



Census of Biodiversity in Sans Souci County Park

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Materials and Methods:

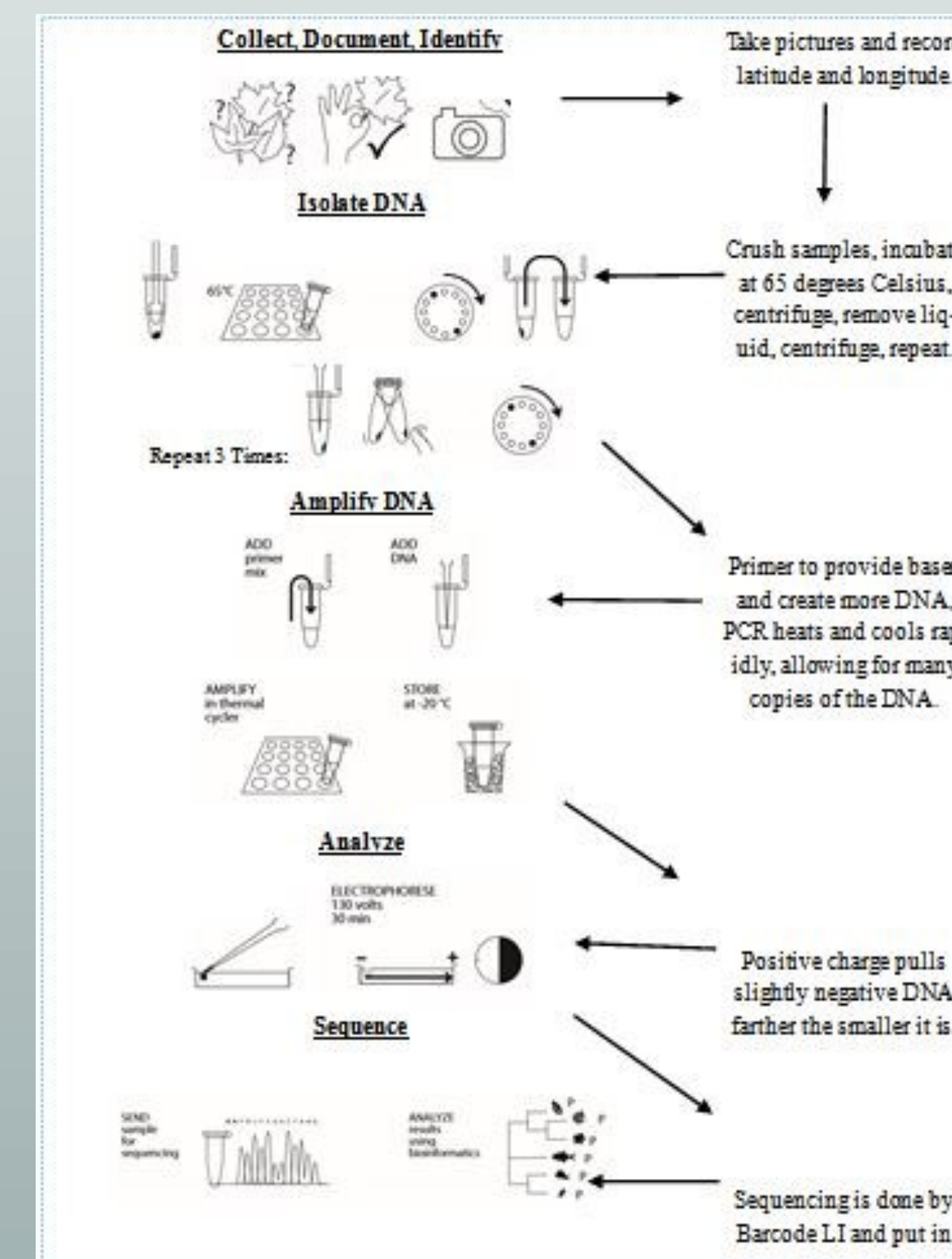


Figure 1: diagram of DNA isolation, extraction, amplification, and analysis.

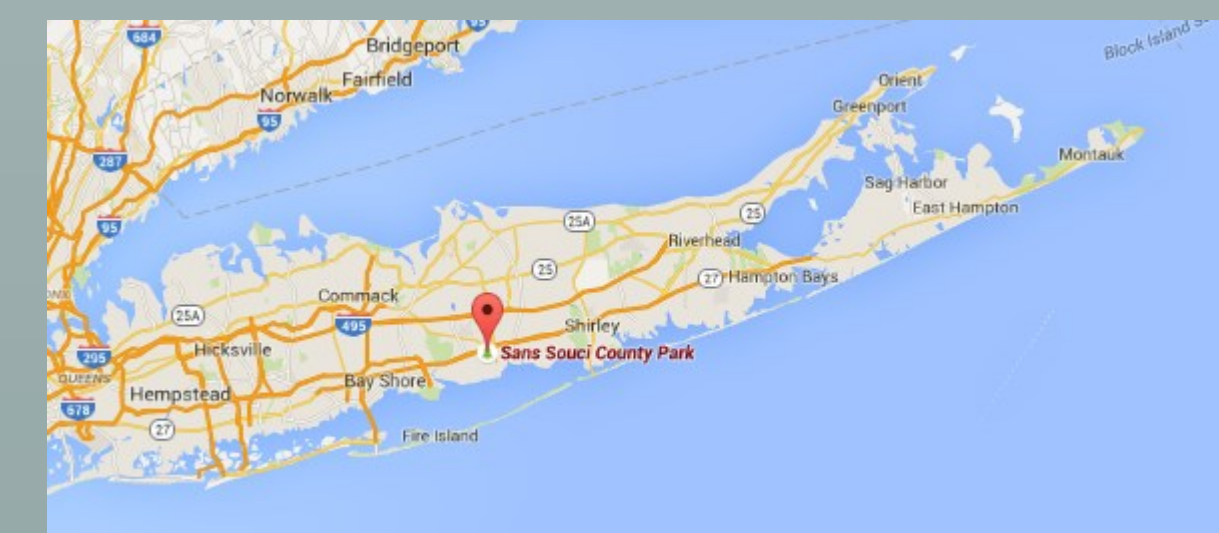


Figure 2: map of Long Island, with a mark on Sans Souci Park, our area of interest and collection site

Results:

#	Accession #	Details	Align. Length	Bit Score	E	Mismatches
1/1	gi69584747gskJ01345	<i>Gaultheria procumbens</i> - rbcL1-1.5. longifolia subunit 1 (COI) gene, partial cds, chloroplast	537	969	0.0	0
2/2	gi84299309gskJ053430	<i>Gaultheria procumbens</i> - rbcL1-1.5. longifolia subunit 1 (COI) gene, partial cds, chloroplast	537	969	0.0	0
3/3	gi84299311gskJ053430	<i>Gaultheria procumbens</i> - rbcL1-1.5. longifolia subunit 1 (COI) gene, partial cds, chloroplast	537	969	0.0	0
4/4	gi79557324gskJ022007	<i>Gaultheria procumbens</i> - rbcL1-1.5. longifolia subunit 1 (COI) gene, partial cds, chloroplast	537	969	0.0	2

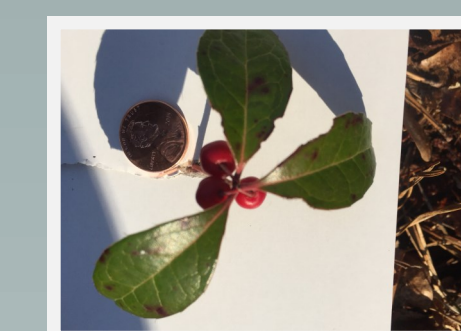


Figure 4: picture of plant sample NYZ-002, with BLAST results. The results show that sample NYZ-002 is most likely a member of *Gaultheria procumbens*.



Figure 5: picture of insect sample NYZ-008 and *Limodromus assimilis*, the closest match to sample NYZ-008 in the database.

#	Accession #	Details	Align. Length	Bit Score	E	Mismatches
1/1	gi69584747gskJ01345	<i>Limodromus assimilis</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	494	738	0.0	34
7/7	gi69584747gskJ01345	<i>Limodromus assimilis</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	494	733	0.0	35

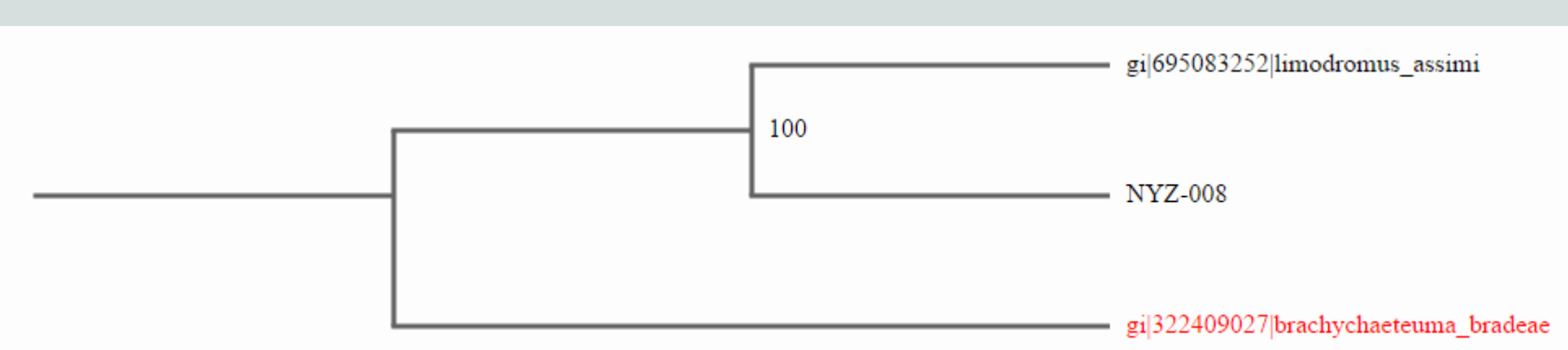


Figure 6: The BLAST results and phylogeny of sample NYZ-008. The results show that *Limodromus assimilis* is the closest match to our sample, but 34 mismatches may indicate the need for further investigation.



Figure 3: Samples collected in Sans Souci County Park

#	Accession #	Details	Align. Length	Bit Score	E	Mismatches
1/1	gi69584747gskJ01345	<i>Idia lubricalis</i> - BOLD:AAA2330 vracher CNL2EP00092022 cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	647	1162	0.0	1



Figure 7: picture of insect sample NYZ-009, with BLAST results. The results indicate that sample NYZ-009 is likely a member of *Idia lubricalis*.

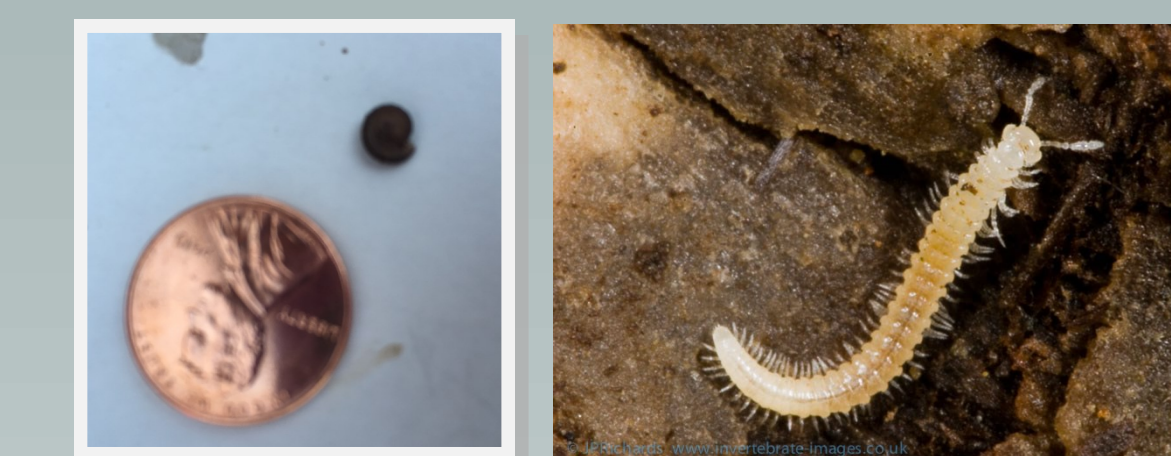


Figure 8: picture of insect sample NYZ-012 and *Brachychaeteuma bradeae*, the closest match to NYZ-012 in the database.

#	Accession #	Details	Align. Length	Bit Score	E	Mismatches
1/1	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
2/2	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
3/3	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
4/4	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
5/5	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
6/6	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
7/7	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
8/8	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
9/9	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79
10/10	gi332409027gskJ062142	<i>Brachychaeteuma bradeae</i> - cytochrome oxidase subunit 1 (COI) gene, partial cds, mitochondrial	523	623	0.0	79

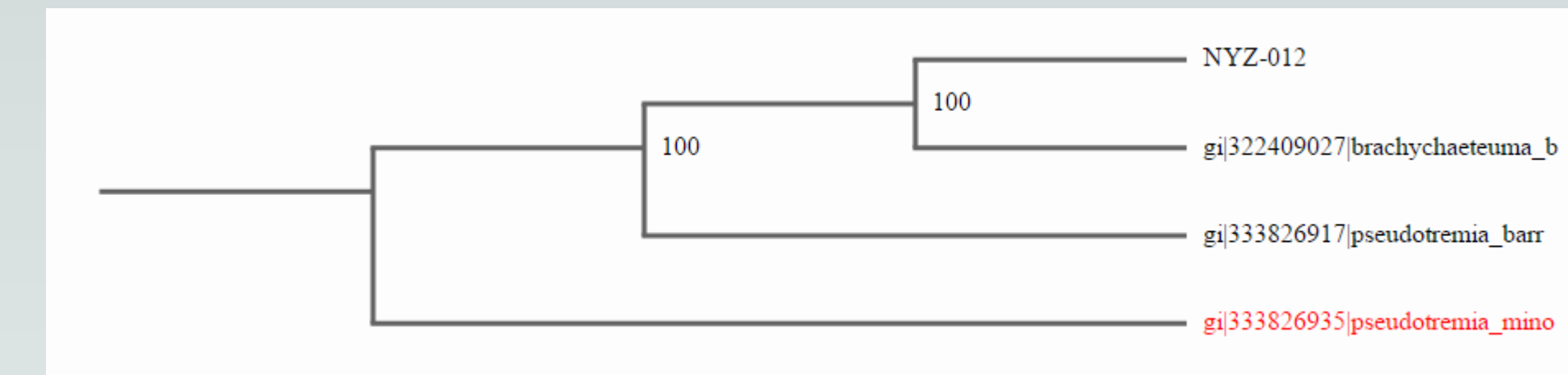


Figure 9: BLAST results and phylogeny of sample NYZ-012. The results show that sample NYZ-012 and *Brachychaeteuma bradeae* are very different and our sample is most likely not a member of *Brachychaeteuma bradeae*, so further investigation is needed.

Discussion:

The BLAST results for sample NYZ-002 showed that its closest match in the database is the *Gaultheria procumbens*, a small, low-growing shrub. More specifically, it is a wintergreen that is a vital food source to a handful of organisms, mainly deer. The database showed no mismatches of the rbcL DNA sequence to the same sequence of *Gaultheria procumbens*. This means that all of the nitrogenous bases for both DNA strands of the target gene, rbcL, were the same. This suggests that the samples are very similar and supports the likelihood of our sample being a member of the *Gaultheria procumbens* species. Sample NYZ-002 had a bit score of 969, indicating that our sample DNA and the *Gaultheria procumbens* rbcL sequence were moderately aligned, but not completely as the score is under 1,000. The e-score of 0 (less than 1) indicates that we can be very confident that our sample and the *Gaultheria procumbens* are closely related and have a very recent common ancestor. Based on this data, this sample is most likely closely related to or a member of *Gaultheria procumbens*.

Sample NYZ-009, also an insect sample, was found to be most similar to *Idia lubricalis*, a species of moth. The Bit-score of 1162, over 1000, indicates that our sample DNA and the *Idia lubricalis* DNA from the database are very well aligned. The e-score of 0 also supports that sample NYZ-009 and *Idia lubricalis* are closely related. There was only one mismatch between our sample and the *Idia lubricalis* DNA, suggesting that NYZ-009 and *Idia lubricalis* are very similar. Due to this information, we can conclude that sample NYZ-009 is likely to be a member of *Idia lubricalis*.

Sample NYZ-008, an insect sample, was most similar to *Limodromus assimilis*, a species of ground beetle. This beetle does not have a specific environmental role, but remains active during the winter and is a food source of larger organisms. This sample had a lower Bit-score of 738, indicating that the samples were not aligned perfectly. The e-score of 0 showed that we can be confident that our sample and *Limodromus assimilis* are closely related. However, there are 34 mismatches between our sample DNA of the target gene and the DNA found in the database for *Limodromus assimilis*. This leads us to believe that our sample may be part of a species that has not yet been sequenced and uploaded into the database or could possibly be a novel species, but further investigation is needed.

Sample NYZ-012 was found to be the most similar to *Brachychaeteuma bradeae*, a species of millipedes. The Bit-core of 628 suggests that our sample DNA sequence and the DNA sequence of *Brachychaeteuma bradeae* were not well aligned. There were 70 mismatches between our sample and the DNA sequence of *Brachychaeteuma bradeae*, showing that they are most likely not closely related. The e-score was 1e-177, meaning that our sample and *Brachychaeteuma bradeae* are distantly related and do not have a recent common ancestor. Thus, we cannot conclude that sample NYZ-012 is a member of *Brachychaeteuma bradeae*. Therefore, there is a possibility that with further investigation our sample may be a member of a species that has not yet been sequenced and uploaded into the database, or is a novel species.

Acknowledgements:

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References

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