

**POJAVA RANIJE NEPOZNATE I ČESTO TEŠKE MULTISISTEMSKE BOLESTI
KOD PASA KOJU IZAZIVA AMDOPARVOVIRUS RAKUNOLIKOG PSA I LISICE**

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Kratak sadržaj

Cilj ovog saopštenja je da obavesti naučnu i stručnu javnost o pojavi nove, do sada nepoznate bolesti kod pasa u Srbiji, a koja je istovremeno detektovana i širi se i u drugim zemljama. Prvi otkriveni slučajevi oboljenja, dostupni autorima ovog rada, koje je pratila teška klinička slika, ustanovljeni su u smeštaju za pse profesionalnog trenera pasa u blizini Grada Novog Sada (mesto Čortanovci, opština Indija). Epizootiološkim istraživanjem, o putu unošenja infekcije ustanovljeno je da je do izbijanja zaraze došlo nakon uvoza dva psa iz Rusije. Klinički znaci prvo su se pojavili kod jedne od dve uvezene kuje rase Doberman, koja je bila stara 7 meseci, 10 dana po prispeću u smeštaj.

Tokom marta i aprila 2026. godine, uzorci obolelih dobermana iz pomenutog objekta poslati su na laboratorijska ispitivanja u Naučni institut za veterinarstvo „Novi Sad“. Kod obolelih jedinki, oboljenje je proticalo u hroničnom toku, a kao klinički sindrom dominirao je mukopurulentni konjunktivitis sa ili bez rinitisa, subsklernalne hemoragije, progresivno mršavljenje uz poremećaj hepatograma i zamućenje rožnjače "plavo oko". Od ostalih simptoma uočeni su artritis, orožavanje sluzokože nosne pećurke, sa ili bez ragada, orožavanje mekušića šapa "hard pad" i u krajnjem stadijumu bolesti kaheksija i neurološki poremećaji uključujući paraplegiju. Nakon negativnog laboratorijskog nalaza na adenovirus, koronavirus, herpesvirus, parvovirus, virus štenećaka, virus gripa A, leptospirozu i lajšmanijazu, izvršeno je NGS-metagenomsko sekvenciranje na odabranim tkivima uginulih odraslih životinja i štenaca, nakon čega je usledila bioinformatička analiza. Sekvenciranjem je generisano 434.220 nukleotidnih sekvenci a među njima višestruke genomske sekvence amdoparvovirusa rakunolikog psa i lisice (*Raccoon dog and fox amdoparvovirus* - RFAV). Bioinformatičkim alatima je sklopljen genom od 4.799 baznih parova detektovanog virusa sa približno 97% sličnosti sa poznatim sojevima RFAV u banci gena i organizacijom genoma u skladu

sa rodnom Amdoparvovirus. Do sada, RFAV je utvrđen samo kod rakunolikog psa i lisica, ali slučaj prirodne infekcija kod domaćih pasa nije dokumentovan. Konstruisani kompletan genom je objavljen u *NCBI GenBank* (broj unosa: [PZ348355](#)). Pored toga, u skladu sa poznatim genomom virusa i dostupnim podacima iz literature, dizajniran je dijagnostički protokol za PCR specifičan za RFAV. Tokom perioda od maja do jula 2026.godine, prisustvo RFAV je naknadno detektovano pomenutim PCR testom kod epidemiološki povezanih pasa i u različitim tipovima uzoraka, uključujući krv, urin, u bubrezima, slezini, mozgu, plućima, testisima, spermi, ileocekalnim limfnim čvorovima i nosnim i oro-faringealnim brisevima, ali i u uzorcima drugih dobermana sa kliničkim znacima koji nisu bili epidemiološki povezani sa populacijom pasa u kojoj smo utvrdili prvi slučaj oboljenja. Istovremeno, klinički zdravi doberman koji nisu bili epizootički povezani sa obolelim životinjama, kao i psi drugih rasa koji su bili u kohabitaciji ili u kontaktu sa obolelim dobermanima, kao i druge životinje različitih vrsta reagovali su negativno u PCR testu.

Dobijeni podaci i saznanja stečena do sada jasno ukazuju na „*spillover*” i prenos RFAV-a sa jedne na drugu vrstu životinja, odnosno sa divljih mesojeda ili gajenih divljih mesojeda na pse. Rasa doberman, verovatno zbog svoje genetske predispozicije, je izgleda podložna ovoj infekciji. Do ovog trenutka, nakon više od 100 testiranih životinja, a među njima i većeg broja pasa drugih rasa koji su bili u kohabitaciji ili u kontaktu sa zaraženim dobermanima, samo su psi rase doberman bili pozitivni na prisustvo RFAV, zaraženi sa ili bez prisustva kliničkih znakova bolesti. Na mnoga pitanja još uvek nemamo odgovor, potrebno je više vremena i istraživanja. Naša istraživanja su još uvek u toku i uskoro će biti dostupno više podataka.

Ključne reči: amdoparvovirus, infekcija, *Canis lupus familiaris*, metagenomska analiza, sekvenciranje, *spillover*, prenos virusa na novu vrstu domaćina, novi domaćin, divlje životinje, Srbija

Zahvalnica

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**AN OUTBREAK OF A PREVIOUSLY UNRECOGNIZED, OFTEN SEVERE
MULTISYSTEMIC DISEASE IN DOGS CAUSED BY THE RACCOON DOG AND FOX
AMDOPARVOVIRU**

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Summary

The aim of this report is to inform the scientific and professional community about the outbreak of a new previously unrecognized disease in dogs in Serbia but also detected and spreading in the other counties. The first discovered cases of the disease, available to the authors of this paper, which were accompanied by a severe clinical picture, were found in the dog shelter of a professional dog trainer near the City of Novi Sad (town of Čortanovci, municipality of Indija). Epizootiological research on the route of infection established that the outbreak of infection occurred after the importation of two dogs from Russia. Clinical signs first appeared in one of the two imported Doberman bitches, which was 7 months old, 10 days after arrival at the shelter.

During March and April 2026, samples from affected Dobermann dogs from afore mentioned kennel were submitted for laboratory investigation to Scientific Veterinary Institute "Novi Sad". In affected animals, the disease followed a chronic course, and the dominant clinical syndrome was mucopurulent conjunctivitis with or without rhinitis, subscleral hemorrhages, progressive weight loss accompanied by abnormal liver function tests, and corneal opacity known as 'blue eye'. Among the other symptoms observed are arthritis, hyperkeratosis of the nasal planum mucosa, with or without rhagades, hyperkeratosis of the paw pads ('hard pad'), and in the final stage of the disease, cachexia and neurological disorders including paraplegia. After negative testing for canine adenovirus, canine coronavirus, herpesvirus, parvovirus, distemper virus, influenza A virus, leptospirosis and leishmaniasis, NGS-metagenomic sequencing was performed on selected tissues from succumbed adult animals and puppies, followed by bioinformatic analysis. Sequencing generated 434,220 reads and identified multiple raccoon dog and fox amdoparvovirus (RFAV) hits. Pooled assembly produced a 4,799-bp consensus genome with approximately 97% similarity to known RFAV strains and genome organization consistent with the genus *Amdoparvovirus*. RFAV has been reported in raccoon dogs and foxes, but natural infection in domestic dogs has not previously been documented. The

constructed full genome was published in NCBI GenBank (Access No: [PZ348355](#)). In addition, according to the known virus genome and available literature data RFAV specific PCR protocol was designed. During period from May to July, RFAV DNA was subsequently detected by virus-specific PCR in a epidemiologically linked dogs and across diverse specimen types including blood, urine, kidney, spleen, brain, lung, testicle, ileocecal lymph node, and throat swabs, but also in different type of samples of other Dobermans with clinical signs that were not epidemiologically connected to the kennel where study started, whereas clinically healthy unrelated Dobermans and dogs in cohabitation and other animals of different species were PCR-negative.

The obtained data and knowledge acquired until now clearly suggest the spillover and cross-species transmission of RFAV from wildlife or wild animals kept in captivity to dogs. Among dog breeds, probably due to their genetic predisposition, the Doberman breed seems susceptible to this disease for now. Until this moment, after more than 100 tested animals and among them a lot of dogs from other breeds that were in contact/cohabitation with infected Dobermans, only the dogs of Doberman breed were found positive for virus presence, infected with or without visible clinical signs of disease. A lot of questions are still not answered, both more time and research are needed. Our research is still in progress, and more data will be available soon.

Keywords: amdoparvovirus; infection; *Canis lupus familiaris*; metagenomic analysis; sequencing; cross-species transmission; novel host; wildlife; spillover; Serbia

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