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WPRS *International Organisation for Biological and Integrated Control
West Palaearctic Regional Section*

SROP *Organisation Internationale de Lutte Biologique et Intégrée
Section Régionale Ouest Palaéarctique*

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New insights into the microbiome of apple fruit surface “cv. Pinova” through metagenomics

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Plant microbial communities (microbiota) living at the surface of fruit have been the source of the majority of biocontrol agents (BCAs) but their role as a community has been poorly studied so far. A pioneering assay using high-throughput sequencing (HTS) has been carried out to get insight into the microbiota of apple surface through metagenome sequencing. Apple from cv. Pinova were sampled in Belgium during Autumn 2013 and then the microbiota was isolated. After DNA extraction, the HTS assay generated 14.5 Gbases which were assembled in 133,888 contigs. These contigs provided useful information on taxonomic composition of the microbiota. Our results demonstrated high fungal and bacterial diversity on conventionally treated apple cv. Pinova. A total of 1398 bacterial species and 397 fungal species have been identified. Among the detected fungi, the phylum *Ascomycota* prevailed on the surface of fruits whilst *Bacteroides* were dominant in the bacterial population. Some contigs appear to be closely related to apple pathogenic fungi like *Aspergillus* spp., *Botrytis* spp., *Sclerotinia* spp. and *Penicillium* spp. and apple associated pathogenic bacteria like *Erwinia* spp. and *Agrobacterium* spp. Others were assigned to species of known BCA strains like *Cryptococcus* spp., *Talaromyces* spp, *Candida* spp., *Saccharomyces* spp., *Bacillus* spp. and *Enterobacter* spp. These results underline a very diverse microbial community whose role needs to be characterized.

Key-words: microbiota; apple; high-throughput sequencing