Poster Presentation

BM.P06

Importin alpha and nonclassical nuclear localization signal

C. Chang[1, 2], R. Couñago[1, 2], S. Williams[1, 2], M. Bodén[1, 3], B. Kobe[1, 2]

[1]*School of Chemistry and Molecular Biosciences and Institute for Molecular Bioscience, University of Queensland, Brisbane, Qld 4072, Australia,*
[2]*Australian Infectious Diseases Research Centre, University of Queensland, Brisbane, Qld 4072, Australia,* [3]*School of Information Technology and Electrical Engineering, University of Queensland, Brisbane, Qld 4072, Australia*

In the classical nuclear import pathway, the specific recognition between the nuclear receptor (importin-α) and the nuclear localization signals (NLSs) plays an essential role on facilitating the cargo import process. Importin-α has two separate NLS-binding sites (the major and the minor sites), accommodate NLSs, comprising of one (monopartite) or two clusters (bipartite) of basic residues connected by a 10 - 12 residue linker. The major NLS-binding site is the preferential binding site for most of the monopartite NLSs characterized to date. By screening random peptide libraries using importin-α variants as bait, the bound NLS sequences could be divided into six classes [1]. The class-3 minor site-specific NLSs and class-5 plant-specific NLSs feature a shorter basic cluster. The molecular basis of the specific binding between these non-classical NLSs and importin-α was not known and in particular, there was a lack of crystal structures of plant importin-α. Here, we present the first crystal structure of plant importin-α, and explain the differential binding specificity between the class-5 plant-specific NLSs and importin-α variants [2]. The binding conformation of the class-3 minor site-specific NLSs features an α-helical turn, that is distinct from the other NLSs reported structurally [3]. Comparative bioinformatic screens not only indicate both plant-specific and minor site-specific NLSs are much less prevalent than the classical NLSs, but also reveal a greater prevalence of these two classes of non-classical NLSs in rice the proteome, compared to the others from yeast, mammals, and even other plant species. Together, our data can help to characterize novel proteins containing non-classical NLSs destined for the cell nucleus by the classical nuclear import pathway.

[1] S. Kosugi, M. Hasebe, N. Matsumura, et al, J Biol Chem., 2009, 284, 478-85., [2] C.-W. Chang, R. L. M. Counago, S. J. Williams, et al, The Plant Cell, 2012, 24, 5074-5088., [3] C.-W. Chang, R. L. M. Counago, S. J. Williams, et al, Traffic, 2013, 14, 1144-1154.

Keywords: nuclear import, Plant importin alpha, nuclear localization signal