



Nov 24, 2022

Fluorescent image acquisition and processing using Axiovert 200M microscope and ImageJ software

DOI

dx.doi.org/10.17504/protocols.io.ewov1o98plr2/v1

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DOI: <https://dx.doi.org/10.17504/protocols.io.ewov1o98plr2/v1>

External link: <https://doi.org/10.3390/cells12030343>

Protocol Citation: Electra Brunialti, Alessandro Maria Villa, Paolo Ciana 2022. Fluorescent image acquisition and processing using Axiovert 200M microscope and ImageJ software. **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.ewov1o98plr2/v1>

Manuscript citation:

Brunialti E, Villa A, Toffoli M, Pozzo SLD, Rizzi N, Meda C, Maggi A, Schapira AHV, Ciana P, Sex-Specific Microglial Responses to Glucocerebrosidase Inhibition: Relevance to GBA1-Linked Parkinson's Disease. Cells 12(3). doi: [10.3390/cells12030343](https://doi.org/10.3390/cells12030343)



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Protocol status: Working

We use this protocol and it's working

Created: November 24, 2022

Last Modified: November 24, 2022

Protocol Integer ID: 73221

Keywords: primary fluorescent microglia, dynamic changes of primary fluorescent microglia, imagej software fluorescent image acquisition, using axiovert, imagej software

Funders Acknowledgements:

The work was supported by the EU Joint Programme - Neurodegenerative Disease Research (JPND) project GBA-PaCTS, 01ED2005B

Abstract

Fluorescent image acquisition and processing using Axiovert 200M microscope and ImageJ software to analyze morphological and dynamic changes of primary fluorescent microglia.

Troubleshooting

Step 1: Acquire live microglia images using Axiovert 200M microscope with dedicated software (AxioVision Rel 4.9, Zeiss)

- 1 Insert the cell culture plate in the microscope holder, and set chamber parameters: T 37°C and CO2 5%.
- 2 Using X20 magnification chose 20 random fields;
- 3 Set exposition of the fluorescent channel to have a sharp image of microglia bodies and branches;
- 4 Records the live fluorescent microglia for 2 h taking a picture every 5 min.
- 5 Save the recorded file as a ".zvi".

Step 2: Elaborate the acquired images using Fiji software (ImageJ, NIH, version 2.0.0)

- 6 Open ".zvi" file with Fiji software as hyperstack and tick the "split channel" option;
- 7 close the bright field channel and start to elaborate the fluorescent channel (microglia);
- 8 subtract the background using "Process > Subtract Background"(identifier: legacy:ij.plugin.filter.BackgroundSubtracter);
- 9 defined threshold (foreground) that corresponds to green fluorescent objects using "Image > Adjust > Threshold" (identifier: legacy:ij.plugin.frame.ThresholdAdjuster). Keep the threshold consistent between acquisitions;
- 10 apply despeckle function "Process > Noise > Despeckle" (identifier:legacy:ij.plugin.filter.RankFilters("despeckle"));
- 11 apply smoothing function "Process > Smooth" (identifier: legacy:ij.plugin.filter.Filters("smooth"));

- 12 set the measurement: "Analyze > Set Measurements" (identifier: legacy:ij.plugin.filter.Analyzer("set")), and tick "Area", "Center of Mass", "Feret's Diameter" and "Shape Descriptors";
- 13 for each microglia select the area that contains the microglia in each time-frames using "Edit > Options > Roi Defaults" (identifier: legacy:ij.gui.RoiDefaultsDialog);
- 14 run analyze particles "Analyze > Analyze Particles" (identifier: legacy:ij.plugin.filter.ParticleAnalyzer), set size (micron²):130-infinity, circularity: 0.00-1.00; tick "display results";
- 15 process "all images";
- 16 copy the data in an Excell file;
- 17 repeat the steps from 13 to 16 for each microglia.
- 18 Among the "Shape Descriptors", keep the values of "Area", "Solidity", "FeretAngle", "XM" and "YM";
- 19 to calculate the distance covered by the cell during the time-lapse use the coordinates of the center of mass and sum the distance covered in each time frame assuming that the distance between frames corresponds to the cathetus of a right triangle made by X-axis and Y-axis displacement;
- 20 to calculate the rotation sum the "FeretAngle" taking into account that it is the angle among Ferret's diameter and parallel line to the cell contour only on x-axis;
- 21 calculate the median and the CV% of "Solidity" and "Area";
- 22 to perform the cluster analysis use each parameter obtained from the analysis; use the values of the vehicle and treated cells and identify the median parameter for the experiment;
- 23 use the identified median as a threshold to cluster the cells in two groups (over or under the median);
- 24 combine two parameters to generate four different clusters.

