

Navigating Obstacles in Exosome and Cell-Free RNA Extraction Protocols

Anna Sekyrova¹, Pavel Stejskal¹, Josef Srovnal¹, Marian Hajduch¹

¹Laboratory of Experimental Medicine, Institute of Molecular and Translational Medicine, Faculty of Medicine and Dentistry, Palacky University and University Hospital in Olomouc, Czech Republic

INTRODUCTION

Cell-free circulating RNA (cfRNA), particularly when encapsulated in exosomes, represents a promising avenue for minimally invasive cancer biomarker discovery. **Exosomes** (30–150 nm) carry a diverse array of RNA molecules that mirror the physiological and pathological states of their cells of origin, underscoring their potential in cancer diagnostics and prognostics. However, the translation of exosome-derived cfRNA into clinical practice is contingent upon the reproducibility and standardization of isolation and extraction techniques.

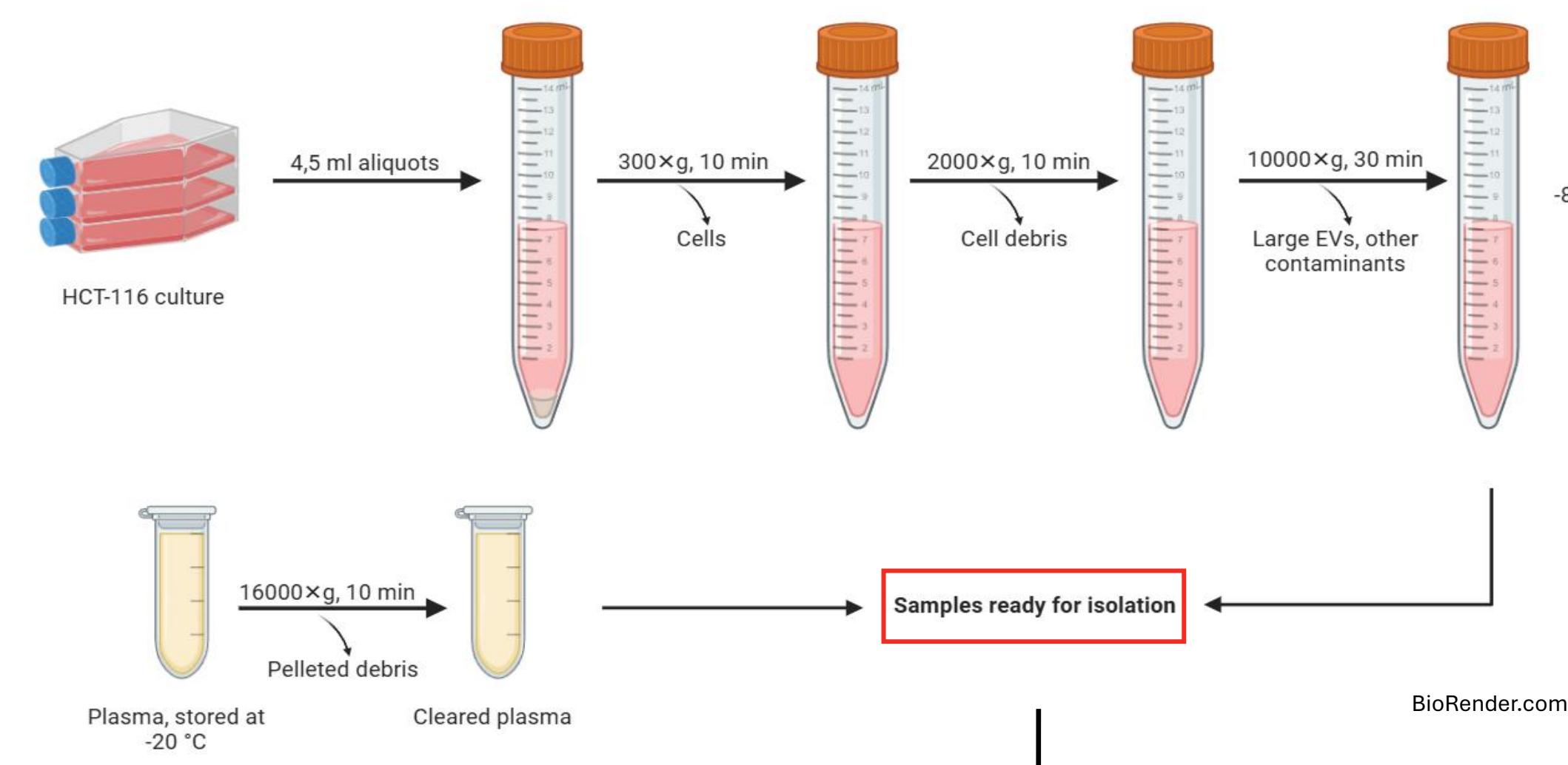
Aim

→ small EVs (preferentially exosomes) extraction and non-coding RNA extraction from within them

METHODS

Materials

cell culture-conditioned medium (CCM) from HCT-116 cells, 2–4 mL of **plasma** from healthy donors



Ultracentrifugation (UC) 100.000 x g, 90 min, 4 °C

—38,5 mL open-top tubes
—1,5 mL UC tubes with adaptors*
1 x 90 min*
2 x 90 min*
Beckman Coulter Optima XPN-100
SW 32 Ti rotor
50.2 Ti Fixed-Angle rotor

Commercial kits

—Norgen ExtraClean Plasma/Serum Exosome Purification (part one) and RNA Isolation Kit
—Qiagen exoRNeasy
—Qiagen exoEasy*

- Part one (exosome purification)*
- Complete protocol with RNA extraction
- Complete protocol + DNase treatment

*RNA isolation

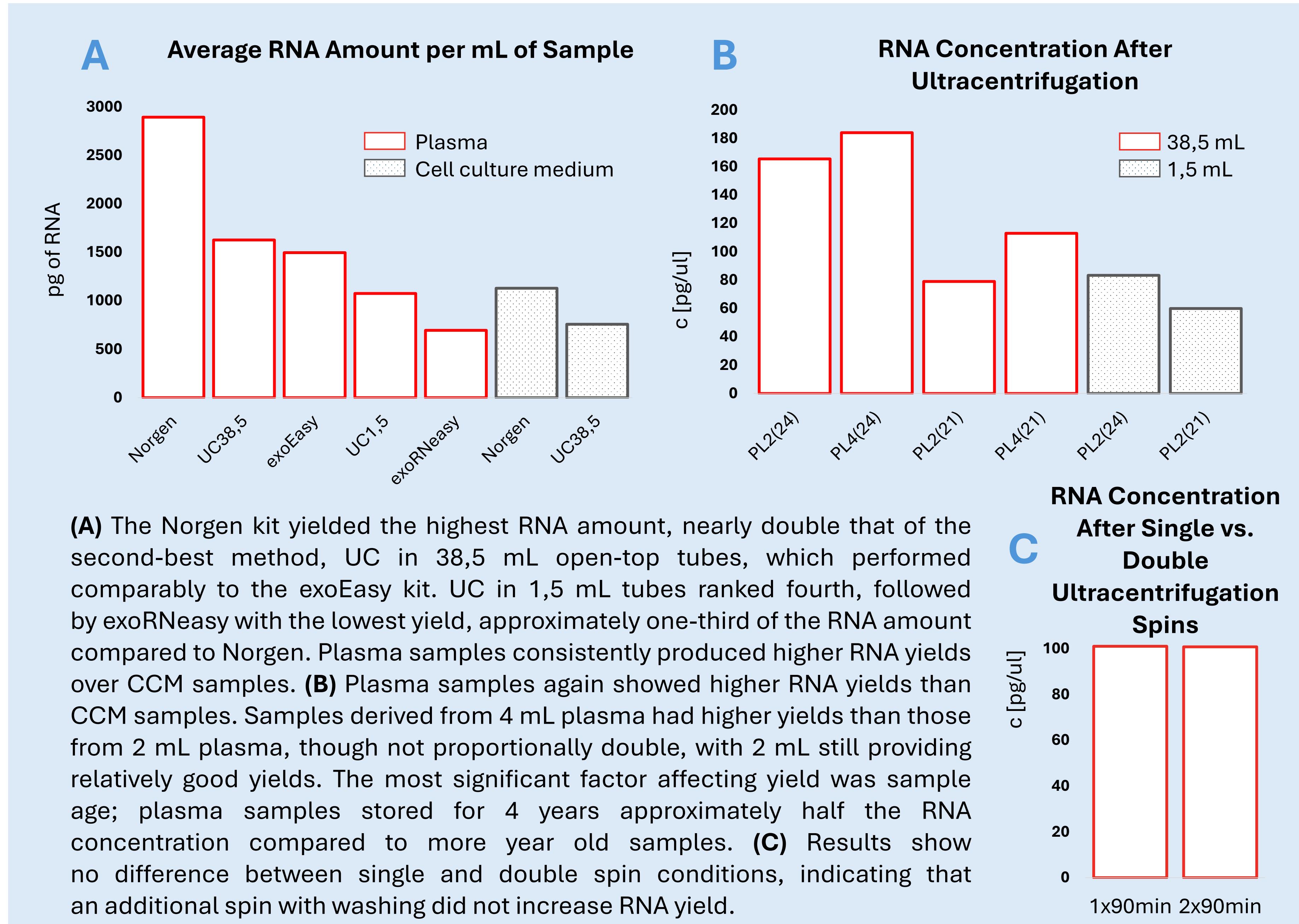
Qiagen miRNeasy

RNA quantification
Agilent Bioanalyzer RNA 6000 Pico Kit

ACKNOWLEDGEMENTS

This work was supported by Ministry of Health of the Czech Republic (No. NV18-03-00470), Ministry of Education, Youth and Sport of the Czech Republic (Nos. BBMRI – LM2023033, NCMG – LM2023067, EATRIS-CZ – LM2023053), Palacky University Olomouc (No. LF 2025_006), National Institute for Cancer Research (Programme EXCELES, ID Project No. LX22NPO5102) - Funded by the European Union - Next Generation EU and the SALVAGE project (CZ.02.01.01/00/22_008/0004644) supported by OP JAK, with co-financing from the EU and the State Budget.

RESULTS

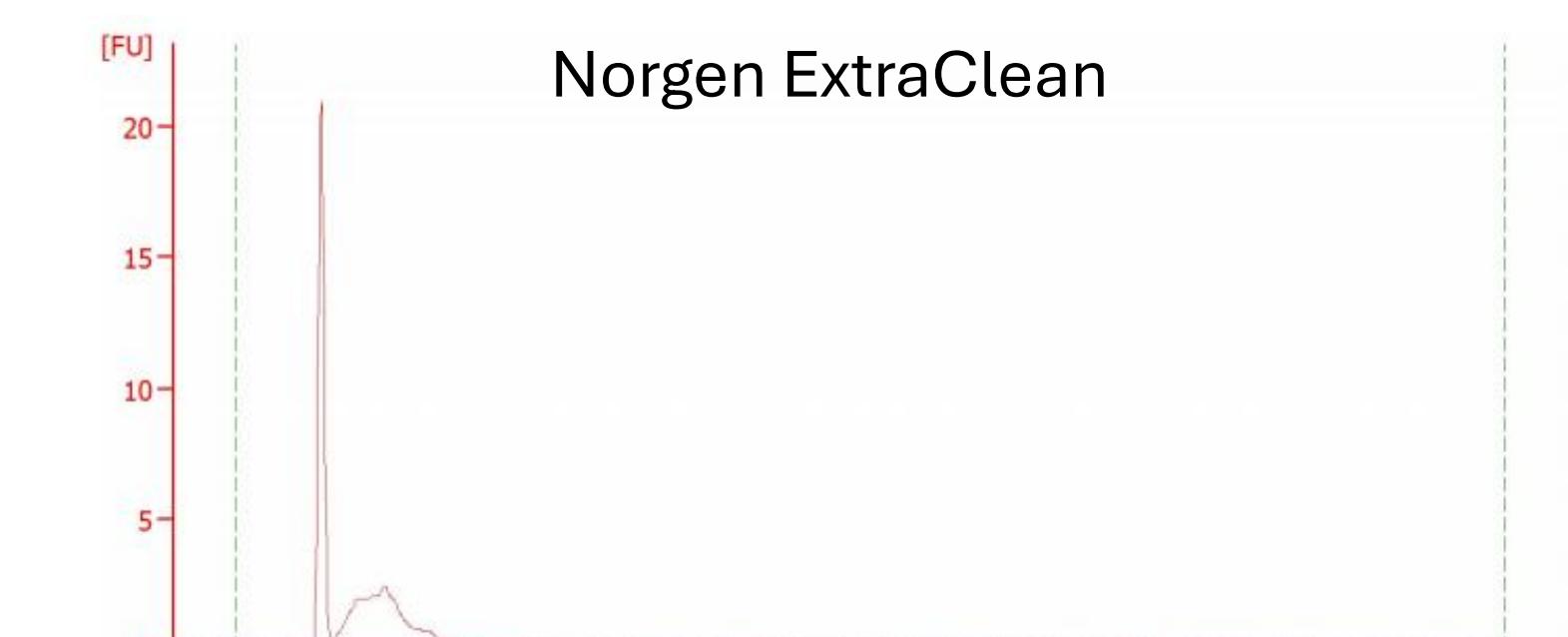


(A) The Norgen kit yielded the highest RNA amount, nearly double that of the second-best method, UC in 38,5 mL open-top tubes, which performed comparably to the exoEasy kit. UC in 1,5 mL tubes ranked fourth, followed by exoRNeasy with the lowest yield, approximately one-third of the RNA amount compared to Norgen. Plasma samples consistently produced higher RNA yields over CCM samples. **(B)** Plasma samples again showed higher RNA yields than CCM samples. Samples derived from 4 mL plasma had higher yields than those from 2 mL plasma, though not proportionally double, with 2 mL still providing relatively good yields. The most significant factor affecting yield was sample age; plasma samples stored for 4 years approximately half the RNA concentration compared to more year old samples. **(C)** Results show no difference between single and double spin conditions, indicating that an additional spin with washing did not increase RNA yield.

Norgen ExtraClean Plasma/Serum Exosome Purification and RNA Isolation Kit

- Inconsistent results
- Good RNA amounts (larger elution volume), but poor quality
- Great losses with DNase treatment

Norgen ExtraClean

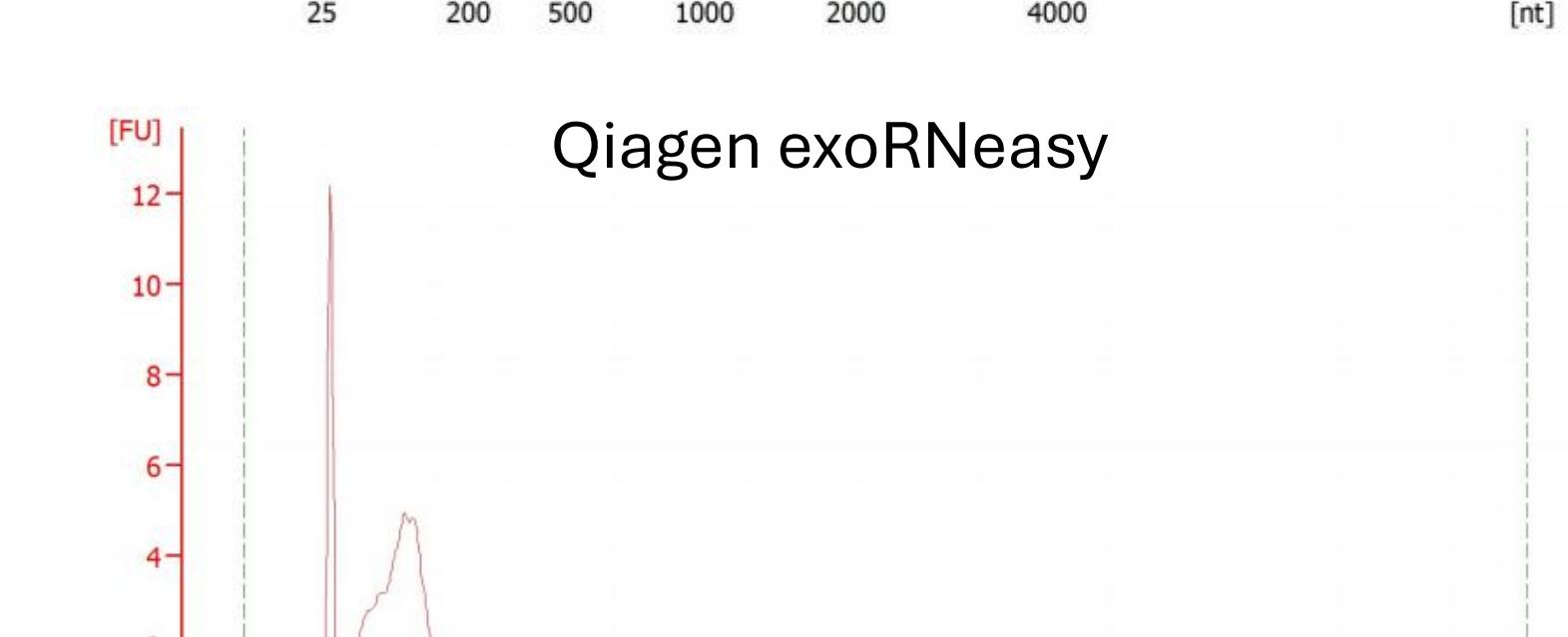


Qiagen exoEasy

- Mainly short fragments

Qiagen exoRNeasy

- Also yields short fragments



Bioanalyzer as a tool for RNA quality assessment

- Not suitable as RIN (RNA integrity number) algorithm depends on intact 18S and 28S rRNA peaks
- rRNA usually absent or depleted in EV RNA

RNA Electropherogram of Norgen ExtraClean and Qiagen exoRNeasy kits Isolated RNA (Agilent Bioanalyzer)

CONCLUSION & FUTURE PERSPECTIVES

- **Isolation method critical:** Norgen ExtraClean highest yield, but significant losses with DNase treatment
- **Qiagen exoEasy/exoRNeasy:** predominantly enrich short RNA fragments, limiting full-length RNA applications
- **Sample type:** plasma yields superior to CCM; larger plasma volumes improve yield but not proportionally
- **Sample age fundamental:** older samples show significantly reduced RNA concentrations
- **Ultracentrifugation:** 38,5 mL tubes overall better, extra spin + wash do not improve yield
- **Bioanalyzer:** not the optimal tool for EV RNA quality assessment (no RIN) due to lack of rRNA peaks

Next steps

SEC and **magnetic immunocapture** for higher purity/yield + **PCR-based quantification** to improve sensitivity

References

- Welsh, J. A., et al. (2024). Minimal information for studies of extracellular vesicles (MISEV2023): From basic to advanced approaches. *Journal of extracellular vesicles*, 13(2).
- Elkommoss-Zakhary, M., Rajesh, N., & Beljanski, V. (2022). Exosome RNA sequencing as a tool in the search for cancer biomarkers. *Non-coding RNA*, 8(6).
- Grätz, C., et al. (2024). A pipeline for the development and analysis of extracellular vesicle-based transcriptomic biomarkers in molecular diagnostics. *Molecular Aspects of Medicine*, 97.



LET'S CONNECT

anna.sekyrova02@upol.cz