BROAD SURVEY OF BARUCH'S AUTOSOMAL DNA

Summary and Conclusion

A comparison of the Baruch Lousadas who lack Barrow ancestry with those having Barrow ancestry might show characteristics independent of the Baruch Lousadas, and eventually provide means of segregating Barrow ancestors like Baruch. We have at present (July 2024) 12 probable Baruch Lousada descendants – 5 without Barrow ancestry (Bob, Jeannine, MD, TPhelan, and Jeremy), and 7 with Barrow ancestry (Julian, JG, SW, Ed, RF, RM, and Allan). Of the latter, SW may not be a descendant of Baruch but is sure to have connections with those who are.

From observations 1-4 below we confirm our view of the significance of the 4 Lousada indicator segments. And from observation 7 below, we have 6 possible non-Lousada indicator segments. A summary of these 6 interesting matches, together with a preliminary view as to the significance of each, is in Attachment 1. Attachment 2 shows the 3 most promising (a,d,e) of these 6 interesting multiples.

And from Attachment 3, which shows the most complex of the 6 interesting matches (f), we see it divides into 3 - each part of which has matches from outside the Barrow subset; but one these 3 is a MD/JG/Ed/Allan/RM pentuple at 32.5-33.6 which might merit attention as an additional Baruch Lousada indicator but the examination is disappointing with only one more single match possibly emerging. Baruch Lousada matches in fact accompany all promising Barrow potential indicators, while there is no standout Barrow indicator.

Observations

The 5 non-Barrows generate 55 segment matches, and the 7 Barrows generate 129. We used Q-Match from GEDmatch set at 3cM minimum segment size with Precision set at 7. This gives reliable statistics and good family match detection but does not exclude pre-genealogical matches (sometimes called Identical by State – IBS). Possible IBS matches need to be treated with due scepticism, because even random samples can generate impressive multiple matches – especially weak and (both types of) strong triple matches, quadruple matches with 2 unconnected pairs, and even sextuple matches with 3 unconnected pairs.

In the Barrow 7 by 7 matches, the 1st cousin match of Julian and Allan was not included – it is by far the biggest match we have and would dominate the individual segment match count. Similarly, the large RF and RM match was not included as it reflects the highly connected Central European Jewish milieu. But all other matches were included so Allan, RF and RM are consequently well represented.

We can thus readily demonstrate where our key matches occur, but we do not reproduce our full analysis as we ignore in this study the related (but more uncertain) matches which only emerge at smaller segment size and/or lower Precision.

What we observe is:

- 1. The Cr2 Lousada segment at 218-220m shows up in both samples as weak triples, but overlapping each other. (This segment showed up much more strongly in previous work when mixed matches were considered and when we also used P=3).
- 2. The Cr5 Lousada segment at 79-82m appears only once in the non-Barrows and not at all in the Barrows. (Previous work showed more matches but few Barrows perhaps this segment could be deleted).
- 3. The Cr8 Lousada segment at 50-52m appears only once in the non-Barrows and much more strongly in the Barrows. (Previous work showed many more matches including mixed matches, but as the Cr8 segment was also shown to appear in other Barrow and Baruch Lousada matches with random people it may not have value except in conjunction with the Cr2 segment).
- 4. The Cr21 segment at 37-39m does not appear in the non-Barrows, and only once in the Barrows. (Previous work showed many matches, and this segment remains potentially useful).
- 5. We ignore the 1 Lousada weak triple (Cr3) and the 9 Barrow weak triples (Cr4,6,13,16,17,19,20).
- 6. We ignore the 10 mixed weak quadruples (Cr 2,6,7,9,10,10,12,12,17,19) and the Barrow weak quadruples (Cr 2,8,9).
- 7. From this culling we are left with only a few interesting multiples all in the Barrow sub-sample see the Attachment 1 for details:
 - a. A pentuple at Cr1 1-14m
 - b. A sextuple at Cr4 183-191m
 - c. A quadruple at Cr5 228-320m
 - d. A quadruple at Cr 6 14-17m
 - e. A quadruple at Cr 6 39-42m
 - f. A pentuple at Cr 17 14-35m (includes an adjacent weak triple).
- 8. The multiple match a (and perhaps d or e) appears worth pursuing. In the first place it is important to see whether there are any mixed or Baruch Lousada matches.
- 9. In fact, as shown in Attachment 2, there are additional mixed matches as follows:
 - i. a has 2 such matches additional to the 4 already found
 - ii. d has 2 such matches additional to the 3 already found
 - iii. e has 2 such matches additional to the 3 already found

- 10. Thus, we cannot conclude that a, d, and e are Barrow matches they might be additional unproven Baruch Lousada matches!
- 11. Match f is analysed in Attachment 3, and breaks down into 3 multiples, the most compelling is the MD/JG/Ed/Allan/RM pentuple at 32.5-33.6. But neither this, nor the other 2 lesser possibilities, are pure Barrow they all have a contribution from the Baruch Lousada sample.

ATTACHMENT 1

6 Interesting Barrow segments - a to f

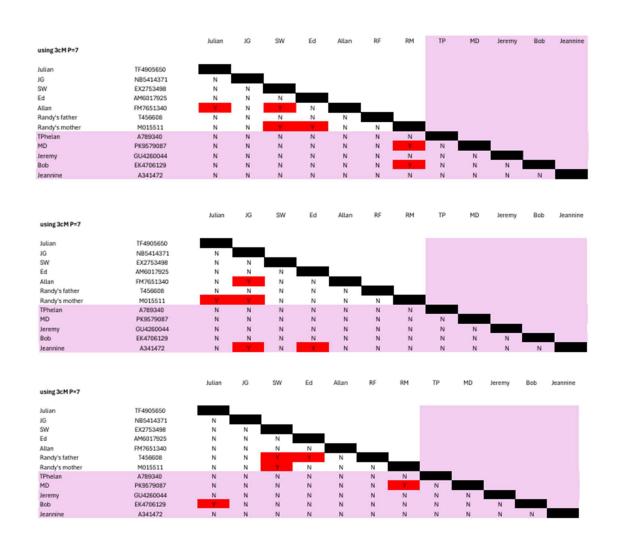
| Julian/Allan | 1 | 1079198 | 14518979 | 30.7 | 1276 | 37.9 | 37.9 |
|--------------|----|-----------|-----------|------|------|-------|-------|
| SW/Allan | 1 | 10808587 | 14195122 | 7.5 | 234 | 0.81 | 0.81 |
| Ed/RM | 1 | 10935232 | 12267464 | 3.6 | 307 | 3.26 | -2.14 |
| SW/RM | 1 | 11007159 | 12718815 | 4.7 | 412 | 5.28 | 5.28 |
| Julian/RF | 4 | 183141735 | 184285017 | 3.8 | 257 | 1.21 | 1.21 |
| SW/RM | 4 | 183666740 | 185111580 | 4.8 | 361 | 5 | 5 |
| Ed/Allan | 4 | 184573015 | 190937862 | 18.5 | 681 | 17.78 | 17.78 |
| SW/Allan | 5 | 22817855 | 26888460 | 4 | 227 | 0.11 | 0.11 |
| SW/Ed | 5 | 23261792 | 26207219 | 3.1 | 335 | 3.65 | 3.65 |
| SW/RF | 5 | 26555788 | 31920340 | 5.9 | 1074 | 27.38 | 27.38 |
| JG/Ed | 6 | 14014793 | 16017042 | 3.6 | 250 | 0.8 | 0.8 |
| Julian/RM | 6 | 14203502 | 16598133 | 4.3 | 499 | 9.69 | -2.52 |
| JG/RM | 6 | 14345024 | 16104631 | 3.1 | 360 | 3.43 | -2.13 |
| SW/RM | 6 | 39150098 | 41519522 | 4.6 | 666 | 14.1 | -1.43 |
| SW/RF | 6 | 39763506 | 41404666 | 3.4 | 473 | 8.15 | 8.15 |
| Ed/RF | 6 | 39907809 | 41377992 | 3 | 293 | 3.05 | 3.05 |
| Julian/RM | 17 | 14277843 | 14857236 | 3.3 | 203 | 0.05 | 0.05 |
| Julian/SW | 17 | 14601455 | 15333562 | 3.1 | 243 | 1.15 | -2.76 |
| Ed/Allan | 17 | 15099857 | 34819191 | 17.3 | 849 | 24.26 | 24.26 |
| SW/RM | 17 | 16407478 | 20823268 | 3.5 | 577 | 11.35 | 11.35 |
| Allan/RM | 17 | 31853074 | 33622774 | 4.3 | 204 | 0.01 | 0.01 |
| Ed/RM | 17 | 31978888 | 33718077 | 4.1 | 414 | 6.81 | 6.81 |

The importance of these 6 interesting matches is gauged as follows:

- a. Linked weak triples plus an overlap perhaps at least one IBS
- b. Possibly 3 overlapping unconnected IBS
- c. Not quite a strong triple as there is a non-overlap
- d. Linked weak triples perhaps at least one IBS (note no SW)
- e. Linked weak triples perhaps at least one IBS
- f. Needs analysis see Attachment 3

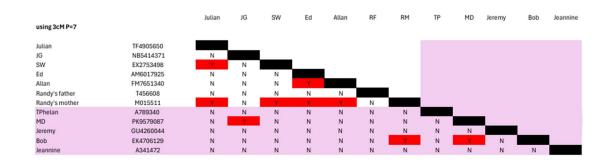
ATTACHMENT 2

Do the interesting Barrow segments - a, d and e have further matches?



ATTACHMENT 3

Another interesting Barrow segment -f?



This match is messy – the large Ed/Allan segment overlaps 3 different segment matches:

- 1. The lowest is the Julian/SW segment match, then
- 2. The SW/RM segment match, and finally
- 3. The Ed/Allan/RM weak triple making it a strong triple.

The extra matches contributed by the non-Barrow sample are the MD/JG match at 32.5-34.2m, which overlaps the Ed/Allan/RM strong triple at 32-33m, the Bob/RM match at 15-19m which only overlaps the Julian/SW segment match at 14.6-15.3m and of course the Ed/Allan match, and the Bob/MD match at 34.4-37m which only overlaps the Ed/Allan match. At P=3 only one further match was found – MD/Jeremy. This does not suggest that this (most interesting of the Cr17 matches) match is useful.

