Genotype 2: Prevalence, Cure and Viral Diaspora

This article which originally appeared in the HCV Advocate, discusses hepatitis C genotype 2.

February 25, 2015 By Alan Franciscus

In the past, genotype 2 and 3 information has been lumped together. More recent information has emerged that there are clear differences between these two genotypes with respect to prevalence, disease progression and treatment cure rates. Interestingly, there is also substantial data about how genotype 2 migrated from Africa to other parts of the world via the slave trade in the 16th, 17th, and 18th centuries.

Prevalence

There are 7 HCV genotypes identified numbered 1 through 7. The most common genotypes worldwide include:

- Genotype 1 (46.2%)
- Genotype 3 (30.1%)
- Genotype 2 (9.1%)
- Genotype 4 (8.3%)
- Genotype 6 (5.4%)
- Genotype 5 (.8%)

So far, there has only been 1 person identified with genotype 7. Thirteen to 15% of people with hepatitis C in the United States are infected with genotype 2.

As noted above, 9.1% of the population worldwide has genotype 1. This translates to about 16.5 million people infected with HCV genotype 2 globally. Areas that have a prevalence of 10% or greater include:

- Central Latin America— 19.3%
- East Asia—15.3%
- High-income Asia Pacific—24.5%

- High-income North America—12.0%
- Southeast Asia—18.2%
- Western Europe—10.8%
- West Sub-Saharan Africa—23.0%

Subtype
The most common genotype 2 subtypes include 2a, 2b, 2c, but there have been 15 other subtypes identified.

Origins
Technology is amazing! Science can analyze the genetic make-up of hepatitis C virus to estimate the origin, date it and track the viral migration. Previous studies were able to deduce that genotype 2 originated in West Africa at least 500 years ago.

In the current study "Phytogeography and molecular epidemiology of hepatitis C virus genotype 2 in Africa," by P.V. Markov et al., the authors wanted to understand where genotype 2 originated. The study group looked at all the known subtypes of genotype 2, then concentrated on the geographical area of Guinea-Gambia, which had been theorized as the origin of genotype 2. Using a process called the molecular clock the authors confirmed that Guinea-Gambia was indeed the source of genotype 2. Genotype 2 then spread from West Africa to Central Africa.

Blood-to-blood contact transmits hepatitis C. This being the case, it is likely that the spread of hepatitis C through Africa occurred over hundreds of years. So what made hepatitis C increase in such large numbers and spread throughout all of West Africa and Central Africa faster? It is most likely that hepatitis C was spread throughout Africa by European campaigns to treat endemic diseases in Africa with injectable medications. Trypanosomiasis (sleeping sickness), syphilis, yaws, malaria, and leprosy were (and some still are) rampant in Africa. Treating these and other diseases was well-intentioned but, unfortunately, the needles were reused or not properly cleaned. Millions of unsafe injections were given in Africa before the advent of disposal needles, which contributed to the spread of hepatitis C in Africa.

With regard to how genotype 2 was spread beyond Africa that question has also been answered based on the same genetic technology. The introduction of genotype 2 into America—particularly in Central and South America—was the result of the transatlantic slave trade from West Africa. This is called viral migration.

This is the same way that yellow fever (in the same viral family as the hepatitis C virus—flavivirus family) and other diseases common in Africa were introduced into the Americas by the same transatlantic slave trade. Similarly, European diseases such as smallpox, measles, tuberculosis, and influenza were introduced into the Americas by the Europeans.

Genotype 2 is also common in Europe not only because of the slave trade, but also due to immigration. France is believed to have contributed to the migration of genotype 2 from their West African colonies to other colonies in Morocco, Quebec, and Vietnam (French Indochina). It appears that genotype 2 in France was introduced by West African conscripts trained and stationed in southern France during World

War I—but this needs to be confirmed by larger studies.

Genotype 2 did not only migrate from Africa to the Americas and Europe, it also migrated from South America to Asia. This occurred by way of the slave trade from Java, Indonesia to Surinam (South America) and then back to Indonesia in the 20th century.

Disease Progression
Genotype 2 does not increase the risk for HCV disease progression. This is in stark contrast to genotype 3, which has been found to increase the risk for steatosis (fatty liver) and HCV disease progression, including higher rates of fibrosis and steatosis.

Treatment
The American Association for the Study of Liver Diseases (AASLD) and the Infectious Disease Society of American (IDSA) recommend that genotype 2 should be treated with the combination of Sovaldi (sofosbuvir a pill taken once-a-day) plus ribavirin (a pill taken twice daily—dosage based on a person's body weight). The duration of treatment with Sovaldi is 12 weeks. The cure rates are:

- Treatment naïve: 97% (no cirrhosis 97%; cirrhosis 100%)
- Treatment experienced: (no cirrhosis 91%; cirrhosis 88%)

AASLD/IDSA also recommend that previous non-responders to therapy can include peginterferon in the 12 weeks of therapy. Patients who were previous non-responders with cirrhosis may benefit by extending treatment duration to 16 weeks.

There is such a high cure rate for genotype 2 that there is very little research looking at new therapies to treat HCV genotype 2. However, due to the high cost of current treatments, newer inexpensive therapies would be a welcome addition to the treatment landscape of genotype 2, especially in resource-poor countries.

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