

**SESSION 5 - CAROTENOIDS - ORAL COMMUNICATION****Ilya Vasilyev - Abstract n° C4**

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**Title of abstract:** First identification of C<sub>50</sub> carotenoids biosynthesis gene cluster in nematode-associated bacterium *Agreia bicolorata* strain VKM AC-1804 and its abundance in coryneform actinobacteria group

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**Key words:** C<sub>50</sub> carotenoids, whole-genome sequencing, coryneform bacteria, actinobacteria

**Abstract:** *Agreia* spp. are high-%GC aerobic coryneform bacteria found in different psychrotolerant environments such as soils, permafrost ices, air etc. Most of coryneform bacteria produce yellow or pale pigments while *Agreia bicolorata* strain VKM AC-1804 synthesizes orange and red compounds, probably isoprenoids. The strain AC-1804 was originally isolated from narrow reed grass (*Calamagrostis neglecta*) infected by the plant-parasitic nematode (*Heteroanguina graminophila*) in Moscow region, Russia (1). We have performed the de novo whole-genome sequencing of the strain VKM AC-1804 in order to reconstruct the possible pathway of the pigment biosynthesis (2). The processed genome sequence contained predicted genes involved in MEP/DOXP pathway of isoprenoid biosynthesis. We also found a gene cluster encoded certain enzymes of carotenoid biosynthesis: a phytoene synthase (*crtB*), phytoene desaturase (*crtI*), C<sub>50</sub> carotenoid epsilon cyclase (*crtYe/f*), lycopene elongase (*crtEb*). The metabolic role of these predicted proteins are related to biosynthesis of probably C<sub>40</sub> and C<sub>50</sub> carotenoids – acyclic lycopene, flavuxanthin and epsilon-cyclic decaprenoxanthin. The structure of the found gene cluster is considered to be common within coryneform bacteria group since discovered in *Corynebacterium glutamicum* (3). The phylogenetic analysis of the gene cluster has revealed the close affiliation between the strain VKM AC-1804 and *Rathayibacter toxicus*, an infective agent causing mass neurological disease of livestock known as annual ryegrass toxicity (ARGT). *A. bicolorata* VKM AC-1804 and *R. toxicus* have similar cultural properties and are vectored by *Anguina*-form nematode (4). Moreover, homologous gene clusters were found in a variety of known and possible human or plant pathogens such as *Kocuria rhizophila*, *Micrococcus luteus*, *Corynebacterium atypicum*, *Clavibacter michiganensis* subsp. *michiganensis*, and in completely free-living bacteria as well.

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