THE KING’S SON
(The Evidence)
(3rd Edition)
(APPENDIX No.1)
(April 2018)

By
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ABOUT THE AUTHOR

Brad Michael Little is the youngest grandson of William James Shepherd. He lives in the United States and was born in Australia.

At the end of 2010 he accidently stumbled on to an old family rumor that his maternal Grandfather was somehow related to the British Royal Family.

The more he started to dig in to the mystery, the more he found it was possible.

This had to be a mistake.

However, he kept on investigating. The more evidence he found the more it pointed to it being true. It was truly a personal "out of body" experience to discover such a possible connection.

He had to get to the truth.

And finally during 2017 the truth was proven as to who his maternal Grandfather’s family line really was. He was indeed related to the British Royal Family.
PROLOGUE

This is the ultimate cold case, a 125 year old mystery hidden in plain sight.

This book pieces the evidence together that William James Shepherd was closely related to a member of the British Royal Family.

The case is built-up and includes clues that lead to a clear path forward - readied for a compelling conclusion and resolution to the mystery.

If you like puzzles and a story that twists and turns with lots of detail – then you have the right book. If you like analysis with just a touch of mystery, then you also have the right book. If you want an “easy read” book, you may have the wrong book.

This book is about determination to get to the bottom of a family rumor and mystery.

This is a story of intrigue and challenge about a man who left enduring clues during his lifetime about his origins. The clues appear to have been left in a subliminal manner, and at times it was like participating in a movie somewhat like the “Da Vinci Code”, with clue after clue being uncovered together with their meaning.

This book is about how my maternal Grandfather William James Shepherd mysteriously arrives in Australia in the early 1900’s, with the skills to be able to play the Double
Bass and then goes on to become Australia’s No. 1 performer.

And yet in 1901, he is Census listed as a “Pauper Inmate” (age 10) in a London Workhouse orphanage - straight out of the pages of the book “Oliver Twist”.

William throughout his life, due to his looks and mannerisms, is often compared to various members of the then British Royal Family born in the late 1800’s / early 1900’s.

Even today some of William’s descendants continue to have comparisons made with various members of the current British Royal Family.

DNA tests are used to set a test to prove the link, including the invention of a system and process that enables the parsing of atDNA in to the component ancestors of the DNA tester. It is a system and process that DNA testing companies may be interested to implement as a tool – refer Chapter 8.3.

The suspense in determining what is true and what is false – together with the patience needed to try to obtain DNA matches, makes for very interesting twists and turns, as the story progresses.

So based on the evidence collected and presented in this book …… Was William James Shepherd indeed related to the British Royal Family?

Please read on ……
The Puzzle as to who my Grandfather’s paternal family line was is ultimately solved in the new Parts 4, 5 and 6 of this 3\textsuperscript{rd} Edition of this book. It was solved after years of part time investigation and the initial 1\textsuperscript{st} and 2\textsuperscript{nd} Editions of this book being published.

This 3\textsuperscript{rd} Edition proves William James Shepherd’s close relationship to the British Royal Family, as my Grandfather is shown to be a maleline descendant of the House of “xyz” – refer Chapters 8 onwards for the answer.

If you have previously read the 2\textsuperscript{nd} Edition of this book, you may wish to skip forward to Chapter 7, and pick up the story from there with all its new material. The 2\textsuperscript{nd} Edition was 200 pages whereas this 3\textsuperscript{rd} Edition is 550 pages – noting they are small 9” x 6” pages.

As a result of this investigation additional Royal Haplogroups have now been discovered and are documented in Chapter 10. There are some major surprises.

This 3\textsuperscript{rd} Edition is now available for the wider Genealogical Community to review; critique and hopefully agree with my conclusions regarding who William James Shepherd’s father was.

Brad Michael Little - September 2017
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APPENDICES
APPENDIX 1 –

CHAPTER 10.15 FOLLOW-ON (V2)

1. Ancient DNA – More Information

Coincidently, after I had published my 3rd Edition of “The King’s Son (The Evidence)”, I noticed an increase in weblog postings on Ancient DNA. This is fantastic, as it will enable us to better align my work in determining the YDNA SNP’s of European Royalty with this Ancient DNA information. It will help us better join the dots on the Origins of Mankind in Europe.

I therefore decided to publish on my www.the-kings-son.com website an extract of Chapter 10.15 - Ancient DNA, as I wanted to see what ideas or thoughts would come back as a result. I then advertised this on the various Yahoo DNA Ancestry blogs that I was a member of.

One important piece of information came back almost straight away, from Vince Tilroe:

“Your chr6 matches wouldn't happen to be between hg38 coordinates chr6:29723340-32896489 by any chance? This region contains the HLA series of genes, which are infamously known for having an extremely high conservation rate, extending far beyond the age of the Wettin Cluster. 23andMe had reported that mine have matches with East Indians, which I presume goes back to a common ancestry existing thousands to tens of thousands
of years ago (since I also have a nearly 100% European makeup).

HLA genes are commonly genotyped for compatibility between tissue and organ donors and recipients.”

So I relooked at the Ancient DNA results and compared them against Chromosome No.6 on the FTDNA Chromosome Browser – and the answer was “Yes” – the Chromosome 6 matches I was seeing were in the range 29723340-32896489. I found this answer both exciting and very interesting.

**However the experts assessed that there was no relationship between this HLA region and the DF98 (or FGC5494) SNP alignment hypothesis that I had posed in this Appendix 1.**

As a reminder to folks who haven’t read Chapter 10.15, [Gedmatch](http://gedmatch.com) manages a tool that enables you to compare your atDNA (Autosomal DNA) against Ancient DNA samples that have been collected and stored in their system.

Previously I had compared the results of all my close family members plus Simon Coburg (my ~6th cousin) and my friend Wayne Smulan (my ~10th cousin) to see what comes up regarding any matching – just for fun. The detailed pictures of how the results showed up on the Chromosome
browser can be found in Attachment 15.19, and are restated in this Appendix 1.

It is very important to note that only 4 out of 10 of my close family members (who are descended from my maternal GF William James Shepherd) showed this Chromosome 6 segment match. In other words, assuming this ratio is standard across other families who take the test – that there is a high probability that you may not show a Chromosome 6 segment match – even if you are known to be related to a DF98 SNP ancestor.

Additionally, this Chromosome 6 Ancient DNA test won't be exclusive to DF98 only. As a for instance, my maternal GF is L21 > FGC5494. I just happen to now know he has Wettin ancestors (per all my research in my 3rd Edition book) and only a tiny small 0.000001% or so of the population would know this (unless they are Royalty). The rest of us “mere mortals” have to derive a result to demonstrate such royal connections – hence our shared interest in this DNA Ancestry hobby.

The only other folks who really then know for sure they are descended from a. ancestors of the Wettin line OR b. are from the Wettin line itself (i.e. subclades near “Wettin Man”), are the DF98 men.

Remember, I am triangulating from THREE Royal Houses (Hesse (mine), Wettin (Simon Coburg's etc) and a 3rd “Big Name Brand). The only commonality I detect ends up
being the Wettin line’s ancestors (aka DF98 subclades) between the three of them.

What I am expecting to see, IF my hypothesis is right, is a higher % hit ratio with DF98 men (& associated relatives) vs non-DF98 men (& associated relatives). I was not able to make this assessment, based on the additional data I collected as a result of publishing V1 of this paper.

By way of this Appendix 1, I had as part of V1, asked the following three groups of people to “take the test” using Gedmatch by setting the cM filter to cM = 2:

1. U106 > DF98 (i.e. The King’s Cluster) men and their relatives as shown by atDNA matching,
2. FGC5494 men and their close relatives (i.e. my Royal Hesse line) who also have DF98 Wettin ancestors, and
3. Non-DF98 or non- FGC5494 men (i.e. anybody else who isn’t Nos 1 and 2 above).

Almost immediately, after putting out the initial V1 request - I got some additional Ancient DNA results from readers - that helped me hone my DF98 hypothesis as to what it all meant. They are included in this Appendix 1.

I did not get a huge response for additional data though – I had hoped this paper would garner more interest. As they say “it is what it is”.

This didn’t happen.
2. “The Test” - Results

Attachment 15.21 shows the screenshots of the results from the initial 5 additional new testers – who tested positive. Let me summarize the positive results I have received, so far:

<table>
<thead>
<tr>
<th>Name</th>
<th>Country</th>
<th>Age</th>
<th>Markings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hixton-3</td>
<td>UK</td>
<td>1.3 ky</td>
<td>WS, BW</td>
</tr>
<tr>
<td>Ajvide58</td>
<td>Sweden</td>
<td>5.0 ky</td>
<td>J, RR, WS, BW</td>
</tr>
<tr>
<td>NE5, Hungary</td>
<td></td>
<td>7.1 ky</td>
<td>J, RR, WS, BW, RS</td>
</tr>
<tr>
<td>NE7, Hungary</td>
<td></td>
<td>6.4 ky</td>
<td>J, RR</td>
</tr>
<tr>
<td>CO1, Hungary</td>
<td></td>
<td>4.8 ky</td>
<td>J, RR, WS</td>
</tr>
<tr>
<td>Gokhem2, Sweden</td>
<td></td>
<td>5.0 ky</td>
<td>RR</td>
</tr>
<tr>
<td>NE1, Hungary</td>
<td></td>
<td>7.2 ky</td>
<td>BW</td>
</tr>
</tbody>
</table>

Legend 1: J = Jeff Harp, RR = Reinhard Rueckemann, WS = Wolfgang Steinwachs, BW = FTDNA Kit No.542289, RS = FTDNA Kit No.136272

Also let me repeat the summary of the results I showed in Chapter 10.15, so we have all the data in one paper:

<table>
<thead>
<tr>
<th>Name</th>
<th>Country</th>
<th>Age</th>
<th>Markings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hixton-3</td>
<td>UK</td>
<td>1.3 ky</td>
<td>S</td>
</tr>
<tr>
<td>Ajvide58</td>
<td>Sweden</td>
<td>5.0 ky</td>
<td>S, K</td>
</tr>
<tr>
<td>NE5, Hungary</td>
<td></td>
<td>7.1 ky</td>
<td>S, K, T, L, D, W</td>
</tr>
</tbody>
</table>
Legend 2: S = Simon Coburg, K = Kevin Howes, T = Thelma Shepherd, L = Lorraine Bruce, D = Denise Lawrence, W = Wayne Smulan

The Table below provides details relating to all the Ancient people with whom the above testers are related to (albeit very distantly):

<table>
<thead>
<tr>
<th>Sample Name</th>
<th>Sample Location</th>
<th>GED Match</th>
<th>Sex</th>
<th>Y-DNA</th>
<th>Mt-DNA</th>
<th>Approx. Age by authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hinxton-3</td>
<td>Cambridge, UK</td>
<td>F999922</td>
<td>F</td>
<td>K1a4a1a2b</td>
<td></td>
<td>1300 years</td>
</tr>
<tr>
<td>Ajvide58</td>
<td>Sweden</td>
<td>F999924</td>
<td>M</td>
<td>I-CTS772</td>
<td>U4d</td>
<td>5000 years</td>
</tr>
<tr>
<td>NE5</td>
<td>Kompolt - Kigyósér, Hungary</td>
<td>F999927</td>
<td>M</td>
<td>C-F3393</td>
<td>J1c</td>
<td>4990-5210 BC</td>
</tr>
<tr>
<td>NE7</td>
<td>Apc-Berekalja I., Hungary</td>
<td>F999928</td>
<td>M</td>
<td>I-L1228</td>
<td>N1a</td>
<td>4360-4490 BC</td>
</tr>
<tr>
<td>CO1</td>
<td>Apc-Berekalja I., Hungary</td>
<td>F999930</td>
<td>F</td>
<td>H</td>
<td></td>
<td>2700-2900 BC</td>
</tr>
<tr>
<td>Gökhem2</td>
<td>Sweden</td>
<td>F999934</td>
<td>F</td>
<td>H1c</td>
<td></td>
<td>5000 years</td>
</tr>
<tr>
<td>NE1</td>
<td>Polgár-Ferencihát, Hungary</td>
<td>F999937</td>
<td>F</td>
<td>U5b2c</td>
<td></td>
<td>5070-5310 BC</td>
</tr>
</tbody>
</table>

Source: Gedmatch.com – Ancient DNA
3. “The Test” - Categorization

I have parsed the results in to three groups of people, as I mentioned above:

1. U106 > DF98 (i.e. The King’s Cluster) men and their relatives:
   J, RR, WS, S
   
   Note 1: Jeff Harp subsequently performed a one to many match using Gedmatch, and discovered some of the folk who were atDNA related to him – were also showing the same Chromosome 6 segment matching. Jeff is also discovered he was a distant relative of my close family.

2. FGC5494 men and their close relatives (i.e. my Royal Hesse line) and “others” (refer Note 2) who have DF98 Wettin ancestors:
   
   K, T, L, D and
   BW, RS, W
   
   Note 2: BW is being currently being tested as to whether he is a Plantagenet (refer Chapter 10.16), RS is a Royal “Big Name Brand” – whose details and associated evidence will be revealed in an up and coming Appendix 2, and W is highly likely to be descended from the Oldenburg line – via multiple female /

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male lineages (not the maleline only) going back 500 years or so.

Note 3: A number of FGC5494 men undertook the test, including Rob Dixon (who is the closest FGC5494 member with my Uncle Eric Shepherd). Some other FGC5494 men did match on Chromosome 6 though.

3. Non-DF98 or non-FGC5494 men (i.e. anybody else who isn’t in Category 1 and Category 2 above):

This could be a large group. I don’t know how big though, as it is highly likely that many folks took the test, and weren’t a match - and didn’t report back.

3. “The Test” – What does this all mean?

In Chapter 10.9 of “The King’s Son (The Evidence)”, I wrote the following:

“Let me just explain a little bit better re this term “atDNA Magnification”, which I am using – and have mentioned multiple times throughout this book.

What happens as atDNA is passed down from the father and mother to a child is that ~50% comes from each parent. However it isn’t a precise split. Think of a bag of confetti (confetti acting as the strands of atDNA) that is spliced in half with a sword. Not all the confetti strands will
be touched by the sword and approximately half of the confetti will be left in the bag – completely untouched. This process happens time and again as the children become parents and again reproduce.

Now normally, if all the ancestors of a person were completely independent of each other (i.e. there was zero in-breeding) than a GGGG-Grandchild will only have 0.049% (i.e. ~3.5 cM) of the atDNA from any of his / her 2048 ancestors. Note that there are a total of 7098 cM’s on the FTDNA “chip” across all 22 Chromosomes.

However, if there is a lot of inbreeding, then there is a heightened chance that some of the atDNA segments from the multiple occurring GGGG-GP’s may have been “missed the knife” over multiple generations – as there are so many multiple segments of atDNA that are common that there is an increased probability that the segment isn’t cut. Hence this is what is happening with the atDNA from Christian III b.1503 (King of Denmark and Norway) (House of Oldenburg) (17 times via different ancestors to PLB) and Philip I, Landgrave of Hesse b.1504 (47 times via different ancestors to PLB). We are also getting these highly inbred ancestors breeding with other highly inbred ancestors due to PLBs ancestors marrying within their “class”, which magnifies the situation.

Some of these in-bred segments are coming through to today - and often showing up as greater than 8 cM in length - therefore giving a signal that the Family Finder cousin is a 5th or 6th cousin - whereas they may actually be a 10th to 12th
cousin. I have used the term “atDNA Magnification” to describe this phenomenon.”

Now, for this Gedmatch test and Appendix 1 – what we are seeing is EXTREME “atDNA Magnification”, for the atDNA to be able to remain intact on a small 2.5 cM segment of Chromosome 6 over a period of 7000 years.

This indicates, based on my Wettin DF98 hypothesis – these folk stayed together as a group for an incredibly long period of time. Is this really possible?

Well – as you will see when we publish Appendix 2, it will show that the pre-Wettin line and another Royal “Big Name Brand” stayed together for 2000 years. It is a beginning and gets us part way towards the 7000 years that we need to find – so as to fully prove the hypothesis.

So - what does all this mean? I think we still don’t fully know. More data in a scientifically controlled study may be useful – particularly from DF98, FGC5494 and others - to see if there is any correlation between these “funny little Chromosome 6 segments”.

I do not have the resources or skills to take on such a study.

It still remains curious that the data that did come back kept on showing this small Chromosome 6
segment match only across 7 of the Ancient DNA samples.

I do want to thank the folks who sent their screenshots in answer to my call for additional data as part of V2. However, the sample is just too small. Some of the additional folks had the Chromosome 6 segment, some didn’t. I am unable to assess what the additional data means or shows, as I don’t have a “control group”.

I also discovered that this paper became a bit controversial – this is okay - 

**occasionally.** However if I then move in to being seen as hysterical or sensationalist - then I kill my credibility. This is not okay. In this V2 of Appendix 1, I have tried to add in some additional balance.

To this end, Debbie Kennett provided the following useful information, which I have included as follows:

“Autosomal DNA is not restricted to the last four or five generations. Our genomes are made up of a patchwork of DNA from different periods. Some sections of our DNA can go back thousands of years and others can go back millions of years.

However, for genealogical purposes autosomal DNA cannot be reliably be used beyond about five or six
generations. This is because there are two components to genetic genealogy – genetics and genealogy. It is the genealogy that limits our research because few people are able to trace all their ancestors back beyond about four or five generations. Also, as we go further back in time our pedigrees start to collapse and you only have to go back 1000 years to reach a point where all Europeans share the same common ancestors. This means that even if you share a genealogical ancestor with someone and you can identify that you both share a segment of DNA you cannot be certain that the DNA is inherited from the ancestor of interest. You could just as easily be sharing by virtue of a common ancestor from several hundred years ago that you haven’t been able to identify.

A further difficulty is that once you go back beyond five or six generations we have some ancestors with whom we share no DNA at all:

https://isogg.org/wiki/Cousin_statistics

Clearly it is going to be highly unlikely that two men will share the same Y-DNA signature and also share autosomal DNA as a result of a documented genealogical relationship going back beyond about four or five generations.

The HLA region on chromosome 6 is not the only part of our genome where the DNA is “conserved”. The technical name for this is excess IBD (identity by descent). Colloquially we use the term “pile-up regions”. Some of these regions have been documented in the scientific
literature. You’ll find a list of papers on this page in the IOSGG Wiki:

https://isogg.org/wiki/Identical_by_descent#Excess_IBD_sharing

However, that list is probably just the tip of the iceberg.

Ancestry DNA has a proprietary filter known as Timber which down-weights regions of the genome that are prone to over-matching - but they have not published the data.”

So there we have it. The results are curious, but not scientifically verified – by any stretch of the imagination. In fact the experts have stated their views which I inserted in a few places above.

The puzzle is not solved, and only partly answered, in this Appendix 1, is my conclusion.

However, I decided I would leave this V2 paper hanging out there - just in case in the future an Ancient DNA expert picks it up - they might find it useful.

Or – they might not. 😊
15. ATTACHMENTS

15.21 Ancient DNA – More Info

Jeff Harp (The King’s Cluster)

Haplogroup: R-U106 > DF98 > FGC51008 > FGC51005

Gedmatch Code: A982634

Note 4: Jeff Harp also had the same Chromosome 6 match on F999915 La Brana, Spain – 7 ky

Note 5: Jeff Harp co-incidentally discovered he is a distant atDNA cousin to my close family and Wayne Smulan.
Reinhard Rueckemann (The King’s Cluster)

Haplogroup: R-U106 > DF98 > S18823 > FGC15238

Gedmatch Code: H431049

Note 6: Reinhard’s brother also has the same Chromosome 6 pattern, as does both his father and mother (his parents are known to be distantly related using their ancestral paper trail).

Note 7: Reinhard co-incidentally discovered he is a distant atDNA cousin to my close family – via the Frey line. Refer Chapters 9.1 and 10.6.
Wolfgang Steinwachs (The King’s Cluster)

Haplogroup: R-U106 > DF98

Gedmatch Code: H697195
FTDNA Kit No.542289 (Plantagenet?)

Haplogroup: P312 > ZZ11 > DF27 > Z195 > FGC15710

Gedmatch Code: F231054
FTDNA Kit No.136272 (“Big Name Brand?”)

Haplogroup: P312 > DF19

Gedmatch Code: T498233

Note 8: Appendix 2 is currently being written that will provide details and evidence as to which Royal “Big Name Brand?” this person may be a member of.