

Editorial

Dear reader,

The number of communications in the field of forensic haemogenetics on stain analysis is continually on the increase. One part of such communications deals especially with population genetics of selected STRs in selected populations. Since this is on the one hand of paramount importance in our field but on the other hand ten thousands of such interesting systems exist, certain limitations need to be addressed.

Please observe the following rules:

1. If multiplexing has been used a subdivision into single locus communications does not make sense. The focus should preferably be on multiple loci.
2. Refer to the literature whenever possible. Key references summarising 2 or more references should be preferred. The number of references should not exceed 6 per single locus paper.
3. Statistics should include: check for Hardy-Weinberg equilibrium (exact test or tests with similar sensitivity), heterozygosity (observed and expected), allele frequencies, population size and 2 forensic efficiency values e.g. DI and exclusion chance.
4. Repetitions should be strictly avoided, also in the abstract. All basic information should be contained in one table and not repeated in the text.
5. Ideally, the whole content should not exceed 1–1.5 typewritten pages including references, tables etc. If 3–4 loci are combined, the number of manuscript pages can be approximately 4. The number of references allowed can then be up to 15.
6. The text dedicated to each section should be extremely short (abstract, introduction, materials and methods, statistics: each two lines, results and discussion: max. 100 words; data can briefly be compared to results on other selected populations).
7. Standards to be met if not referenced:
 - allelic ladder,
 - precision and accuracy of allele determination,
 - resolution of the system used,
 - definition of the electrophoretic system (e.g. native/denaturing).
8. Comparisons to other populations are not necessary but 2–3 such informative comparisons can be briefly performed.

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