BLEMMYES ANALYSIS GAPS

What Was Not Examined — With Emphasis on Genetic Screening for Developmental Variants

Summary of Existing Analysis (Flakstad and Related Sites)

The primary published work (Naumann et al. 2014) focused on three main areas: (1) neck trauma interpreted as decapitation, (2) stable isotope analysis for diet, and (3) limited ancient mitochondrial DNA (mtDNA) analysis for maternal lineage relatedness. This created a strong interpretive framework of "decapitated slaves / grave gifts." Several important areas received little or no attention.

1. Genetic Analysis — What Was Done vs. What Was Missed

What Was Done:

- Ancient mitochondrial DNA (mtDNA) fragments only — used exclusively to test maternal relatedness between individuals buried together.
- Limited haplogroup identification (primarily European lineages H, J, U).
- No whole-genome sequencing.
- No screening for autosomal mutations, developmental genes, or inbreeding coefficients.

What Was Not Done (Critical Gaps):

- No screening for developmental mutations — No analysis of genes known to affect craniofacial development, skull formation, or neck/shoulder morphology.
- No inbreeding coefficient calculation — No assessment of runs of homozygosity (ROH) or other measures that would indicate multi-generational inbreeding.
- No whole-genome or nuclear DNA analysis — Only mtDNA was used. This misses the vast majority of the genome where developmental and structural genes reside.
- No comparison to known congenital disorder databases — No cross-referencing with genetic conditions involving craniofacial relocation or neck abnormalities.
- No population-level genetic diversity assessment — Limited sample and limited markers made it impossible to evaluate whether this group showed unusual genetic patterns consistent with a reproductively isolated or highly inbred population.

Implication:

The existing genetic work was narrowly scoped to support a social/status interpretation. It was never designed to test whether these individuals belonged to a population with significant developmental or genetic differences. This is a major gap for any hypothesis involving inbreeding-driven anatomical variants.

2. Skeletal Analysis — Areas That Received Minimal Attention

- Shoulder / Clavicle / Supraclavicular Region: No targeted examination for sockets, depressions, remodeling, or structural adaptations that could relate to eye placement.
- Upper Chest / Upper Rib Area: Not systematically reviewed for cavities or developmental features.
- Cervical Vertebrae Structure (Beyond Trauma): Cuts were documented, but the vertebrae were not deeply assessed for developmental shortening, fusion, or malformation.
- Overall Craniofacial Development: With most skulls missing, there was no opportunity to examine whether facial bones were reduced or absent in the normal head position.
- Taphonomic vs. Developmental Distinction: Subtle changes in bone structure were likely attributed to normal postmortem degradation rather than possible developmental variation.
- Broader Pathology Screening: Basic health markers were noted but not pursued in depth for the headless individuals or framed within a developmental variant context.

3. Methodological / Interpretive Gaps

- Strong prior assumption of "normal humans who were decapitated" shaped what was looked for and what was considered significant.
- The "clean C3 cuts" became the dominant piece of evidence early, locking in the decapitation narrative and reducing openness to alternative explanations.
- The fundamental question "Where are the skulls?" was answered with "They were removed during execution" rather than being held open as a genuine anatomical unknown.
- Standard osteological priority (trauma + burial context) meant areas not directly related to the decapitation hypothesis received far less attention.
- No deliberate re-examination protocol was applied to test alternative hypotheses against the same physical evidence.

4. Recommended Genetic Work for Future Analysis

- Whole-genome sequencing or targeted enrichment of developmental genes (especially those involved in craniofacial and axial skeleton formation).
- Calculation of inbreeding coefficients and runs of homozygosity (ROH) to assess multi-generational inbreeding levels.
- Screening for known pathogenic variants associated with severe craniofacial or neck developmental disorders.
- Comparison of genetic profiles against reference populations to identify unusual patterns consistent with a reproductively isolated or highly inbred group.
- If possible, ancient DNA extraction focused on any remaining cervical or shoulder-region bone to look for localized developmental signals.

5. Recommended Skeletal Re-Examination Priorities

- Targeted visual and metric examination of the clavicle, supraclavicular fossa, and upper shoulder region for any sockets, depressions, or remodeling.
- Detailed assessment of cervical vertebrae morphology (not just cut marks) for signs of developmental variation.
- Review of any available upper chest / upper rib fragments for unusual features.
- Explicit comparison of observed features against both "normal decapitation" and "developmental variant" expectations.
- Documentation of any subtle changes previously attributed to taphonomy that could alternatively reflect developmental processes.