

Recent Advances in Aminocoumarin Antibiotic Biosynthesis: Pyrroles, Adenylating Enzymes and MbtH-like Proteins

Lutz Heide

Professor

Pharmaceutical Biology, Pharmaceutical Institute
Eberhard-Karls-Universität Tübingen, Germany

Date: Tuesday, November 20, 2012

Time: 9:30 - 11:30

**Venue: 10F. Conference Room, Faculty of Pharmaceutical Science Research Bldg.,
the University of Tokyo**



The aminocoumarin antibiotics are characterized by their 3-amino-4,7-dihydroxycoumarin moiety. This family of antibiotics comprises highly potent gyrase inhibitors, including novobiocin and the structurally related compounds clorobiocin and coumermycin A1. These compounds interact with the B subunit of bacterial gyrase and inhibit ATP-dependent supercoiling of DNA. The structurally more complex simocyclinone D8, which contains two polyketide moieties, inhibits gyrase by a completely different mechanism, i.e. via interaction with the A subunit. Rubradirin and its aglycone, which contain an ansamacrolide moiety, interfere with protein or RNA synthesis, respectively. The biosynthetic gene clusters of all five aminocoumarin antibiotics have been identified, and the gene functions have been studied by genetic and biochemical methods. The biosynthesis of novobiocin and clorobiocin is now one of the best-understood pathways of secondary metabolism in streptomycetes.

**Organizer: GCOE Program Center for Medical System Innovation through Multidisciplinary Integration,
the University of Tokyo**

Ikuro Abe, Professor,

Graduate School of Pharmaceutical Sciences, the University of Tokyo

**Cooperation: Graduate Program for Leaders in Life Innovation, the University of Tokyo
Center for NanoBio Integration, the University of Tokyo**

For Further Information Contact: Kiyoko Jarnes at CMSI Office

Phone: 03-5841-1509 / Fax: 03-5841-1510

E-mail: jarnes@cnbi.t.u-tokyo.ac.jp

Registration: <http://park.itc.u-tokyo.ac.jp/CMSI/>