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# Sir model of hepatitis B disease in the North Tongu district

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**Abstract**
In this paper, we consider the prediction and the spread of the infectious disease (Hepatitis B) and develop a model based on the Susceptible-Infected-Recovered (SIR). The North Tongu District was considered as the host population. The district is assumed to have a constant population size. A system of non-linear differential equations is used to model the spread of the disease in the district. We solve the system numerically using the fourth-order Runge-Kutta method. Simulation and sensitivity analyses were also performed on the model equations to determine the effect of different parameter values on the spread of the disease. It was shown that the global dynamics are completely determined by the basic reproductive number $R_0$. If $R_0 < 1$, the disease-free equilibrium is globally stable and the disease always dies out. On the other hand, if $R_0 > 1$, an endemic equilibrium exists and is globally stable in the interior of the feasible region, and the disease persists in an endemic equilibrium state if it initially exists. This paper indicates that the people of North Tongu would be at high risk if there should be an outbreak of the Hepatitis B. It was therefore recommended that vaccination of the more susceptible populace should to be done, since it will give immunity to the individual

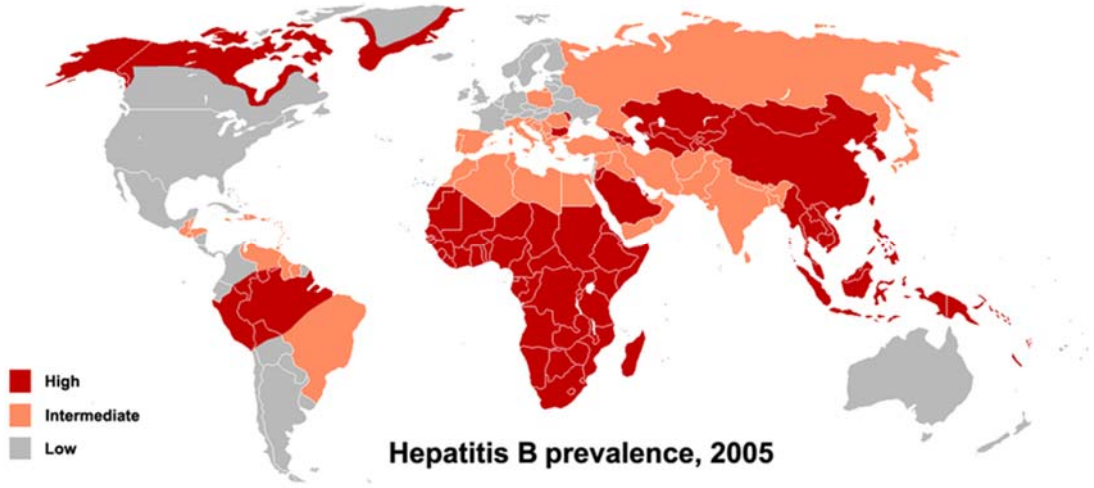
**Keywords:** Hepatitis B, SIR, epidemiology, simulation and sensitivity analysis

## 1. Introduction
Hepatitis B is one of the major health problems in the world. The World Health Organization (WHO) reported that over one-third of the world's population (more than 2 billion people) has been or is actively infected with HBV; more than 350 million have chronic (lifelong) infections and 25-40 percent of these chronic infection carriers die from liver cirrhosis or primary hepatocellular carcinoma. HBV is the 10th leading cause of death worldwide (World Health Organization, 1997). The hepatocellular cancer (HCC) alone accounted for more than 500,000 deaths per year, making it the 3rd most common cause of cancer death worldwide (Parkin, Bray *et al*. 2005) [11].

National and regional prevalence ranges from over 10% in Asia to under 0.5% in the United States and northern Europe. Routes of infection include vertical transmission (such as through childbirth), early life horizontal transmission (bites, lesions, and sanitary habits), and adult horizontal transmission (sexual contact, intravenous drug use).

The primary method of transmission reflects the prevalence of chronic HBV infection in a given area. In low prevalence areas such as the continental United States and Western Europe, injection drug abuse and unprotected sex are the primary methods, although other factors may also be important. In moderate prevalence areas, which include Eastern Europe, Russia, and Japan, where 2–7% of the population is chronically infected, the disease is predominantly spread among children. In high prevalence areas such as China and South East Asia, transmission during childbirth is most common, although in other areas of high endemicity such as Africa, transmission during childhood is a significant factor. The prevalence of chronic HBV infection in areas of high endemicity is at least 8%.

The HBV disease burden are generally classified as percentage of Hepatitis B surface antigen (HBsAg) carriers in the population and categorized as; low($< 2\%$), intermediate ($2 - 7\%$) or high ($> 8\%$), as shown in Figure 1.1




**Source:** http://en.wikipedia.org/wiki/File:HBV_prevalence_2005.png

**Fig 1:** Global Hepatitis B virus prevalence

Hepatitis B virus is a Deoxyribonucleic acid (DNA) virus with a remarkably compact genomic structure; it has a relaxed circular (but not covalently closed), partially double stranded DNA genome. The complete genome is approximately 3200 nucleotides (3.2 kilobases or kb) long. There are four sets of HBV DNA codes for viral products with a complex, multiparticle structure. HBV achieves its genomic economy by relying on an efficient strategy of encoding proteins from four overlapping genes: the envelope (S); core (C); polymerase (P); and X regions (Scanglioni, Melegari *et al*. 1996) [13]. See Figure 1.2.

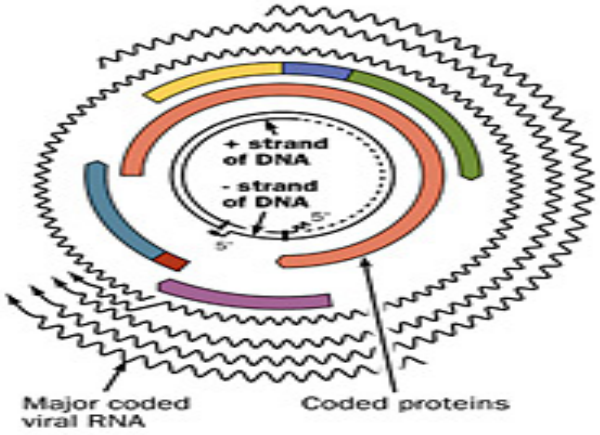



**Fig 2:** Genomic organization of Hepatitis B virus

### 1.1 Epidemiology of Hepatitis B

In order to reproduce, the virus belongs to the Hepadnaviridae family. Its members are divided into two genera; Orthohepadnaviruses infecting mammals, and Avihepadnaviruses affecting birds. The two genera of HBV, all have the same distinctive three morphologic forms, and counterparts to the envelope and nucleocapsid virus antigens of HBV. They replicate in the liver, but exist in extrahepatic sites, contain their own endogenous DNA polymerase and have partially double-strand and partially single-strand genomes.

The hepatitis B virus consists of an outer 42nm diameter spherical lipoprotein envelope and an inner 27nm diameter icosahedral nucleocapsid core enclosing the DNA genome, polymerase and a protein Kinase (Dane et al, 1970). The outer envelope contains embedded proteins which are involved in viral binding off, and entry into, susceptible cells. The virus is one of the smallest enveloped animal viruses with a virion diameter of 42 nm, but pleomorphic forms exist, including filamentous and spherical bodies lacking a core. These particles are not infectious and are composed of the lipid and protein that forms part of the surface of the virion, which is called the surface antigen (HBsAg), and is produced in excess during the life cycle of the virus.

Hepatitis B virus, must first attach onto a cell which is capable of supporting its replication. Though the liver is the most effective cell type for replicating HBV, other extrahepatic sites have been found to be able to support replication to a lesser degree. HBV replicative intermediates and/or viral transcripts have been found in mononuclear cells, bile duct epithelial, endothelial, pancreatic acinar cells, and smooth muscle tissue, as well as in the adrenal glands, gonads, cultured bone marrow, kidneys, lymph nodes, spleen and thyroid glands of acute hepatitis B infected patients (Dienstag, 2008) [3]. Although the virus does not appear to be associated with tissue injury in any of these extrahepatic sites, its presence in these “remote” reservoirs has been invoked to explain the recurrence of HBV infection after orthotopic liver transplantation.

Hepadnaviruses rely on a replicative strategy unique among DNA viruses, but typical of retroviruses. Instead of DNA replication directly from a DNA template, hepadnaviruses rely on reverse transcription (effected by the DNA polymerase) of minus-strand DNA from a “pregenomic” Ribonucleic acid (RNA) intermediate. The plus-strand DNA is transcribed from the minus-strand DNA template by the DNA dependent DNA polymerase and converted in the hepatocyte nucleus to a covalently closed circular DNA (cccDNA) by host proteins called chaperones, which serves as a template for messenger RNA and pregenomic RNA. Viral proteins are translated by the messenger RNA, and the proteins and genome are packaged into virions and secreted from the hepatocyte. Although HBV is difficult to cultivate in vitro in the conventional sense from clinical material, several cell lines have been transfected with HBV DNA. Such transfected cells support in vitro replication of the intact virus and its component proteins.

## 2. Method

### 2.1 Area of Study

North Tongu District is one of the twenty five (25) Municipalities and Districts in the Volta Region of Ghana, with its Administrative capital known as Battor. The people of North Tongu District are mainly in subsistence farming and petty trading. There are 5 Senior High Schools 53 Junior High Schools, 119 primary schools and 79 preschools. North Tongu District Assembly has 12 health facilities spread across the District. These facilities under the Ghana Health Service and Christian Health Association of Ghana provide health services to the citizens. The District has one hospital (Battor Catholic Mission Hospital), six (6) Health Centres, three (3) CHPS Zones and one (1) private clinic.

### 2.2 Study Design

We employ the Susceptible-Infective-Recovered (SIR) compartmental model which was developed by Karnack and McKendrick in 1927. This model would be used to describe the epidemiology to compute the amount of susceptibles, infectives and recovered people in a population. The model equations are solved numerically using the fourth-order Runge-Kutta method. All algorithms employed were implemented using MATLAB. Simulation and sensitivity analysis are then performed on the model equations to determine the effect of the parameter values on the spread of the disease. Epidemiology has provided valuable insights for analysis of different types of diseases in the world.

## 3. Sir Model

### 3.1 Description of SIR Model of Hepatitis B

The model is divided into three classes: Susceptible class (S), Infective class (I) and Removal class (R). This is represented as:

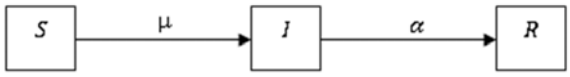



**Fig 3:** is the flowchart of the SIR model of Hepatitis B without vital dynamics, where proportionality constant μ and $\alpha$ are the infection and removal rates respectively. When the disease persists in a population for a longer period of time than we have.

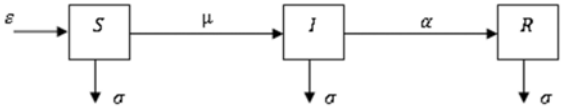



**Fig 4:** represents the flow chart of the SIR model of Hepatitis B with vital dynamics, with a natural death rate of $\sigma$ and birth rate of $\varepsilon$.

The stability of the disease free equilibrium depends on the values of $\sigma, \alpha$ and $\mu$, given the equation $\lambda_1 = -\sigma < 0$ and $\lambda_2 = \mu - \sigma - \alpha$. (3.1)

The basic reproductive ratio ($R_0$) of Hepatitis B with vital dynamics, conclude that the average time of an infection is $\frac{1}{\alpha+\sigma}$, and as infectious individuals infect others at rate $\mu$, the basic reproductive number becomes

$$R_0 = \frac{\mu}{\alpha + \sigma} \quad 3.2)$$

Similarly, the stability of the endemic equilibrium depends on the values of $\sigma, \alpha, \mu$ and $\varepsilon$ given the equation

$$\lambda_{1,2} = \frac{\frac{-\mu\varepsilon}{\sigma+\alpha} \pm \sqrt{\left(\frac{\mu\varepsilon}{\sigma+\alpha}\right)^2 - 4(\mu\varepsilon - \sigma(\sigma+\alpha))}}{2} \quad (3.3)$$

## 4. Results and Discussions

### 4.1 Simulations and Results of SIR model with vital dynamics

Considering the SIR model with vital dynamics we use the estimated parameters in table 1

**Table 1:** Parameter values of the SIR model with vital dynamics

| Description | Parameter | Value |
|---|---|---|
| Birth rate | $\varepsilon$ | 0.03 |
| Infectious rate | $\mu$ | 0.13 |
| Recovered rate | $\alpha$ | 0.085 |
| Natural death rate | $\sigma$ | 0.03 |

**Source:** Battor Catholic Hospital, Battor.

From equation (3.2), we obtained the reproductive number to be

$$R_0 = \frac{0.13}{0.085 + 0.03} = 1.1304$$

This means that on the average, one hepatitis B patient contacts 1.1304 susceptible people in the population during his/her infectious period. Since the reproductive number $R_0 = 1.1304 > 1$, an outbreak of hepatitis B will result in an epidemic in the North Tongu District.

Figure 6 below depicts the dynamics of the various compartments (susceptible, infectives and recovered) during the outbreak, where $S(t) = 0.95, I(t) = 0.05$ and $R(t) = 0.00$. When the initial infectives is 0.05, the proportion of the susceptibles declines from an initial value of 0.95 to an approximate minimum value of 0.83 from the first week to the sixtieth week and begins to increase gradually afterwards, reaching a value of 0.89.

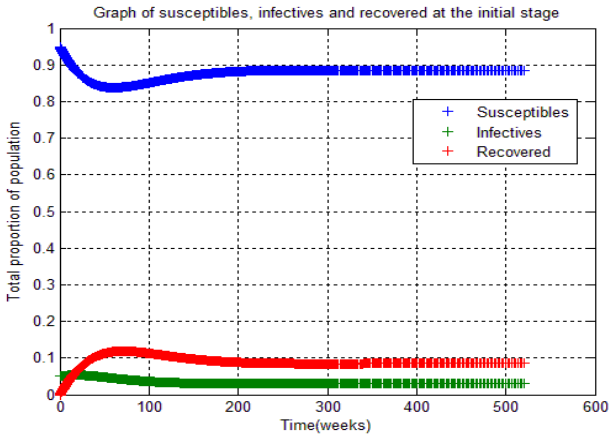



**Fig 6:** The dynamics of the various compartments during the outbreak.

The population of the infectives declines asymptotically from the first week, reaching a minimum value of 0.03 on the 160th week and maintaining that value onwards. Also, the proportion of the recovered population increased after the initial week and reaches a maximum value of 0.12 on the 70th week and then declining steadily with time until it reaches a value of 0.08 on the 180th week and maintaining that value afterwards.

### 4.2 Effects of initial infectives on the various compartments.

Experiments were performed to verify the effect of varying initial infectives on the dynamics of the susceptible, infective, and recovered populations. Table 2 contains the various instances considered for the initial number of infectives. The number of susceptibles varies appropriately with change in the number of infectives.

**Table 2:** Varying the initial number of infectives

| Infectives | Susceptibles | Recovered |
|---|---|---|
| 0.05 | 0.95 | 0.00 |
| 0.10 | 0.90 | 0.00 |
| 0.20 | 0.80 | 0.00 |
| 0.30 | 0.70 | 0.00 |

From Figure 7 below, when the initial proportion of the infectives is 0.05, the proportion of the susceptibles declined from an initial value of 0.95 to an approximate minimum value of 0.84 from week one to week 60 and then began to increase until attaining a constant value of 0.89 at week 200.

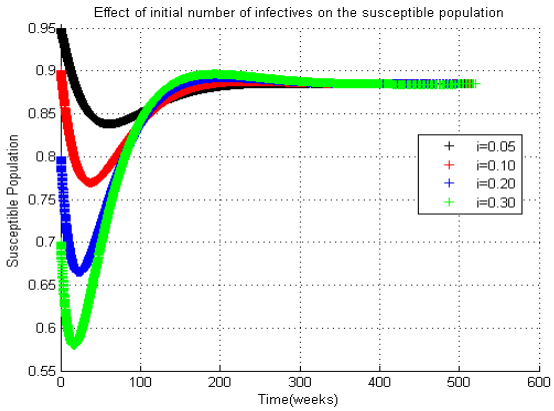



**Fig 7:** Effects of initial infectives on the susceptible population with vital dynamics.

When the initial proportion of infectives is increased to 0.10, 0.20 and 0.30, the proportion of the susceptibles declined from an initial value of 0.90, 0.80 and 0.70 to a minimum value of 0.77 in 40 weeks, 0.67 within 30 weeks, and 0.58 within 20 weeks respectively. After week 340, they all attained a steady state of 0.89.

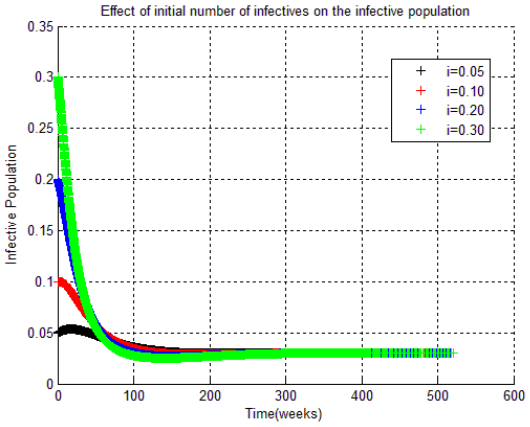



**Fig 8:** Effects of initial infectives on the infective population with vital dynamics

In Figure 4.3 above, as the initial proportion of infectives is 0.05, the proportion of the infectives declines from its initial value of 0.05 to its minimum value of 0.03 within 160 weeks. With the initial proportion being 0.10, 0.20 and 0.30, the infective populations exhibited similar behavior by declining exponentially to 0.03 by week 150. It is observed that the higher the initial proportion of the infectives, the faster the declination.

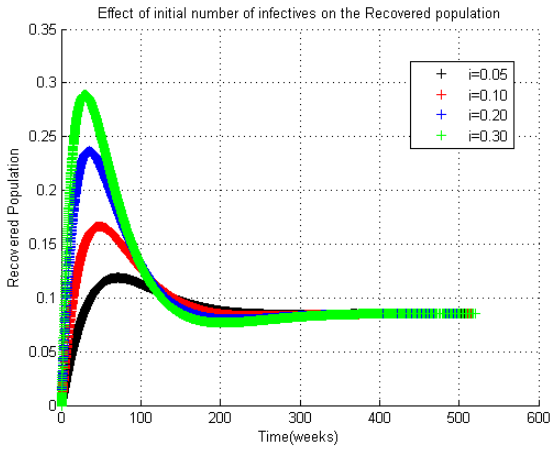



**Fig 9:** Effects of initial infectives on the recovered population with vital dynamics

From Figure 4.4, as the initial proportion of infectives is 0.05, the proportion of the recovered population rises exponentially from zero at week one to a peak value of 0.12 on week 70 before reducing gradually to 0.08 on week 210 and remained stable at that value as the weeks go by. As the initial proportion of the infectives is increased to 0.10, the maximum value of 0.17 was reached on week 50.

Similar observations are made for the increasing number of initial proportion of infectives. However, each proportion of the recovered population attains different peak values, but at different times with all declining to a minimum of 0.08.

### 4.3 Stability Analysis of the model with vital dynamics

We now look at the linear stability of the infectious free equilibrium point$E_0(S^*, I^*) = (1,0)$. By substituting the parameter values in table 4.1 into equation (3.1), the eigenvalues corresponding to the infectious free equilibrium are $\lambda_1 = -0.03$ and

$\lambda_2 = 0.015$. Because the two eigenvalues are both real, one is positive and the other negative, it implies the disease free equilibrium is a saddle point, therefore unstable. The unstable equilibrium implies that the presence of a Hepatitis B positive patient in North Tongu will eventually result in an outbreak of the disease. The endemic equilibrium point occurs at a time where all the compartments of the population coexist in the population. The introduction of an infected person will infect others, therefore changing the health condition of a lot of people. Substituting the parameter values in Table 4.1 into equation (3.2), we obtain the eigenvalues corresponding to the endemic equilibrium. This is given by

$$\lambda_{1,2} = \frac{\left(\frac{\mu\varepsilon}{\sigma+\alpha}\right) \pm \sqrt{\left(\frac{\mu\varepsilon}{\sigma+\alpha}\right)^2 - 4\left(\mu\varepsilon - \sigma(\sigma+\alpha)\right)}}{2}$$

$$\lambda_{1,2} = \frac{-\left(\frac{0.13\times0.03}{0.03+0.085}\right) \pm \sqrt{\left(\frac{0.13\times0.03}{0.03+0.085}\right)^2 - 4\left(0.13\times0.03 - 0.03(0.03+0.085)\right)}}{2}$$

$$\lambda_{1,2} = \frac{-0.0339 \pm \sqrt{(0.0339)^2 - 0.0018}}{2}$$

$$\lambda_1 = -0.01695 + 0.01276i \text{ and } \lambda_2 = -0.01695 - 0.01276i$$

Since the eigenvalues have real negative parts with complex conjugates, it implies the endemic equilibrium is asymptotically stable.

**4.4 Sensitivity Analysis of the model with Vital Dynamics**

Vital dynamics is introducing birth and death into a population when a disease persists for a long period of time.

**Table 3:** Parameter values, Eigenvalues and classification of the disease free equilibrium with Vital Dynamics.

| $\varepsilon$ | $\mu$ | $\alpha$ | $\lambda_1$ | $\lambda_2$ | $\sigma$ | $R_0$ | Nature of the equilibrium |
|---|---|---|---|---|---|---|---|
| 0.03 | 0.095 | 0.085 | -0.03 | -0.02 | 0.03 | 0.8261 | Stable sink |
| 0.03 | 0.130 | 0.085 | -0.03 | 0.015 | 0.03 | 1.1304 | Unstable saddle |
| 0.03 | 0.085 | 0.085 | -0.03 | -0.03 | 0.03 | 0.7390 | Stable improper sink |
| 0.03 | 0.115 | 0.085 | -0.03 | 0 | 0.03 | 1.000 | Neutrally stable |

**Source:** Battor Catholic Hospital, Battor.

From equation (3.1), we could observe that the eigenvalues, $\lambda_1 = -\sigma$ and since $\sigma > 0$, it implies that $\lambda_1 < 0$.Considering the second eigenvalue, $\lambda_2 = \mu - \sigma - \alpha$, stability can only be obtained if $\lambda_2 < 0$. Thus $\mu < \sigma + \alpha$, and $\frac{\mu}{\sigma+\alpha} < 1$ implying $R_0 < 1$. The disease free equilibrium will be stable if the reproductive number is less than unity, i.e. $R_0 < 1$, whilst the disease free equilibrium is unstable if the reproductive number is greater than unity.

**Table 4:** Parameter values, Eigenvalues and classification of equilibrium points of the endemic equilibrium with Vital Dynamics

| $\varepsilon$ | $\mu$ | $\alpha$ | $\lambda_1$ | $\lambda_2$ | $\sigma$ | $R_0$ | Nature of the equilibrium |
|---|---|---|---|---|---|---|---|
| 0.03 | 0.095 | 0.085 | 0.01506 | -0.03984 | 0.03 | 0.8261 | Unstable saddle |
| 0.03 | 0.130 | 0.085 | 0.02090 | -0.04307 | 0.03 | 0.7391 | Unstable saddle |
| 0.03 | 0.085 | 0.085 | -0.01696 + 0.01275i | -0.01696 -0.01275i | 0.03 | 1.1304 | Stable spiral sink |
| 0.03 | 0.115 | 0.085 | 0 | -0.03 | 0.03 | 1.000 | Neutrally stable |

**Source:** Battor Catholic Hospital, Battor.

From the above table, it is observed that the endemic equilibrium is stable when the reproductive number is greater than unity, i.e. $R_0 > 1$, and unstable when the reproductive number is less than unity, i.e. $R_0 < 1$.

## 5. Conclusion and Recommendations

The infectious rate and the recovery rate play the dominant role in determining the outcome of Hepatitis B virus in the North Tongu District of Ghana when there happens to be an outbreak. In the absence of vaccination, the susceptible population will reduce sharply when an infective is introduced into the population. The rate of decrease is directly proportional to the number of infectives introduced into the population. With time, the infective population will reduce as more and more infectives recover from the disease and become immune.

The calculated reproductive ratio was 1.1304 and this suggests that the North Tongu District is in danger should there be an outbreak. There is therefore the need to reduce the reproductive ration to less than one. To do this vaccination of the more susceptible populace needs to be done, since it will give immunity to the individual. Also, awareness campaigns need to preached about the silent killer and by the campaign, horizontal transmission will be reduced since more and more people would be aware of the seriousness and consequence of sharing household items like toothbrush, towels and partially eaten candies with a brother or a sister whose HBV status is not known.

## 6. Acknowledgement

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