetinae Karyotype with 2n=48–54. This variation in diploid number is the result of uncertainty concerning the number of segments of *M. musculus* (MMU) 14 and 15, that is, their presence in the karyotype as one or two fragments (Supplement Data 4, 5). Another problem is the association MMU 11/5/14. It is currently not possible to ascertain whether there was only one chromosome combining segments MMU 5, 11 and 14, or two chromosomes homologous to MMU 5/14 and MMU5/11. However, as Arvicolinae species (see below) have two segments homologous to MMU 5 in their karyotypes, the presence of MMU 11/5/14 seems more likely. Consequently, an Ancestral Cricetinae Karyotype with 2n=48 containing MMU 1/17, 2, 3, 4, 4, 5/16, 6, 6/17, 7, 7/19, 8, 8/2/13, 9, 10, 10/17, 11/5/14, 11/17/16, 12, 12/17, 13/15, 15/1/17, 17/1/10/17, 18, X and Y is proposed.

Arvicolinae

The subfamily includes voles and lemmings. Diploid numbers range from 2n=17 in *Ellobius lutescens* and *Microtus oregoni* to 2n=64 in *M. longicaudus.* G-banded chromosomes of 50 arvicoline species were summarized in the Atlas of Mammalian Chromosomes (2006). The subfamily includes species with several striking cytogenetic features: the presence of B-chromosomes in some, unusual systems of sex chromosomes in others (*Dicrostonyx, Ellobius* and *Microtus*) and giant sex chromosomes in *Microtus agrestis* (Supplement Data 1).

Most representatives of *Microtus* have been included in comparative painting investigations. The limited variation in external morphology has been a significant challenge in *Microtus* classification and this has made cytogenetic data important for solving problems of vole taxonomy. A comparison of eight *Microtus* species using *M. agrestis* painting probes allowed reconstruction of a putative ancestral karyotype and insights to karyotype evolution within the taxon (Lemskaya *et al*., 2010). Surprisingly, cross-species chromosome painting in *Microtus* revealed no rearrangements that clearly support the branching pattern depicted in the molecular tree (see Lemskaya *et al*., 2010). Karyotypes of grey voles are generally characterized by the conservation of large ancestral syntenies suggesting that Robertsonian translocations predominate in the karyotype evolution of these species (Li *et al*., 2006b; Lemskaya *et al*., 2010).

Reorganization of several ancestral chromosomes occurred during formation of modern *Ellobius* karyotypes. The genus comprises five species (Carleton and Musser, 2005) whose diploid numbers vary from 17 (*E. lutestens*) to 54 (*E. talpinus*). The species *E. lutestens*, *E. talpinus*, and *E. tancrei* were compared using chromosome painting (Romanenko *et al*., 2007a; unpublished data) and its clear that *E. lutestens* has undergone a 'catastrophic' reshuffling of its chromosomes during its evolution. In spite of the high number of fusions, fissions and inversions detected, it was nonetheless possible to identify conserved elements that could be considered ancestral for *Ellobius*. In the case of *E. tancrei* and *E. alaicus*, a 'Robertsonian fan' was described (Lyapunova *et al.,* 1980). Chromosome painting showed that *E. tancrei* (2n=30–54) has a complex karyotypic structure formed by racial hybridization, and that chromosomal diversity was accompanied by independent and repeated Robertsonian rearrangements (single and multiple), and possibly by whole-arm reciprocal translocations (Bakloushinskya *et al.,* 2010).

On the basis of the signatures revealed in different arvicolines, the ancestral karyotype of the Arvicolinae (2n=56) appears to be identical to that proposed for *Ellobius* (Romanenko *et al*., 2007a). It comprises: MMU 1/14/1, 1/17, 1/17/7/5/10/17, 2, 2, 2/13, 3, 3, 4, 4, 5/11, 5/16, 6, 6/12/17, 7, 7/19, 8, 8, 9, 10, 11/17/16, 12, 13/15, 14, 15, 17/1/10/17, 18, X and Y. The ancestral *Microtus* karyotype (AMiK, Lemskaya *et al*., 2010) can therefore be derived by one fusion, that of MMU 6 and MMU 6/12/17, which resulted in the formation of MMU 6/17/12/6.

Sigmodontinae

A high degree of karyotype conservation was revealed for eight species of *Sigmodon* (Swier *et al*., 2009). In contrast, the karyotypes of *Akodon, Necromys* and *Thaptomys* are highly rearranged. For example, Robertsonian and tandem fusion rearrangements, pericentric inversions and/or centromere repositionings, paracentric inversions, translocations and insertions were observed in *Akodon* species (Hass *et al*., 2008; Ventura *et al*., 2009). Cross-species FISH using murine probes suggest that MMU 8/13 may be a signature for the Sigmodontinae (Hass *et al*., 2011; Supplement Data 3). Syntenies such as MMU 3/18 and 6/12 are combined in *Akodon* and *Necromys*. However, as most painting data for the group are incomplete we cannot draw definitive conclusion on the composition of a putative Sigmodontinae ancestral karyotype.

Neotominae

Although previously included in Sigmodontinae, 16 genera (many of New World rats and mice) are grouped in the Neotomyinae within the New World Cricetidae. Of these, conventional banding analysis showed a high degree of karyotypic conservation within *Peromyscus*: all species have 2n=48. The number of chromosomal arms ranges from 52 to 92 because of variation attributable to heterochromatin additions and pericentric inversions (Robbins and Baker, 1981; Rogers *et al*., 1984). On the basis of the painting data, it seem reasonable to consider the *P. eremicus* karyotype as being close to the putative ancestral state for Muroidea (Romanenko *et al*., 2007b). However, there is some disagreement on the murine signatures found in *P. eremicus* and *P. maniculatus* (Romanenko *et al*., 2007b; Mlynarski *et al*., 2008) and broader taxon sampling is necessary for reconstructing the ancestral karyotype of the subfamily.

Calomyscidae

Mouse-like hamsters of the genus *Calomyscus* represent a striking example of speciation underscored by cytogenetic characters—morphologically similar species of mouse-like hamsters have different diploid and fundamental numbers, and specific sets of translocations (Graphodatsky *et al*., 2000). Current cytogentic data confirm conclusions based on molecular studies that show *Calomyscus* to be the most basal clade within Muroidea (Jansa and Weksler, 2004; Romanenko *et al*., 2007b).

Muridae

Muridae comprises ~730 species and is larger than any other mammalian family. The examination of murid chromosomes using

conventional cytogenetics allowed the detection of some notable features in their karyotypes including (i) extensive variation in diploid numbers—from 2n=14 (*Taterillus tranieri*) to 2n=74 (*Gerbillus latastei*), (ii) considerable interspecific differences in the amount and distribution of heterochromatin (Graphodatsky, 1989), (iii) the presence of supernumerary chromosomes in many species (Trifonov *et al.*, 2002) and (iv) sex chromosomes systems that differ from the conventional XX/XY.

Representatives of the Muridae were the first rodents studied by chromosome painting (Scherthan *et al.*, 1994) and today some 29 species from three subfamilies have been investigated (Table 1) using different sets of probes. Generally, murid genomes have been extensively reorganized during evolution. However, some species with conserved genomes have been identified. For example, a single chromosomal rearrangement distinguishes *Apodemus* (Matsubara *et al.*, 2004; Stanyon *et al.*, 2004) and relatively high genome conservation was established for species within *Rattus* and *Tokudaia*, representatives of the tribe Rattini (Guilly *et al.*, 1999; Stanyon *et al.*, 1999; Cavagna *et al.*, 2002; Nakamura *et al.*, 2007; Badenhorst *et al.*, 2011).

The most likely Ancestral Murinae Karyotype had 2n=46 and contained following associations of mouse chromosomes: MMU 1, 2, 2/13, 3, 4, 5/6, 5/11, 7/19, 8, 8, 9, 10/17, 10/17, 11/16, 12/17, 13/15, 14, 14, 15, 16, 17/1/17, 18, X and Y. However there could be three segments of MMU 5 and MMU 10, and MMU 4 and MMU 9 may have been present in two fragments and not in one (Supplement Data 5), thereby collectively increasing the ancestral 2n to 54.

OVERVIEW OF KARYOTYPE EVOLUTION IN RODENTS

In order to reconstruct the putative ancestral karyotypes at some of the major nodes of the Rodentia tree, we combined all available painting data and attempted to identify shared syntenic associations between lineages. These shared ancestral (and hence symplesiomorphic) elements were considered to be a part of the ancestral karyotype under consideration. In those instances where syntenic arrangements were different between closely related taxa (for example, chromosomal segments 1 and 2 were fused in species A, but disrupted in its sister species B) outgroup comparisons were used (Dobigny *et al.* 2004) to determine the ancestral state. In this example, the fused presence of chromosomal segments 1 and 2 in a distantly related species C, suggests that this is the ancestral condition shared with species A.

An Ancestral Karyotype of Rodentia (RAK) was proposed (Graphodatsky *et al.*, 2008) that suggested the associations HSA 8/12 and 15/20 may define rodents. Originally, HSA 1/10p and 9/11 were considered ancestral for Glires (the cohort combining Rodentia and Lagomorpha). However, the most recent glirid painting data showed the absence of HSA 9/11 and 3/19 in *Eliomys*. In the light of these findings, we concur with Sannier *et al.* (2011) that the occurrence HSA 9/11 cannot be unequivocally explained. It could be a result of convergence in some lagomorphs, sciurids and myomorphs, or it may represent an ancestral feature that was lost in certain branches. The association HSA 3/19 was found in all Carnivora and one eulipotyphlan species, as well as in all studied species of Sciuridae and Anomaluromorpha. Consequently questions about its presence in the RAK remain open. Syntenies such as HSA 3/21, 4/8p, 7/16, 12/22, 14/15, 16/19 are shared with other eutherians (Ferguson-Smith and Trifonov, 2007). We consequently placed the RAK at the base of the tree and tracked its reorganization during rodent evolution.

Molecular phylogenies are not universally consistent, but they all consider Sciuromorpha as a basal clade within Rodentia (Huchon *et al.*, 2002; Adkins *et al.*, 2003; Debry, 2003; Blanga-Kanfi *et al.*, 2009; Churakov *et al.*, 2010). The fusion HSA 8/12 (resulting in the HSA 8/4/8/12/22 association) could be the single rearrangement distinguishing the Ancestral Sciuromorpha Karyotype from RAK. All sciurids share following associations: HSA 1/8, 2/17, 7/22, 10/13, 15/20 (Richard *et al.*, 2003; Li *et al.*, 2004, 2006a; Graphodatsky *et al.*, 2008; Beklemisheva *et al.*, 2011). Thus, only five fusions are needed to explain the derivation of the Sciuridae Ancestral Karyotype from that of the putative ancestral Sciuromorpha karyotype. Many more rearrangements (12 fissions and 12 fusions) are needed to form a putative ancestral Rodentia karyotype from that of the ancestral Gliridae (Sannier *et al.*, 2011).

Suborders Anomaluromorpha, Hystricomorpha, Myomorpha and Castorimorpha form a single clade based on the presence of HSA 1/7, the disruption of the HSA 7/16 synteny, and the fissions of HSA 1, 4, 5, 6, 11, and 15 in karyotypes of all studied representatives. There is also a possibility that the HSA 10/16 association may be ancestral for the clade. The HSA 8 and HSA 19 association was found in different rodent species (that is, *Castor fiber, P. capensis*), but this involved different non-homologous fragments of HSA 8 so it cannot be considered ancestral for the group. The absence of HSA 1/10 was previously proposed as a signature for a clade comprising Anomaluromorpha+Myomorpha+Castorimorpha but this association was subsequently detected in karyotypes of *M. musculus* and *R. norvegicus* (Ensembl Mouse web site (http://www.ensembl.org); Nilsson *et al.*, 2001). HSA 1/10 was not present in the *Cavia* karyotype. Finally, we conclude that the putative ancestral karyotype of Anomaluromorpha, Hystricomorpha, Myomorpha and Castorimorpha had a 2n=60 (or 2n=62 if the HSA 1/10 association in myomorphs and sciuromorphs is convergent) that consisted of HSA 1, 1/7, 1/10, 2, 2, 3, 3/19, 3/21, 4, 4, 4/8, 5, 5, 6, 6, 7, 8, 9/11, 10/16, 11, 12/22 (twice), 13, 14/15, 15, 16/19, 17, 18, 20, X and Y.

The following rearrangements offer a striking confirmation of the close evolutionary relationship of Myomorpha and Castorimorpha: HSA 5/17 (it is absent in *Mus* and *Rattus,* but present in *Sicista*), HSA 11/15 and fission of HSA 14/15 (Graphodatsky *et al.*, 2008). However, the use of different methods of analysis (DNA sequences for myomorph genomes and chromosome painting for castorimorphs) could give inconsistent results because of resolution differences of the analyses. For example, HSA 5/17 was not detected in the mouse and rat karyotypes by FISH and a disruption of ancestral eutherian synteny HSA 14/15 occurred in hystricomorphs (*Cavia*). Moreover, all representatives of Hystricomorpha, Myomorpha and Castorimorpha studied have three fragments of HSA 12 in their karyotypes. These features corroborate our suggestion that Hystricomorpha is intermediate between Anomaluromorpha and Myomorpha+Castorimorpha. Although such an arrangement contradicts the latest data based on painting with human probes, sequencing of nuclear genes and the distribution of short interspersed elements all place Hystricomorpha in a basal position to the Anomaluromorpha+Myomorpha+Castorimorpha clade (Ferguson-Smith and Trifonov, 2007; Blanga-Kanfi *et al.*, 2009; Churakov *et al.*, 2010; Horn *et al.*, 2011). We therefore consider the fission of HSA 14/15 and the disruption of HSA 12 onto three fragments as convergent events that took place independently in hystricomorphs, myomorphs and castorimorphs.

Despite some gaps in *Cavia* and human whole genome homology maps, we were able to demonstrate a 'catastrophic' reorganization of the hystricomorph karyotype—as many as 29 fusions and 31 fissions were detected when compared with the RAK. The evolution of the *C. fiber* karyotype was accompanied by a smaller number of rearrangements—these included disruptions to HSA 1/7, 1/10, 3/19, 9/11, 16/19 and the presence of 8 fusions.

Within Myomorpha the karyotype of only one species (*Sicista betulina*) was studied using human painting probes (Graphodatsky *et al*., 2008). This species falls within Dipodoidea, which represents a basal branch in Myomorpha (Jansa and Weksler, 2004; Steppan *et al*., 2004). Two other species (*M. musculus* and *R. norvegicus*) were compared with human using non-painting approaches (that is, based on full genome sequencing data) but the resolution of the methods differs greatly thus precluding the construction of an ancestral karyotype for Myomorpha.

As a result of the extent of genomic reshuffling in muroid rodents, conserved syntenies are referenced to mouse rather than to human chromosomes. Reciprocal chromosome painting between mouse/golden hamster and golden hamster/field vole (Romanenko *et al*., 2006; Lemskaya *et al*., 2010) provided an opportunity to include cricetid and arvicolin comparisons in the myomorph investigation. Here, we examined the karyotype evolution of Muroidea based solely on mouse chromosome associations.

The analysis of chromosomal signatures in different muroid karyotypes suggests a 2n=52 for the Ancestral Muroidea Karyotype (AMK) (Figure 1). The AMK differs from the one proposed earlier based on a wide range of hamster species comparison but that included few murids (Romanenko *et al*., 2007b). It is also possible that MMU 5/14 and MMU 11, which were syntenic in the AMK were disrupted in the *Calomyscus* branch. In this case, the AMK was identical to the common ancestral karyotype of Cricetidae and Muridae. The 2n=52 karyotype of *Calomyscus* sp. differs from the proposed AMK by four fusions and four fissions.

The evolution of the Ancestral Cricetidae Karyotype (Figure 1) was accompanied by a small number of fissions (MMU 17 twice) and fusions (MMU 17/1+MMU 10/17, MMU 1+17 and MMU 6+17) of ancestral chromosomes. If MMU4 was present as two segments, then Ancestral Cricetidae Karyotype would have been 2n=50.

In view of the disagreements in painting results obtained for two Neotomyinae species (Mlynarski *et al*., 2008; Romanenko *et al*., 2007b), it was not possible to unequivocally define the type and number of rearrangements for *Peromyscus*. The partial hybridization of *M. musculus* probes to four *Akodon* species does not provide sufficient data to reconstruct the ancestral karyotype for Sigmodontinae, and to define the number and types of rearrangements for the different branches.

The ancestral karyotype common to the Arvicolinae and Cricetinae probably had 2n=52 or 50 (it depends on the number of segments homologous to MMU14) and contained the following associations: MMU 1/17, 1/17, 2, 3, 4, 4, 5/16, 6, 6/17, 7, 7/19, 8, 8/2/13, 9, 10, 10/17, 11/5/14, 11/17/16, 12, 12/17, 13/15, 14, 15, 17/1/10/17, 18, X and Y. The subsequent formation of the Ancestral Cricetinae Karyotype was accompanied by two fusions (Romanenko *et al*., 2007b). As mentioned above, the putative ancestral karyotype of Arvicolinae may be

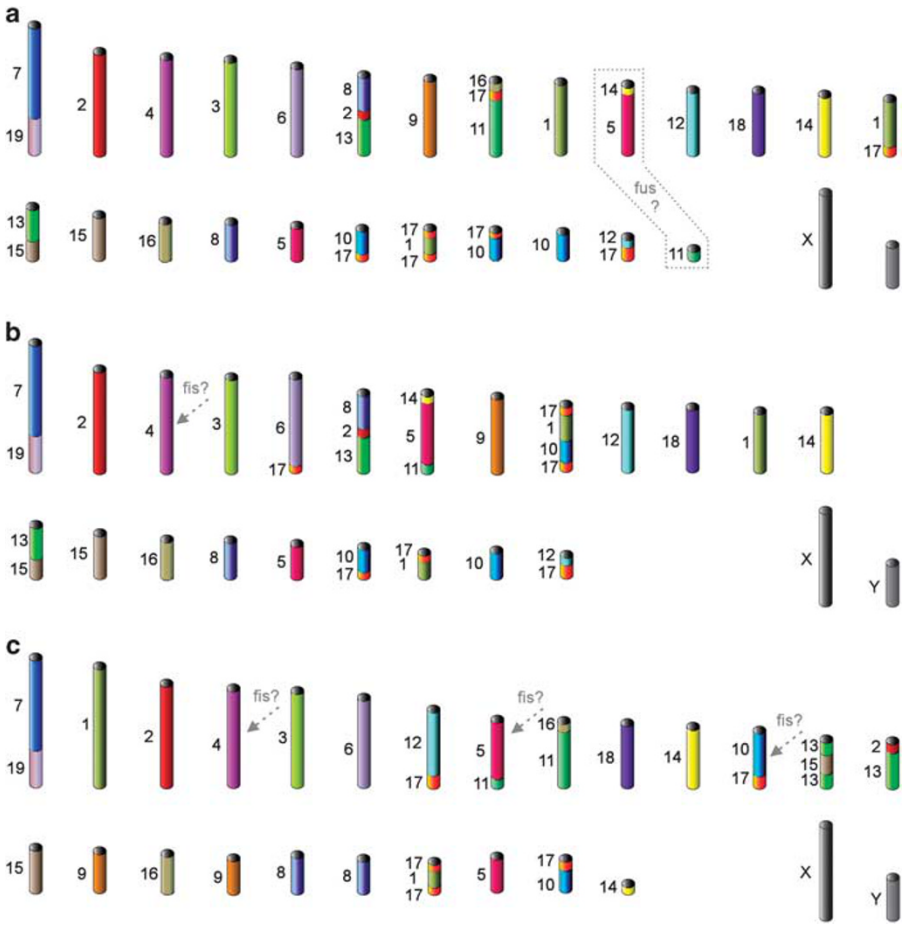

Figure 1 Putative ancestral karyotypes: (**a**) AMK–ancestral Muroidea karyotype, (**b**) ACdK—ancestral Cricetidae karyotype, (**c**) AMdK—ancestral Muridae karyotype. Different colors correspond to separate mouse chromosomes. Dashed gray frame and arrows mark elements whose state in the AKs was not ambiguously determined. fis, fission; fus, fusion. See comments in the text.

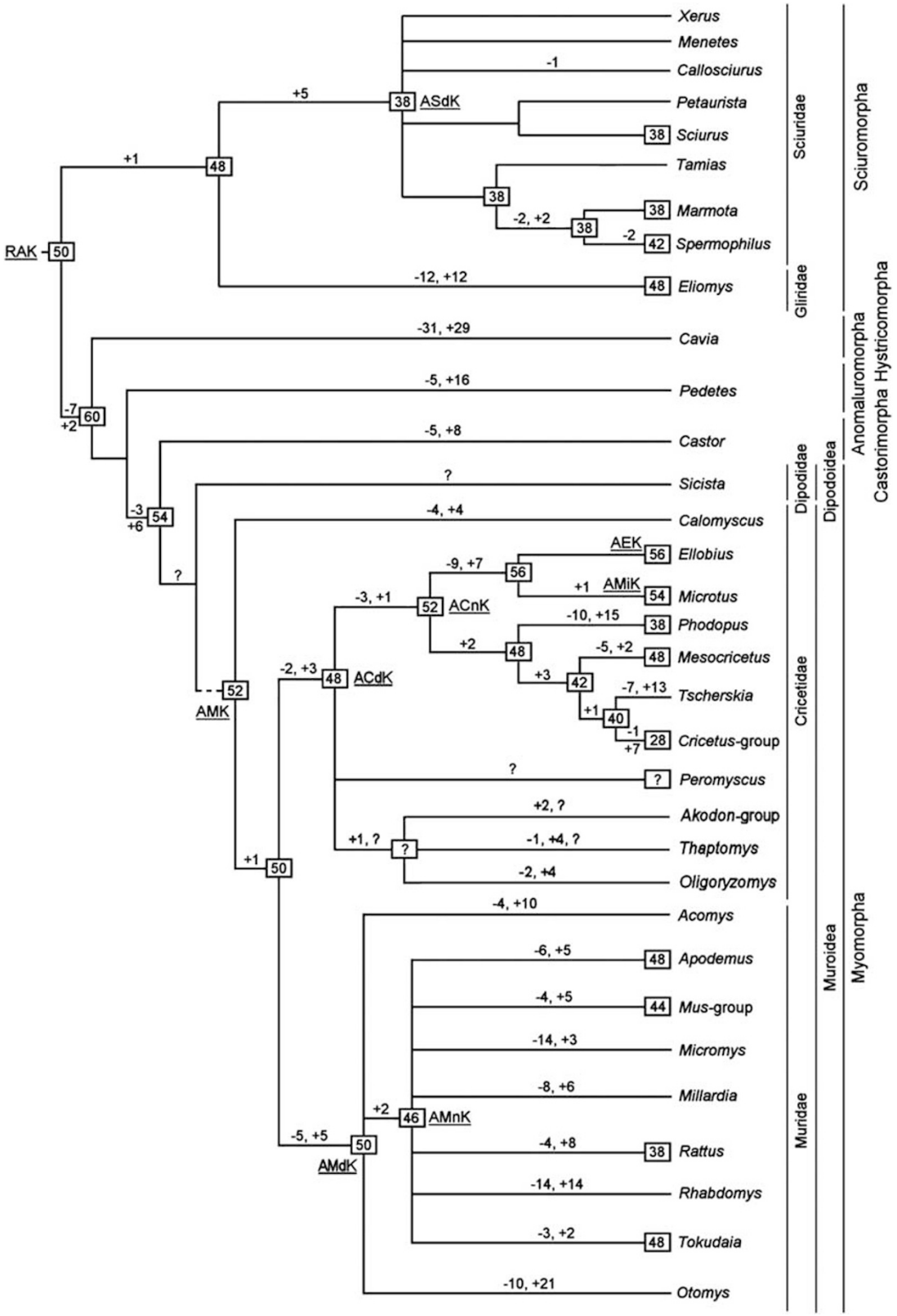

Figure 2 Putative scheme of chromosome evolution in Rodentia to the genus level. RAK—ancestral Rodentia karyotype; ACdK—ancestral Cricetidae karyotype; ACnK—ancestral Cricetinae karyotype; AEK—ancestral *Ellobius* karyotype; AMdK—ancestral Muridae karyotype; AMK—ancestral Muroidea karyotype; AMiK—ancestral *Microtus* karyotype; AMnK—ancestral Murinae karyotype; ASdK—Sciuridae ancestral karyotype. Presumable ancestral diploid number characters for node are shown in black frames. Minus sign indicates chromosome fissions, plus sign indicates chromosome fusions, and question mark indicates unresolved positions. See comments in the text.

identical to that of *Ellobius* and can be derived from the Ancestral Cricetidae Karyotype by nine fissions and seven fusions (Romanenko *et al*., 2007a).

The Ancestral Muridae Karyotype (Figure 1) differs from that of the common ancestor of Cricetidae and Muridae by at least five fissions and five fusions. The chromosome number of Ancestral Muridae Karyotype ranges from 2n=50 to 2n=56 because of variable interpretations of the number of segments homologous to MMU 4, 5 and 10. Although the sequence-based Muridae phylogeny is controversial (Conroy and Cook, 1999; Martin *et al*., 2000; Michaux *et al*., 2001; Jansa and Weksler, 2004; Steppan *et al*., 2004; Blanga-Kanfi *et al*., 2009), we propose that two fusions (synteny MMU 5/6 and fusion of two segments homologous to different parts of MMU 9) occurred during the formation of the Ancestral Murinae Karyotype (with 2n=46–52). The various generic associations suggested in Murinae by sequence-based phylogenies could not be verified using painting data. The types and numbers of rearrangements that are thought to lead to the ancestral karyotypes of each genus are shown in Figure 2. These data prompted us to revise the diploid chromosome number previously proposed for the *Mus*-group (2n=46 to 2n=44 and which combines subgenera *Coelomys*, *Nannomys*, *Mus* and *Pyromys*). It seems more plausible that the ancestor of the subgenera had three segments homologous to MMU 5 as reported by Veyrunes *et al*. (2006). Considering that most Murinae have the MMU 13/15 association in their karyotypes, we suggested that MMU 13/15 was present in the ancestral karyotype of the *Mus*-group, and not the MMU 13/15/13 configuration suggested by Veyrunes *et al*. (2006).

A high number of species and elevated rates of chromosomal change make rodent karyotypes particularly informative for building and improving existing phylogenies. However, it is clear that the incorporation of new species in future molecular cytogenetic studies and the application of new molecular markers would result in better understanding of rodent evolution.

RATES OF KARYOTYPE EVOLUTION

Although the numbers of autosomal segments scored in comparative chromosome painting experiments include hemiplasic (Avise and Robinson, 2008) and homoplasic segments, they nonetheless remain good indicators of the level of genome conservation. The numbers of human autosomal conserved segments detected in sciurid genomes vary from 35 to 36 (Table 1). Generally, the genomes of sciurids are highly conserved and most closely reflect the putative ancestral genome of all rodents. Investigations of glirids, castorimorphs and anomaluromorphs detected slightly higher numbers of human autosomal segments in their karyotypes. Hystricomorph painting indicated a high level of *Cavia* genomic reshuffling (>71 conserved segments). The only representative myomorph species (*Sicista betulina*; Graphodatsky *et al*., 2008) had 62 autosomal conserved segments when analyzed by FISH using human probes.

Generally, the rates of karyotype evolution differ in various branches of rodent phylogenetic tree. Even within a single family it is not unusual to find genera with low rates of reorganization (for example, *Apodemus* species) and those whose genomes are extensively rearranged (*Mus* species). Rough estimates show that rates may vary as much as 10 times across different branches of the muroid tree (Veyrunes *et al*., 2006).

CONCLUSIONS

In recent years, modern cytogenetics has contributed significantly to studies of evolutionary relationships among mammals. Chromosome painting has resulted in novel discoveries and has extended previous conclusions drawn from conventional comparative banding data. Nowhere is this more apparent than in rodents where high species diversity and extensive genome reshuffling has produced unparallel opportunities for studying chromosomal evolution in mammals.

It is clear, however, that future studies should focus on problematic and uninvestigated branches in Rodentia, particularly in Myomorpha. These should include pivotal lineages such as *Laonastes* and gundis, basal murids and jerboas and combine refinements in methodology that would permit the detection of smaller rearrangements (such as multicolor banding and mapping using bacterial artificial chromosomes). Importantly, the absence of reciprocal painting in most studies makes it currently difficult to unambiguously define chromosomal characters because of the questionable homology of supposedly syntenic fragments. Finally, although prospective studies will undoubtedly benefit greatly from the whole genome analysis of different rodents (see the Genome 10K Project proposed by the Genome 10K Community of Scientists, 2009), their selection will, in part, be directed by detailed karyotypic descriptions resulting from molecular cytogenetic investigations such as those outlined in this paper.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ACKNOWLEDGEMENTS

This study was funded in part by programs MCB and SB RAS Programs and research grants of Russian Fund for Basic Research.

Adkins RM, Walton AH, Honeycutt RL (2003). Higher-level systematics of rodents and divergence time estimates based on two congruent nuclear genes. *Mol Phylogenet Evol* **26**: 409–420.

Atlas of mammalian chromosomes (2006). Stephen J. O'Brien, Joan C. Menninger, William G. Nash (eds). A John Wiley & Sons: Hoboken, NJ, USA.

Avise JC, Robinson TJ (2008). Hemiplasy: a new term in the lexicon of phylogenetics. *Syst Biol* **57**: 503–507.

Badenhorst D, Dobigny G, Adega F, Chaves R, O'Brien PCM, Ferguson-Smith MA *et al*. (2011). Chromosome evolution in Rattini (Muridae, Rodentia). *Chromosome Res* **19**: 709–727.

Bakloushinskya IYu, Romanenko SA, Graphodatsky AS, Matveevsky SN, Lyapunova EA, Kolomiets OL (2010). The role of chromosome rearrangements in the evolution of mole voles of the genus *Ellobius* (Rodentia, Mammalia). *Russ J Genet* **46**: 1143–1145. (In Russian).

Beklemisheva VR, Romanenko SA, Biltueva LS, Trifonov VA, Vorobieva NV, Serdukova NA *et al*. (2011). Reconstruction of karyotype evolution in core Glires. I. The genome homology revealed by comparative chromosome painting. *Chomosome Res* **19**: 549–565.

Benton MJ, Donoghue PC (2007). Paleontological evidence to date the tree of life. *Mol Biol Evol* **24**: 26–53.

Blanga-Kanfi S, Miranda H, Penn O, Pupko T, DeBry RW, Huchon D (2009). Rodent phylogeny revised: analysis of six nuclear genes from all major rodent clades. *BMC Evol Biol* **9**: 71.

Carleton MD, Musser GG (2005). Order Rodentia. In: Wilson DE, Reeder DM (eds). *Mammal Species of the World: A Taxonomic and Geographic Reference*. Johns Hopkins University Press: Baltimore. pp 745–1601.

Cavagna P, Stone G, Stanyon R (2002). Black rat (*Rattus rattus*) genomic variability characterized by chromosome painting. *Mamm Genome* **13**: 157–163.

Churakov G, Sadasivuni MK, Rosenbloom KR, Huchon D, Brosius J, Schmitz J (2010). Rodent evolution: back to the root. *Mol Biol Evol* **27**: 1315–1326.

Conroy CJ, Cook JA (1999). MtDNA evidence for repeated pulses of speciation within arvicoline and murid rodents. *J Mamm Evol* **6**: 221–245.

Dawson WD, Young SR, Wang Z, Lui LW, Greenbaum IF, Davis LM *et al*. (1999). *Mus* and *Peromyscus* chromosome homology established by FISH with three mouse paint probes. *Mamm Genome* **10**: 730–733.

DeBry RW (2003). Identifying conflicting signal in a multigene analysis reveals a highly resolved tree: the phylogeny of Rodentia (Mammalia). *Syst Biol* **52**: 604–617.

Deuve JL, Bennett NC, Britton-Davidian J, Robinson TJ (2008). Chromosomal phylogeny and evolution of the African mole-rats (Bathyergidae). *Chromosome Res* **16**: 57–74.

Deuve JL, Bennett NC, O'Brien PC, Ferguson-Smith MA, Faulkes CG, Britton-Davidian J *et al.* (2006). Complex evolution of X and Y autosomal translocations in the giant mole-rat, *Cryptomys mechowi* (Bathyergidae). *Chromosome Res* **14**: 681–691.

Dobigny G, Ducroz JF, Robinson TJ, Volobouev V (2004). Cytogenetics and cladistics. *Syst Biol* **53**: 470–484.

Engelbrecht A, Doigny G, Robinson TJ (2006). Further insights into the ancestral murine karyotype: the contribution of the *Otomys-Mus* comparison using chromosome painting. *Cytogenet Genome Res* **112**: 126–130.

Ferguson-Smith MA, Trifonov V (2007). Mammalian karyotype evolution. *Nat Rev Genet* **8**: 950–962.

Ferguson-Smith MA, Yang F, O'Brien PC (1998). Comparative mapping using chromosome sorting and painting. *ILAR J* **39**: 68–76.

Fredga K (1983). Aberrant sex chromosome mechanisms in mammals. Evolutionary aspects. *Differentiation* **23**: 23–30.

Genest FB, Morisset P, Patenaude RP (1979). The chromosomes of the Canadian Beaver *Castor canadensis*. *Can J Genet Cytol* **21**: 37–42.

Genome 10K Community of Scientists (2009). A proposal to obtain whole genome sequence for 10,000 vertebrate species. *The Journal of Heredity* **100**: 659–674.

Graphodatsky AS (1989). Conserved and variable elements of mammalian chromosomes. In: Halnan CRE (eds). *Cytogenetics of Animals*. CAB International Press: UK, pp 95–123.

Graphodatsky AS, Sablina OV, Meyer MN, Malikov VG, Isakova EA, Trifonov VA *et al.* (2000). Comparative cytogenetics of hamsters of the genus *Calomyscus*. *Cytogenet Cell Genet* **88**: 296–304.

Graphodatsky AS, Yang F, Dobigny G, Romanenko SA, Biltueva LS, Perelman PL *et al.* (2008). Tracking genome organization in rodents by Zoo-FISH. *Chromosome Res* **16**: 261–274.

Grutzner F, Himmelbauer H, Paulsen M, Ropers HH, Haaf T (1999). Comparative mapping of mouse and rat chromosomes by fluorescence *in situ* hybridization. *Genomics* **55**: 306–313.

Guigo R, Dermitzakis ET, Agarwal P, Ponting CP, Parra G, Reymond A *et al.* (2003). Comparison of mouse and human genomes followed by experimental verification yields an estimated 1,019 additional genes. *Proc Natl Acad Sci USA* **100**: 1140–1145.

Guilly MN, Fouchet P, de Chamisso P, Schmitz A, Dutrillaux B (1999). Comparative karyotype of rat and mouse using bidirectional chromosome painting. *Chromosome Res* **7**: 213–221.

Hass I, Muller S, Artoni RF, Sbalqueiro IJ (2011). Comparative chromosome maps of neotropical rodents *Necromys lasiurus* and *Thaptomys nigrita* (Cricetidae) established by ZOO-FISH. *Cytogenet Genome Res* **135**: 42–50.

Hass I, Sbalqueiro IJ, Muller S (2008). Chromosomal phylogeny of four Akodontini species (Rodentia, Cricetidae) from southern Brazil established by Zoo-FISH using *Mus musculus* (Muridae) painting probes. *Chromosome Res* **16**: 75–88.

Helou K, Walentinsson A, Levan C, Stahl F (2001). Between rat and mouse ZOO–FISH reveals 49 chromosomal segments that have been conserved in evolution. *Mammalian Genome* **12**: 765–771.

Horn S, Durka W, Wolf R, Ermala A, Stubbe A, Stubbe M *et al.* (2011). Mitochondrial genomes reveal slow rates of molecular evolution and the timing of speciation in beavers (*Castor*), one of the largest rodent species. *PLoS One* **6**: e14622.

Huchon D, Madsen O, Sibbald MJ, Ament K, Stanhope MJ, Catzeflis F *et al.* (2002). Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear genes. *Mol Biol Evol* **19**: 1053–1065.

Jansa SA, Weksler M (2004). Phylogeny of muroid rodents: relationships within and among major lineages as determined by IRBP gene sequences. *Mol Phylogenet Evol* **31**: 256–276.

Lemskaya NA, Romanenko SA, Golenishchev FN, Rubtsova NV, Sablina OV, Serdukova NA *et al.* (2010). Chromosomal evolution of Arvicolinae (Cricetidae, Rodentia). III. Karyotype relationships of ten *Microtus* species. *Chromosome Res* **18**: 459–471.

Li T, O'Brien PC, Biltueva L, Fu B, Wang J, Nie W *et al.* (2004). Evolution of genome organizations of squirrels (Sciuridae) revealed by cross-species chromosome painting. *Chromosome Res* **12**: 317–335.

Li T, Wang J, Su W, Nie W, Yang F (2006a). Karyotypic evolution of the family Sciuridae: inferences from the genome organizations of ground squirrels. *Cytogenet Genome Res* **112**: 270–276.

Li T, Wang J, Su W, Yang F (2006b). Chromosomal mechanisms underlying the karyotype evolution of the oriental voles (Muridae, *Eothenomys*). *Cytogenet Genome Res* **114**: 50–55.

Lyapunova EA, Vorontsov NN, Korobitsina KV, Ivanitskaya EYu, Borisov YuM, Yakimenko LV *et al.* (1980). A Robertsonian fan in *Ellobius talpinus*. *Genetica (The Hague)* **52**: 239–247.

Martin Y, Gerlach G, Schlotterer C, Meyer A (2000). Molecular phylogeny of European muroid rodents based on complete cytochrome b sequences. *Mol Phylogenet Evol* **16**: 37–47.

Matsubara K, Nishida-Umehara C, Kuriowa A, Tsuchiya K, Matsuda Y (2003). Identification of chromosome rearrangements between the laboratory mouse (*Mus musculus*) and the Indian spiny mouse (*Mus platythrix*) by comparative FISH analysis. *Chromosome Res* **11**: 57–64.

Matsubara K, Nishida-Umehara C, Tsuchiya K, Nukaya D, Matsuda Y (2004). Karyotypic evolution of *Apodemus* (Muridae, Rodentia) inferred from comparative FISH analyses. *Chromosome Res* **12**: 383–395.

Matthey R (1972). Chromosomes and evalution. *Triangle* **11**: 107–112.

Michaux J, Reyes A, Catzeflis F (2001). Evolutionary history of the most speciose mammals: molecular phylogeny of muroid rodents. *Mol Biol Evol* **18**: 2017–2031.

Mlynarski EE, Obergfell CJ, Rens W, O'Brien PC, Ramsdell CM, Dewey MJ *et al.* (2008). *Peromyscus maniculatus-Mus musculus* chromosome homology map derived from reciprocal cross species chromosome painting. *Cytogenet Genome Res* **121**: 288–292.

Montgelard C, Forty E, Arnal V, Matthee CA (2008). Suprafamilial relationships among Rodentia and the phylogenetic effect of removing fast-evolving nucleotides in mitochondrial, exon and intron fragments. *BMC Evol Biol* **8**: 321.

Murphy WJ, Eizirik E, Johnson WE, Zhang YP, Ryder OA, O'Brien SJ (2001). Molecular phylogenetics and the origins of placental mammals. *Nature* **409**: 614–618.

Nakamura T, Kuroiwa A, Nishida-Umehara C, Matsubara K, Yamada F, Matsuda Y (2007). Comparative chromosome painting map between two Ryukyu spiny rat species, *Tokudaia osimensis* and *Tokudaia tokunoshimensis* (Muridae, Rodentia). *Chromosome Res* **15**: 799–806.

Neumann K, Michaux J, Lebedev V, Yigit N, Colak E, Ivanova N *et al.* (2006). Molecular phylogeny of the Cricetinae subfamily based on the mitochondrial cytochrome b and 12S rRNA genes and the nuclear vWF gene. *Mol Phylogenet Evol* **39**: 135–148.

Nilsson S, Helou K, Walentinsson A, Szpirer C, Nerman O, Stahl F (2001). Rat-mouse and rat-human comparative maps based on gene homology and high-resolution zoo-FISH. *Genomics* **74**: 287–298.

Patton JL, Sherwood SW (1982). Genome evolution in pocket gophers (genus *Thomomys*). I. Heterochromatin variation and speciation potential. *Chromosoma* **85**: 149–162.

Petit D, Couturier J, Viegas-Péquignot E, Lombard M, Dutrillaux B (1984). Great degree of homeology between the ancestral karyotype of squirrels (Rodents) and that of Primates and Carnivora. *Ann Genet* **27**: 201–212.

Radjabli SI (1975). The karyotypic differentiation of Palaearctic hamsters (Rodentia, Cricetidae). *Reports AS USSR* **225**: 697–700. (In Russian).

Rambau RV, Robinson TJ (2003). Chromosome painting in the African four-striped mouse *Rhabdomys pumilio*: detection of possible murid specific contiguous segment combination. *Chromosome Res* **11**: 91–98.

Richard F, Messaoudi C, Bonnet-Garnier A, Lombard M, Dutrillaux B (2003). Highly conserved chromosomes in an Asian squirrel (*Menetes berdmorei*, Rodentia: Sciuridae) as demonstrated by ZOO-FISH with human probes. *Chromosome Res* **11**: 597–603.

Robbins LW, Baker RJ (1981). An assessment of the nature of chromosomal rearrangements in 18 species of Peromyscus (Rodentia: Cricetidae). *Cytogenet Cell Genet* **31**: 194–202.

Rogers DS, Greenbaum IF, Gunn SJ, Engstrom MD (1984). Cytosystematic value of chromosomal inversion data in the genus *Peromyscus* (Rodentia, Cricetidae). *J Mammal* **65**: 457–465.

Romanenko SA, Lemskaya NA, Beklemisheva VR, Perel'man PL, Serdyukova NA, Graphodatsky AS (2010). Comparative cytogenetics of rodents. *Russian J Genet* **46**: 1138–1142.

Romanenko SA, Perelman PL, Serdukova NA, Trifonov VA, Biltueva LS, Wang J *et al.* (2006). Reciprocal chromosome painting between three laboratory rodent species. *Mamm Genome* **17**: 1183–1192.

Romanenko SA, Sitnikova NA, Serdukova NA, Perelman PL, Rubtsova NV, Bakloushinskaya IY *et al.* (2007a). Chromosomal evolution of Arvicolinae (Cricetidae, Rodentia). II. The genome homology of two mole voles (genus *Ellobius*), the field vole and golden hamster revealed by comparative chromosome painting. *Chromosome Res* **15**: 891–897.

Romanenko SA, Volobouev VT, Perelman PL, Lebedev VS, Serdukova NA, Trifonov VA *et al.* (2007b). Karyotype evolution and phylogenetic relationships of hamsters (Cricetidae, Muroidea, Rodentia) inferred from chromosomal painting and banding comparison. *Chromosome Res* **15**: 283–297.

Sannier J, Gerbault-Seureau M, Dutrillaux B, Richard FA (2011). Conserved although very different karyotypes in Gliridae and Sciuridae and their contribution to chromosomal signatures in Glires. *Cytogenet Genome Res* **134**: 51–63.

Scherthan H, Cremer T, Arnason U, Weier HU, Lima-de-Faria A, Fronicke L (1994). Comparative chromosome painting discloses homologous segments in distantly related mammals. *Nat Genet* **6**: 342–347.

Scalzi JM, Hozier JC (1998). Comparative genome mapping: mouse and rat homologies revealed by fluorescence *in situ* hybridization. *Genomics* **47**: 44–51.

Sitnikova NA, Romanenko SA, O'Brien PC, Perelman PL, Fu B, Rubtsova NV *et al.* (2007). Chromosomal evolution of Arvicolinae (Cricetidae, Rodentia). I. The genome homology of tundra vole, field vole, mouse and golden hamster revealed by comparative chromosome painting. *Chromosome Res* **15**: 447–456.

Stanyon R, Stone G, Garcia M, Froenicke L (2003). Reciprocal chromosome painting shows that squirrels, unlike murid rodents, have a highly conserved genome organization. *Genomics* **82**: 245–249.

Stanyon R, Yang F, Cavagna P, O'Brien PC, Bagga M, Ferguson-Smith MA *et al.* (1999). Reciprocal chromosome painting shows that genomic rearrangement between rat and mouse proceeds ten times faster than between humans and cats. *Cytogenet Cell Genet* **84**: 150–155.

Stanyon R, Yang F, Morescalchi AM, Galleni L (2004). Chromosome painting in the long-tailed field mouse provides insights into the ancestral murid karyotype. *Cytogenet Genome Res* **105**: 406–411.

Steppan S, Adkins R, Anderson J (2004). Phylogeny and divergence-date estimates of rapid radiations in muroid rodents based on multiple nuclear genes. *Syst Biol* **53**: 533–553.

Svartman M, Stone G, Stanyon R (2005). Molecular cytogenetics discards polyploidy in mammals. *Genomics* **85**: 425–430.

Swier VJ, Bradley RD, Rens W, Elder FF, Baker RJ (2009). Patterns of chromosomal evolution in *Sigmodon*, evidence from whole chromosome paints. *Cytogenet Genome Res* **125**: 54–66.

Trifonov VA, Kosyakova N, Romanenko SA, Stanyon R, Graphodatsky AS, Liehr T (2010). New insights into the karyotypic evolution in muroid rodents revealed by multicolor banding applying murine probes. *Chromosome Res* **18**: 265–275.

Trifonov VA, Perelman PL, Kawada SI, Iwasa MA, Oda SI, Graphodatsky AS (2002). Complex structure of B-chromosomes in two mammalian species: *Apodemus peninsulae* (Rodentia) and *Nyctereutes procyonoides* (Carnivora). *Chromosome Res* **10**: 109–116.

Ventura K, O'Brien PC, Yonenaga-Yassuda Y, Ferguson-Smith MA (2009). Chromosome homologies of the highly rearranged karyotypes of four *Akodon* species (Rodentia, Cricetidae) resolved by reciprocal chromosome painting: the evolution of the lowest diploid number in rodents. *Chromosome Res* **17**: 1063–1078.

Veyrunes F, Dobigny G, Yang F, O'Brien PC, Catalan J, Robinson TJ *et al.* (2006). Phylogenomics of the genus *Mus* (Rodentia; Muridae): extensive genome repatterning is not restricted to the house mouse. *Proc Biol Sci* **273**: 2925–2934.

Viegas-Péquignot E, Petit D, Benazzou T, Prod'homme M, Lombard M, Hoffschir F *et al.* (1986). Phylogénie chromosomique chez les Sciuridae, Gerbillidae et Muridae, et étude d'espèces appartenant à d'autres familles de Rongeurs. *Mammalia* **50**: 164–202.

Waddell PJ, Kishino H, Ota R (2001). A phylogenetic foundation for comparative mammalian genomics. *Genome Inform* **12**: 141–154.

Ward OG, Graphodatsky AS, Wurster-Hill DH, Eremina VR, Park JP, Yu Q (1991). Cytogenetics of beavers: a case of speciation by monobrachial central fusions. *Genome* **34**: 324–328.

Yang F, O'Brien PCM, Ferguson-Smith MA (2000). Comparative chromosome map of the laboratory mouse and Chinese hamster defined by reciprocal chromosome painting. *Chromosome Res* **8**: 219–227.

Supplementary Information accompanies the paper on Heredity website (http://www.nature.com/hdy)