P05-004

Investigating the Relationship between the Growth of Wild-simulated Ginseng and the Soil Bacterial Community

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Background and Objectives

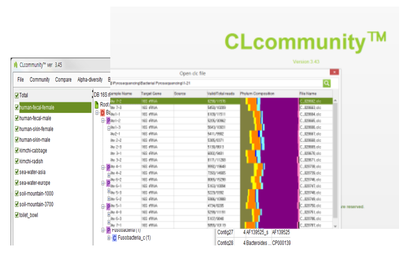
- ❖ **Wild-simulated ginseng (*Panax ginseng* C.A. Meyer) is one of the worldwide medicinal plants cultivated in forestry environment.**
- ❖ **The growth of wild-simulated ginseng can be affected by various factors, such as soil chemical properties, physiognomy, and soil microbial community.**
- ❖ **The aim of this study was to investigate the relationship between growth characteristics of wild-simulated ginseng and soil bacterial community living in rhizosphere environment.**

Materials and Methods

- ❖ **Subjects : 7- and 13-year-old wild-simulated ginseng (Pyeongchang, Yeongju, Muju)**
- ❖ **Growth characteristics : stem length, stem diameter, flower stalk length, number of leaflets, petiole length, leaflet length, leaflet width, rhizome length, root diameter, root length, number of rootlets, total weight, root weight, dry weight**
- ❖ **Soil bacterial community analysis : Next generation sequencing, Mothur application**
- ❖ **Relationship analysis : Relative abundance (Phylum level), Principal coordinate analysis (PCA)**

Next generation sequencing to Bioinformatics Workflow

Illumina



Results

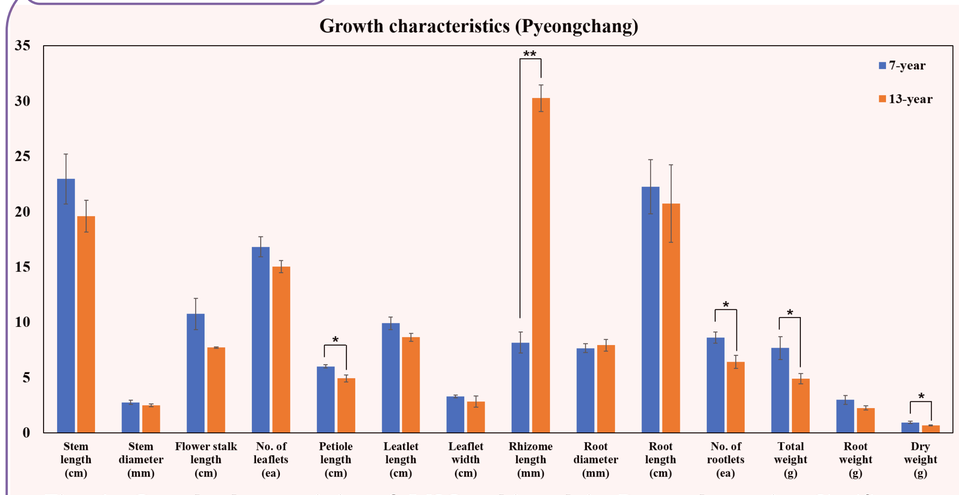


Fig. 1. Growth characteristics of WSG cultivated in Pyeongchang site. Significant differences were shown in petiole length, rhizome length, number of rootlets, and total weight.

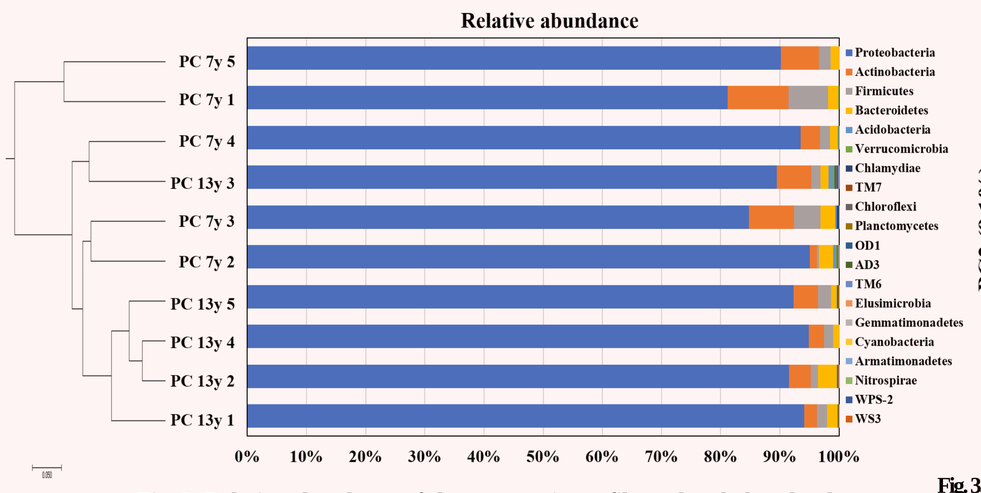


Fig. 2. Relative abundance of the taxonomic profile at the phylum level for bacteria in rhizosphere soils of Pyeongchang WSG cultivation site.

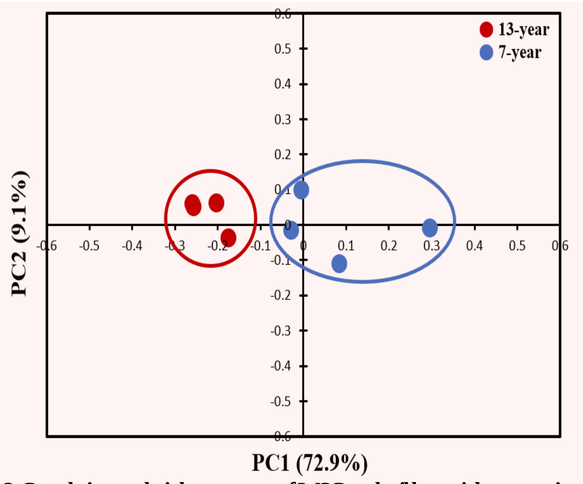


Fig. 3. Correlation analysis between age of WSG and soil bacterial community obtained from Principal coordinate analysis (PCA) in Pyeongchang cultivation site. Soil bacterial community was clustered by age of WSG.

Pyeongchang			
	Genus name	13-year	7-year
1	Methylotenera	0.0000	0.1763
2	Polaromonas	0.0025	0.1136
3	Candidatus_Rhabdochlamydia	0.0156	0.0902
4	Rubrivivax	0.0005	0.0686
5	Ochrobactrum	0.0000	0.0672
6	Aquicella	0.0078	0.0606
7	Faecalibacterium	0.0000	0.0564
8	Microbacterium	0.0000	0.0554
9	Microbulbifer	0.0000	0.0497
10	Epulopiscium	0.0000	0.0487

Pyeongchang			
	Genus name	13-year	7-year
1	Dyadobacter	0.4526	0.0000
2	Prevotella	0.1295	0.0000
3	Cupriavidus	0.0827	0.0000
4	Enterobacter	0.0657	0.0000
5	Carnobacterium	0.0624	0.0000
6	Bacteroides	0.0524	0.0000
7	DA101	0.0446	0.0207
8	Aeromonas	0.0428	0.0000
9	Ktedonobacter	0.0362	0.0000
10	Bdellovibrio	0.0351	0.0000

Fig. 4. Bacterial compositions of different WSG ages in Pyeongchang cultivation site. The most predominant genus of 7- and 13-year-old WSG was *Methylotenera* and *Dyadobacter*, respectively.

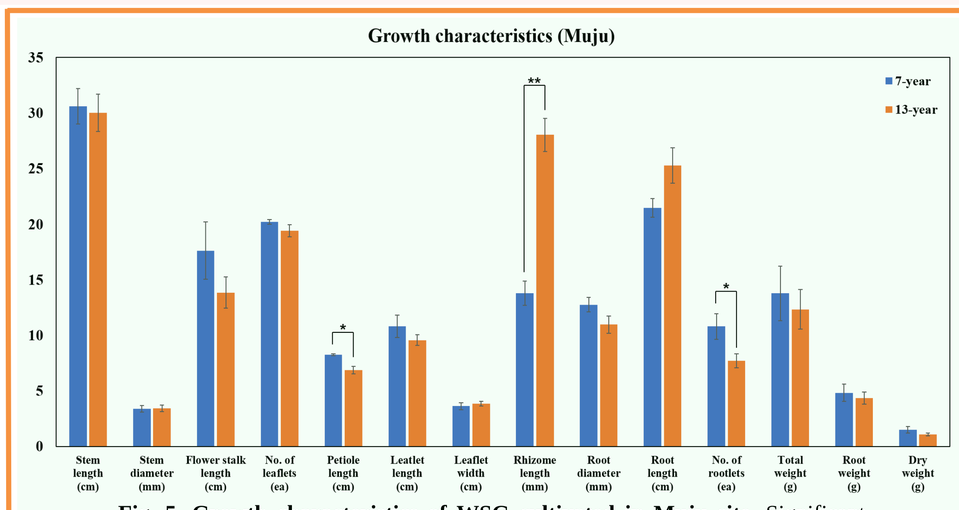


Fig. 5. Growth characteristics of WSG cultivated in Muju site. Significant differences were shown in petiole length, rhizome length, and number of rootlets.

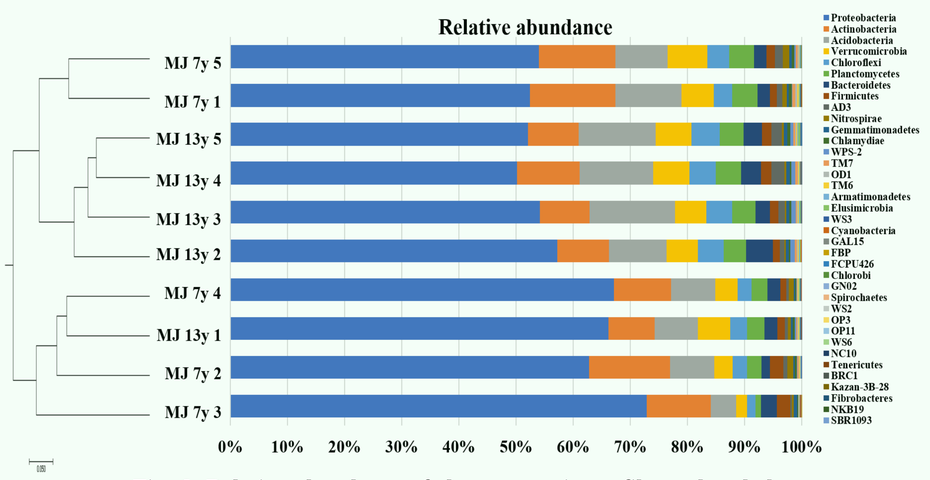


Fig. 6. Relative abundance of the taxonomic profile at the phylum level for bacteria in rhizosphere soils of Muju WSG cultivation site.

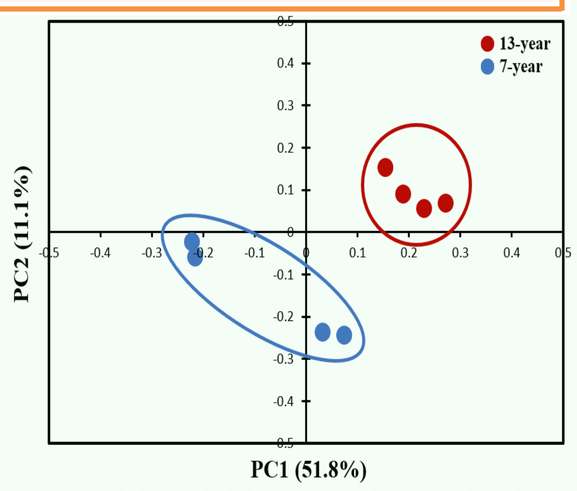


Fig. 7. Correlation analysis between age of WSG and soil bacterial community obtained from PCA in Muju cultivation site. Soil bacterial community was clustered by age of WSG.

Muju			
	Genus name	13-year	7-year
1	Peredibacter	0.0000	0.1332
2	Luteolibacter	0.0040	0.0538
3	Niabella	0.0000	0.0455
4	Pseudoxanthomonas	0.0000	0.0446
5	Telluria	0.0000	0.0396
6	Staphylococcus	0.0000	0.0381
7	Streptococcus	0.0000	0.0375
8	Microlunatus	0.0013	0.0346
9	Singulisphaera	0.0026	0.0320
10	Pseudoramibacter_Eubacterium	0.0000	0.0312

Muju			
	Genus name	13-year	7-year
1	Rhodopila	0.0767	0.0041
2	Geothrix	0.0347	0.0000
3	Archangium	0.0317	0.0000
4	Rhodanobacter	0.0288	0.0000
5	Haliangium	0.0259	0.0016
6	Dactylosporangium	0.0246	0.0016
7	heteroC45_4W	0.0193	0.0045
8	Perlucidibaca	0.0180	0.0000
9	Asticcacaulis	0.0176	0.0005

Fig. 8. Bacterial compositions of different WSG ages in Muju cultivation site. The most predominant genus of 7- and 13-year-old WSG was *Peredibacter* and *Rhodophila*, respectively.

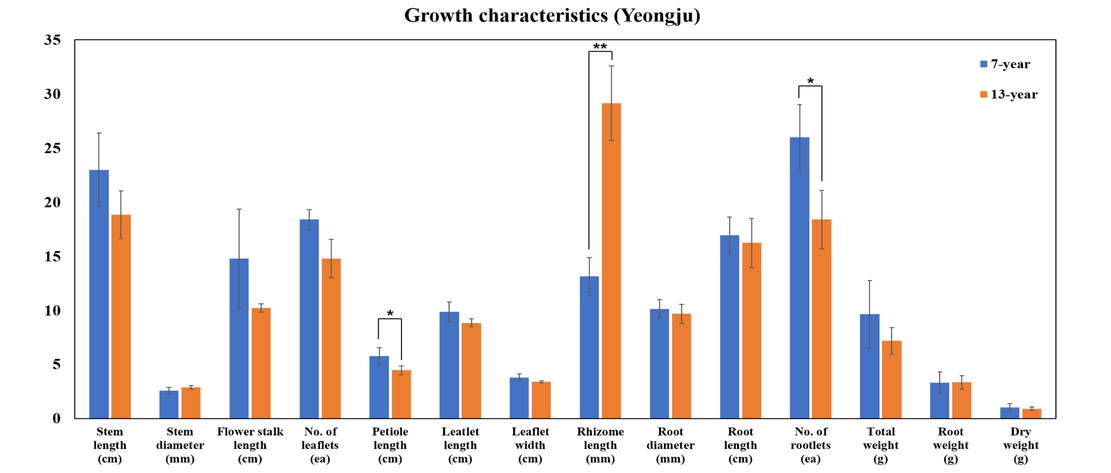


Fig. 9. Growth characteristics of WSG cultivated in Yeongju site. Significant differences were shown in petiole length, rhizome length, and number of rootlets.

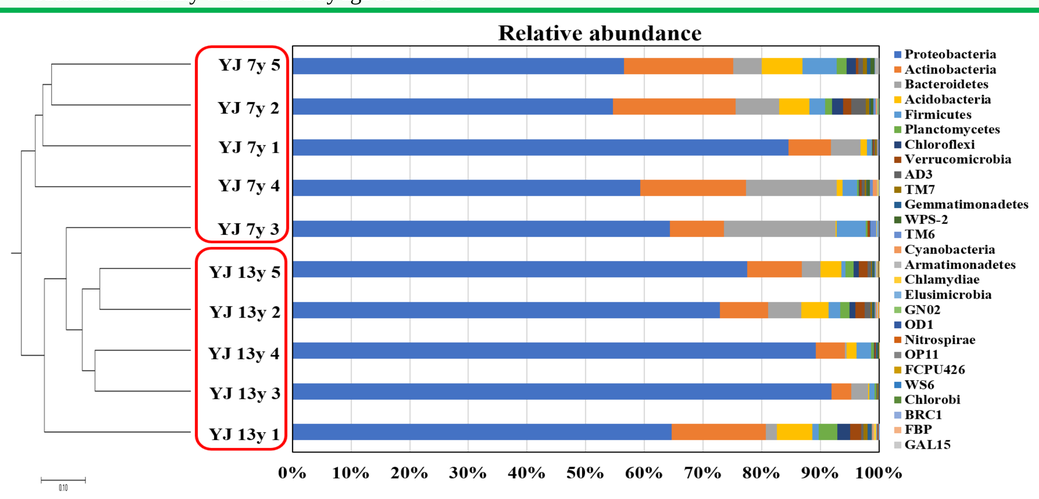


Fig. 10. Relative abundance of the taxonomic profile at the phylum level for bacteria in rhizosphere soils of Muju WSG cultivation site. Soil bacterial communities were grouped according to the age of WSG.

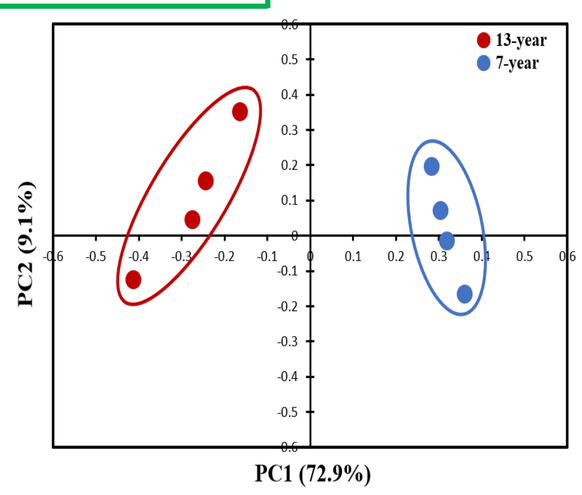


Fig. 11. Correlation analysis between age of WSG and soil bacterial community obtained from PCA in Yeongju cultivation site. Soil bacterial community was clustered by age of WSG.

Yeongju			
	Genus name	13-year	7-year
1	Paracoccus	0.0003	2.6757
2	Deinococcus	0.0000	1.8323
3	Chryseobacterium	0.0003	1.6499
4	Lutibacterium	0.0000	0.9846
5	Micrococcus	0.0000	0.7958
6	Microbacterium	0.0013	0.3276
7	Bergeyella	0.0000	0.3203
8	Enterococcus	0.0000	0.1614
9	FFCH10602	0.0000	0.1143
10	Amaricoccus	0.0000	0.1064

Yeongju			
	Genus name	13-year	7-year
1	Planctomyces	0.1868	0.0000
2	Labrys	0.1908	0.0000
3	Rahnella	0.1355	0.0000
4	Pelosinus	0.0393	0.0000
5	Cupriavidus	0.0442	0.0000
6	Clostridium	0.0461	0.0000
7	Alistipes	0.0371	0.0000
8	Nocardia	0.0376	0.0000
9	Phycicoccus	0.0371	0.0000
10	Paucibacter	0.0371	0.0000

Fig. 12. Bacterial compositions of different WSG ages in Yeongju cultivation site. The most predominant genus of 7- and 13-year-old WSG was *Paracoccus* and *Planctomyces*, respectively.

Conclusion

Rhizome length and the number of rootlets were proportional and inversely proportional to age of WSG, respectively. The relative abundance of soil bacterial community was clustered through the age of WSG in Yeongju cultivation site. *Cupriavidus* genus, commonly found in 13-year-old WSG in PC and YJ, has resistance to heavy metals and plant growth-promoting activity. In future study, it will be necessary to isolate soil microorganism living in the WSG cultivation sites and then confirm their growth-promoting effects on WSG.