The Honorable Tuilaepa Aiono Sailele Malielegaoi
Prime Minister
Independent State of Samoa

November 19th, 2019

Dear Honorable Prime Minister,

I write with profound sadness to offer my condolences for the measles outbreak that has recently affected your country and taken the lives of precious Samoan children. These deaths are a personal tragedy for their bereaved families and for all the people of your tight-knit nation.

I was dismayed—but not surprised—to see media reports that linked the current measles outbreak to the so-called "anti-vaccine" movement. While we can expect pundits to engage in uninformed finger-pointing, Samoa's public health officials must undertake the serious tasks of containing the infection and—equally importantly—to thoroughly understand its etiology. To safeguard public health during the current infection in and in the future, it is critical that the Samoan Health Ministry determine, scientifically, if the outbreak was caused by inadequate vaccine coverage or alternatively, by a defective vaccine.

There are three questions that Samoan Health Officials must answer if they are to make a science-based determination.

1) **What were the ages of the victims?**

Media reports from Samoa suggest that the infection is targeting young infants who are not yet of age to receive the measles vaccine. If true, the culprit is most likely a vaccine that failed to produce antibodies in the vaccinated mothers sufficient to provide the infant with maternal immunity. Young infants contracting measles is a relatively new phenomena first recognized in the 1990's. Prior to the development and widespread use of Merck's measles, mumps and rubella (MMR) vaccine, mothers passed protection to their infants via passive immunity derived from the placenta and breast milk. In contrast, mothers vaccinated with a defective Merck vaccine provide inadequate passive immunity to their babies. Merck's version of the MMR has created a crisis where infants under the age of one are now highly vulnerable to these infections. These young infants suffer a much higher morbidity and mortality compared to populations historically impacted by wild measles later in childhood.

When it first introduced its measles vaccine in 1963, Merck promised that a single dose of its vaccine would provide lifetime immunity and maternal immunity equivalent to that provided by wild measles. Merck predicted that its vaccine would eradicate measles by 1967, so long as 55% of children were immunized. Leading scientists including the world's preeminent

bacteriologist, Sir Graham Wilson and Harvard Virologist John Enders, who first isolated measles, warned against introducing a vaccine unless it provided lasting life-long immunity, as Merck promised. Measles, they cautioned, would rebound with increased virulence and mortality as the vaccine shifted outbreaks away from children—biologically evolved to handle measles—to young infants with inadequate maternal immunity and senior citizens vulnerable to measles-induced pneumonia. Unfortunately, we are now seeing the global emergence of the exact pattern that scientists cautioned against.

2) **Were Samoa's fatal measles cases caused by strains of measles not targeted by Merck's vaccine?**

Both Dr. Enders and Dr. Wilson and other leading Virologists warned Merck that in addition to shifting the disease to vulnerable infants and the elderly, a defective vaccine with high initial failure rate, or substantial long-term waning, would provoke the evolution of more virulent measles strains.

American public health officials have recently admitted that, instead of providing lifetime immunity, Merck's vaccine failed in about 10% of vaccine individuals within seven years. And, as scientists predicted, the measles virus has therefore mutated. Two new strains of measles that are not included in the current vaccine are now spreading like wildfire among populations worldwide. Global Public Health Officials have recently identified these deadly new rogue strains as measles genotype D4.1 and D4.2. The vaccine genotype A in the current MMR vaccine cannot adequately neutralize new strains. Merck cannot claim that this development is a surprise. Virologists have long known that viruses with multiple strains often shift to evade a vaccine that targets just a few strains. This is the reason that public health officials develop new flu vaccines each year to target the emerging viral strains.

3) **Were the fatal Samoan infections from a vaccine strain?**

There is also the possibility that children who received the live measles virus during Samoa's recent vaccination drive may have shed the virus and inadvertently infected vulnerable children. It is a regrettable possibility that these children are causalities of Merck's vaccine. Alarmed CDC officials documented this emerging phenomenon during the measles outbreak in California in 2015. Federal epidemiological investigations found that at least 1/3 of Californian cases were vaccine strain. In fact, CDC identified 73 of the 194 measles virus sequences obtained across the entire United States in 2015 as vaccine strain A sequences. This means that those children contracted measles from vaccination or from someone who received the vaccine.

For obvious reasons, it is critical for Samoa's public health officials to quickly determine if the Samoan children who recently died suffered measles from the Merck vaccine or from a mutant strain that evolved to evade the Merck vaccine. In each of those cases, Samoa's public health officers would react with a very different strategy than if the lethal measles genotype was a wild strain that spread due to inadequate vaccine coverage.

Therefore, it is critical to obtain timely and accurate information regarding gene sequencing of the measles infections that now threaten the health of your citizens. If any genotypes identified

include wild-type virus, it is also critical that they be sequenced to determine whether they are emergent resistant D 4.1, and D 4.2 strains. If these strains caused the deaths, further boosting with MMR vaccine might only exacerbate the situation and further spread the disease.

Because of the widely-recognized importance of making these determinations with each new measles outbreak, reputable laboratories around the globe now specialize in routinely identifying measles genotypes. To that end, we are offering information below for options for obtaining this critical information. Please do not hesitate to contact me if I can be of any assistance. You and the wonderful citizens of Samoa will continue to be in my thoughts and prayers.

Sincerely,

Robert F. Kennedy Jr.
Chairman, Children's Health Defense

cc. Dr. Leausa Take Naseri, Director General of Health

Information Regarding Measles Virus Sequencing

Measles virus strain-determination by gene sequencing is a straightforward, tried-and-tested routine laboratory practice. [1-4] The key to the success of the molecular assay is the quality of the starting genetic material isolated from clinical samples. Successful sequence analysis has been conducted in measles sufferers on urine, throat swabs, and peripheral blood mononuclear cells, isolated from a venous blood draw.

Measles is an RNA (as opposed to a DNA) virus. RNA is prone to rapid degradation after the sample has been taken and must be preserved adequately to protect it from enzymatic destruction of the measles virus genomic RNA. This can be achieved by rapid isolation of the cells from the sample and freezing and maintaining the sample at -70 to -80 degrees centigrade. Alternatively, and much more conveniently, preservation reagents like RNALater can be added to the sample according to the manufacturer's instructions. See ThermoFisher Scientific for additional information at the link below. https://www.thermofisher.com/us/en/home/brands/product-brand/rnalater.html?gclid=EAIaIQobChMIsKa_r4Hv5QIVxR6tBh3BFgSLEAAYASAAEgICzfD_BwE&s_kwcid=AL!3652!3!352479661678!e!!g!!rnalater&ef_id=EAIaIQobChMIsKa_r4Hv5QIVxR6tBh3BFgSLEAAYASAAEgICzfD_BwE:G:s&s_kwcid=AL!3652!3!352479661678!e!!g!!rnalater

Samples need to be sent to laboratory willing and able to perform the necessary analysis. Here is a promising option: CD Genomics, https://www.cd-genomics.com/Viral-Genome-Sequencing.html?gclid=EAIaIQobChMIkO6L4IDv5QIVyB6tBh0A4AyZEAAYAyAAEgJBnPD_BwE

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