

**A bipartite module in the pericentriolar matrix scaffold mediates phosphoregulated binding to the  $\gamma$ -tubulin complex**

**Midori Ohta**

(Centrosome Dynamics and Evolution Group, Okinawa Institute of Science and Technology)



**Generation of a micro-intestine system by reproducing interstitial flow and its application in viral infectious disease**

**Sayaka Deguchi**

(Department of Synthetic Human Body System, Medical Research Institute, Institute of Integrated Research, Institute of Science Tokyo)



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**13:00-14:00 JST**



← via Zoom Register here

\*Those who are not affiliated with BDR are required to pre-register.  
The deadline for registration is **April 21 at 9:00.**

<https://riken-jp.zoom.us/meeting/register/ML1H4yZXROK57vjvoKCggg#/registration>

### **A bipartite module in the pericentriolar matrix scaffold mediates phosphoregulated binding to the $\gamma$ -tubulin complex**

Centrosomes consist of a centriolar core surrounded by a pericentriolar material (PCM) matrix that docks  $\gamma$ -tubulin complexes ( $\gamma$ TuCs) to nucleate microtubules. During mitotic entry, Polo-Like Kinase 1 (PLK1) phosphorylates the N-terminus of the PCM scaffold protein SPD-5 to promote  $\gamma$ TuC recruitment essential for chromosome segregation. Here, we show that the SPD-5 N-terminus exhibits two phosphoregulated  $\gamma$ TuC binding elements, PRGB1 and PRGB2, both of which independently bind  $\gamma$ TuCs upon PLK1 phosphorylation. Selective inhibition of either element impairs  $\gamma$ TuC recruitment, while deleting both elements increases centrosome separation defects, recapitulating the complete loss of  $\gamma$ TuCs. In the absence of PLK1, monomeric PRGB1 interacts with dimeric PRGB2, forming an autoinhibited conformation that prevents  $\gamma$ TuC binding. PLK1 phosphorylation disrupts this interaction and relieves the autoinhibition through a conformational change without altering its oligomerization status. These results reveal a bipartite phosphoregulated module within the PCM scaffold that mediates  $\gamma$ TuC recruitment to activate microtubule nucleation at mitotic centrosomes.

### **Generation of a micro-intestine system by reproducing interstitial flow and its application in viral infectious disease**

Recent advances have enabled in vitro modeling of the human intestine, but it remains a challenge to recapitulate fully its structural and functional characteristics. We hypothesized that interstitial flow plays a vital role in intestinal development. We aimed to construct an in vivo-like multilayered intestinal tissue model (micro-intestine system) by differentiating human ES/iPS cells into intestinal cells on a microfluidic device. Numerical simulations demonstrated that interstitial flow could be replicated by gently perfusing medium through the microfluidic device's pores. Single-cell RNA-sequencing analysis revealed that intestinal epithelial cells, fibroblasts, and enteric neurons were simultaneously differentiated from human ES/iPS cells in micro-intestine systems. Interstitial flow within the microfluidic device enhanced the maturation of intestinal cells, leading to the development of a villi-like epithelium and an aligned mesenchymal layer. Furthermore, enterovirus infection studies showed that the micro-intestine system would be a useful tool for recapitulating the pathophysiology of infectious diseases. Our micro-intestine system not only overcomes the limitations of conventional intestine models but also offers a unique opportunity to study the pathophysiology of intestinal disease.