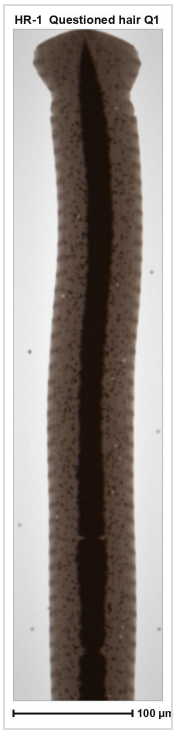
How to compare hairs under a microscope

Keep this card next to you while you work.

CLAIM CEILING. READ THIS FIRST.

- **Polygraph.** It records breathing and heart rate. A change in either one is a physiological response. It is not a measurement of lying, and nothing in this unit produces a deception call.
- **Hair.** Microscopic similarity can support consistency or support exclusion. It cannot identify one person.
- **Fingerprint.** Pattern class can narrow a field or exclude a person. By itself it cannot name a source, and it never says when or why a finger touched something.
- **Timeline.** A scheduled event is not proof the person was there. Time of death is not established in the early case evidence.



A hair at the magnification you will work at. Scale bar is 100 micrometres.

Method card for HR-1, HR-2, HR-3, and HR-4.

What this test can and cannot tell you

- **Claim ceiling.** Microscopic hair comparison supports one of three words: consistent, excluded, or inconclusive. It never identifies a person.
- It can exclude, and exclusion is the stronger result. One feature that sits clearly outside the range of every hair in the known sample rules that source out.

- It cannot name a person. In one examined casework set, mitochondrial DNA excluded 9 of 80 hairs that had already been associated under a microscope (Houck-2002). That 9 of 80 shows limited resolving power in that casework set. It is not a universal error rate.
- It cannot tell you how the hair got where it was found. A hair on a jacket may have arrived from a hug that morning.

Before you start: what you need

- The printed micrograph of the questioned hair, with a labelled scale bar
- The printed known sample sheet, all hairs, same magnification, same scale bar
- One blank sheet of paper, big enough to cover the whole known sample page
- A clear plastic ruler with millimetre marks
- A sharp pencil and an eraser
- Your HR feature sheet, or a blank page you can rule into rows
- A calculator
- A partner who has not seen your work

The steps

1. Check the hair is usable. Hold the questioned micrograph flat and look at the whole shaft from one end to the other. Check three things by eye. Is the shaft in focus for most of its length, is there a scale bar with a number on it, and are both ends visible or is the hair broken off. Write "usable" or "not usable" at the top of your sheet, and if it is not usable write the reason in five words or fewer. You are done with this step when: the word "usable" or "not usable" is at the top of your sheet with a reason beside it.

2. Cover the known sample. Lay the blank sheet of paper over the known sample page so that none of it shows. Then write ten feature names down the left side of your page: colour, shaft diameter, diameter variation, cuticle, pigment density, pigment distribution, medulla type, medullary index, root type, tip type. Do this before you look at anything else. Once your eye has seen the known hair, it starts hunting for that hair's features in the questioned hair instead of recording what is actually in front of you. You are done with this step when: the known sample is fully covered and ten blank feature lines are written on your page.

3. Read the cuticle and the shaft. Look along the outside edge of the shaft, not down the middle. The cuticle is the outer scale layer, and at the edge it shows as fine serration, like the teeth of a very small saw. Then lay your ruler across the hair and measure the shaft width in millimetres at three places, near the top, the middle, and the bottom of the frame. You are done with this step when: you have written whether the serration is visible, and three shaft widths in millimetres.

4. Read the pigment in the cortex. The cortex is the main body of the hair between the edge and the centre, and it holds the pigment granules. The granules look like fine dark specks. Judge how many there are and write light, medium, or heavy. Then judge where they sit and write one word: uniform if they are spread evenly, peripheral if they are pushed toward both edges, one-sided if they are heavier along one edge only, or clustered if they gather in patches. You are done with this step when: one density word and one distribution word are written on your sheet.

5. Name the medulla type. The medulla is the central canal that runs down the middle of the shaft. Put your pencil tip at one end and trace the middle of the hair all the way to the other end. Decide which of four words fits: absent if there is no canal at all, fragmented if there are short specks with long gaps, interrupted if there are long runs broken by regular short gaps, or continuous if it is unbroken along the whole shaft. If you genuinely cannot tell, write the two words you are choosing between. You are done with this step when: one of the four medulla words is circled, or two words are written with "cannot tell" beside them.

6. Measure the medullary index. Pick one clear spot on the shaft and mark it lightly with your pencil. At that exact spot, measure the medulla width in millimetres, then the shaft width in millimetres, without letting the ruler slide off that line. Divide medulla width by shaft width and write the answer to two decimal places. Then measure the printed scale bar in millimetres and use it to convert your shaft width into micrometres. You are done with this step when: a medullary index to two decimals and a shaft diameter in micrometres are both written, taken at the same marked spot.

7. Read the root and the tip. Go to each end of the hair and look at it directly. A root is anagen if it is elongated and narrow with a soft sheath around it, catagen if it is an elongated club, and telogen if it is a rounded pale bulb shaped like a tiny club. A tip is tapered if it narrows to a natural point and was never cut, cut if it ends square, abraded if it is worn and rough, and split if it has separated into strands. If an end is broken off, write "not available" instead of guessing. You are done with this step when: a root word and a tip word are written, with "not available" used for any end that is missing.

8. Uncover and read every known hair. Take the paper off the known sample. Fill in the same ten features for every hair in the known sample, one hair at a time, in the same order you used for the questioned hair. Do not skip a hair because it looks obviously different, and do not stop at the one that looks closest to your questioned hair. When every hair has a full row, write the lowest and the highest value the known hairs gave you for shaft diameter and for medullary index. You are done with this step when: every known hair has a complete feature row, and a low-to-high range is written for shaft diameter and for medullary index.

9. Hunt for the feature that does not fit. Read back through your rows looking for one feature where the questioned hair sits outside the known range rather than inside it. Spend a full minute on this on purpose. Your eye has been looking for agreement for the last ten minutes and it will keep finding agreement unless you point it the other way. If you find a candidate, re-measure it once and refocus the image before you accept it, because some apparent differences move when the focus moves. You are done with this step when: you have written either the name of one feature that falls outside the known range, or the sentence "no feature falls outside the known range" plus the names of the two features you checked hardest.

10. Call it and get it checked. Write one of three words: consistent, excluded, or inconclusive. Excluded needs at least one feature clearly outside the range of every hair in the known sample. Inconclusive is a real answer, and it is the right answer when too few features are readable to support either of the other two. Hand your sheet to a partner who has not seen your call, have them read the same questioned hair cold, and list every feature where the two of you disagree. You are done with this step when: your word, your partner's word, and every disagreement by feature name are all written on the sheet.

Worked example, done all the way through

Questioned hair Q-3 came off a jacket. The known sample K-B holds three hairs, B1, B2, and B3, all taken from one person's head.

Q-3 was in focus for most of its length and the scale bar was labelled 100 micrometres. I measured the scale bar with my ruler and it was 21 mm long on the page, so 1 mm on the page equals 4.76 micrometres on the hair. One end of Q-3 was broken off, so there was no root. I wrote "usable, no root" and went on.

I covered K-B with a sheet of paper before doing anything else, then ruled my ten feature lines.

Working down Q-3: colour medium brown. Serration was visible along both edges, so the cuticle was readable. Shaft width at three points was 15.0 mm, 15.5 mm, and 14.5 mm, which converts to 71, 74, and 69 micrometres. Pigment density medium, distribution uniform. The medulla ran unbroken from one end to the other with one narrow pinch about a third of the way down, so I called it continuous. At the 15.0 mm spot I marked, the medulla measured 4.5 mm, so the medullary index was 4.5 divided by 15.0, which is 0.30. The index came out the same whether I used millimetres on the page or micrometres on the hair, because it is a ratio and the scale bar cancels. The shaft diameter is not a ratio, so that one needed the scale bar. Root not available. Tip cut square.

Then I uncovered K-B and read all three known hairs in the same order.

- B1: medium brown, shaft 15.5 mm which is 74 micrometres, medulla continuous, medulla 4.5 mm, index 4.5 divided by 15.5 which is 0.29, pigment medium and uniform, telogen club root, tapered tip.
- B2: medium brown, shaft 14.5 mm which is 69 micrometres, medulla continuous, medulla 4.8 mm, index 4.8 divided by 14.5 which is 0.33, pigment medium and uniform, no root, cut tip.
- B3: medium brown, shaft 16.0 mm which is 76 micrometres, medulla continuous with a longer pinch, medulla 4.2 mm, index 4.2 divided by 16.0 which is 0.26, pigment medium and uniform, telogen root, abraded tip.

Known ranges: shaft diameter 69 to 76 micrometres, medullary index 0.26 to 0.33.

Here is where I got stuck. Q-3 came out at 0.30 and B3 came out at 0.26. That is a gap of 0.04, and my first thought was that a gap is a difference and a difference means exclude. I nearly wrote excluded. What stopped me was looking at the knowns against each other instead of against Q-3. B1, B2, and B3 all came off one head, and on their own they spread from 0.26 to 0.33, a spread of 0.07. The gap between Q-3 and B3 was smaller than the gap between two hairs that definitely came from the same person. So the gap could not carry an exclusion.

I also checked how much of that spread was me. I re-measured B3's medulla and got 4.3 mm the second time, which gives 0.27 instead of 0.26. My partner measured Q-3's medulla and got 4.6 mm, which gives 0.31 instead of 0.30. So two careful people measuring the same hair land about 0.01 apart. That is much smaller than the 0.07 spread across one person's own hairs, which told me the spread is real biology and not sloppy measuring.

Then I hunted for a feature that did not fit. In the lower third of Q-3 the pigment looked heavier along one edge, which would have been one-sided distribution and would have been a real difference from three uniform knowns. I turned the fine focus and the heavy edge moved to the other side. It tracked the focus, not the hair, so I recorded uniform with a note about the artefact. The one thing that stayed a limit was coverage. Q-3 had no root at all and a cut tip, so root type could not be compared and tip type only told me the hair had been cut at some point. Two of my ten features were unavailable.

Call: **consistent**, with limited features. Q-3 sits inside the known range on shaft diameter, medullary index, medulla type, colour, pigment density, and pigment distribution, and no feature falls outside that range. Two features could not be compared. This does not identify anyone.

My partner read Q-3 cold and also wrote consistent. We disagreed on medullary index by 0.01 and on nothing else. Both numbers went on the sheet.

How to write your conclusion

Fill in one of these three. Use the same words every time.

1. "Questioned hair _____ is microscopically consistent with the known sample from _____ on the features I could read, which were _____, _____, and _____. Features _____ and _____ could not be compared. Microscopic consistency does not identify a person."
2. "Questioned hair _____ is excluded as coming from the same source as the known sample from _____, because _____ measured _____ and falls outside the range of _____ to _____ shown by all _____ hairs in the known sample."
3. "No conclusion is supported for questioned hair _____, because _____. I am recording this as inconclusive."

Two sentences to never write:

"**The hair from the jacket is a match to Suspect B, so Suspect B was at the scene.**" Two separate problems. The word "match" claims the hair came from one specific person, and a microscope cannot support that, no matter how many features agree. The second half is a bigger jump than the first. Even a correct source conclusion says nothing about how the hair arrived. It could have transferred from a coat rack, a shared car seat, or a hug that morning.

"**Hair 3 is different from hair B3, so they came from different people.**" This treats one difference as an exclusion without checking the known sample against itself. In the worked example, B1, B2, and B3 all came from one head and their medullary indices spread from 0.26 to 0.33. A difference only supports exclusion when it falls outside the range of every hair in the known sample, and this one did not.

The three mistakes that cost people most

Comparing to the best-matching known hair only. There are three hairs in the known sample for a reason. If you pick the one that agrees with your questioned hair and quietly stop reading the other two, you have chosen the answer you liked rather than measured anything. The fix is mechanical and it works. Fill in a complete feature row for every known hair before you compare anything, then write the low-to-high range for each measured feature, and compare the questioned hair to the range, never to a single hair.

Treating within-person variation as between-person difference. Hairs from one head are not copies of each other. Shaft diameter, medullary index, and even medulla type can shift along a single hair and between hairs from the same person on the same day. In the worked example one person's three hairs spread 0.07 in medullary index while two careful students measuring the same hair landed 0.01 apart. If you do not know how wide one person's own spread is, you cannot tell a real difference from ordinary variation, so measure the knowns against each other before you measure the questioned hair against them.

Overstating to identification. This is the error with the longest record. An FBI and DOJ review of microscopic hair comparison testimony documented widespread overstatement in historical testimony, and it reinforced the need for bounded language and for DNA testing alongside the microscope (FBI-Hair-Review). In one study, experienced examiners made accurate inclusion or exclusion assessments in 85 percent of selected pairwise comparisons, and performance varied with hair length and with how familiar the examiner was with the populations represented (Koch-2021). That 85 percent is the share of those selected comparisons in that one study. It is not the chance that a hair came from a particular person. Keep the word "consistent" and retire the word "match".