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EDITED AND REVIEWED BY
Francisco Javier Salguero,
UK Health Security Agency (UKHSA),
United Kingdom

*CORRESPONDENCE
Mark Gray
mark.gray@ed.ac.uk

†These authors have contributed equally to this work

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Corrigendum: Comparative analysis of the development of acquired radioresistance in canine and human mammary cancer cell lines

Mark Gray[1*†], Arran K. Turnbull[2,3†], James Meehan[2†], Carlos Martínez-Pérez[2,3], Charlene Kay[2,3], Lisa Y. Pang[1] and David J. Argyle[1]

[1]The Royal (Dick) School of Veterinary Studies and Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom, [2]Translational Oncology Research Group, Institute of Genetics and Molecular Medicine, Western General Hospital, University of Edinburgh, Edinburgh, United Kingdom, [3]Breast Cancer Now Edinburgh Research Team, Institute of Genetics and Molecular Medicine, Western General Hospital, University of Edinburgh, Edinburgh, United Kingdom

KEYWORDS

canine breast cancer models, human breast cancer, radioresistance, global gene analysis, characterization of radioresistant cell lines, comparative oncology

A Corrigendum on
Comparative analysis of the development of acquired radioresistance in canine and human mammary cancer cell lines

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In the original article, images of spheroids and a scratch assay from a previous publication from our group in the journal Radiation Oncology were re-used (publication: https://ro-journal.biomedcentral.com/articles/10.1186/s13014-019-1268-2). Whilst this related publication was referenced in the manuscript, the re-use of the figures in their legends was mistakenly not acknowledged. The authors have confirmed that they retain the rights for re-publication/re-use of the images included in the Radiation Oncology publication. The figures in question are 4Ci (images of the MCF-7 and ZR-751 radiosensitive and radioresistant spheroids) and 6A (image of the MDA-MB-231 radioresistant scratch assay). The amended legends appear below.

The caption of Figure 4 previously stated:

Figure 4. Radioresistant cell lines have modified basal proliferation rates relative to their parental cells. **(A)** SRB assays showing differences in proliferation rates between MCF-7, ZR-751, MDA-MB-231, and REM-134 cell lines and their derived RR cell lines grown in 2D cultures (2-way ANOVA with Holm-Šídák multiple comparisons test; data expressed as mean ± SEM, $n = 3$, $^{****}p \leq 0.0001$; $^{***}p \leq 0.001$). **(B)** Heatmap showing log2 mean-centered gene expression profiles of proliferation genes in parental and RR cell lines showing key G1/S phase regulators taken from the KEGG database cell cycle pathway (55); red = higher expression, black = no change, green = lower expression. Heatmap clustering was carried out using Pearson correlation with average linkage. The gene list is shown in **Supplementary Table 3**. **(Ci)** IHC of MTS stained for Ki67 using MCF-7, ZR-751,

and REM-134 parental and RR cell lines. **(Cii)** Quantitative analysis of the % of cells with Ki67 staining (unpaired, two tailed *t*-test; data expressed as mean ± SEM, $n = 3$, $^{****}p \leq 0.0001$).

The caption has been corrected to:

Figure 4. Radioresistant cell lines have modified basal proliferation rates relative to their parental cells. **(A)** SRB assays showing differences in proliferation rates between MCF-7, ZR-751, MDA-MB-231, and REM-134 cell lines and their derived RR cell lines grown in 2D cultures (2-way ANOVA with Holm-Šídák multiple comparisons test; data expressed as mean ± SEM, $n = 3$, $^{****}p \leq 0.0001$; $^{***}p \leq 0.001$). **(B)** Heatmap showing log2 mean-centered gene expression profiles of proliferation genes in parental and RR cell lines showing key G1/S phase regulators taken from the KEGG database cell cycle pathway (55); red = higher expression, black = no change, green = lower expression. Heatmap clustering was carried out using Pearson correlation with average linkage. The gene list is shown in **Supplementary Table 3**. **(Ci)** IHC of MTS stained for Ki67 using MCF-7, ZR-751 [images reproduced from (34)], and REM-134 parental and RR cell lines. **(Cii)** Quantitative analysis of the % of cells with Ki67 staining (unpaired, two tailed *t*-test; data expressed as mean ± SEM, $n = 3$, $^{****}p \leq 0.0001$).

The caption of Figure 6 previously stated:

Figure 6. Radioresistant cell lines have increased migration and invasion potential. **(A)** Images of 2D migration and 3D MTS invasion assays comparing the parental and the derived RR cell lines. **(B)** Graphs exhibiting the migration **(Bi)** and invasion assay **(Bii)** results. For the migration assays the relative migratory distance was calculated at each time point up to 48 h and expressed as a % area devoid of cells based on the initial scratched area at day 0. Invasion was assessed up to 96 h post-seeding. Area of MTS at each time point was calculated and expressed as a % of initial MTS area at day 0 (2-way ANOVA with Holm-Šídák multiple comparisons test; data expressed as mean ± SEM, $n = 3$, $^{****}p \leq 0.0001$; $^{***}p \leq 0.001$; $^{*}p \leq 0.05$.

The caption has been corrected to:

Figure 6. Radioresistant cell lines have increased migration and invasion potential. **(A)** Images of 2D migration and 3D MTS invasion assays comparing the parental and the derived RR cell lines [MDA-MB-231 image reproduced from (34)]. **(B)** Graphs exhibiting the migration **(Bi)** and invasion assay **(Bii)** results. For the migration assays the relative migratory distance was calculated at each time point up to 48 h and expressed as a % area devoid of cells based on the initial scratched area at day 0. Invasion was assessed up to 96 h post-seeding. Area of MTS at each time point was calculated and expressed as a % of initial MTS area at day 0 (2-way ANOVA with Holm-Šídák multiple comparisons test; data expressed as mean ± SEM, $n = 3$, $^{****}p \leq 0.0001$; $^{***}p \leq 0.001$; $^{*}p \leq 0.05$).

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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