





Response to "Technical approaches to reduce interference of Fetal calf serum derived RNA in the analysis of extracellular vesicle RNA from cultured cells"

Dear Editor

We read with great interest the article by Driedonks and colleagues (2019) on "Technical approaches to reduce interference of fetal calf serum derived RNA in the analysis of extracellular vesicle RNA from cultured cells" [1]. We would like to comment on our experience utilizing FBS-EV "depletion" protocols, in the hope that such a dialogue might be constructive to others investigating EVs derived from cultured cells, and the future evolution of FBS-EV "depletion" protocols.

Foetal bovine serum (FBS) extracellular vesicle (EV) contamination in FBS-supplemented culture media is of great concern to the EV-field, especially those assessing in vitro EV (and exosome) cargo composition and characterization from cultured cells [2]. We recognize the valiant effort put forth by our colleagues, modifying existing EV "depletion" protocols [3] and maximizing reductions in residual FBS-EVs (and RNA species) within supplemented culture media. Our concern remains, however, that despite the authors' technical modifications (i.e. adjusting serial serum dilutions and supernatant removal techniques - decant versus pipette) of existing protocols, there remain significant quantities of FBS-EVs (and RNA species) present in the supernatant used for culture that is difficult to isolate and remove. Using nanoparticle tracking analysis with ZetaVIEW[®], our group has shown that a large population (10⁹ EVs/ml) of residual FBS-derived EVs persist in EV- "depleted" FBS using a similar 18-h ultracentrifugation protocol (20% FBS dilution, 100,000 $\times g$ with an SW41 Ti Rotor, k factor = 124) [4]. Additionally, previous reports have demonstrated that FBS EVs may alter phenotype (and likely genotype) of cultured cells [5-8]. We have also shown that FBS-EV-"depleted" media provides suboptimal conditions for primary astrocyte growth and viability in culture [4].

Thus, these contaminant EVs not only influence the ability to characterize the EVs isolated from conditioned in vitro culture media but also may affect the underlying cellular processes of those cells, including EV release dynamics and EV cargos. More importantly, our field is at the mercy of existing technological capabilities. There remain relevant issues regarding limits of detection in available technologies that reportedly quantify differences at the nano (10^{-9}) scale [9,10]. Further, current technologies available for EV quantification (e.g. NanoSight, ZetaVIEW, qNano, High-Resolution Flow Cytometry) produce inconsistent and unreliable results, varying across institutions and laboratories [11,12]. Therefore, we contend that it remains impossible to confidently assert that using existing methodologies for FBS EV-depletion (i.e. ultracentrifugation [3], chemicalbased precipitation, size-exclusion chromatography, ultrafiltration [13]) can reduce the number of FBS EVs present within the resultant supernatant used to supplement culture media to non-confoundable levels.

Based on our experience and perspective, we would ask the EV-research field to reconsider the continued use of FBS EV-"depletion" protocols for in vitro EV (and exosome) analyses, and increase the focus towards serum-free media alternatives [14,15]. Advancing towards utilizing serum-free media, supplemented with a necessary cocktail of growth factors to support in vitro cell growth, may result in a better indication of both physiologic and pathobiologic cellular processes, in the absence of influential exogenous EVs [16]. Such an approach may allow for more relevant understandings of differential EV cellular dynamics and cargos within specific cell types, leading towards novel diagnostic and/or therapeutic health-care options [17].

Disclosure statement

Dr. Fiandaca reports intellectual property related to exosomes as diagnostics. No additional potential conflicts of interest were reported by the authors.

References

- [1] Driedonks TAP, Nijen Twilhaar MK, Nolte-'T Hoen ENM. Technical approaches to reduce interference of Fetal calf serum derived RNA in the analysis of extracellular vesicle RNA from cultured cells. J Extracell Vesicles. 2019;8 (1):1552059.
- [2] Lötvall J, Padula MP, Lu JF, et al. Minimal experimental requirements for definition of extracellular vesicles and their functions: a position statement from the International

- Society for Extracellular Vesicles. J Extracell Vesicles. 2014;3. DOI:10.3402/jev.v3.26913
- [3] Thery, C, Amigorena S, Raposo G, et al. Isolation and characterization of exosomes from cell culture supernatants and biological fluids. Curr Protoc Cell Biol. 2006; Chapter 3: Unit 3 22.
- [4] Lehrich BM, Liang Y, Khosravi P, et al. Fetal bovine serum-derived extracellular vesicles persist within vesicle-depleted culture media. Int J Mol Sci. 2018;19 (11):3538.
- [5] Eitan E, Zhang S, Witwer KW, et al. Extracellular vesicledepleted fetal bovine and human sera have reduced capacity to support cell growth. J Extracell Vesicles. 2015;4:26373.
- [6] Angelini F, Ionta V, Rossi F, et al. Foetal bovine serum-derived exosomes affect yield and phenotype of human cardiac progenitor cell culture. Bioimpacts. 2016;6(1):15-24.
- [7] Aswad H, Jalabert A, Rome S. Depleting extracellular vesicles from fetal bovine serum alters proliferation and differentiation of skeletal muscle cells in vitro. BMC Biotechnol. 2016;16:32.
- [8] Beninson LA, Fleshner M. Exosomes in fetal bovine serum dampen primary macrophage IL-1beta response to lipopolysaccharide (LPS) challenge. Immunol Lett. 2015;163(2):187-192.
- [9] van der Pol E, Coumans FAW, Grootemaat AE, et al. Particle size distribution of exosomes and microvesicles determined by transmission electron microscopy, flow cytometry, nanoparticle tracking analysis, and resistive pulse sensing. J Thromb Haemost. (7):1182-1192.
- [10] Vestad B, Llorente A, Neurauter A, et al. Size and concentration analyses of extracellular vesicles by nanoparticle tracking analysis: a variation study. J Extracell Vesicles. 2017;6(1):1344087.
- [11] Maas SL, de Vrij J, van der Vlist EJ, et al. Possibilities and limitations of current technologies for quantification of biological extracellular vesicles and synthetic mimics. J Control 2015;200:87-96.
- [12] Akers JC, Ramakrishnan V, Nolan JP, et al. Comparative analysis of technologies for quantifying Extracellular Vesicles (EVs) in Clinical Cerebrospinal Fluids (CSF). PLoS One. 2016;11(2):e0149866.

- [13] Kornilov R, Puhka M, Mannerström B, et al. Efficient ultrafiltration-based protocol to deplete extracellular vesicles from fetal bovine serum. J Extracell Vesicles. 2018;7(1):1422674.
- [14] Zhang Y, Chen K, Sloan SA, et al. An RNA-sequencing transcriptome and splicing database of glia, neurons, and vascular cells of the cerebral cortex. J Neurosci. 2014;34(36):11929-11947.
- [15] van der Valk J, Bieback K, Buta C, et al. Fetal Bovine Serum (FBS): past - present - future. Altex. 2018;35 (1):99-118.
- [16] Cahoy JD, Emery B, Kaushal A, et al. A transcriptome database for astrocytes, neurons, and oligodendrocytes: a new resource for understanding brain development and function. J Neurosci. 2008;28(1):264-278.
- [17] Fiandaca MS, Kapogiannis D, Mapstone M, et al. Identification of preclinical Alzheimer's disease by a profile of pathogenic proteins in neurally derived blood exosomes: a case-control study. Alzheimers Dement. 2015;11(6):600-607. e1.

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