

Special Issue on
**Advances in Genetics, Biochemistry, Genomics,
 Bioinformatics, and Agricultural-Veterinary Applications
 of Antimicrobial Peptides**

CALL FOR PAPERS

Emergence and spread of pathogens of multiple antibiotics resistance evoke public concerns. From human clinical aspects methocillin-resistant *Staphylococcus aureus* (MRSA); extended spectral beta-lactamase (ESBL) producing Enterobacteriaceae; carbapenem-resistant *Klebsiella pneumoniae*, and multidrug-resistant *Pseudomonas* and *Acinetobacter* are the best known examples. From veterinary aspects the pathogenic prokaryotic *Clostridium* and the eukaryotic Coccidia species could be defeated by appropriate antibiotic treatments, but emerging multiple resistances in microbes may result in ineffectiveness of treatment. From medicinal plant aspect the streptomycin-resistant *Erwinia amylovora*, causing fire blight disease in Rosacea, is an example indicating how imperative is to develop new antimicrobial agents to face new challenges. Another “time bomb” is the eukaryotic oomycetal pathogen genus *Phytophthora*, the different species of which cause time-to-time dramatic damages in agriculture and forestry. A multidisciplinary effort is required to combat these infections. The comprehensive strategy includes developing of new antimicrobial agents effective against multiresistant pathogens. This motivates research toward introducing environmentally-friendly medicinal plants of novel mode of action. The resistance toward antibiotics is a phenotypic consequence of mutation or a resistance plasmid with mobile element leading either to enzymatic destruction or blocking permeation of pumping out antibiotics.

The antibacterial peptides (AMP) especially those acting at membrane level have a potential to kill multidrug resistant cells. Knowledge regarding the relationship between peptide structure and function as well as their mechanism of action is being applied in designing antimicrobial peptide variants as novel therapeutic agents against selected pathogenic targets. AMP are produced, for instance, by the bacterium (EPB) partner of entomopathogenic nematode/bacterium (EPN/EPB) symbiotic associations. The latter is to protect the monoxenic symbiotic complex in polyxenic conditions. They are in most cases enzymatically synthesized (nonribosomal, NRP) peptides. Biosynthesis gene clusters encoding NRP synthetases have been identified. The end product classes exhibit large structural heterogeneity and target spectra and are potential candidates for agricultural/plant protection application.

High-quality omics datasets have been providing valuable insights into the structure/activity relations of AMP of several EPB species and enabled the possibility of cross-species comparisons to identify and forecast active but environmentally friendly AMP molecules of shared and distinct chemical structures. The permanent efforts of producing, annotating and exploring draft genomes, transcriptomes, and proteomics, and designing classic genetic protocols to improve AMP production of a given AMP producer strain may lead to developing of novel broad-spectrum therapeutics of agricultural and maybe veterinary use against multidrug resistant pathogens.

Into this special issue, we invite original research papers as well as review articles that promote the field of chemistry, biochemistry, biosynthetic pathways, genetics, genomics, bioinformatics, and agricultural-veterinary applications of natural antimicrobial peptides.

Potential topics include but are not limited to the following:

- ▶ Screening natural symbiotic associations as a potential source of novel AMPs
- ▶ Discovery, bioassay, purification, and identification
- ▶ Chemistry, biochemistry, structure/activity relations
- ▶ Biosynthetic pathways
- ▶ Genetics, genomics, and bioinformatics of novel AMP
- ▶ Bioinformatics and approaches to analyze and compare the following:
 - ▶ NRP-AMP and RP-AMP omics datasets from different EPN/EPB associations
 - ▶ Omics database production or expansion using the *Xenorhabdus* database as a cornerstone
 - ▶ AMP/target identification based on high-throughput datasets
 - ▶ Evolutionary, coevolutionary, and comparative genomic/transcriptomic/proteomic studies
 - ▶ Clade-specific gene family expansions, reductions, or variations

Authors can submit their manuscripts through the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/bmri/biochemistry/agg/>.

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First Round of Reviews

Friday, 25 August 2017

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