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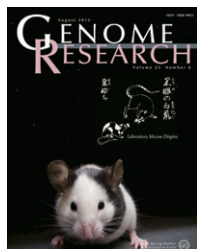
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^{OA}Open Access paper



Cover Photograph of an inbred mouse strain, JF1/Ms, which is now widely used in genomic imprinting and other epigenetic studies. Its ancestor was found in Denmark and then transferred to the National Institute of Genetics in Japan (1987). Recent whole-genome sequencing uncovered that the classical inbred strains have long consecutive genome segments with extremely high similarity to JF1/Ms. A Japanese mouse-breeding guidebook, *Chingan-sodategusa (How to breed fancy mice)* published in 1787, described a small spotted mouse (*lower left* in the drawing represented as a constellation). “Japanese waltzing mice” with a similar coat color were reported in European literature to be imported from Japan in the 19th Century and crossed with European fancy mice for early studies of “Mendelism.” The descendants of these mice were most likely established as the classical inbred strains. (Photo: Toyoyuki Takada © 2013. Drawing courtesy of Kouwa-shuppan. [For details, see Takada et al., pp. 1329–1338.]