

New insights into distribution range of the novel rustrela virus in its putative reservoir, the yellow-necked field mouse (*Apodemus flavicollis*)

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In 2020, the first relatives of rubella virus in mammals, ruhugu virus (RuhV) and rustrela virus (RusV), were described. RuhV was found in oral swabs of apparently healthy cyclops leaf-nosed bats (*Hipposideros cyclops*) in Uganda, Africa. RusV was detected in brain tissues of zoo animals from Germany with acute neurological disease: a donkey (*Equus asinus*), a capybara (*Hydrochoeris hydrochaeris*) and a red-necked wallaby (*Macropus rufogriseus*). Furthermore, RusV was detected in brain tissues of yellow-necked field mice (*Apodemus flavicollis*) on the premises of the zoo and within 10 km around it (Bennett et al., 2020, Nature). Recently, we have tested brain tissues of more than 1,400 additional rodents from different parts of Germany. RusV RNA was exclusively detected in yellow-necked field mice originating from Mecklenburg-Western Pomerania and the Northwest of Brandenburg, but not in other species, even in sympatric occurrence with RusV-positive mice. Phylogenetic analysis of partial E1 gene nucleotide sequences identified three major clades, representing locations in the West, North or East of the distribution area. Analysis of viral tissue distribution revealed the highest RusV RNA levels in the central nervous system, lower levels in the peripheral nervous system, and only rare detection in other tissues. The widespread occurrence of RusV in yellow-necked field mice and its absence in other small mammals indicates this species to be a major RusV reservoir host.