

Regulation of the Wnt signaling pathway

Summary

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Supervisor: Prof. Dr. Tobias Madl
Availability: This position is available.
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Description

Background:

The canonical Wnt signaling pathway plays a pivotal role in a wide range of developmental and physiological processes. Wnt signaling controls essential cellular decisions on growth and differentiation during embryonic development and in adult tissue homeostasis (1,2). Inappropriate activation of the Wnt pathway due to mis-regulation - caused for example by mutations - is frequently linked to a plethora of human diseases such as cancer (1-5).

A key event of the Wnt pathway is the regulated degradation of the transcription co-activator β -catenin by the β -catenin destruction complex, consisting of Glycogen synthase kinase 3 β (GSK3 β), Casein Kinase 1 (CK1), Adenomatous Polyposis Coli (APC), the scaffold protein Axin-1 and the transcription co-factor β -catenin (6; Fig. 1). In the absence of Wnt ligand, free cytoplasmic β -catenin is trapped in the destruction complex, phosphorylated by GSK3 β (Ser33/Ser37/Thr41) (7-11) following priming phosphorylation by CK1,11 (Ser45), ubiquitinated, and degraded via the proteosomal pathway (12,13). The Wnt pathway gets activated upon binding of a Wnt ligand to the cell-surface receptor Frizzled (Fz) and low-density lipoprotein receptor-related protein (LRP) 5/6, resulting in the deactivation of the β -catenin phosphorylation/degradation cascade (2,14-17). The resulting increase in the cytoplasmic and subsequently also the nuclear levels of free β -catenin leads to transcription activation of Wnt target genes by binding of β -catenin to the Tcf (T-cell factor)/Lef (lymphoid enhancing factor) family of transcription factors (12,13,17).

Hypothesis and objective:

Based on our recent studies and supported by our preliminary data, we propose to study key elements of the Wnt pathway and their regulation by post-translational modifications. We propose to reveal the structural and functional mechanisms of Wnt pathway and to develop drugs targeting newly discovered key interactions by:

Aim 1) studying interaction, structure and function of the novel protein complexes

Aim 2) studying regulation of the novel protein complexes by post-translational modifications, disease mutations, and co-factors

This will set the base for the development discovery of early-stage drugs for the treatment of a plethora of diseases, such as human cancers related to distortions in Wnt signaling.

Methodology:

The PhD candidate will make use of our recent methodological achievements for studying structure of large protein complexes by combining solution Nuclear Magnetic Resonance (NMR) spectroscopy, and molecular modeling (18-23), and extend it with complementary approaches such as Mass Spectrometry (MS) and cell biology.

References:

1. Logan CY, Nusse R. The Wnt signaling pathway in development and disease. *Annu Rev Cell Dev Biol.* 2004; 20:781-810
2. MacDonald BT, Tamai K, He X. Wnt/beta-catenin signaling: components, mechanisms, and diseases. *Dev Cell.* 2009; 17:9-26

3. Clevers H. Wnt/beta-catenin signaling in development and disease. *Cell*. 2006; 127:469-80
4. Clevers H, Nusse R. Wnt/beta-catenin signaling and disease. *Cell*. 2012; 149:1192-1205
5. Polakis P. Wnt signaling and cancer. *Genes Dev*. 2000; 14:1837-51
6. Stamos JL, Weis WI. The beta-catenin destruction complex. *Cold Spring Harb Perspect Biol*. 2013; 5:a007898
7. Liu C, Li Y, Semenov M, Han C, Baeg GH, Tan Y, Zhang Z, Lin X, He X. Control of beta-catenin phosphorylation/degradation by a dual-kinase mechanism. *Cell*. 2002; 108:837-47
8. Ikeda S, Kishida S, Yamamoto H, Murai H, Koyama S, Kikuchi A. Axin, a negative regulator of the Wnt signaling pathway, forms a complex with GSK-3beta and beta-catenin and promotes GSK-3beta-dependent phosphorylation of beta-catenin. *EMBO J*. 1998; 17:1371-84
9. Yost C, Torres M, Miller JR, Huang E, Kimelman D, Moon RT. The axis-inducing activity, stability, and subcellular distribution of beta-catenin is regulated in *Xenopus* embryos by glycogen synthase kinase 3. *Genes Dev*. 1996; 10:1443-54
10. Peifer M, Pai LM, Casey M. Phosphorylation of the *Drosophila* adherens junction protein Armadillo: roles for wingless signal and zeste-white 3 kinase. *Dev Biol*. 1994; 166:543-56
11. Gao C, Xiao G, Hu J. Regulation of Wnt/beta-catenin signaling by posttranslational modifications. *Cell Biosci*. 2014; 4:13
12. Jiang J, Struhl G. Regulation of the Hedgehog and Wingless signalling pathways by the F-box/WD40-repeat protein Slimb. *Nature*. 1998; 391:493-6
13. Liu C, Kato Y, Zhang Z, Do VM, Yankner BA, He X. beta-Trcp couples beta-catenin phosphorylation-degradation and regulates *Xenopus* axis formation. *Proc Natl Acad Sci U S A*. 1999; 96:62738
14. Cong F, Schweizer L, Varmus H. Wnt signals across the plasma membrane to activate the beta-catenin pathway by forming oligomers containing its receptors, Frizzled and LRP. *Development*. 2004; 131:5103-15
15. Hernandez AR, Klein AM, Kirschner MW. Kinetic responses of beta-catenin specify the sites of Wnt control. *Science*. 2012; 338:1337-40
16. Kim SE, Huang H, Zhao M, Zhang X, Zhang A, Semenov MV, MacDonald BT, Zhang X, Garcia Abreu J, Peng L, He X. Wnt stabilization of beta-catenin reveals principles for morphogen receptor-scaffold assemblies. *Science*. 2013; 340:867-70
17. Li VS, Ng SS, Boersema PJ, Low TY, Karthaus WR, Gerlach JP, Mohammed S, Heck AJ, Maurice MM, Mahmoudi T, Clevers H. Wnt signaling through inhibition of beta-catenin degradation in an intact Axin1 complex. *Cell*. 2012; 149:1245-56
18. Gobl C, Madl T, Simon B, Sattler M. NMR approaches for structural analysis of multidomain proteins and complexes in solution. *Prog Nucl Magn Reson Spectrosc*. 2014; 80:26-63
19. Huang JR, Warner LR, Sanchez C, Gabel F, Madl T, Mackereth CD, Sattler M, Blackledge M. Transient electrostatic interactions dominate the conformational equilibrium sampled by multidomain splicing factor U2AF65: a combined NMR and SAXS study. *J Am Chem Soc*. 2014; 136:7068-76
20. Karagoz GE, Duarte AM, Akoury E, Ippel H, Biernat J, Moran Luengo T, Radli M, Didenko T, Nordhues BA, Veprintsev DB, Dickey CA, Mandelkow E, Zweckstetter M, Boelens R, Madl T, Rudiger SG. Hsp90-Tau complex reveals molecular basis for specificity in chaperone action. *Cell*. 2014; 156, 963-74
21. Lorenz OR, Freiburger L, Rutz DA, Krause M, Zierer BK, Alvira S, Cuellar J, Valpuesta JM, Madl T, Sattler M, Buchner J. Modulation of the Hsp90 chaperone cycle by a stringent client protein. *Mol Cell*. 2014; 53:941-53
22. Madl T, Gabel F, Sattler M. NMR and small-angle scattering-based structural analysis of protein complexes in solution. *J Struct Biol*. 2011; 173:472-82
23. Muller R, Grawert MA, Kern T, Madl T, Peschek J, Sattler M, Groll M, Buchner J. High-resolution structures of the IgM Fc domains reveal principles of its hexamer formation. *Proc Natl Acad Sci U S A*. 2013; 110:10183-8



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