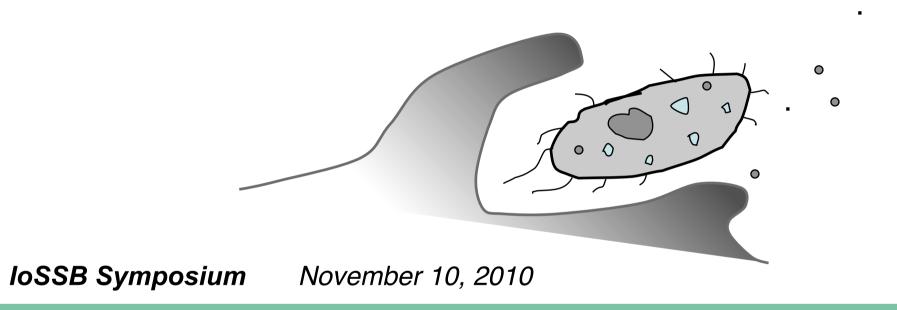
How one cell eats another

Physical principles in phagocytic uptake



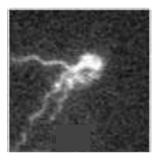
Robert Endres Imperial College London

http://www3.imperial.ac.uk/biologicalphysicsr.endres@imperial.ac.uk

Where physics meets biology....

Chemosensing and motility

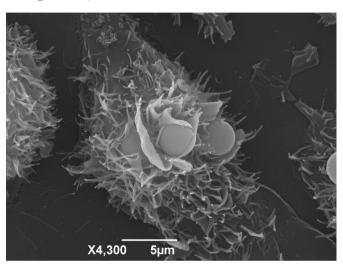
bacteria



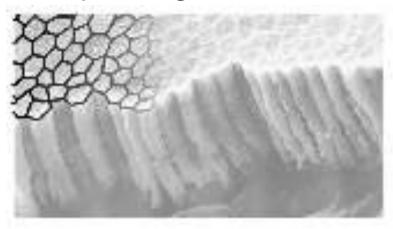
amoeba



Eating, uptake, and destruction



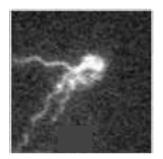
Cell packing



Where physics meets biology....

Chemosensing and motility

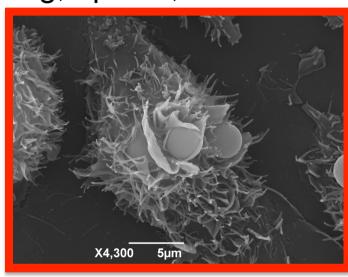
bacteria



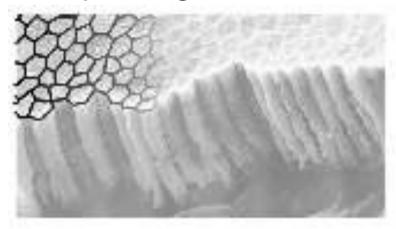
amoeba



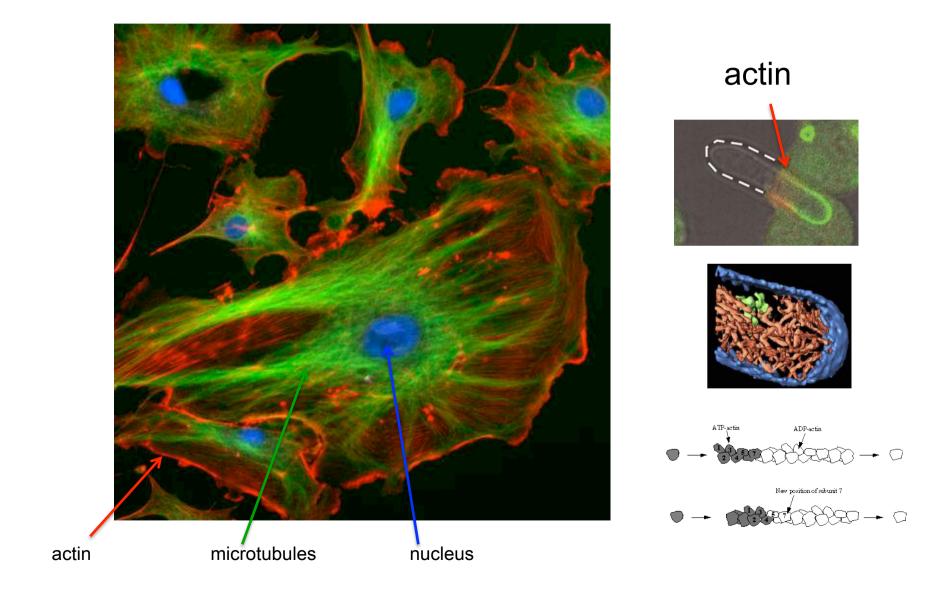
Eating, uptake, and destruction



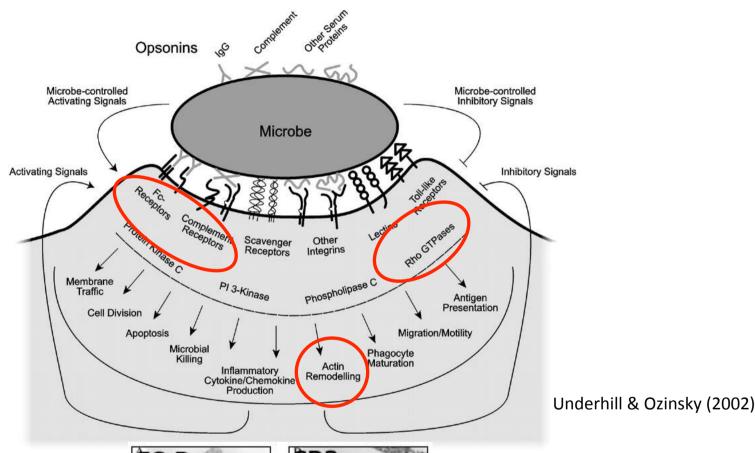
Cell packing



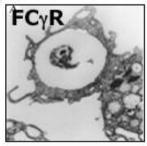
Cell cytoskeleton – very dynamic and versitile for cell-shape changes in phagocytosis, migration, adhesion, and packing

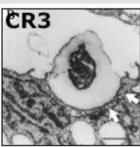


Daunting signalling complexity in phagocytosis



about 140 different molecular species are involved

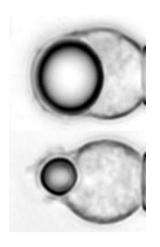




Allen & Aderem (1996)

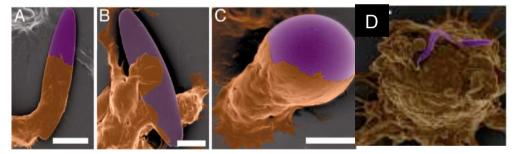
Geometric and biophysical aspects of phagocytosis

1. Particle-size independence



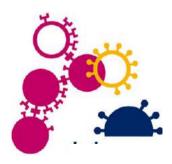
Herant et al. (2006)

- 2. Shape dependence
- 3. Elastic properties



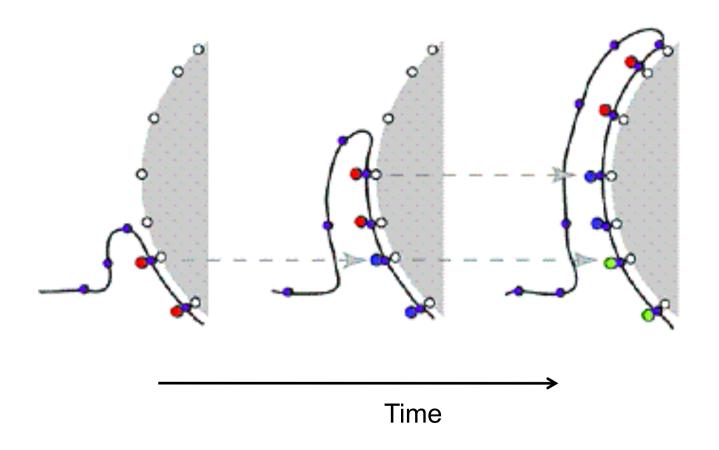
Champion et al. (2006,2009)

4. Ligand density



Conceptual Zipper mechanism

for explaining dependence on ligand density



Griffin et al. (1975), Swanson (2008)

Can the Zipper mechanism explain?

Geometric requirements of particle?

Size independence

Shape dependence



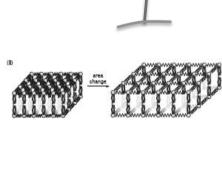
Energetic requirements of cell?

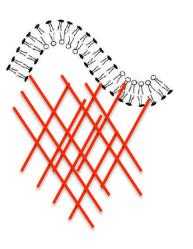
Ligand-receptor binding

Surface tension

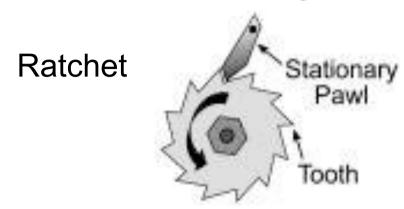
Membrane bending

Remodelling of cytoskeleton

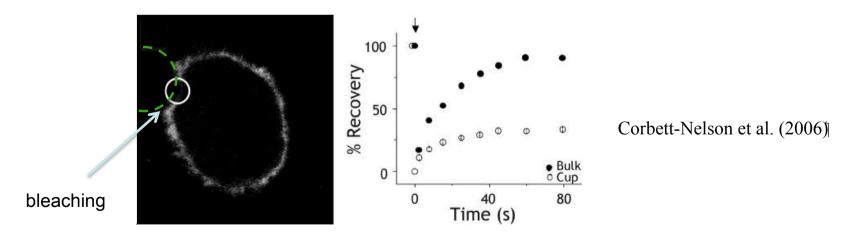




Mechanistic idea for modelling Zipper mechanism

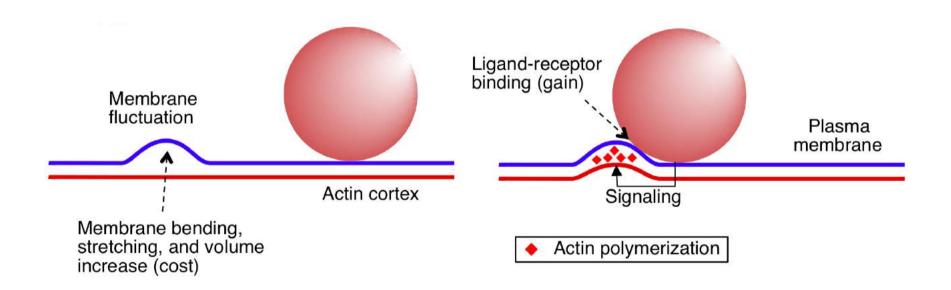


- 1. Unidirectional engulfment, even without pauses
- 2. Immobilization of proteins and lipids in cups from FRAP



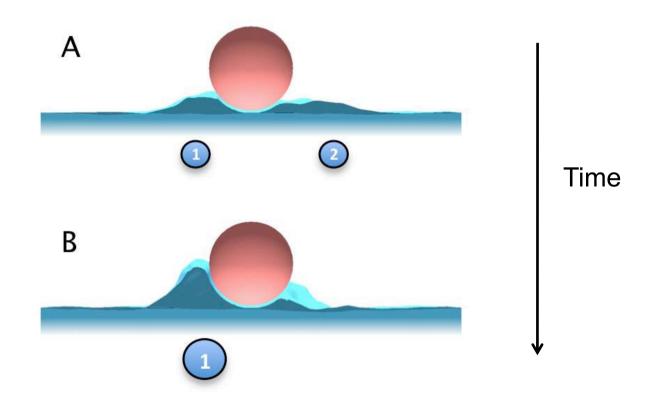
3. Ratchets used before in modelling actin-driven motility

Implementation of zipper mechanism



Ligand-receptor binding induces actin polymerization, making membrane deformation effectively irreversible \rightarrow ratchet.

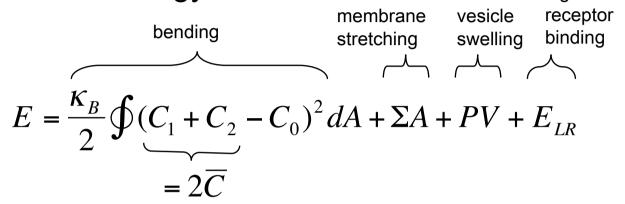
Ratchet model in action



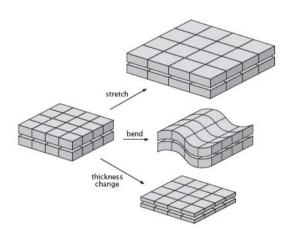
- 1 Membrane deformation near particle is stabilized.
- (2) Membrane deformation far from particle is retracted later.

Model for cell membrane

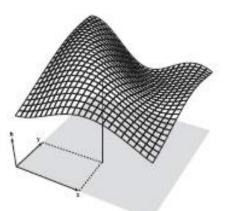
Cell-membrane energy:



membrane deformations

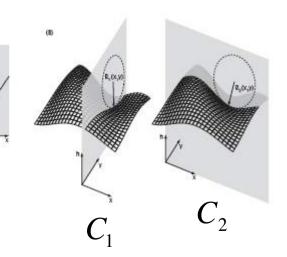


height profile h(x,y)



membrane curvature

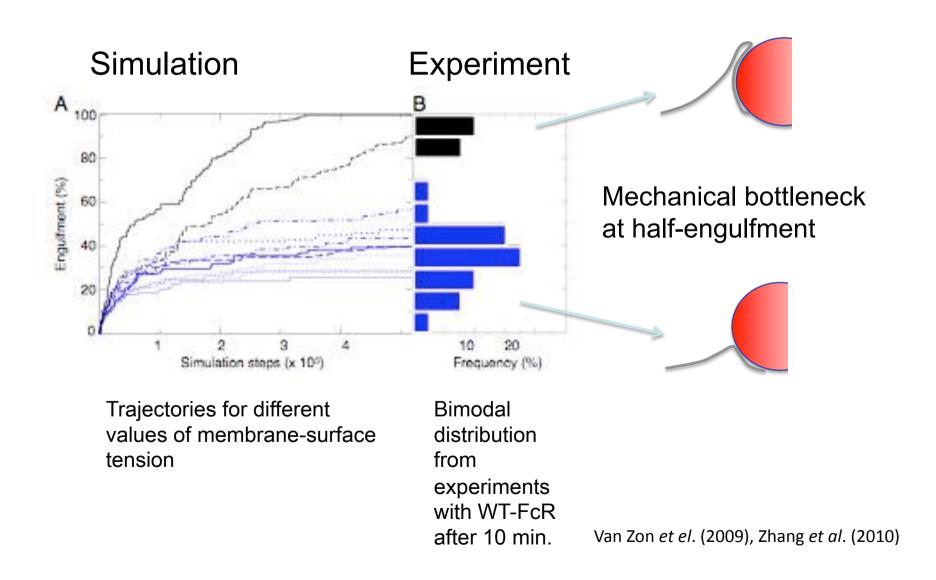
Ligand-



Engulfment for wide range of parameters

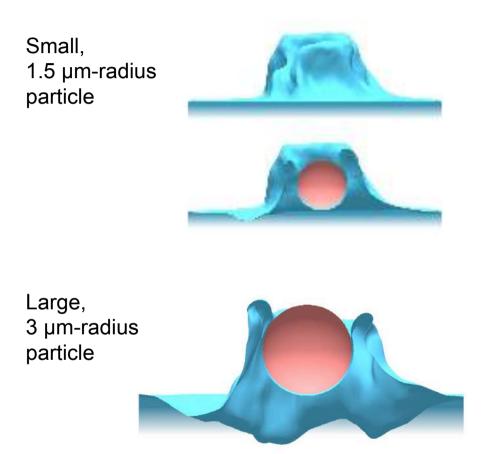
A Surface tension Cup shape constraint K Parameter range Bending K Fold change of 0.01 0.1 10 100 Standard C Parameters (SP) Particle size Particle shape and orientation 7 µm not engulfed!

Bistability: a means of decision making?



Energetic requirements:

Active zipper



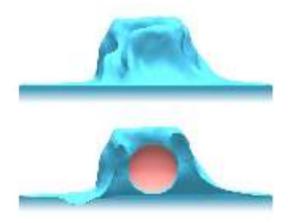
Active zipper easily engulfs small and large particles

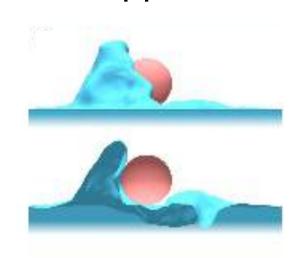
Energetic requirements:

Active zipper

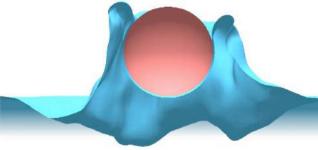
Passive zipper

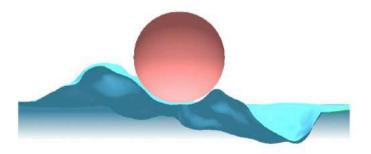
Small, 1.5 µm-radius particle





Large, 3 µm-radius particle

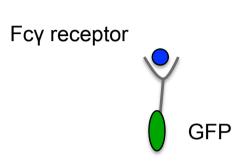


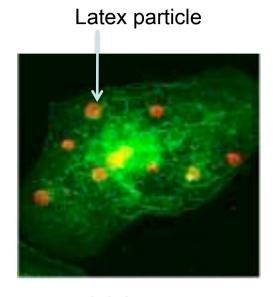


Active zipper easily engulfs small and large particles Passive zipper ONLY engulfs small particles - slowly with highly variable cups

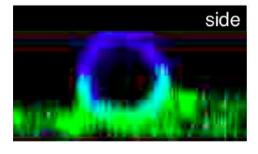
3D imaging with confocal microscopy







COS-7 cell



Phagocytic cup

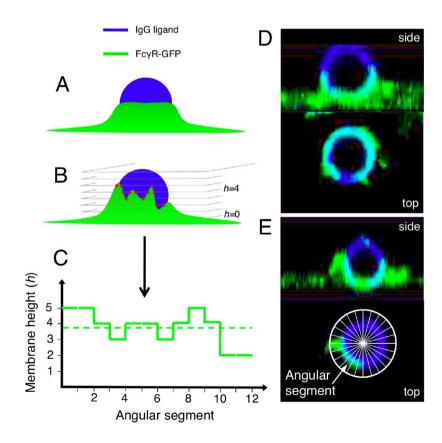
Experimental implementation of two zippers

Active zipper: cells expressing wild-type Fcy receptor

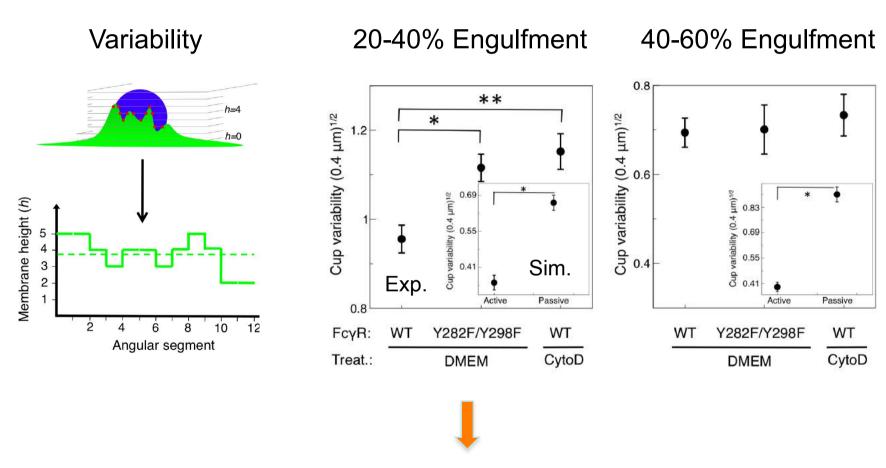
Passive zippers

cells expressing signalling-dead mutant receptor cells transfected with cytochalasin D

Cup height and variability



Variability of cup shape



Passive zipper produces more variable cup shapes than active zipper initially.

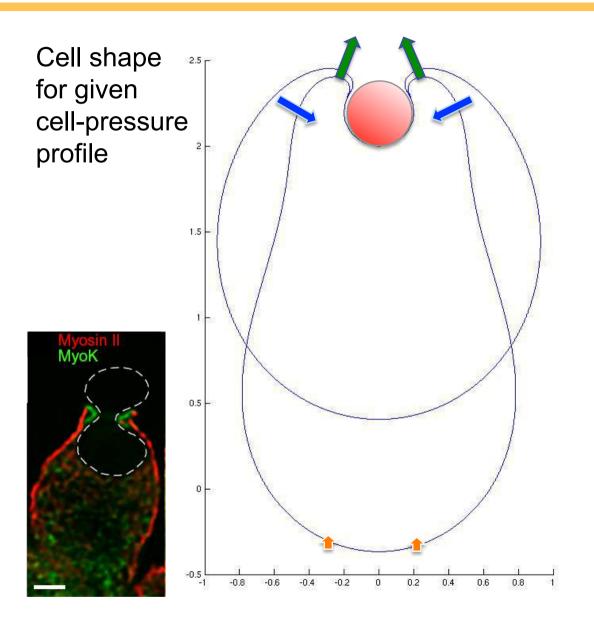
Engulfment time

Simulation **Experiment** В Α Small particles 60 WT-FcyR Small particle WT-FcyR+CytoD Active zipper Passive zipper Surface engulfed (%) Surface engulfed (%) Y282F/Y298F-FcyR Time (min) Time (min) C D Large particles WT-FcyR -Active zipper Large particle Surface engulfed (%) Surface engulfed (%) Passive zipper 4 6 Time (min) 4 6 Time (min) 10 8 10 2

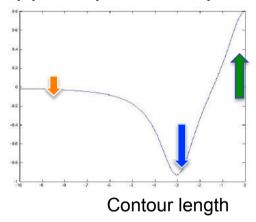


Active zipper engulfs significantly faster than passive zipper

Outlook: role of contraction in cup closure and shape

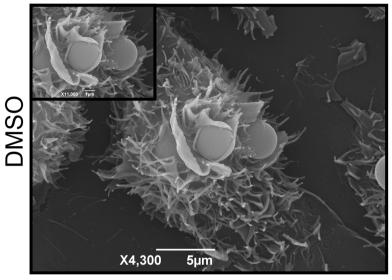


Applied pressure profile

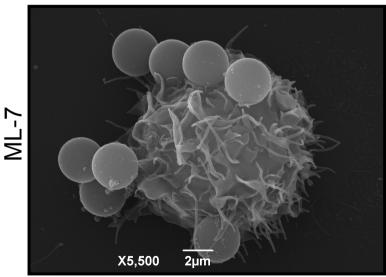


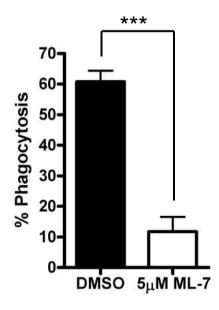
Need to calculate pressure from model for acto-myosin cytoskeleton and signalling

Myosin inhibitor ML-7 turns phagocytosis off



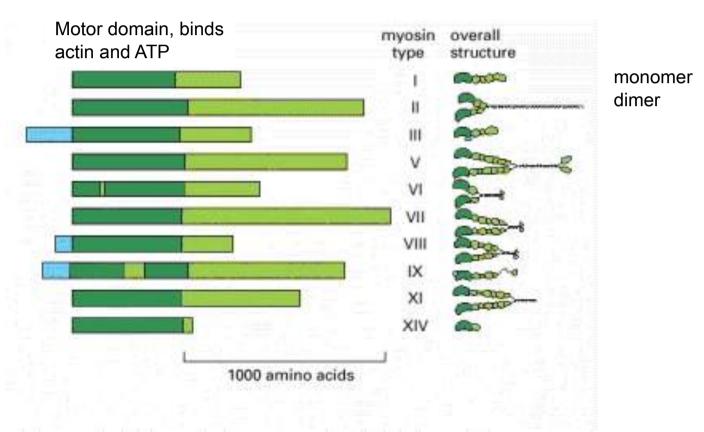
ML-7 is an inhibitor of myosin-light-chain kinase → perturbation of myosin-II





Domain structure of myosins

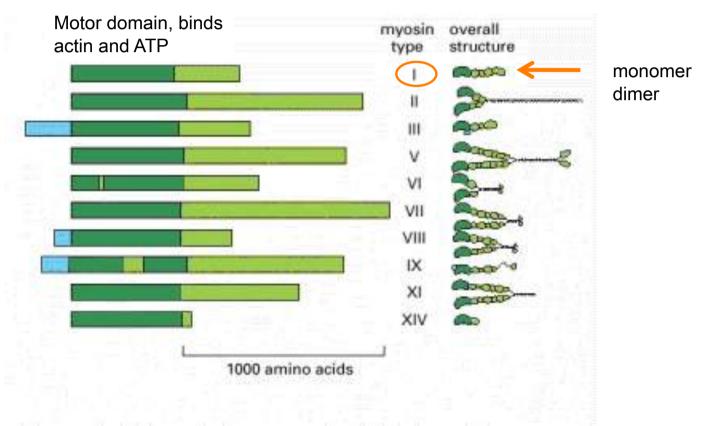
Motor proteins show diverse N- and C-terminus tails



Regulate membrane tension, purse-string contraction, pseudopod extension, transport, e.g. of membrane, and cell elasticity.

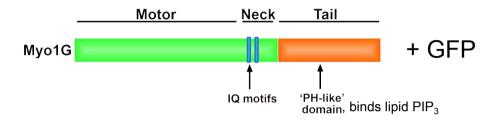
Domain structure of myosins

Motor proteins show diverse N- and C-terminus tails

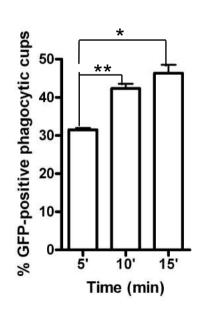


Regulate membrane tension, purse-string contraction, pseudopod extension, transport, e.g. of membrane, and cell elasticity

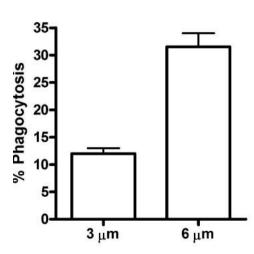
Myosin 1G – new role in phagocytosis



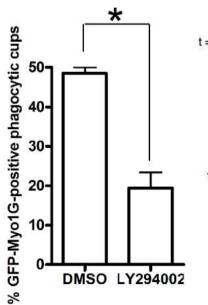
Recruited to cups



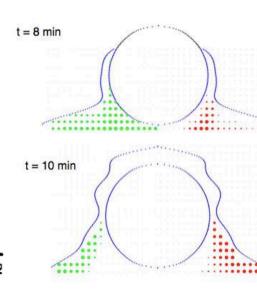
Required for uptake of large particles



Downstream of kinase PI3K

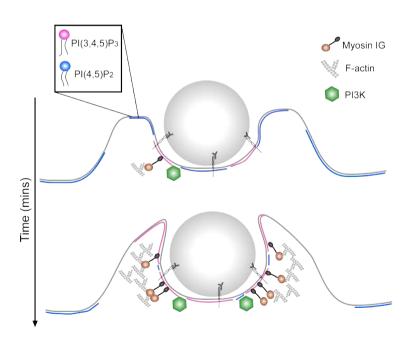


Myo1G and actin colocalise



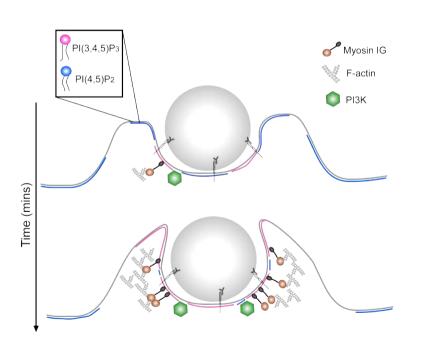
Myosin 1G – dynamic linking of actin and lipids

Conceptual model: PI3K produces PIP₃ lipids, a second messenger for Myo1G and cup closure



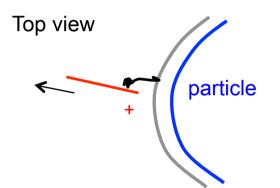
Myosin 1G – dynamic linking of actin and lipids

Conceptual model: PI3K produces PIP₃ lipids, a second messenger for Myo1G and cup closure

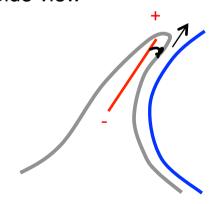


Role of Myo1G motor?

1) Radial force for cup closure

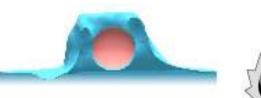


Transport of PIP₃ to cup rim
 Side view



Summary of phagocytosis work

• Implemented a 3D ratchet model for Zipper mechanism.



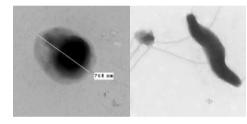
Ratchet
Stationary
Pawl
Tooth

 Particle size does not matter for active zipper, but for passive zipper.

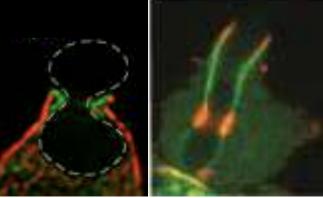
 Biochemical signalling pathways added by evolution for additional robustness?

Shape and orientation matter for active zipper:
 Potentially important for host-pathogen interactions and efficient drug design.

 Current model does not close cups well, contraction by motor proteins necessary?
 Wave-like nature of actin polymerization?



Coccoid and helical shapes



Acknowledgements

Biological Physics group:

- Sylvain Tollis (Postdoc)
- Anna Dart (Postdoc, experiment)
- Gerardo Aquino (Postdoc)
- Diana Clausznitzer (PhD)
- Luke Tweedy (PhD)



Collaborators:

- Gadi Frankel
- Brian Robertson
- Vania Braga
- Tony Magee/Martin Spitaler
- Sally-Ann Cryan (Dublin)
- Thierry Soldati (Geneva)

Tollis S, Dart A, Tzircotis G, Endres RG, BMC Syst Biol 4: 149 (2010); http://arxiv.org/abs/1011.0370.

£££:



