Notes from Dr. James Freed's Presentation, August 21, 2004:

GENETIC GENEALOGY: Fracturing Brick Walls

- DNA studies can be a valuable tool in fracturing (not destroying) brick walls
- DNA studies should be pursued only after:
    - Exhausting traditional genealogical research
    - Developing a specific testable hypothesis

- DNA Success Stories
    - Jefferson – Hemings Story – Hypothesis was that Thomas Jefferson fathered sons with his slave (Sally Hemings) after his wife died. Used a **10 marker** test and was able to conclude that the male descendants of Sally Hemings had definitely inherited Jefferson DNA. (a male descendant of Thomas' cousin was tested in addition to one of the male descendants of Sally Hemings). However, it is not possible to state that Thomas Jefferson was the father based on the DNA test **alone** as the DNA profile would match that of other males in Thomas Jefferson's family (brothers, cousins). **When the DNA test results are COMBINED with oral history and verifiable facts**, there seems to be little doubt that Thomas Jefferson fathered children with Sally Hemings. Some evidence has been reported that Thomas Jefferson was the only male Jefferson in the vicinity nine months prior to each birth.

    - McCabe Family – (Dr. Freed's wife's family) Hypothesis was that James J. McCabe was the son of James B. McCabe. No records of any type had been found earlier for the names of the parents of James J., born in 1843, and he was assumed to be an orphan. Census records were finally found to locate the mother in 1850 and other records showed that she died in 1852. Earlier records showed that the mother had been married to James B. at the age of 17, but after having two daughters, she sued for divorce when James B. abandoned her and moved to another state with another woman. Afterwards, the mother had 3 sons with different surnames, James J. being the second son. DNA samples were taken from male descendants of James B.'s other sons and compared to a sample of one of James J.'s male descendants. The perfect match on 25 markers (plus other very strong circumstantial evidence) strongly indicates that James B. was the father of James J. It was determined that James B. had in fact left his second wife and probably returned briefly to his first wife, siring James J. before he moved farther west, finally reaching Kansas.

    - Lorentz/Lawrence family – The Lawrence family in America wanted to confirm their relationship with what was thought to be a distant Lorentz cousin in Germany to pinpoint the local origin of their immigrant ancestor. DNA from two Americans was compared with the DNA of a present day male Lorentz family member. The DNA of the initiator of the test did not match that of the German Lorentz; however, the other DNA from the American participant did closely match the German Lorentz. The test initiator ended up not being related to either of the other test participants, his ancestors came from a different part of Germany.

    - Dillman/Stillman family – Dr. Freed found the matches between the Dillman and the Stillman DNA to be most interesting. Information collected so far in terms of the missing and presumed dead, Georg Adam Dillman having been taken prisoner by the British and forced into the 84th Regiment to fight on the British side adds to the picture. George Adam is clearly documented as being a son of Hans Georg Dillman (comment raised by Earl). The 25 marker test results showing that Andrew and Frank Stillman perfectly matched Earl, Robert, Don, and Philip Dillman show that they are related. The 37 marker test results (35 matches out of 37) for Andrew (and Frank) Stillman and Earl Dillman indicate a close relationship. The recent 37 marker test results for Don Dillman, which came in at 36 matches out of 37, show that Don's DNA profile is what is known as an **"intermediate"**

profile. This is because it is almost certain that Don's DNA profile, given the markers involved and their respective values, indicates that it is the profile of the common ancestor. A single change to Marker CDY-b in Andrew's DNA profile would render it an exact replica of Don's. Again, a single change to Marker 576 in Earl's DNA profile would render it an exact replica of Don's. Clearly, the DNA profile of Earl and Andrew diverged, differently, from that of Don and the Common Ancestor. **Dr. Freed stated that he would conclude that George Stillman aka Georg Adam Dillman, Georg Michael Dillman, and Andrew Dillman were brothers. While he said he was prepared to make this statement, he hesitated in doing so because there wasn't solid documentation even though there was oral history.** At this point, Earl mentioned that the baptismal and birth records for Georg Adam Dillman have been found indicating that he is a son of Hans Georg Dillmann, researched by Barbara Jensen. Dr. Freed suggested possibly finding the descendants of Conrad Dillman, another son of Hans Georg Dillman to have a test performed on that branch.
(While this was discussed later in the actual presentation, the following is added here since it reinforces this discussion.)
To address any concerns with the number of mutations found in the two Dillman lines and the Stillman Line, Dr. Freed pointed out the following mathematical formula and the concept of the number of expected mutations. The idea is that if the number of observed mutations (2 in this case) is greater than the number of expected mutations, then there should be concern about relatedness. **The number of expected mutations is simply:**

(Mutation rate) X (# of Markers) X (transmission events)

The average mutation rate is 0.002. However, it is known that some Markers mutate at a much faster rate, which can be as high as 0.005-0.006, 2.5-3 times the average rate. **It is also known that the mutations found in the Dillman/Stillman DNA matches were only on those markers which do mutate faster**, not on those that mutate at a slower rate. For this formula, though, the average rate needs to be used.

The # of markers is 37, since the testing that we are currently looking at are the 37 marker tests.

The # of transmission events is the number of father and son relationships, or rather, the number of times DNA was passed to an individual. In this case, Dr. Freed counted 27 down the Stillman Line to both 37-marker participants, down the Georg Michael line, and down the Andrew Dillman line. He based his count on the hypothesis that the common ancestor was the father of all three lines.

The expected number of mutations becomes:

(0.002) x (37) x (27) = 1.998 which is effectively 2, the number of observed mutations. **The number of mutations we observe is the expected number of mutations**.

(NOTE: However, there were 2 "boxes" too many on his family charts and the number of transmission events therefore should have been 25, producing an expected number of mutations of 1.85. But this again rounds to 2 – you either have a mutation or you don't. There are no half or partial mutations. Hence the conclusion is clearly the same) [Further note added 11/6/04 in support of the above provided by Dr. Freed: The most recent reports, October 2004, of mutation rates do not support the expected low mutation rate of 0.002. The mutation rates range from 0.00399 for the 1^{st}-12^{th} markers, 0.00481 for the 12^{th}-25^{th} markers to 0.00748 for the 26^{th}-37^{th} markers for an overall average of 0.0058.)

- Details of DNA Testing (Y chromosome)
    - Every cell in the body (except the sex cells) contains 46 chromosomes, or 23 pairs. The pairs are identical in length and the type of genes, except for the pair that determines a person's sex. Females have two X chromosomes and males have one X and one Y chromosome. The presence of a Y chromosome determines that the individual will be a male. The X chromosome is much longer than the Y chromosome and contains hundreds of very important genes.
    - The Y chromosome is much shorter and has very few genes. Most of the Y chromosome is considered as "junk" or non-coding regions. In the non-coding regions are segments from which DNA is extracted and tested for genealogical purposes, so that **NO GENES** are being tested in these DNA tests. The values for genealogical research are determined by the number of repeated sequences of bases. Bases are the generic building blocks of DNA and are identified as A, G, C, and T. The sequences can consist of 2 up to 6 bases, e.g., ACT would be a sequence. The number of repeats in ACTACTACTACT would be 4. Hence, if this were a marker, its value would be 4. This value can be compared to the value for the same marker at the same site on the Y chromosome on another male's DNA that may have five repeats of ACT These repeated sequences are also known as Short Tandem Repeats, or STR for short.
    - Dr. Freed talked about the different DNA testing companies and the tests they offered.
    - He also showed what a DNA test kit looks like, for those who haven't seen them.

- Dr. Freed talked about mitochondrial testing and how that can be used. Generally, it is most appropriate for determining ancestry over thousands of years, also known as deep ancestry. Mitochondrial DNA is strictly passed down from mother to daughter and is strictly for maternal lines. Y-Chromosome testing is more applicable for genealogical research but is strictly for paternal lines.

--- notes summarized by Andrew Stillman, and reviewed for accuracy by Dr. Freed, 11/6/04