

Reporting of pre-analytical variables in RNA-focused blood plasma studies: a prerequisite for quality assessment and replication

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Pre-analytical variables impact extracellular RNA (exRNA) research results

see the extracellular RNA quality control (exRNAQC) study

- blood collection tube
- time interval between blood collection and plasma preparation
- RNA purification method



Oral presentation in session 4 at this meeting
Full details? Scan me!

To what extent are pre-analytical variables reported in literature?

2 literature searches in Web of Science

selection of 100 most recent publications in 2018 and 2023*

screened for 22 pre-analytical variables



keywords: 'plasma' and 'RNA'

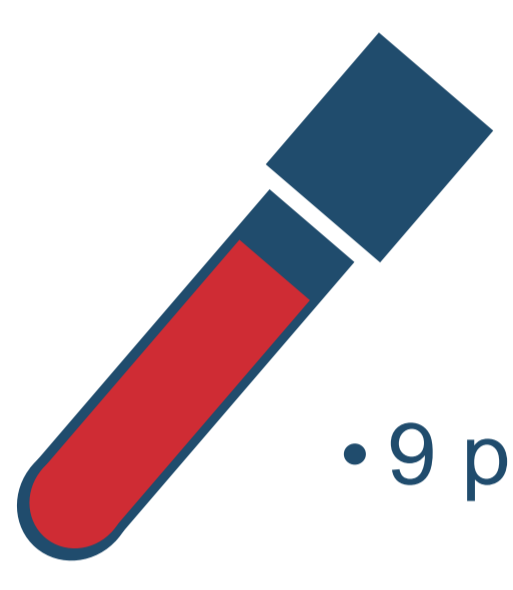


* analysis ongoing



blind evaluation by ≥ 2 researchers

Blood collection



• 9 pre-analytical variables

- 55.0% of the publications reports on the tube anticoagulant, whereby 92.8% uses EDTA tubes. Additional specifications on the type of blood collection tube are lacking or no insightful information is provided.
- the other variables are sparsely reported in literature, i.e. in 0 to 20.0% of the included studies.

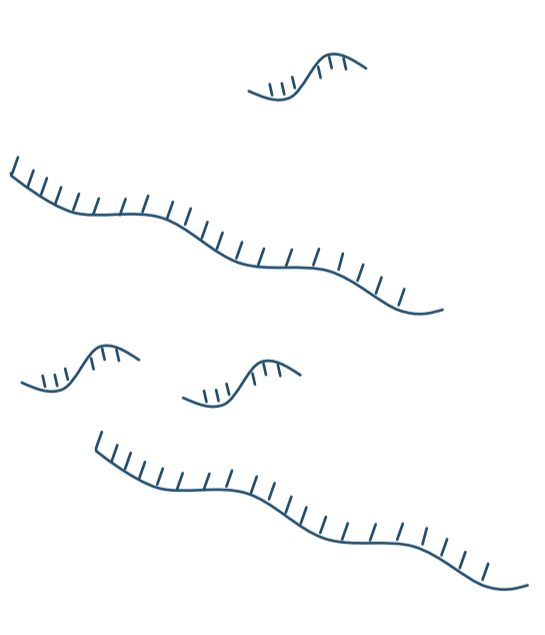
Plasma preparation



• 4 pre-analytical variables

- centrifugation summarizes the reporting of the specifications of the different centrifugation steps. For 28.3% of the studies, the information is incomplete or unclear. Most of the studies prepare single-spun (43.5%) or double-spun (52.2%) plasma.
- plasma QC (by hemolysis measurement) is only assessed in 10.0% of the studies.

RNA purification



• 9 pre-analytical variables

- for 5 publications, it is unclear whether exRNA purification from plasma is performed or not.
- 89.0% of the studies uses neat plasma, while 14.0% uses a specific plasma fraction (i.e. extracellular vesicles) for RNA purification.
- plasma input volume and RNA purification method are amongst the most frequently annotated variables, in 61.5% and 90.5% of the publications, respectively.
- only few articles report on the performance of an extra RNA purification step (7.4%) and/or DNase treatment (8.4%), although gDNA removal is crucial for certain exRNA analyses.

Conclusions

Only 6/22 variables are adequately reported in more than half of the publications. These variables are most frequently investigated in literature and as such a certain level of awareness of the importance on reporting them exists within the research community. For other variables, also documented to significantly affect exRNA results, there is still much room for improvement. In more recent years, multiple guidelines were developed that advocate for standardized reporting, but these clearly need to be further fine-tuned and implemented to allow meaningful interpretation and critical comparison of experimental designs and research results.

