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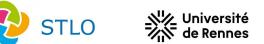


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P213

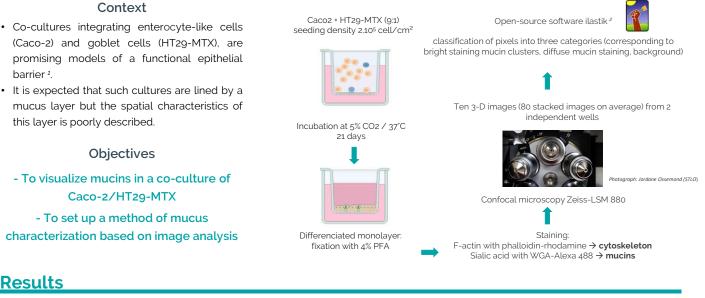
Characterization of the mucus lining a co-culture model of Caco-2/HT29-MTX cells

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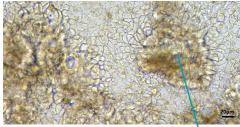
Introduction

Materials and methods



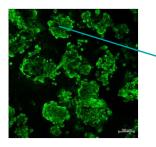
Results

1- Uneven distribution of the mucus



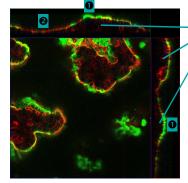
Observation of cultures by optical microscopy (X20)

Cells are confluent and they form a monolyer but some cells are grouped and lined with a blurry material.



Observation of cultures after staining of sialic acid





Observation of one stack of a 3-D reconstituted

3- Development of an image analysis workflow to characterize the mucus structure

Machine learning: annotation of pixels representative of bright / diffuse staining on a subset of images, followed by automatic classification on all images.

Extraction of quantitative data

	Dense mucin clusters	Loose mucus
verage thickness	6.9 µm	21.2 µm
verage volume	183000 µm ³	7502000 µm ³

The culture is not planar. Domes (visible on z-views) are present.

Mucins are present mainly at the apical sides of domes (see bright staining: sites of secretion) but also between

domes (see **2**diffuse staining: secreted mucins spreading over

the culture, loose mucus)

Height up to 135 µm.

On-going: segmentation and classification of cells

Conclusions

· Staining of sialic acid and confocal microscopy enable three-dimensional visualization of the mucus layer

Mucins are abundantly

expressed as clusters

- The mucus on the co-culture model is heterogenous in density
- The protocol of image analysis is suitable to extract quantitative data on the mucus layer (NB: lower thickness than in vivo data)

image

These methodological developments open the way to studying the impact of digested food constituents or digested foods on the intestinal mucus

References: (1) Béduneau et al. 2014. A Tunable Caco-2/HT29-MTX Co-Culture Model Mimicking Variable Permeabilities of the Human Intestine Obtained by an Original Seeding Procedure. Eur J Pharm Biopharm 87 (2), 290-298 (2) Berg et al. 2019. A. Ilastik: Interactive Machine Learning for (Bio)Image Analysis. Nat Methods 16 (12), 1226–1232.

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