Protein Science Best Paper awards to Chih-Chia (Jack) Su and Minttu Virkki

Warmest congratulations to Jack Su and Minttu Virkki (Figure 1), the recipients of the Protein Society's Year 2014 "Best Paper" awards.

At the beginning of each year, two "best papers" are selected from articles published in *Protein Science* during the preceding 12 months. A junior author (typically the first author) is designated as the award winner and invited to give a talk at the following Annual Protein Society Symposium.

Jack Su received his Bachelor's degree in Life Science from National Dong-Hwa University, Taiwan. He received his Ph.D. in the Department of Biochemistry, Biophysics and Molecular Biology from Iowa State University (ISU). Currently, he is an assistant research scientist at ISU, working on the structure/function relationships of bacterial antimicrobial efflux proteins, which include the *C. jejuni* CmeABC, *N. gonorrhoeae* MtrCDE and *E. coli* CusCBA tripartite efflux systems. He uses X-ray crystallography, single-molecule FRET, isothermal titration calorimetry, and drug accumulation and efflux assays to elucidate the action mechanisms of these protein machines. Ultimately, he would like to pursue a career in academic research and study disease-related proteins using biophysical techniques.

Jack's award-winning work¹ is directed toward a major pathogen, *C. jejuni*, which is particularly devastating toward children. The pathogen has developed resistance to many antimicrobial compounds *via* the so-called CmeABC drug efflux system which actively extrudes antibiotics. The award-winning paper, reporting work carried out in the lab of Edward Yu at Iowa State University, describes the three-dimensional structure of CmeC, which is the outer membrane channel of CmeABC. This is the only part of the overall CmeABC tripartite complex system for which structural information is available. As seen in Figure 2, the CmeC structure, which is made up of three polypeptide chains, forms a 130 Å long tunnel (or "cannon") through which

antimicrobials are exported. There are two "gates" which presumably open to allow passage of these small molecules. It is hoped that knowledge of the structure will allow rational design of agents to block the export activity.

According to Dr. Yu, Jack is very passionate about his work. He has lots of ideas and always wants to improve his understanding of basic science. He was the key person in determining the CmeC structure. Jack has also supervised a number of postdoctoral fellows, graduate students and undergraduates in Dr. Yu's lab.

Minttu Virkki's path to her award-winning manuscript² was not entirely straightforward. She was born and attended school in Finland and planned to go to medical school. While studying for the entrance exams, however, she "fell in love" with cells, which led her to take a course in molecular biology in Sweden at Stockholm University. This led to further courses on a variety of subjects with her interest focusing more and more on proteins. After obtaining her Master's degree she began Ph.D. studies on membrane proteins with Arne Elofsson.

Aquaporin is an α -helical integral membrane protein. Most such proteins fold in a two-step manner. First, individual transmembrane helices are inserted into the membrane by the Sec translocan. Then these helices fold into the final overall conformation of the protein. Aquaporin follows a more convoluted process during which one of the α -helices is inserted into the membrane in one orientation but then ends up with the opposite alignment. Minttu and her coauthors use a variety of experimental and computational approaches to describe how this realignment occurs.

According to both Minttu and Arne Elofsson, the aquaporin study was very much a collaborative, multi-faceted effort. Anni Kauko, the last author on the manuscript, came up with the original idea for the folding process and with her student Nitin Agrawal used molecular dynamics to see if it seemed feasible. Arne Elofsson also contributed using bioinformatics analysis. All of the experimental work was

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Figure 1. Award winners. (A) Chih-Chia (Jack) Su. (B) Minttu Virkki.

Figure 2. Structure of the *C. jejuni* Cme channel protein. The three polypeptide chains are colored, respectively, red, blue and green. From Su et al. ¹, with permission.

done by Minttu, with help from student Elin Edsbäcker under Minttu's supervision. According to Elofsson, it is possible that Minttu did not realize the challenges she entered when she decided to do a Ph.D. in his group. "The group is almost completely bioinformatical and for the last three years she has been running the entire lab all by herself. During this time she has not only handled her own projects

but also taken care of all practical issues such as ordering and handling chemical registers. She has also supervised a number of master students. She has also been one of the most appreciated teacher assistants at the department during her Ph.D. studies."

Background Information

All articles published in *Protein Science* are candidates for the "Best Paper" awards. No nomination statement is required. At the same time, if authors submitting a manuscript feel that it will be a strong candidate for a "best paper" award, they are very welcome to include a brief note in the submission letter explaining why the contribution is especially worthy of consideration.

Brian W. Matthews
Editor

References

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2. Virkki MT, Agrawal N, Edsbäcker E, Cristobal S, Elofsson A, Kauko A (2014) Folding of Aquaporin 1: Multiple evidence that helix 3 can shift out of the membrane core. *Protein Sci.* 23:981–992.