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Defining glial cell self-alignment parameters for 3D CNS tissue models.

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INTRODUCTION: Recreating the 3D spatial environment of the CNS allows neural cells in vitro to behave more like their counterparts in vivo, providing robust and controllable model systems that mimic key aspects of the cell biology of the nervous system ¹. The overall aim is to develop engineered neural tissue models to resemble functional CNS tissue, with anisotropic tracts of neurons and glia arranged within a robust collagen hydrogel, at a scale suitable for drug screening. To establish viable production technology for the manufacture of CNS tissue models, the parameters, cell density and contraction, that govern glial cell self-alignment have been optimised.

METHODS To achieve consistent predictable glial cell alignment, an assay system was developed for determining optimal glial cell seeding density. 24-well and 96-well plate contraction profiles were conducted using C6 glioma cells in free-floating round collagen gels at 0.1 to 6 million cells/ml. Specific seeding densities were then used in alignment assays using tethered rectangular collagen gels ². Tethered gels were fixed and stained using Haematoxylin and Eosin and micrographs were analyzed to assess cellular alignment in 2 regions with characteristic alignment patterns (side and middle) and a control region, in which cells are randomly oriented ².

RESULTS: The two contraction profiles (Fig 1) follow a similar pattern, illustrating that a satisfactory profile can be constructed in either a 96-well or a 24-well plate. Contraction reached a plateau at 3 x 10⁶ cells/ml. A significant degree of alignment was measured using cell densities of 2, 3 and 4 x 10⁶ cells/ml in both middle and side regions, whereas 0.5 and 1 x 10⁶ cells/ml only produced significant alignment in the side region (Table 1).

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DISCUSSION & CONCLUSIONS: A two-stage approach was developed to determine the optimal glial cell seeding density to achieve consistent, predictable alignment. The establishment of the relationship between contraction and alignment will allow the optimal seeding density for alignment to be predicted using a small number of cells, regardless of the cell source.

REFERENCES: