Ray C T Hung et al., Metabolomics 2014, 4:2
http://dx.doi.org/10.4172/2153-0769.S1.024

OMICS Group Conferences
Accelerating Scientific Discovery

3rd International Conference and Exhibition on
Metabolomics & Systems Biology
March 24-26, 2014 Hilton San Antonio Airport, San Antonio, USA

Using neurotoxin proteolytic activity and mass spectrometry to determine botulinum neurotoxin A (BoNT/A) in pharmaceutical products

Ray C T Hung and **Ella L M Wong**
Government Laboratory, China

Neurotoxins consisting mainly of botulinum neurotoxin A (BoNT/A) produced by anaerobic bacterium *Clostridium botulinum* are the most lethal known poisons. Although BoNT/A has high lethal toxicity (LD_{50}=0.8 μg for a 70 kg human by inhalation), it has been used as a versatile substance for muscle spastic disorder treatments in clinical settings. BoNT/A also gains its worldwide popularity in cosmetic surgery to relieve facial wrinkles in recent years. The potency of therapeutic BoNT/A is usually tested using *in vivo* mouse bioassays as stated in British Pharmacopoeia and European Pharmacopoeia, or alternatively, *in vitro* enzymatic or immunoassay methods.

Botulinum toxin itself comprises a single heavy chain of ~100 kDa linked to a ~50 kDa light chain by a disulfide bond. The breaking of the disulfide bond can release the light chain, which can target a soluble *N*-ethylmaleimide-sensitive attachment protein (SNARE protein)–either synaptosomal-associated protein-25 (SNAP-25) or vesicle-associated membrane protein 2 (VAMP2), leading to a series of biological processes for its medicinal and cosmetic effects. Different botulinium toxins (serotype A-H) cleave uniquely on a specific site of SNAP-25 or VAMP2. In this paper, we attempt to develop a sensitive chemical method to analyse BoNT/A in pharmaceutical products and the detection mechanism is based on the unique BoNT/A neurotoxin proteolytic activities on the synthetic peptide SNAP-25. The specifically cleaved peptide fragments from SNAP-25 are then determined using liquid chromatography coupled with high resolution tandem mass spectrometry.

cthung@govtlab.gov.hk