

# GENOME RESEARCH

## Errata

*Genome Res.* 2008 18: 1680-1681

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## Errata

**Genome Research 17:** 1319–1326 (2007)**Direct linkage of mitochondrial genome variation to risk factors for type 2 diabetes in conplastic strains**

Michal Pravenec, Masaya Hyakukoku, Josef Houstek, Vaclav Zidek, Vladimir Landa, Petr Mlejnek, Ivan Miksik, Kristyna Dudová-Mothejzíkova, Petr Pecina, Marek Vrbacký, Zdenek Drahota, Alena Vojtiskova, Tomas Mracek, Ludmila Kazdova, Olena Oliarynyk, Jiaming Wang, Christopher Ho, Nathan Qi, Ken Sugimoto, and Theodore Kurtz

The authors have discovered an error in the presentation of the mitochondrial DNA haplotyping analysis described in Table 2 and wish to correct the data. The row that displays genotypes at nucleotide position 11,374 is incorrect and should be replaced by a new row that displays genotypes at nucleotide position 11,360. The corrected Table 2 is reprinted below. The authors apologize for any inconvenience this error may have caused other investigators in the field.

**Table 2.** Mitochondrial DNA haplotype grouping of 43 strains of rats

Nucleotide	Genotype <sup>a</sup>			
	Group 1	Group 2	Group 3	Group 4
1716	BN	SHR	SHR	BN
1918	SHR	SHR	SHR	BN
4352 <sup>b</sup>	BN	SHR	SHR	BN
5200	BN	SHR	SHR	BN
5237	BN	SHR	SHR	BN
5269	BN	SHR	SHR	BN
5326 <sup>b</sup>	SHR	SHR	SHR	BN
7930 <sup>b</sup>	SHR	SHR	SHR	BN
8021 <sup>b</sup>	BN	SHR	SHR	BN
11,194	BN	SHR	SHR	BN
11,360 <sup>b</sup>	BN	BN	SHR	BN
13,647 <sup>b</sup>	BN	SHR	SHR	BN
13,693	BN	SHR	SHR	BN
13,974 <sup>b</sup>	SHR	SHR	SHR	BN
15,135 <sup>b</sup>	SHR	SHR	SHR	BN
15,400	SHR	SHR	SHR	BN

We identified four haplotype groups by genotype analysis of 16 mitochondrial DNA polymorphisms in 43 rat strains including the SHR and BN progenitor strains. The specific variants present at each nucleotide site in the SHR and BN strains are listed in Tables 1 and Supplemental Table 1.

<sup>a</sup>Haplotype Group 1 consisted of 20 strains: ACI/Ztm, BC/CpbU, BDE/Han, BDIV/Ifz, BDIX/Han, BH/Ztm, BUF/Han, COP/OlaHsd, DA/Han, F344/Han, NAR/SaU, NEDH/K, PVG/OlaHsdCp, R/A, RHA/Kun, SDL/lpvc, SPRD-Cu3/Han, SR/lrlpvc, SS/lrlpvc, WF/Han. Group 2 consisted of 17 strains: AS/Ztm, AVN/Orl, BBWB/Mol, BDII/Han, BS/Ztm, LE/Han, LEW/OlaHsd, LOU/C, MNS/Gro, MW/Hsd, OM/Han, SD/Rij, SDH/Ztu, WF/Gut, WIST/Nhg, WOK.1A/K, WOK/w/K. Group 3 consisted of four strains: SHR/Ola, OKA/Wsl, GC/Kun, WKY/M. Group 4 consisted of two strains: BN/Ola, DZB/Gro. The DZB/Gro strain was derived by a cross of BN rats with AO rats.

<sup>b</sup>Nucleotides causing amino acid substitutions.

**Genome Research 18:** 729–741 (2008)

**Insights from the complete genome sequence of *Mycobacterium marinum* on the evolution of *Mycobacterium tuberculosis***

Timothy P. Stinear, Torsten Seemann, Paul F. Harrison, Grant A. Jenkin, John K. Davies, Paul D.R. Johnson, Zahra Abdellah, Claire Arrowsmith, Tracey Chillingworth, Carol Churcher, Kay Clarke, Ann Cronin, Paul Davis, Ian Goodhead, Nancy Holroyd, Kay Jagels, Angela Lord, Sharon Moule, Karen Mungall, Halina Norbertczak, Michael A. Quail, Ester Rabbinowitsch, Danielle Walker, Brian White, Sally Whitehead, Pamela L.C. Small, Roland Brosch, Lalita Ramakrishnan, Michael A. Fischbach, Julian Parkhill, and Stewart T. Cole

FadB was inadvertently omitted from the sentence on page 731 describing the enzymes involved in beta-oxidation in *M. tuberculosis*. The sentence should have read:

“FadD (acyl-CoA synthetase) catalyses the formation of acyl-CoA thioesters that are then processively oxidized by FadE, EchA, FadB, and FadA (Cole et al. 1998).”

In addition, the page range for the Hagedorn and Soldati 2007 reference was incorrect, the corrected reference is as follows:

Hagedorn, M. and Soldati, T. 2007. Flotillin and RacH modulate the intracellular immunity of *Dictyostelium* to *Mycobacterium marinum* infection. *Cell Microbiol.* **9**: 2716–2733.

The authors apologize for any confusion these errors may have caused.