In the news

MEASLES INCREASES THE RISK OF OTHER INFECTIONS

Measles, which is caused by the measles virus, is a highly contagious infectious disease, and measles-related morbidity and mortality have been linked to an increased susceptibility to secondary bacterial and viral infections, even years after initial infection. Previous studies have suggested that measles induces prolonged impairment of acquired immunological memory that renders individuals more susceptible to other pathogens, although the underlying mechanisms were not well understood. The introduction of the measles–mumps–rubella (MMR) vaccine has been implicated in the reduction of childhood morbidity and mortality caused by non-measles pathogens; however, globally the number of cases of measles has increased, owing to a reduction in vaccine uptake, which might increase the incidence of secondary infections and mortality risk.

Two recent studies provide further evidence that measles induces 'immunological amnesia'; that is, long-term immune memory loss. Mina et al. analysed the antibody repertoire in unvaccinated children before and after natural measles virus infection as well as in vaccinated children and found that measles caused a reduction of the antibody repertoire in unvaccinated children (11–73%), whereas a similar loss of antibodies was not observed in vaccinated children (Science 1 Nov. 2019). Petrova et al. showed that measles virus infection causes changes in the diversity of naive and memory B lymphocytes that persist after the resolution of clinical symptoms (Science Immunol. 1 Nov. 2019). Together, the studies provide mechanistic insights into the immunological mechanisms whereby measles virus infection contributes to prolonged immunosuppression that alters previously acquired immune memory. Moreover, the findings further highlight the importance of vaccination and the need to increase vaccination rates.

The global decline in vaccine coverage is particularly worrying in the developing world, where the number of measles cases is rising, children are exposed to various infectious agents, and measles-related immunological amnesia might cause more deaths. In response to the ongoing measles outbreak in the Democratic Republic of the Congo, where more than 200,000 cases and about 4,000 deaths have been reported since January 2019, UNICEF is vaccinating thousands of children against measles and supplying life-saving medicines to care for infected individuals. In the developed world, the number of routine childhood vaccinations (including MMR) is falling, and countries, including the UK, have lost their eradication status. Anti-vaccination campaigns and misinformation are considered to be major factors contributing to the decline in vaccine uptake; the National Audit Office in the UK identified additional reasons, such as the timing and availability of appointments at the general practitioner, parents needing childcare as well as the reorganization of the National Health Service in England in 2013, which led to an inconsistent national approach to delivery of the vaccination programme (The Guardian). Thus, various factors need to be taken into account to ensure that high vaccination rates are recovered and maintained and to prevent measles outbreaks and measles-related complications and deaths.

Andrea Du Toit

PARASITE EVOLUTION

A sequence of unfortunate events

Plasmodium falciparum, the most prevalent and lethal of human malaria parasites, is thought to have evolved after transmission from gorillas. Reticulocyte-binding protein homologue 5 (RH5) is an essential adhesin for invasion of erythrocytes and has been implicated in host specificity of *P. falciparum*. Introgression (the movement of genomic regions from one species to another) of *rh5* into an ancestor of *P. falciparum* enabling infection of humans is thought to be a key event in the origin of *P. falciparum* in humans, but the molecular events of zoonosis were unknown. Now, Galaway et al. report the resurrection of ancestral RH5, providing a molecular explanation for the origin of human *P. falciparum*.

The authors used a genomic probabilistic-based approach and the sequences of extant species to infer the probable sequence of the ancestral introgressed *rh5* gene (*IntRH5*). *IntRH5* was expressed and purified and, using surface plasmon resonance (SPR), was found to bind to human and gorilla basigin (the erythrocyte receptor) with similar affinities. The promiscuous binding of IntRH5, which contrasts with the observed human-specificity of *P. falciparum* RH5, suggested a mechanism by which a gorilla parasite infected humans.

Next, the authors tested whether promiscuous binding was unique to IntRH5 by determining the RH5–basigin tropism for extant members of the *Laverania*,

MICROBIOME

At the root of the problem

Many studies have investigated the highly complex microbial assemblages that are associated with different plants and specific plant compartments, such as the rhizosphere, phyllosphere and endosphere. Although it is becoming increasingly clear that the plant microbiome has important functions in plant growth, development and health, a clear understanding of the functional role of plant-associated microorganisms and their functional capacity in promoting distinct plant phenotypes is lacking. Some soils were previously shown to protect plants from root pathogens. This effect, referred to as 'disease-suppressiveness', is partially conferred by microorganisms found in the rhizosphere, which provide a first line of defence against plant disease. In this study, Carrión et al. investigated how the endophytic root microbiome forms a second line of defence against the fungal root pathogen *Rhizoctonia solani* and report that *Chitinophaga* and *Flavobacterium* species and their functional traits have a role in plant protection from disease.

The authors grew sugar beet seedlings in field soil that was either conducive or suppressive to fungal disease and

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