

## Addressing social contexts and determinants of health in Marshallese communities

We read with great interest the Article by Virgie Fields and colleagues,<sup>1</sup> which describes a mumps outbreak in an Arkansas (USA) Marshallese community. They analysed relevant Arkansas Department of Health data from Aug 5, 2016, to Aug 6, 2017. The authors recognised that other social factors, such as health illiteracy, poor access to health care, and overcrowding, might explain the high prevalence of infectious disease in Marshallese people.

The authors conclude that the 2016–17 mumps outbreak underscored the need for an “interdisciplinary, culturally sensitive, outbreak response team”.<sup>1</sup> A social determinant of health that should be accounted for in this description is health-care access, perhaps through health-care facilitators. Although recognising the exclusion of Marshallese people from some federal health benefits, the authors neglect health-care access disparities in Arkansas itself. Arkansas’ children’s health insurance programme, ARKids First, is not available to Compact of Free Association migrants living in Arkansas, consequently leaving many Marshallese children without health insurance.<sup>2</sup> This unavailability could further explain why most mumps infections in this outbreak occurred in children.

Fields and colleagues note that investigators at the Arkansas Department of Health did interviews to obtain standardised demographic and exposure information, among other factors. Despite acknowledging the role of poverty in heightening the opportunity for disease spread in the Marshallese community, income was not stratified for. Poverty, a

function of low income and other social factors, leads to escalated health risks. For example, the working environments of poorer people often hold more environmental risks for illness and disability, and other environmental factors, such as lack of clean water access, disproportionately affect poor families.<sup>3</sup> This poor environment and contaminated water should be viewed in light of the effect of radioactivity exposure in Marshallese people. Cesium-137, a radioactive isotope with a half-life of about 30 years, was detected in the groundwater at all contaminated atolls in the northern Marshall Islands.<sup>4</sup> Cesium-137 is transported from soil to the edible portions of plants, further contributing to the radioactive dose experienced in the Marshall Islands.<sup>4</sup>

Fields and colleagues’ analysis could be improved by accounting for social determinants of health, such as poor access to health care and socioeconomic poverty, which might affect Marshallese people with disadvantaged status. Improving statistical measurements and analyses of mumps prevalence through addressing health inequities and social contexts governing health will allow infectious disease professionals to improve prevention and more adequately address future outbreak burdens.

We declare no competing interests.

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- 2 McElfish PA. Marshallese COFA migrants in Arkansas. *J Ark Med Soc* 2016; **112**: 259.
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### Authors’ reply

We thank Asghar Shah and colleagues for their comments on our Article<sup>1</sup> reporting a mumps outbreak among the Marshallese community in Arkansas, USA. We agree that social determinants of health, such as access to health care and socioeconomic poverty, within this community are important factors that should be further described. However, during the outbreak, when over 100 individuals per week were interviewed and numerous urgent vaccination clinics were held in a variety of settings, only demographical and epidemiological information essential to controlling transmission were collected. Unfortunately, information about social determinants of health was not collected in this context.

Nonetheless, readers might benefit from additional information about the social determinants of health for the Marshallese community in Arkansas. A 2017 pilot study provided a foundation for understanding the socioeconomic challenges that affect this population.<sup>2</sup> The study found that only half (199/401) of Marshallese participants had a high school education, and among individuals who did, only 15% (60/401) had college education.<sup>2</sup> The vast majority (89%; 191/214) report income that is at or below the federal poverty level (unpublished). Although information about income is sparse, it is known that many Marshallese people in Arkansas work low-wage jobs, without health or retirement benefits, in the poultry industry.<sup>3</sup> In the outbreak we studied, we observed intense disease transmission in crowded homes and other congregate settings.<sup>1</sup> The unifying underlying factor in each of these settings is poverty.

These social determinants of health, along with federal policies

that exclude Marshallese migrants from Medicaid, have restricted their access to health care.<sup>2</sup> Almost half (46%; 183/394) of the adult Marshallese population that was sampled was uninsured.<sup>2</sup> The large majority (80%; 312/392) did not have a primary care provider, and half (196/389) stated they needed to see the doctor in the past year but did not because of cost.<sup>2</sup> As Shah and colleagues point out, Marshallese children were also excluded from the ARKids First programme until 2017 (during the outbreak period). Despite low rates of insurance, the clear majority (92%; 1536/1676) of children aged 5 to 17 years affected in the outbreak were vaccinated with two or more doses of measles, mumps, and rubella vaccination.<sup>1</sup>

Qualitative studies have shown that other social determinants of poor health at multiple levels of the community ecology are barriers to health-care access, including low access to transportation, food insecurity, limited English language proficiency, and scarce Marshallese medical translators.<sup>4</sup> Successful health interventions for reaching the Marshallese community in Arkansas have been culturally adapted and have used community health workers and non-traditional models of care, such as home visiting programmes.<sup>5</sup> These findings reinforce the need for culturally sensitive and informed outbreak-response efforts to engage this marginalised community.

We declare no competing interests.

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## Host genetic factors can impact vaccine immunogenicity and effectiveness

Darren Westphal and Asha Bowen<sup>1</sup> commented on the study of Virgie Fields and colleagues<sup>2</sup> about a mumps outbreak in a highly vaccinated Marshallese community of Arkansas (USA). Their Comment provides an important discussion about the factors that can explain the outbreak in this specific situation. Westphal and Bowen ended their article with the following question: “Is vaccine effectiveness equal among all populations?”

Considering genetic diversity in a broad sense and data about susceptibility and resistance patterns of distinct human populations to different pathogens, we believe that vaccine effectiveness should differ according to the human population targeted. Different patterns of vaccination effectiveness among different populations would result from complex interactions of the host, pathogen, and environmental factors. In this sense, such differential patterns could arise because of (although not exclusively as a result of) distinct or characteristic host genetic factors such as frequencies of specific alleles of, for example, major histocompatibility complex genes in a given human population. As an example, we

would like to call attention to an immune system-related genetic variant that is suggested to affect vaccine immunogenicity. Ganczak and colleagues<sup>3</sup> have shown the homozygous genotype of CCR5Δ32 to be associated with reduced hepatitis B virus (HBV) vaccine immunogenicity. CCR5Δ32 is a 32-base-pair deletion in the coding region of the CCR5 gene that affects CCR5 protein expression. CCR5 is a chemokine receptor involved in various immune reactions and pathological processes, including susceptibility to HIV infection and the inflammatory state seen in rheumatoid arthritis, cancer, and other diseases.<sup>4</sup> Since this genetic variant presents a characteristic distribution, being typically more frequent among populations of European origin,<sup>5</sup> the newly described influence of CCR5Δ32 on HBV vaccine immunogenicity demonstrates how the genetic background of different populations might influence the effectiveness of vaccines. This point highlights the importance of not only ethnic origin but also the geographical distribution of the human population under investigation.

We acknowledge that it is unlikely that a given specific genetic variant would substantially affect the effectiveness of most vaccines. Following this same reasoning, we are not affirming that genetic factors would indeed explain the results of Fields and colleagues. However, the scenario mentioned above reminds us that the influence of human genetic factors on vaccine effectiveness is a neglected issue. Studies exploring the genetic variability of distinct human groups can help us to understand differentiated patterns of vaccine response among different human populations.

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