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Omicron Neutralizing Antibodies and B-cells

Omicron breakthrough infection drives cross-variant neutralization and memory B cell formation

Omicron is the evolutionarily most distinct SARS-CoV-2 variant (VOC) to date and displays multiple amino acid alterations located in neutralizing antibody sites of the spike (S) protein. We report here that Omicron breakthrough infection in BNT162b2 vaccinated individuals results in strong neutralizing activity not only against Omicron, but also broadly against previous SARS-CoV-2 VOCs and against SARS-CoV-1. We found that Omicron breakthrough infection mediates a robust B cell recall response, and primarily expands preformed memory B cells that recognize epitopes shared broadly by different variants, rather than inducing new B cells against strictly Omicron-specific epitopes. Our data suggest that, despite imprinting of the immune response by previous vaccination, the preformed B cell memory pool has sufficient plasticity for being refocused and quantitatively remodeled by exposure to heterologous S protein, thus allowing effective neutralization of variants that evade a previously established neutralizing antibody response.

One Sentence Summary Breakthrough infection in individuals double- and triple-vaccinated with BNT162b2 drives cross-variant neutralization and memory B cell formation.

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Jasmin Quandt

https://de.linkedin.com/in/jasmin-quandt-539625182

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Ukraine Samples

Molecular screening of vector-borne pathogens in ectoparasites from bats in Ukraine
June 2021
DOI:10.13140/RG.2.2.10937.90728
Conference: The Annual Conference of the German Veterinary Medical Society

Bats (Mammalia: Chiroptera) represent the second-most diverse order of mammals after rodents, being described as hosts for a wide range of bloodsucking arthropods that are able to circulate bacterial, protozoal and viral agents. Bats join other mammals in facilitating the spread of pathogens and are natural reservoir hosts of a large variety of zoonotic diseases with the ability to cross species barriers. In addition, due to their migratory habits, bats can facilitate the long-distance dispersal of pathogens. The aim of this study was to perform a molecular screening for selected vector-borne pathogens in ectoparasites collected from bats in Ukraine. Bats from a mine system and from urban (Kharkiv city) and rural areas (Kharkiv region) in Ukraine were captured and checked for ectoparasites. The mines (Liptsy mines) are used by bats for swarming and hibernation. In Kharkiv city area bats were examined during hibernation season, and in countryside areas breeding colonies from buildings were checked. From the total number of collected ectoparasites, so far 143 samples were morphologically identified as Nycteridopsylla eusarca fleas (n=100) and Carios vespertilionis soft ticks (n=43) then screened for pathogens. Nycteridopsylla eusarca fleas were collected only from Nyctalus noctula (urban area) bat species while C. vespertilionis ticks were collected from three different bat species from the mines: Myotis dasycneme (n=28), Myotis daubentonii (n=2) and Plecotus auritus (n=1), and two bat species from rural sites: Pipistrellus kuhlii (n=1) and Pipistrellus pygmaeus (n=11). All ectoparasites were tested individually by PCR for Rickettsia spp., Bartonella spp., Ehlichia/Anaplasma spp. and Babesia spp. while only C. vespertilionis samples were tested by nested PCR for Borrelia spp. The amplified PCR products were sequenced for species identification. Only C. vespertilionis samples were positive for Rickettsia spp. and following sequencing 16.3% (7/43) of samples showed 100% identity to Rickettsia parkeri (GenBank accession number: CP040325.1). Six of the positive ticks were found on Pipistrellus pygmaeus bat species while one sample was found on Pipistrellus kuhlii. Bartonella spp. was detected only in N. eusarca (7%; 7/100) and after sequencing, three samples showed 99 to 99.4% identity to uncultured Bartonella sp. (access. no.: MK140218.1) previously found in C. vespertilionis while the other four samples had 100% identity to uncultured Bartonella sp. (access. no.: AJ871615.1) previously reported in the blood of Nyctalus noctula. Ehrlichia/Anaplasma spp. PCR showed 58 positive samples: 56% (56/100) of N. eusarca and 4.7% (2/43) of C. vespertilionis. Selected Ehlichia/Anaplasma spp. positive samples were sequences and the obtained sequences from N. eusarca were identical to Wolbachia endosymbiont (access. nos.: MH618381.1 and EU315781.1) and an uncultured bacterium clone layman_j06 (access. no.: DQ980970.1). The sequences from C. vespertilionis matched Candidatus Ehrlichia shimanensis (AB074459.1) and uncultured Anaplasma sp. clone Erz1600 (access. no.: MT601947.1). The results for Ehrlichia/Anaplasma spp. might suggest that the used PCR reaction is not specific for the identification of the pathogenic species. All ectoparasite samples were negative for Babesia spp., while Borrelia spp. was detected in 4.7% (2/43) C. vespertilionis samples without identifying the Borrelia species after sequencing. In this study we report for the first time in Ukraine the molecular detection of several bacterial agents in two species of ectoparasites found on six species of bats. The data presented extend the knowledge on the distribution of ectoparasite species on bats and their involvement to potentially circulate pathogenic agents.

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WNV injected into Ticks?

Transstadial Transmission and Replication Kinetics of West Nile Virus Lineage 1 in Laboratory Reared Ixodes ricinus Ticks

September 2020Pathogens 9(780)
DOI:10.3390/pathogens9100780

West Nile virus (WNV) is a mosquito-borne agent that has also been isolated from several tickspecies. Vector competence ofIxodes ricinus, one of the most common tick species in Europe, has beenpoorly investigated for WNV to date. As such, to evaluate the vector competence, laboratory rearedIxodes ricinusnymphs werein vitrofed with WNV lineage 1 infectious blood, allowed to molt, and theresulting females artificially fed to study the virus transmission. Furthermore, we studied the kineticsof WNV replication in ticks after infecting nymphs using an automatic injector. Active replication ofWNV was detected in injected nymphs from day 7 post-infection until 28 dpi. In the nymphs infectedby artificial feeding, the transstadial transmission of WNV was confirmed molecularly in 46.7% ofmales, while virus transmission duringin vitrofeeding ofI. ricinusfemales originating from infectednymphs was not registered. The long persistence of WNV inI. ricinusticks did not correlate with thetransmission of the virus and it is unlikely thatI. ricinusrepresents a competent vector. However,there is a potential reservoir role that this tick species can play, with hosts potentially acquiring theviral agent after ingesting the infected ticks.

https://www.researchgate.net/
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WNV in Germany since 2018 via Mosquitoes???

West Nile Virus Lineage 2 Vector Competence of Indigenous Culex and Aedes Mosquitoes from Germany at Temperate Climate Conditions
May 2020Viruses 12(5):561
DOI:10.3390/v12050561

West Nile virus (WNV) is a widespread zoonotic arbovirus and a threat to public health in Germany since its first emergence in 2018. It has become of particular relevance in Germany in 2019 due to its rapid geographical spread and the detection of the first human clinical cases. The susceptibility of indigenous Culex pipiens (biotypes pipiens and molestus) for a German WNV lineage 2 strain was experimentally compared to that of Serbian Cx. pipiens biotype molestus and invasive German Aedes albopictus. All tested populations proved to be competent laboratory vectors of WNV. Culex pipiens biotype pipiens displayed the highest transmission efficiencies (40.0%–52.9%) at 25 °C. This biotype was also able to transmit WNV at 18 °C (transmission efficiencies of 4.4%–8.3%), proving that temperate climates in Central and Northern Europe may support WNV circulation. Furthermore, due to their feeding behaviors, Cx. pipiens biotype molestus and Ae. albopictus can act as “bridge vectors”, leading to human WNV infections.

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RACOONS

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