GENETIC VOYAGE

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DNA MATCH RESEARCH CHECKLIST

Your complete first-pass workflow for every significant new match

Before you begin — quick glossary:

cM (centimorgan) — the unit for measuring shared DNA. More shared cM points to a closer relationship — see the chart below.

Segment — a continuous stretch of matching DNA on one chromosome. Total cM is the sum of all segments you share with a match.

Shared matches / "In Common With" (ICW) — the list of other people who match both you and a specific match — found on every major testing site.

Run through this list for every significant new match. It takes five to ten minutes and prevents you from re-doing the same detective work twice.

Quick reference — shared cM to likely relationship

Shared cM	Most likely relationship(s)
3,330–3,720 cM	Parent / child, identical twin
2,300–3,400 cM	Full sibling
1,300–2,300 cM	Grandparent/grandchild, aunt/uncle, half-sibling, niece/nephew
575–1,330 cM	1st cousin, great-grandparent, great-aunt/uncle, half-aunt/uncle
200–850 cM	1st cousin once removed, half-1st cousin
90–450 cM	2nd cousin, 1st cousin twice removed
25–200 cM	2nd cousin once removed, 3rd cousin
0–50 cM	3rd cousin once removed, 4th cousin, or more distant

Ranges overlap significantly between relationship types — always cross-check with shared matches, ages, and tree research rather than the cM figure alone.

Step 1 — Record the basics (do this for every match you investigate)

☐ Match name / username — *as displayed on the testing site — copy it exactly, including any numbers appended to duplicate names*

☐ Testing company — *AncestryDNA, 23andMe, MyHeritage, FamilyTreeDNA, LivingDNA — write the exact platform, since cM ranges are calculated slightly differently by each*

☐ Total shared cM — *shown directly on the match card/profile on every platform*

☐ Number of segments — *on Ancestry: click the match → "View shared DNA"; on MyHeritage: click "Review DNA Match" → segment info is below the map; on FTDNA: "Chromosome Browser"*

☐ Largest segment size (cM) — ★ *critical — two matches with the same total cM but very different largest segments often imply different relationship types. Find it in the same chromosome browser/segment view as above*

☐ Estimated relationship range given by the testing company — *note the company's own label (e.g. "1st–2nd cousin") even though you'll refine it yourself using the chart above*

☐ Date first contacted / date match appeared — *add a literal calendar date, not "recently" — you'll need this to judge how long you've waited for a reply*

Step 2 — Investigate the match's tree

☐ Is a family tree attached? Public, private, or none? — *on Ancestry a private tree still shows if it exists; request access via the match's profile page if it's private*

☐ Number of generations shown — *count generations back from the match to their earliest listed ancestor*

☐ Surnames that also appear in your own tree — *check spelling variants too — e.g. Andersson/Anderson, Nilsson/Nelson*

☐ Geographic locations in common — *birthplaces AND places of residence — a shared parish or county is often more useful than a shared country*

☐ Any obvious common ancestor visible from trees alone? — *if yes, note the exact name and approximate birth year of that ancestor*

Step 3 — Cross-reference shared matches

☐ Pull the full shared-matches list — *Ancestry: "Shared Matches" tab on the match page (only shows matches sharing 20 cM+ with both of you); MyHeritage: "Shared DNA Matches"; FTDNA: "In Common With" filter*

☐ Flag shared matches you can already place in your tree — *write the exact relationship next to each name, not just a checkmark*

☐ Group shared matches by suspected shared ancestor — *this group is the seed of a cluster — give it a working label, e.g. "possible Andersson line"*

☐ Note whether the cluster looks maternal, paternal, or unclear — *if you have matches from a known parent tested, compare against their match list to sort maternal vs. paternal instantly*

Step 4 — Reach out (if useful)

☐ Send a short, specific message — *example opener: "Hi — we're DNA matches at [X] cM. I think we may connect through the [surname] family in [place]. Does that name mean anything to you?" — specific beats generic every time*

☐ Ask for their earliest known ancestor in the relevant line — *name + approximate birth year + place, if they have it*

☐ Log the date you messaged and whether you received a reply — *set a literal follow-up date 2–3 weeks out if no reply — see Step 5*

Step 5 — Log and file

☐ Add the match to your master DNA match spreadsheet — *minimum columns: name, company, total cM, largest segment, tree link, suspected ancestor, confidence, date logged*

☐ Record your working hypothesis for the relationship — *write the specific relationship (e.g. "2nd cousin via great-grandmother Elin"), not just "related somehow"*

☐ Note confidence level using these three exact labels: — *Confirmed = paper trail AND DNA both independently support it; Probable = strong DNA cluster evidence but paper trail incomplete; Speculative = a guess based on surname/location overlap alone*

☐ Set a follow-up reminder if the match hasn't replied — *2–3 weeks is a reasonable first follow-up window; after two attempts with no reply, mark as "no response" and move on*

Pro tip: Never rely on the company's relationship estimate alone. A predicted “2nd–3rd cousin” can genuinely be anywhere from a half-first cousin to a third cousin once removed — always sanity-check the estimate against the cM chart above, shared matches, and segment size before writing anything into your tree.