



Proceeding Paper

Metagenomics of Distant Hybrids in the Genus *Ribes* (Grossulariaceae) †

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Abstract: Currant–gooseberry intersectional hybrids were created artificially using the polyploidy method. In terms of morphological, palynomorphological, karyological and other characteristics, currant–gooseberry hybrids are contrasting. We performed a comparative metagenomic analysis of three distant hybrids of known origins and their parental forms using locus-specific NGS sequencing on the Illumina MiSeq platform. The ribotypes of hybrids correspond to those of the parental forms. Ribotypes of unknown origin highly homologous to other currants were found. It has been shown that most pseudogenes are not conserved in hybrids. Comparative plant metagenomics is an informative method for studying hybrids of unknown origin.

Keywords: distant hybrids; intragenomic polymorphism; 35S rRNA; NGS



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1. Introduction

Just as in traditional metagenomics, the species composition of environmental samples is determined according to DNA marker regions, so a comparative analysis of the intragenomic polymorphism of plants based on the same methods shows the presence of a large number of haplotypes of various origins and allows one to study, with some limitations and accuracy, the history of hybridization processes. In this work, we illustrate how the ITS1 5.8S rRNA marker region changes in distant hybrids after a small number of hybridization steps.

The genus *Ribes* L. consists of several subgenera and approximately 150 species [1,2]. Some authors divide the genus into two genera—currants and gooseberries [3–5]. Currant–gooseberry hybrids were created artificially [6,7]. In terms of morphological, palynomorphological, karyological and other characteristics, currant–gooseberry hybrids are contrasting [8,9]. Tetraploid hybrids have pollen grains with an intermediate type of pollen [10,11]. The pollen of the triploid DCGL is not typical for the family; it is ugly and has a warty exine structure [12]. We selected palynomorphologically contrasting hybrids distinguishable from the parental species (*Josta*, *Kroma* and *Dlinnokistnaya* CGL) and their parental forms: *R. niveum* Lindl., *R. reclinatum* L., *R. divaricatum* Douglas and *R. nigrum* L. ssp. *europeum*.

2. Materials and Methods

Plant material from the garden collection of the Komarov Botanical Institute of the Russian Academy of Sciences and a collection of black currant and gooseberry NPB “Pushkin and Pavlovsk laboratory of VIR” (vouchers VIR), St. Petersburg, Russia, were studied.

Kroma (VIR k-32609). Allotetraploid ($4n = 32$). It was bred in Sweden at the agricultural station in Alnarp by crossing hybrid forms (*R. nigrum* × *Grossularia*) × (*R. nigrum* ×

G. nivea). It is of interest for breeding as a source of high resistance to fungal diseases and gall mites, a high content of pectin substances in fruits and ascorbic acid in leaves [11,13].

Jošta (VIR k-34031). Allotetraploid ($4n = 32$). It was created in the 1970s at the Max Planck Institute, initial forms: (*R. nigrum* × *G. reclinata*) × (*R. nigrum* × *G. divaricata*). The variety is of interest for breeding as a source of high resistance to American powdery mildew, anthracnose and gall mites, a high content of pectin substances in fruits (1.12%), ascorbic acid and P-active substances in leaves [11,13].

Dlinskostnaya CGL (VIR k-14550). Triploid ($3n = 24$). It was bred in Michurin FNC; initial forms: Kyzyrgan (*R. altissimum* Turcz.) × Eighth Davison (*R. nigrum* L. ssp. *europium*) [14]. *R. altissimum* is a natural far hybrid of red and black currant [5].

Intragenomic polymorphism was studied with locus-specific NGS sequencing on the Illumina MiSeq using total DNA samples [15] and primers ITS1P [16], ITS2 [17]. Amplification was carried out according to the protocol: initial denaturation at 98 °C for 5 min; 30 cycles (98 °C 5 s, 56 °C 5 s and 72 °C 15 s); final synthesis at 72 °C 1 min; storage at 12 °C.

Data processing was performed using FastQC (Babraham Bioinformatics), Trimmomatic [18], Fastq-join [19], Vsearch [20], SplitsTree [21] and TCSBU [22]. ZOTU filtering was performed manually using Mega 7 [23] and BLAST NCBI.

3. Results

3.1. Pseudogenes

It is well known that almost all gooseberries and currants are hybrids to one degree or another, and in hybrids, some ribotypes are eliminated. The studied samples contain ribotypes with extended deletions, possibly affecting splicing, since it is believed that splicing is associated with the secondary structure of the transcript. There are many pseudogenes in parental forms, but most of them are not preserved in hybrids and cannot be used for the comparative analysis of ribotypes (Table 1, Figure 1).

Table 1. Highly homologous currant ribotypes (pseudogenes) with long deletions.

Deletion	Length (bp)	Start	End	Number of ZOTU	ZOTU
1	4	289	292	425	22, 29
2	5	45	49	1123	8, 27, 37, 46
3	11	56	66	364	23, 35
4	16	153	167	121	38
5	21	99	119	813	16, 20, 47, 50
6	22	33	54	813	16, 20, 47, 50
7	48	72	119	364	23, 35
8	57	190	245	354	32, 40

3.2. Ribotypes

The results of metagenomic analysis of 50 most frequent ribotypes are presented in Figure 1. Zotu1 of the parental form *R. nigrum* was found in all three hybrids in an amount of more than 60% and in a small amount in *R. divaricatum*. The second ribotype of *R. nigrum* (Zotu3) was only found in a small amount in D CGL and *R. divaricatum*. These two ribotypes differ in only one nucleotide substitution C/A. However, their inheritance is asymmetrical, and Josta and Kroma do not have Zotu3. Thus, only two ribotypes of *R. nigrum* were found in Kroma and Josta: Zotu1 and the pseudogene Zotu29.

The other ribotypes of currant–gooseberry hybrids came from gooseberries. Concerning *R. divaricatum*, the ribotypes Zotu13, Zotu19 and Zotu21 found in hybrids are also found in other gooseberries, so it is impossible to reliably trace their inheritance. In addition, *R. divaricatum* differs from other gooseberries by the presence of a number of specific ribotypes (Zotu10, 15, 17, 26, 28, 34 and 43), a small number of *R. nigrum* ribotypes (Zotu1 and 3) and a number of pseudogenes (Zotu8, 22, 37, 40 and 47). This indicates that *R. divaricatum* may be a natural far hybrid, having the parental form *R. nigrum* in its history.

The ribotypes of *R. niveum* and *R. reclinatum* (Zotu2, 6, 7, 9, 11 and others) are well traced in the Kroma and Josta. In D CGL, no gooseberry ribotypes were found.

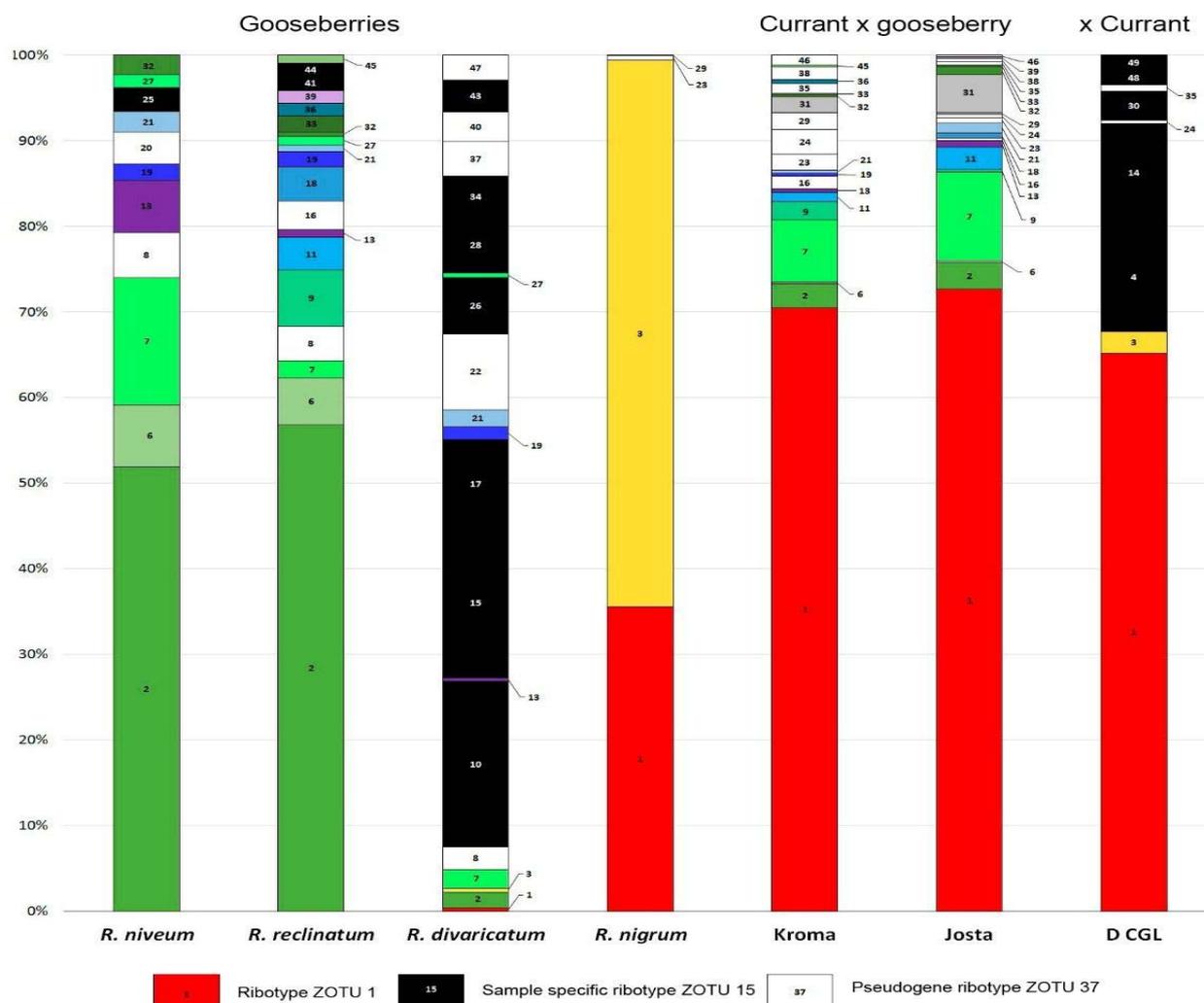


Figure 1. Ribotypes of distant hybrids and parental forms. Numbers and colors indicate comparable ZOTU (Zero-radius Operational Taxonomic Unit). Incomparable sample specific ribotypes are indicated as black, and pseudogenes as white.

4. Discussion

More than half of ribotypes/pseudogenes were found for all seven samples (282 Zotu), and in most cases, multiple deletions were observed. For example, Table 1 lists the deletions for the first 50 Zotu. Only Zotu38 has a unique deletion, and other deletions are characteristic of several ribotypes. Probably, pseudogenes are not inherited, since in most cases they are characteristic of the sample. Therefore, they cannot be used for the comparative analysis of hybrids. It is possible that the elimination of ribotypes in hybrids occurs at a high rate through multiple mutations. Note that long deletions are the only trait indicating that the ribotype is a pseudogene. This cannot be said about ribotypes with many nucleotide substitutions, because even if they are not singletons, their frequency is low, and the variety of substitutions is very high, which significantly reduces homology.

We believe that the first 50 Zotu are sufficient for a comparative metagenomic analysis of distant hybrids and hybrids of unknown origin. For example, in the case of D CGL, it can be seen that there are a large number of specific ribotypes, probably corresponding to the lost parental forms from red and black currants, since they are highly homologous to *R. janczewskii* Pojark., *R. himalense* Royle ex Decne, *R. petraeum* Wulfen, *R. triste* Pall.,

R. mandshuricum Kom. and *R. palczewskii* Pojark. In addition, *R. reclinatum* and Kroma probably contain ribotypes of unknown origin, highly homologous (85%) to *R. andicola* Jancz. Since there is no evidence that the species *R. andicola* could be the parental form of the Kroma, it can be assumed that the ribotypes of this group could have been contained in the earlier parental forms of gooseberries. We believe that a comparative metagenomic analysis of hybrids is quite informative, since it does not contradict the history of hybrids of known origin.

Supplementary Materials: The following are available online at <https://www.mdpi.com/article/10.3390/IECPS2021-11933/s1>.

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References

1. Janczewski, E. Monographie de Groseilliers. *Mém. Soc. Phys. Genève* **1907**, *35*, 24–517.
2. Rehder, A. *Manual of Cultivated Trees and Shrubs*, 2nd ed.; Macmillan: New York, NY, USA, 1954; 996p.
3. Berger, A. *A Taxonomical Review of Currants and Gooseberries*; New York State Agricultural Experiment Station: Geneva, Switzerland; New York, NY, USA, 1924.
4. Lozina-Lozinskaya, A.C. *Ribes* L., *Grossularia* Mill. In *Trees and Shrubs of the USSR, Izdatel'stvo Akad.*, 3rd ed.; Sokolov, S., Ed.; Nauk SSSR: Moscow, Russia; Leningrad, Russia, 1954; pp. 177–225. (In Russian)
5. Pojarkova, A.I. *Ribes* L. In *Flora of the USSR (English Edition)*; Komarov, V.L., Yuzepchuk, S.V., Eds.; U.S. Department of Commerce: Springfield, IL, USA, 1971; pp. 175–208.
6. Brennan, R.M. Currants and gooseberries. In *Fruit Breeding, Vine and Small Fruit Crops*; Janick, J., Moore, J.N., Eds.; Wiley: New York, NY, USA, 1996; pp. 191–295.
7. Sergeeva, K.D. *Gooseberry*; Agropromizdat: Moscow, Russia, 1989; 208p. (In Russian)
8. Knight, R.L.; Keep, E.; Briggs, J.B.; Parker, J.H. Transference of resistance to black-currant gall mite, *Cecidophyopsis ribis*, from gooseberry to black currant. *Ann. Appl. Biol.* **1974**, *76*, 123–130. [[CrossRef](#)]
9. *Pomology*; Sedova, E.N. (Ed.) RAS, State Scientific Institution All-Russian Institute of Breeding of Fruit Crops: Orel, Russia, 2009; Volume 4, 468p. (In Russian)
10. GavriloVA, O.A.; Tikhonova, O.A. Diversity of pollen grain shapes and their distribution across some *Grossulariaceae* species and hybrids. *Trans. Karelian Res. Cent. Russ. Acad. Sci.* **2013**, *3*, 82–92. (In Russian)

11. Tikhonova, O.A.; Gavrilova, O.A.; Pupkova, N.A. Morpho-biological features of blackcurrant-gooseberry hybrids in the North-West of Russia. *Contemp. Hortic. Electron. J. Orel* **2015**, *4*, 42–60. (In Russian)
12. Gavrilova, O.A.; Tikhonova, O.A. On reproductive biology of distant hybrids in the Grossulariaceae family. *Proc. Appl. Bot. Genet. Breed.* **2017**, *178*, 100–118. (In Russian) [[CrossRef](#)]
13. Keep, E. Blackcurrant and gooseberry. In *Breeding of Fruit Culture*; Kolos: Moscow, Russia, 1981; pp. 274–371. (In Russian)
14. Chuvashina, N.P. *Cytogenetics and Selection of Distant Hybrids and Polyploids of Currant*; Nauka: Leningrad, Russia, 1980; 121p. (In Russian)
15. Doyle, J.J.; Doyle, J.L. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem. Bull.* **1987**, *19*, 11–15.
16. Ridgway, K.P.; Duck, J.M.; Young, J.P.W. Identification of roots from grass swards using PCR-RFLP and FFLP of the plastid trnL (UAA) intron. *BMC Ecol.* **2003**, *3*, 8. [[CrossRef](#)] [[PubMed](#)]
17. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In *PCR Protocols: A Guide to Methods and Applications*; Innis, M.A., Gelfand, D.H., Sninsky, J.J., White, T.J., Eds.; Academic Press, Inc.: New York, NY, USA, 1990; pp. 315–322.
18. Bolger, A.M.; Lohse, M.; Usadel, B. Trimmomatic: A flexible trimmer for Illumina sequence data. *Bioinformatics* **2014**, *30*, 2114–2120. [[CrossRef](#)] [[PubMed](#)]
19. Aronesty, E. Comparison of Sequencing Utility Programs. *Open Bioinform. J.* **2013**, *7*, 1–8. [[CrossRef](#)]
20. Rognes, T.; Flouri, T.; Nichols, B.; Quince, C.; Mahé, F. VSEARCH: A versatile open source tool for metagenomics. *PeerJ* **2016**, *4*, e2584. [[CrossRef](#)] [[PubMed](#)]
21. Huson, D.H.; Bryant, D. Application of Phylogenetic Networks in Evolutionary Studies. *Mol. Biol. Evol.* **2005**, *23*, 254–267. [[CrossRef](#)] [[PubMed](#)]
22. Santos, A.M.; Cabezas, M.P.; Tavares, A.I.; Xavier, R.; Branco, M. tcsBU: A tool to extend TCS network layout and visualization. *Bioinformatics* **2016**, *32*, 627–628. [[CrossRef](#)] [[PubMed](#)]
23. Kumar, S.; Stecher, G.; Li, M.; Knyaz, C.; Tamura, K. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Mol. Biol. Evol.* **2018**, *35*, 1547–1549. [[CrossRef](#)] [[PubMed](#)]