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Supporting information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Figure S1 (a) Gross morphology of the stillborn Original Braunvieh calf with ~50 cm body length. Note the round-shaped hydrocephalic-like head with extreme brachygnathia. (b) Genome-wide average read depth analysis (500 kb window size). Note the 1.5-fold increase in coverage of the entire chromosome 29 (red arrow).

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Genotyping *KIF1C* (c.608G>A) mutant reveals a high prevalence of progressive ataxia in Uckermärker cattle

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Source/description Progressive ataxia is a neurodegenerative disease with autosomal recessive inheritance resulting from a mutation within *KIF1C* (c.608G>A, p.R203Q).¹ Clinical signs begin between 1 and 2 years old and in rare cases as early as 6 months.^{1–5} This condition is prevalent at high frequencies in Charolais cattle worldwide.^{2–5} Heterozygous carriers exhibit an advantage in growth rate and muscularity and this may have caused the high frequency of the deleterious *KIF1C* allele in Charolais.¹

In the former Democratic German Republic, a breeding program among Charolais bulls and Fleckvieh cows was initiated between 1971 and 1975 and finalized in 1985 with the aim to establish a beef cattle breed (genotype 67) with optimum meat traits from both breeds.⁶ After this time, the herdbook was closed and selection was only within breeding animals of the genotype 67. In 1993, this breed received official acknowledgement as a cattle breed and was named Uckermärker.⁶

Table 1 Genotype counts of the *KIF1C*:c.608G>A variant in 88 Uckermärker cattle born between 1992 and 2019. Genotyping was done using PCR-RFLP (Table S1). Homozygous mutant animals were between 10 and 15 months old. One sire had heterozygous and homozygous mutant progeny and two sires had only heterozygous progeny.

Genotype	Male	Female	Total	Number of sires of animals genotyped
G/G	21	49	70	14
G/A	7	8	15	3
A/A	2	1	3	2
Total	30	58	88	16

Samples and genotyping We sampled 88 Uckermärker cattle from Germany, including 58 female and 30 male individuals. These animals were sired by 16 Uckermärker bulls. Genotyping of the *KIF1C*:c.608G>A variant was performed with a PCR-based RFLP (Fig. S1) using the restriction enzyme BstUI and primer pairs according to Duchesne *et al.*¹ (Table S1).

Validation of the *KIF1C*:c.608G>A variant We found three homozygous and 15 heterozygous *KIF1C* mutant animals (Table 1). *KIF1C* mutant allele frequency was 0.12 and in HWE. However, one bull, born in 2015, sired two homozygous mutant, 12 heterozygous mutant and 16 homozygous wt progeny. This bull was state champion in 2017. In addition, this bull belongs to the top 25 bulls according to its relative breeding value for meat production according to the official evaluation report by vit/Verden in 2019. The two bulls with homozygous mutant progeny had no common paternal ancestors up to the paternal and maternal grandsires. Our data indicate an introgression of the lethal *KIF1C*:c.608G>A variant through Charolais bulls before 1985, a wide distribution and persistence of this mutation into the actual population. Genetic testing should prevent further dissemination of this lethal variant in the Uckermärker population.

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Table S1 Primer sequences used for validation of the *KIF1C*:g.27041449G>A mutation using an RFLP.

Figure S1 Genotyping using a PCR-RFLP for *KIF1C*:27041449G>A (c.608G>A) for animals 1–3.

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Mitochondrial DNA variation of Nigerian Muscovy duck (*Cairina moschata*)

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The Muscovy duck (*Cairina moschata*) is a roosting duck originating from tropical regions of Central and South America.¹ A single domestication event has been proposed owing to the low genetic diversity in Muscovy duck groups.² Domesticated Muscovy duck is one of the poultry species classified as an indigenous bird in Africa and one of the most common waterfowl species in Nigeria.³ Herein, we compare the mtDNA haplotypes in Nigerian Muscovy ducks with those in other populations.

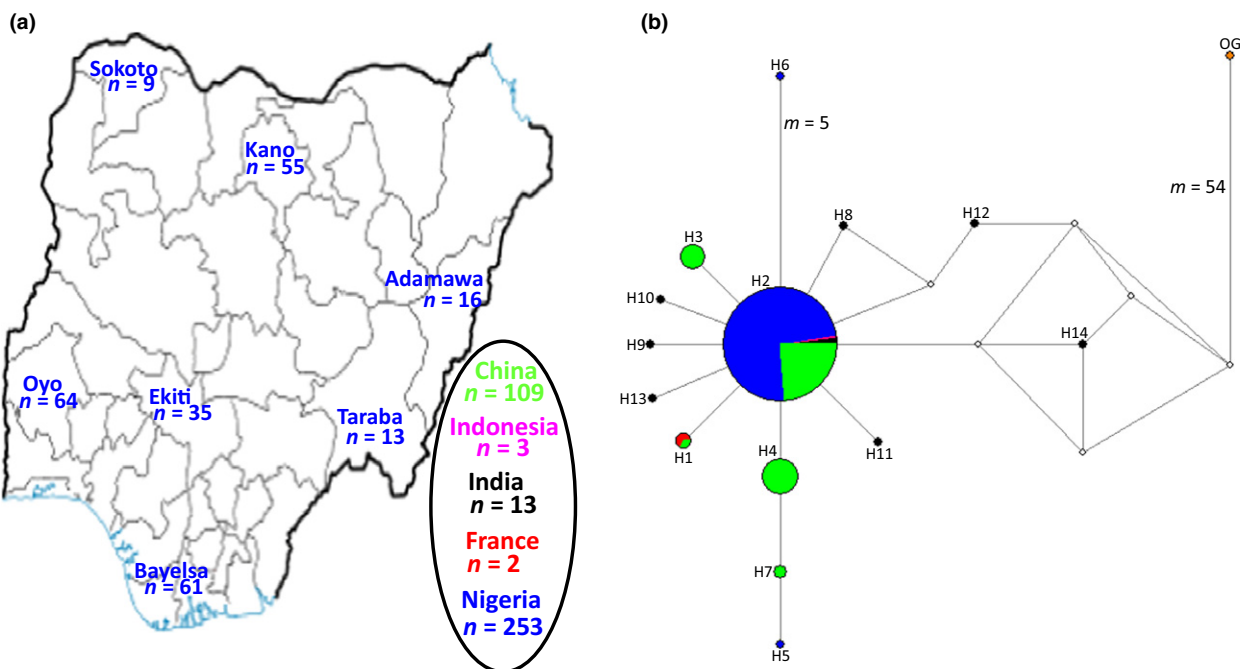


Figure 1 Sampling and network of domesticated Muscovy duck analyzed in this work. (a) Map of individuals sampled and their locations. (b) Median-joining network of 381 domesticated Muscovy duck samples constructed using NETWORK version 4.6.7 The size from each location is indicated. H1–H14 represent haplotypes 1–14. M represents the number of mutation steps whereas those not indicated comprise just one step. Colors are indicated in the figure.