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Rhizosphere bacterial community influence on *Deschampsia antarctica* È Desv. adaptability in context of temperature near plants in local spatial scales of Galindez Island, Argentine Islands (the maritime Antarctic)

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Abstract

The effect of rhizosphere bacterial community index (I^{rb}_{i}) influence on the nine populations of Antarctic hair grass (*Deschampsia antarctica*) adaptability was studied in the Galindez Island (summer season 2017/18). Moreover, the corresponding influence indices I^{rb}_{i} (i=1÷9) and I^{rbp}_{i} (p=1÷5 for the most common bacteria) were evaluated as well. The objective was to compare the I^{rb}_{i} and I^{rbp}_{i} series with the united temperature influence index on plant populations (I^{t1}_{i}(z)) series and the united quality latent index of adaptability I^{q1}_{i}. The study used data on the rhizosphere metagenome composition based on 16S RNA analysis. Methods determining the plant number in populations, and measuring the morphometric indices of *D. antarctica* populations were used. Reserve and protective seed proteins spectra were studied by polyacrylamide gel electrophoresis. Method of extreme grouping the spatial variables of these indices was applied for nine populations to obtain a I^{q1}_{I} and I^{t1}_{i} and I^{rb}_{i}, I^{rbp}_{i}. Sets of united indices were compared by regression technique. A comparative statistical analysis of the I^{t1}_{i} and I^{rb}_{i}, I^{rbp}_{i} sets in this season was carried out. This possible influence appeared to be individual for each *D. antarctica* studied population. In each population, part of the plants reacted positively to the bacteria influence, while the other part either did not react or reacted negatively. Dependence of the plant adaptation indices on rhizospheric bacterial communities z(x) is shown in our data. This means that the rhizosphere bacterial community and temperature-dependent rhizosphere bacteria (x) can play an active role in plant adaptation of *D. antarctica* populations (z) to individual temperature conditions in the microscale of Galindez Island from a biological point of view.

Key words: *Deschampsia antarctica*, I^{q1}_{i}, I^{t1}_{i}, I^{rb}_{i} and I^{rbp}_{i}, Argentine Islands, the maritime Antarctic

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Introduction

The advantages to any organism can be provided by cooperation with other organisms in extreme environmental conditions. This phenomenon is currently being actively studied in the Antarctica with its extremely unfavorable conditions (Gallardo-Cerda et al. 2018, Glick et al. 2007).

In recent research, special attention is drawn to the effect of the bacteria mediating soil processes in the context of the nutrients availability. Moreover there are also functional consequences of these interactions which can have significant influences on nutrient cycling, plant productivity and ecosystem responses to environmental changes, in addition to the roots broad effects on rhizosphere bacterial communities (Ahkami et al. 2017, Garcia and Kao-Kniffin 2018, Paterson and Mwafulirwa 2022).

Colobanthus quitensis and *Deschampsia antarctica* are the only flowering plants that naturally colonize the Antarctica. Current studies explain the ecological success of the two species in Antarctica mainly by their association and root microbiota management which gives the necessary advantage in survival (Ozheredova et al. 2015, Parnikoza et al. 2018). The role of the rhizosphere and endosphere bacterial communities in facilitated uptake of nutrients from the soil or in the ability to tolerate the harsh conditions (salt stress and nutrient deficiency) is reported (*e.g.* Znój et al. 2021). Therefore, the rhizosphere bacterial community can influence the plant adaptability.

Another approach is to describe the habitat rigor characteristics that may affect soil communities at regional and local spatial scales along the Antarctic Peninsula. In particular, it was shown that bacterial communities differed most significantly in soil and climate parameters, and the specific parameters that influenced each taxon differed at regional and local spatial scales (Ball et al. 2023). The authors used bacterial communities from locations of five plant species, including lichens and fungi, soil composition, latitude and regional-scale meteorological conditions including air temperature and precipitation, at 13 sites on the Antarctic Peninsula. It was shown that (i) bacterial communities differed most significantly due to soil and climate parameters, and (ii) specific parameters that influenced each taxon differed at regional and local spatial scales (Ball et al. 2023).

Our previous studies showed that *D. antarctica* rhizosphere microbiomes from two distant regions in the central maritime Antarctica had similar diversity and taxonomic composition (Prekrasna et al. 2022). Therefore, we paid more attention not to the latitudinal gradient, but to the microbiome composition and characteristics of plant population dependence on local conditions in temparature context, accordingly to the influence microbiome had on the plant populations in this study.

Considering this studies results, we have compared the influence of the spatial changes in local temperature near plants and the rhizosphere bacterial community composition on the *D. antarctica* population adaptability in the microscale of Galindez Island within the influence of abiotic and biotic factors on plants.

Material and Methods

The research was conducted during the 22th Ukrainian Antarctic Expedition (UAE) in the 2017/2018 summer Antarctic season. The network of research sites for the regular study of *Deschampsia antarctica* populations is presented in Fig. 1 and in Table 1 (Supplements).

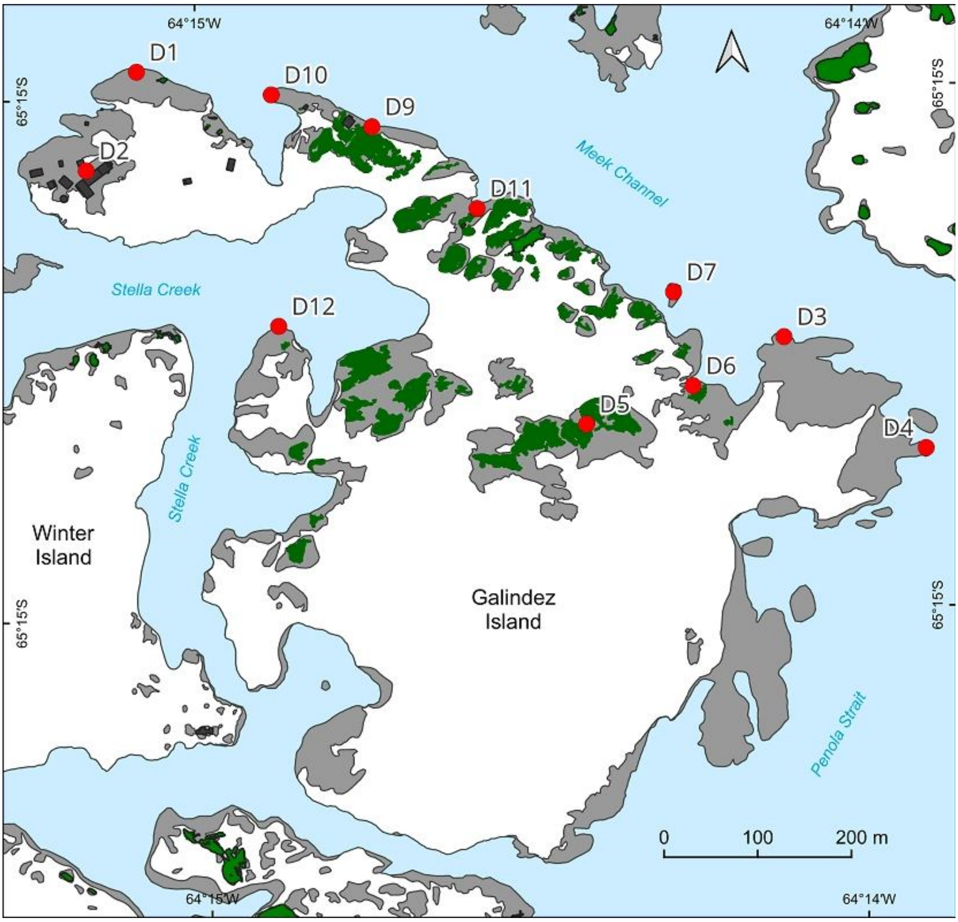

Fig. 1. Map of the location of the researched *D. antarctica* populations and rhizosphere bacterial communities on Galindez Island, Argentine Islands.

Locations of the studied *D. antarctica* populations reflect the growth conditions variety and, we hypothesize, reflect microclimatic conditions in the studied region that support the species successful growth in the region. Sensors and data-loggers that record the local temperature near the plants were installed in all studied populations D1(D_1(1)) to D12 (D_{11}(12)) in Fig. 1, (for installation details, *see* Savenets et al. 2023). For analysis, the temperature data were taken from Miryuta et al. (2019b).

Plants (10 from each population) and soils samples for the rhizosphere bacterial DNA isolation were collected at the D1 to D12 experimental points. Metagenome study of the *D. antarctica* plants rhizosphere was done earlier using 16S RNA metagenomics (Prekrasna et al. 2022). In our recent study, Bacterial DNA of samples D3 (D_3(3)) and D10 (D_9(10)) was not possible to isolate in sufficient amount. Therefore, 9 populations were analyzed instead of 11 in this work.

Shares of bacteria groups within rhizosphere bacterial community the were calculated. We used only bacteria groups which make up at least 10% of bacterial community (data from Prekrasna et al. 2022) for nine studied sampling points (Table 1s) in our work. Moreover, plant number, population morphometric indices and seed protein fractions were studied as well. We marked *Proteobacteria* group as B1, *Actinobacteria* group as B2, *Bacteroidetes* group as B3, *Firmicutes* group as B4, *Cyanobacteria* group as B5. The first three of them depend on the temperature spatial distribution in a microscale (specified as temperature-dependent in the following text), the other two do not (Prekrasna et al. 2022).

The plant population number and plant population morphometric indices such as leaf length, inflorescence length, flower length (on the lower flower scale), and flower number in an inflorescence were evaluated by standart methods. The following parameters in *D. antarctica* populations were marked: plants number (S), leaf length (dl), inflorescence length (dm), flower (lower glume) length (dk), number flowers in an inflorescence (dn). Further Ph is morphometric characteristics set.

Spare and protective seed protein spectra were studied by polyacrylamide gel electrophoresis and analyzed using the ScionImage program[1]. The protective and reserve seed protein fractions are marked: those corresponding to globulins with a molecular weight of more than 150 KDa as >150, glutenins with a molecular weight of 94 to 145 KDa as 94-145, sulfur-poor prolamins from 45 to 80 KDa as 45-80; sulfur-rich prolamins from 20 to 40 KDa as 20-40; parts of sulfur-rich prolamins probably including the IRIP protein (ice recrystallization inhibition protein) from 27 to 31 KDa as 27-31; seed protein characteristic set as Pr according to the classification (Sozinov 1985).

Density functions of a leaf length and flower length of *D. antarctica* plants and values of the different protein fractions in *D. antarctica* seed data were presented in our previous works (Miryuta et al. 2019a, b).

To process and analyze the already published data of plant population number, population morphometric indices, spare and protective seed proteins according to Miryuta et al. (2019a, b), rhizosphere bacterial community according to Prekrasna et al. (2022) and local temperature near the plants according to Savenets et al. (2023) we used regression technique and the extreme grouping method (Pollard 2009, Ayvazyan et al. 1989, Bauman et al. 2008), applied using the algorithm described in the work (Miryuta et al. 2019b). Weighted Unifrac distance matrix between samples, which takes into account the bacterial phylogenetic species kinship/difference in soil samples (Prekrasna et al. 2022), was used to determine the influence rhizosphere bacteria community on the studied *D. antarctica* populations. The use of this matrix and matrices of spatial distances between plant adaptability indices made it possible to determine the portion of each studied plant population that responded to the rhizosphere bacteria community in the particular *D. antarctica* population location.

This was done using the procedure described in Legendre et al. (2015), and Miryuta et al. (2019b). The presence of a positive correlation between the comparison matrices was interpreted as a positive influence, a negative correlation as a negative influence or no influence. The percentage of plant in population that demonstrated a positive or negative dependence on bacteria was determined. It was done during the search for the relationship between the rhizosphere bacterial community or individual bacteria groups with the hairgras adaptability indices by extreme grouping.

To calculate complex index of adaptability (namely a United latent index of adaptability (I^{q1}_{1}) and United temperature influence indices) and rhizosphere bacterial community influence indices on plant adaptability characteristics (I^{t1}_{i} and I^{rb}_{i}, I^{rbp}_{i}) the extreme grouping method was applied to plant adaptability indices spatial distances for nine populations (Ayvazyan et al. 1989). The series comparison of united indices was carried out by regression technique (Pollard 2009, Miryuta et al. 2019a, b). Examples of these algorithm applications are presented in Supplements. In particular, an example of the regression technique and the extreme grouping method (Pollard 2009, Ayvazyan et al. 1989, Bauman et al. 2008) is shown in Fig. 1s, and examples of applied algorithms are shown in Fig. 2s and 3s (Miryuta et al. 2019a, b).

Results

The rhizosphere bacterial community influence on plant adaptability indices

Data about the portion of plant population that responded to the rhizosphere bacteria community in the each studied *D. antarctica* population are shown in Fig. 2.

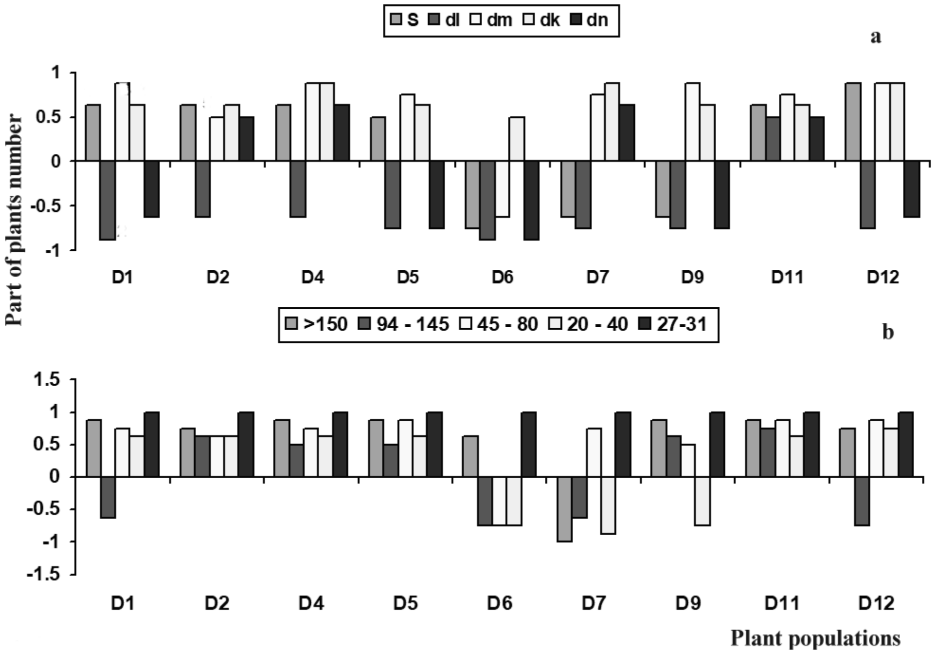

Fig. 2. Plant population portion that responded to the rhizosphere bacteria community in the each studied *D. antarctica* populations locations in Galindez Island, Argentine Islands.

The influence of rhizosphere bacteria community was proven, specifically on plants number (S), leaf length (dl), inflorescence length (dm), flower length (dk), flowers number in an inflorescence (dn) (Fig. 2a); and the content of protective and reserve seeds proteins fractions (Fig. 2b). The fractions correspond to: globulins with a molecular mass more than 150 KDa (>150), glutenins with a molecular mass from 94 to 145 KDa (94-145), sulfur-poor prolamins with a molecular mass from 45 to 80 KDa (45-80); sulfur-rich prolamins with a molecular mass from 20 to 40 KDa

(20-40); part of sulfur-rich prolamins and probably the IRIP protein, with a molecular mass from 27-31 KDa (27-31) in various *Deschampsia antarctica* populations in the Galindez Island microscale.

The rhizosphere bacterial community influenced the adaptation indices of various *D. antarctica* populations in different ways (*see* Fig. 2). United rhizosphere bacterial community influence index on *D. antarctica* populations (I^{rb}_i) is presented in Fig. 3.

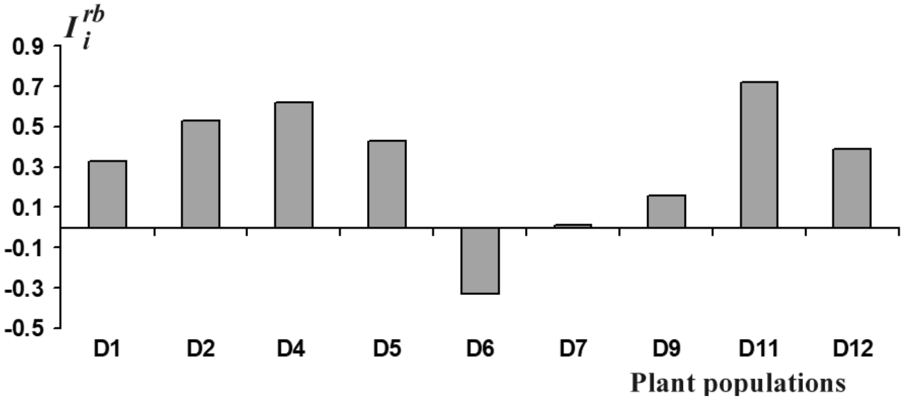

Fig. 3. United rhizosphere bacterial community influence index on *D. antarctica* populations (I^{rb}_i) in micro-scale of Galindez Island, Argentine Islands.

I^{rb}_i reached positive values in most *D. antarctica* populations except for D6 (negative value) and D7 (close to zero value). Table 1 was compiled on the basis of Fig. 2 which gives a general idea of the five most common bacteria groups and their positive influence in the rhizosphere bacterial community on three general plant adaptability characteristics.

The rhizosphere bacteria influence on different characteristics of *D. antarctica* populations (plant number, %) in the scale of Galindez Island is presented in Fig. 4, 5.

Population	Most common bacteria groups in the rhizosphere bacterial community				
	B1	**B2**	**B3**	**B4**	**B5**
D1	S, Ph, Pr	Pr	Pr	S, Pr	Pr
D2	S, Ph, Pr	S, Pr	S, Pr	Ph	
D4	S, Ph, Pr	Ph, Pr	Ph, Pr	S, Ph, Pr	Ph
D5	S, Ph, Pr	Ph, Pr	Ph, Pr	S, Ph	Pr
D6		Pr	Pr	Ph	S, Ph
D7	Ph, Pr	Ph	Ph	Ph	Ph
D9	S, Ph	Ph	Ph	Ph	Ph
D11	S, Pr	Pr	S, Pr		S, Pr
D12	Ph, Pr	Ph, Pr	Ph, Pr	S	Ph

Table 1. Positive influence of the corresponding rhizosphere bacterial community on the most of *Deschampsia antarctica* population of Galindez Island, Argentine Islands. *Notes*: *Proteobacteria* group is marked B1, *Actinobacteria* group is marked B2, *Bacteroi* group is marked B3, *Firmicutes* group is marked B4, *Cyanobacteria* group is marked B5.; Ph is morphometric characteristics set, S is populations set, Pr is seed proteins characteristics set.

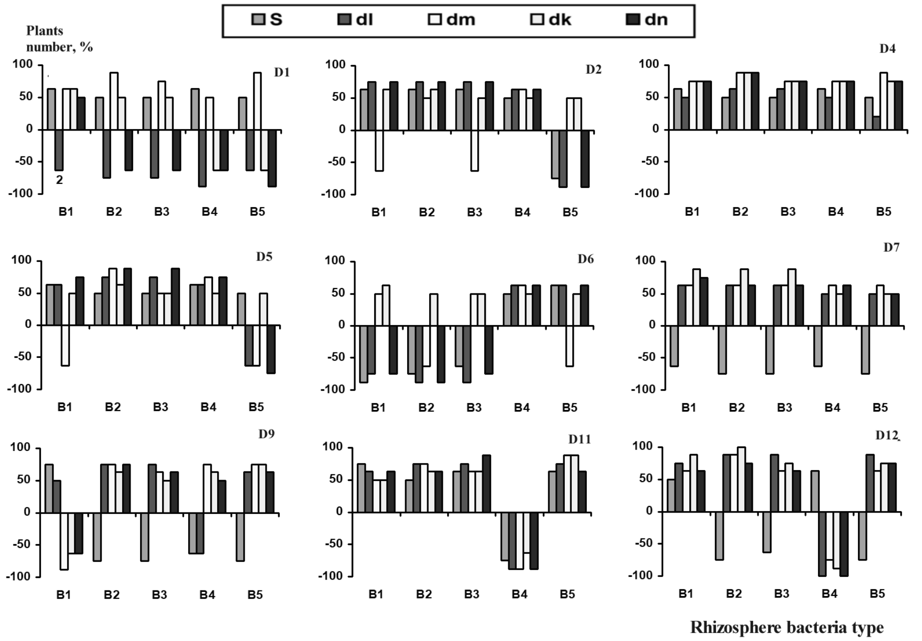

Fig. 4. Positive or negative response probability of plant morphometric indices for different *Deschampsia antarctica* populations on the influence of individual rhizosphere bacteria in the microscale of Galindez Island, Argentine Islands. The influence of *Proteobacteria* group (B1), *Actinobacteria* group (B2), *Bacteroidetes* group (B3), *Firmicutes* group (B4), *Cyanobacteria* group (B5) on the plants number (S), leaf length (dl), inflorescence length (dm), flower length (dk), flowers number in inflorescences (dn) in the *D. antarctica* populations.

United rhizosphere bacteria influence index (for bacteria groups B1÷B5) for *D. antarctica* populations (I^{rbp}_i) in the scale of Galindez Island is presented in Fig. 6.

The soil temperature influens on the rhizosphere bacterial community and plant populations adaptability

Both the rhizosphere bacterial community marked by $x(t_1)$ and the *D. antarctica* populations marked by $z(t_1)$ are shown to depend on local temperature near plants where t_1 is the temperature in the 2017/18 season. The United temperature influence indices $I^{t1}_i(x)$ and $I^{t1}_i(z)$ in x(t1) and z(t1) respectively are shown in Fig. 7.

The indices $I^{t1}_i(x)$ and $I^{t1}_i(z)$ have the opposite sign in some populations as Fig. 2 shows and, in general, have a negative tendency between these values sets which, however, is not statistically reliable ($R^2=0.1355$, $F_{1,7}=1.099$, limit value at $\alpha=0.05$ $F_{1,7}=5.99$).

Rhizosphere bacterial community influence on plant adaptability in context of soil temeperature in local spatial scales is shown in Table 2 ($I^{t1}_i(z)$, I^{rb}_i, and I^{rbp}_i).

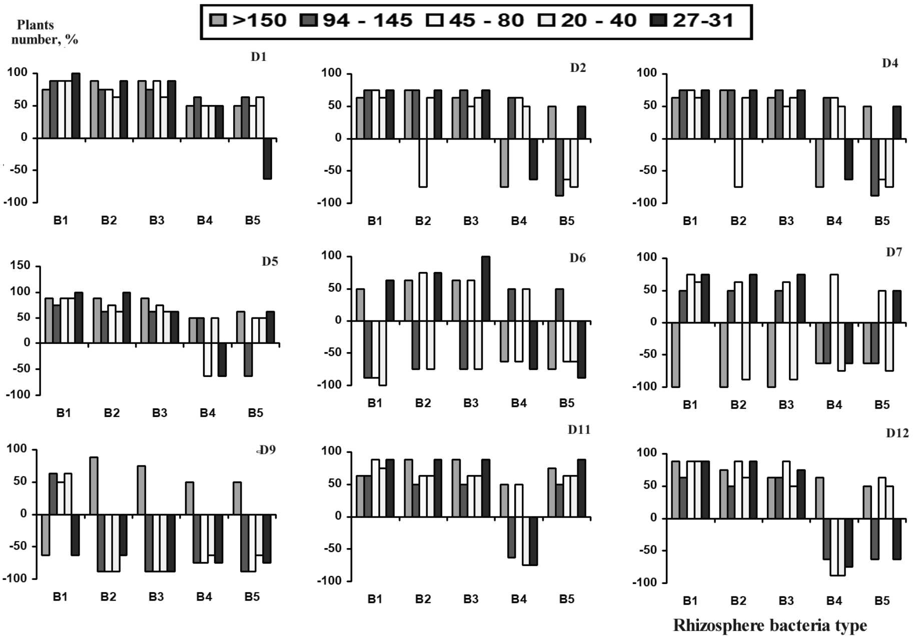

Fig. 5. Positive or negative response of protective and reserve seed protein fractions for different *Deschampsia antarctica* populations to the influence of individual rhizosphere bacteria in the microscale of Galindez Island, Argentine Islands The influence of *Proteobacteria* group (B1), *Actinobacteria* group (B2), *Bacteroidetes* group (B3), *Firmicutes* group (B4), *Cyanobacteria* group (B5) on the content of protective and reserve seed protein fractions which correspond to: globulins with a molecular mass more than 150 KDa (>150), glutenins with a molecular mass from 94 to 145 KDa (94-145), sulfur-poor prolamins with a molecular mass from 45 to 80 KDa (45-80); sulfur-rich prolamins with a molecular mass from 20 to 40 KDa (20-40); part of sulfur-rich prolamins and probably the IRIP protein, with a molecular mass from 27-31 KDa (27-31) in the *D. antarctica* population locations.

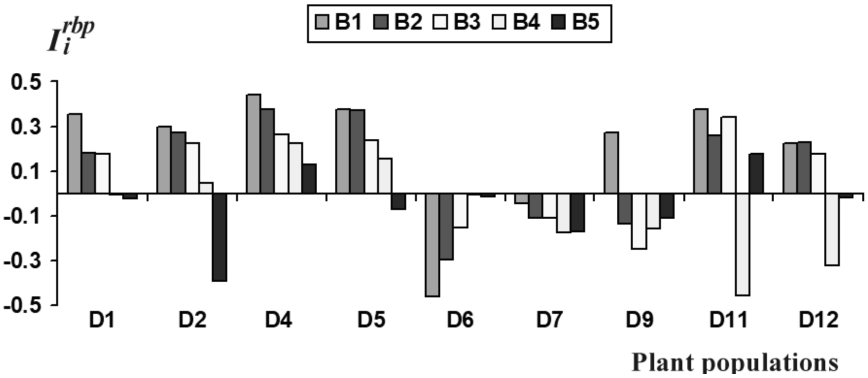

Fig. 6. United rhizosphere bacteria influence index (I^{rbp}_i) (for bacteria groups B1-B5: *Proteobacteria* group is marked B1, *Actinobacteria* group is marked B2, *Bacteroidetes* group is marked B3, *Firmicutes* group is marked B4, *Cyanobacteria* group is marked B5) on *D. antarctica* populations plants on the scale of Galindez Island, Argentine Islands where p=1÷5 is the serial number of tested bacterium group.

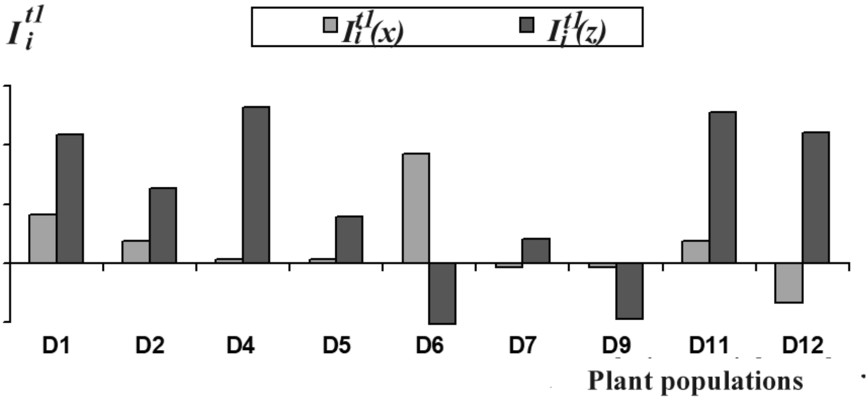

Fig. 7. The United temperature influence indices in the rhizosphere bacterial community x(t_1) I^{t1}_i(x) and the *D. antarctica* populations z(t_1) I^{t1}_i(z) of Galindez Island, Argentine Islands.

Pairs of index sets	**n**	**R^2**	**R**	**$F_{1,n-2}$**	**$F_{1,n-2}$** (α=0.05)
$I^{t1}_i - I^{rb}_i$	9	0.6771	**0.823**	14.679	5.59
$I^{t1}_i - I^{rb1}_i$	9	0.4838	**0.696**	6.559	5.59
$I^{t1}_i - I^{rb2}_i$	9	0.6849	**0.828**	15.218	5.59
$I^{t1}_i - I^{rb3}_i$	9	0.791	**0.889**	26.495	5.59
$I^{t1}_i - I^{rb4}_i$	9	0.0098	0.1	0.070	5.59
$I^{t1}_i - I^{rb5}_i$	9	0.1522	0.390	1.260	5.59

Table 2. Relationships of the United temperature influence index (I^{t1}_i(z)) and the United rhizosphere bacterial community influence index (I^{rb}_i) and United individual rhizosphere bacteria groups influence index (I^{rbp}_i) on these *D. antarctica* populations of Galindez Island, Argentine Islands in the 2017/2018 season.

The series of United temperature influence index (I^{t1}_i(z)), and the United rhizosphere bacterial community influence index (I^{rb1}_i), and United individual rhizosphere bacteria groups (three temperature-dependent bacteria groups with p=1÷3) influence index (I^{rb1p}_i) on *D. antarctica* population adaptability indices are shown to be reliably correlated with each other (Table 2). Moreover, the series of I^{t1}_i and I^{rb2}_i, I^{rb3}_i, I^{rb}_i have the largest positive correlation coefficient (Table 2).

Using the series of United temperature influence index (I^{t1}_i(z)) (Fig. 7), the United rhizosphere bacterial community influence index (I^{rb}_i) (Fig. 4) and United individual rhizosphere bacteria groups B1÷B5 influence index (I^{rbp}_i) (Fig. 6) on *D. antarctica* populations these sets were compared with United quality latent index of *D. antarctica* population adaptability (I^{q1}_i) (Fig 4s) by regression technique. The results are given in Table 3.

Pairs of index sets	**n**	**R^2**	**R**	**$F_{1,n-2}$**	**$F_{1,n-2}$** (α=0.05)
$I^{q1}_i - I^{t1}_i$	11	0.7307	**0.855**	24.417	5.12
$I^{q1}_i - I^{rb}_i$	9	0.728	**0.853**	18.732	5.59
$I^{q1}_i - I^{rb1}_i$	9	0.5486	**0.741**	8.505	5.59
$I^{q1}_i - I^{rb2}_i$	9	0.8205	**0.906**	31.997	5.59
$I^{q1}_i - I^{rb3}_i$	9	0.8226	**0.907**	32.459	5.59
$I^{q1}_i - I^{rb4}_i$	9	0.0877	0.296	0.672	5.59
$I^{q1}_i - I^{rb5}_i$	9	0.1689	0.411	1.421	5.59

Table 3. Contributions of the United temperature influence index (I^{t1}_i), United rhizosphere bacterial community influence index (I^{rb}_i) and United individual rhizosphere bacteria groups influence index (I^{rbp}_i) on *D. antarctica* population adaptability indices to the United quality latent index of *D. antarctica* population adaptability (I^{q1}_i) of Galindez Island, Argentine Islands in the 2017/2018 season.

Sets of United temperature influence index on population adaptability indices (I^{t1}_i) and United rhizosphere bacterial community and individual rhizosphere bacteria groups influence index (I^{rb}_i and I^{rbp}_i) on *D. antarctica* populations are shown to have a reliable contribution to United quality latent index of *D. antarctica* population adaptability (I^{q1}_i) (Table 3). Moreover, almost the same positive contribution to I^{q1}_i is given by the I^{t1}_i and I^{rb1}_i. The I^{rb2}_i (*Actinobacteria* group) and I^{rb3}_i (*Bacteroidetes* group) give a slightly larger contribution to I^{q1}_i.

Discussion

Unfavorable climatic conditions leading to abiotic stress are significant factors contributing to a decrease in plant productivity (Chauhan et al. 2023). Low temperature and episodes of air temperature drop are important drivers for productivity even during the period of climate warming in Antarctica (Bertini et al. 2021). Therefore, our study focused on extreme temperature effects to plant growth and rhizosphere bacterial community role in plant response to temperature changes in nature.

Plant growth-promoting rhizobacteria are microorganisms that may help mitigate abiotic stress effect in Antarctic vascular plants. These microorganisms use different strategies, such as production of phytohormones, ethylene oxide reduction, dehydration response enhancement, and induction of genes encoding antioxidants (Chauhan et al. 2023).

In particular, the temperature-dependent *D. antarctica* rhizosphere bacteria *Proteobacteria* and *Actinobacteria* types found on Galindez Island (Prekrasna et al. 2022), according to our statistical studies, have a different effect on *D. antarctica* populations which are located in places with different condition of soil surface temperature. It is known from the literature that the *Proteobacteria* group functions consist of the IAA synthesis, ACC deaminase production, nitrogen fixation of phosphorus/potassium, and solubilization. The *Actinobacteria* group functions consist of the IAA production, nitrogen fixation, fungicidal and bactericidal action (Chauhan et al. 2023).

In this study, we found positive correlation set between the rhizosphere bacterial communities' composition and the *D. antarctica* plants adaptability indices. Such correlations suggest the contribution of the microbiome composition to the plant adaptability indices.

The relationship between *D. antarctica* rhizosphere microbial communities and plant, is typically explained by mediating role and the influence on soil formation (Hartmann et al. 2009, Cesco et al. 2010, Bulgarelli et al. 2013, Hu et al. 2018). However, the results obtained in our research can indicate possible role of rhizosphere microbial communities in the Antarctic vascular plant adaptation in a way affecting temperature conditions in microscale of Galindez Island at least in 2017/18 season (Tables 2, 3).

We suggest that microbial communities and individual temperature-dependent bacteria groups of the rhizosphere help the *D. antarctica* gene family by the signaling molecules. They encode ice recrystallization inhibitory protein (IRIP) homologues (John et al. 2009). In our study, 100% of the plants responded positively to the rhizosphere bacterial communities only in the case of the seed protein fraction which probably contains the IRIP protein (27-31 KDa). The ice recrystallization inhibitory protein (IRIP) suppresses the small ice crystal growth and potentially impairs formation of large crystals in response to low temperature (*see* John et al. 2009). The protein has a conformation that keeps it between two ice surfaces in the *Deschampsia antarctica* leaves apoplasm. Our statistical analysis suggests that IRIP accumulates not only in the leaves, but also in seeds, although in smaller quantities. In each *D. antarctica* population, part of the plants responded positively to the bacteria influence while the other part either did not react or reacted negatively.

Such differences between individual plants within the same population may be associated with a different state of plant dynamic (functional) hereditary memory. According to Tchuraev's hypothesis (Tchuraev 2006a), the genetic changes acquired through external conditions are saved in dynamic hereditary memory. Dynamic hereditary memory is a way of saving information, in which, unlike structural memory information is recorded in the spatial structure of biopolymers, and is provided by signals circulating in a cyclic system of elements (Tchuraev 2006a, b).

The functional hereditary memory existence probably makes it possible to implement a non-Darwinian evolutionary strategy, when both "successful" and "unsuccessful" steps of evolution are remembered. Their active or latent state is determined by the external conditions under which this state is advantageous or disadvantageous (Tchuraev 2006a). Signaling molecules can play the role of a trigger that switch the corresponding complex cycle (epigene) from one position to another during the exchange between rhizosphere bacterial communities and plant populations. The different response of plants to the temperature influence on the soil surface within the same population may be related to the different epigene state in which bacterial signaling molecules succeeded or failed to turn on in response to temperature changes. Probably, the presence of plants with different states of epigenes in the population allows the population to survive in difficult conditions. This is consistent with Churaev's hypothesis of a non-Darwinian strategy of evolution (Tchuraev 2006a).

All rhizosphere bacterial communities included portions of highly unique amplicon sequence variants (ASVs) and there was a high heterogeneity observed between samples at the ASV, as shown in previous work. The investigated soil parameters do not explain this heterogeneity (Prekrasna et al. 2022). It turned out that bacteria groups belonging to *Proteobacteria*, *Actinobacteria* and *Bacteroidetes* types were sensitive to local soil surface temperature near plants fluctuations.

The value of the United temperature influence indiex in the rhizosphere bacterial community (I^{t1}_i(x)) showed that variations in most of the microbial communities of Galindez Island were related to microscale changes in soil surface temperature (Prekrasna et al. 2022). A similar influence of surface temperature and the investigated soil parameters on *Deschampsia antarctica* populations was shown in our other work (Miryuta et al. 2019b). It was found that there was an influence of spatial microscale temperature changes on plants (I^{t1}_i(z)) which was enhanced by spatial changes in soil composition, but changes in soil composition alone had no significant influence on plants. The series of the United temperature influence indiex on the bacterial community composition ($I^{t1}_i(x)$ and on plant adaptability indices ($I^{t1}_i(z)$) in microscale of Galindez Island did not have a statistically significant correlation as shown above. That's why series of the United temperature influence index and the United rhizosphere bacterial communities influence index on plants populations ($I^{t}_i(z)$ and $I^{rb}_i(z)$ respectively) were compared. The last sets of United temperature and rhizosphere bacterial community influence indices in plant populations had a statistically significant correlation (Table 2). These considerations allowed to conclude that the microbial community has a role in the *D. antarctica* adaptation processes. This conclusion was confirmed by the fact that the sets of United temperature and rhizosphere bacterial community influence indices in *D. antarctica* populations have a significant contribution to the United latent influence index of plant adaptability, calculated according to the algorithm described in the work of Miryuta et al. (2019a). Moreover, as can be seen from the Table 3, similar positive contribution to I^{q1}_i is given by the values of United temperature influence indiex and rhizosphere bacterial community influence indiex. The presented results and conclusions are valid for the studied season (2017/18). This does not mean that the influence of plant populations on the composition of the rhizosphere bacterial community cannot be observed in another season.

Conclusions

1. A comparative statistical analysis of United temperature influence index and rhizosphere bacterial community influence index on the *D. antarctica* population adaptability characteristics in the Antarctic summer season 2017/18 was conducted.

2. The influence of temperature-dependent individual rhizosphere bacteria groups relative content on different *D. antarctica* population plants was statistically investigated taking into account differences between all compared indices in the microscale of Galindez Island, Argentine Islands. This influence appeared to be individual for each *D. antarctica* population. In each population, part of the plants reacted positively to the individual bacteria groups influence while the other part either did not react or reacted negatively.

3. The dependence z(x) is shown to exist by statistical methods. This means that the rhizosphere bacterial community and temperature-dependent rhizosphere bacteria groups (x) can play an active role in plant adaptation of *D. antarctica* populations (z) to individual temperature conditions in the microscale of Galindez Island from a biological point of view.

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Web sources / Other sources

[1] ScionImage program: http://scion-image.software.informer.com/4.0/

Suplements

i	D_i	Localization of the population	S_i, plant population number
1	D_1(D1)	Meteo Point, coastal rocks of Marina Point near the meteorological station, S 65.244780°, W 64.255800°	99
2	D_2(D2)	near main station building (Coronation House), Marina Point, S 65.245700°, W 64.256400°	124
3	D_3(D3)	Leopard Tower, Penguin Point, S 65.247500°, W 64.241200°	106
4	D_4(D4)	Korabel Rock, Penguin Point, S 65.248600°, W64.238230°	80
5	D_5(D5)	the upper terrace of the Hovorukha Dome under the Anna Hill, S 65.248260°; W 64.245240°	91
6	D_6(D6)	near the Antarctic pearlwort (*Colobanthus quitensis* (Kunth) Bartl.) point on the Roztochchia Ridge, S 65.247990°, W 64.242720°	161
7	D_7(D7)	on the Krapla Rock, S 65.247017°, W 64.243167°	500
8	D_8(D9)	on the rocky shore of the Shyia Ridge behind the large magnetic pavilion, S 65.245467°, W 64.249867°	547
9	D_9(D10)	on Magnit Point, S 65.245008°, W 64.253205°	256
10	D_{10}(D11)	on the Cemetry Ridge near the pavilion of Very Low Frequencies (VLF), S 65.246170°, W 64.248250°	242
11	D_{11}(D12)	on the Gull Tower slopes on Stella Point, S 65.247450°, W 64.252740°	300

Table 1s. Localization and plant number (S_i) of *D. antarctica* populations, Galindez Island, Argentine Islands, seasons 2017/18. Microtoponyms of Galindez Island provided according to (Yevchun 2021).

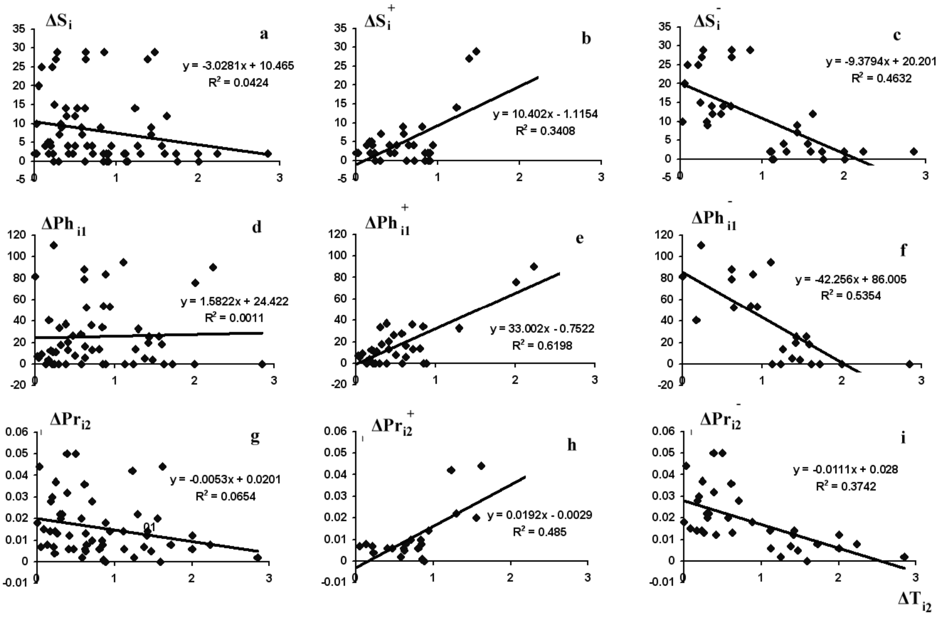

Fig. 1s. An example of dependence of spatial differences sets plant number ($|\Delta S_i|$), leaf length (ΔPh_{i1}) and protein content of 95-145 KDa fraction ($|\Delta Pr_{i2}|$) of *D. antarctica* populations of Galindez Island, Argentine Islands, season 2017/2018, from spatial average temperature differences sets in the 01.2018 : **a**, **d**, **g** – for all points located on the plot between population indices sets paires $|\Delta S_i|$ versus $|\Delta T_{i2}|$, ΔPh_{i1} versus $|\Delta T_{i2}|$, $|\Delta Pr_{i2}|$ versus $|\Delta T_{i2}|$; **b**, **e**, **h** – for points located on plane of the plot which belong to positive group, $|\Delta S^+_i|$ versus $|\Delta T_{i2}|$, ΔPh^+_{i1} versus $|\Delta T_{i2}|$, $|\Delta Pr^+_{i2}|$ versus $|\Delta T_{i2}|$, **c**, **f**, **i** – for points located on plane of the plot which belong to negative group, $|\Delta S^-_i|$ versus $|\Delta T_{i2}|$, ΔPh^-_{i1} versus $|\Delta T_{i2}|$, $|\Delta Pr^-_{i2}|$ versus $|\Delta T_{i2}|$. There are regression equations by the least squares technique and squares of the corresponding correlation coefficients between the above indices values on the charts. The test value of R^2, on the charts: **a** – $F_{1,64}=2.816$, **d** – $F_{1,53}=0.053$, **g** - $F_{1,53}=3.710$ (do not exceed the value of the upper 5% F-distribution limit for N=66 ($F_{1,64}=4.00$), N=55 ($F_{1,53}=4.08$)), **b** – $F_{1,30}=15.510$, **e** – $F_{1,30}=48.900$, **h** – $F_{1,19}=17.898$ (exceed the value of the upper 5% F-distribution limit for N=32 ($F_{1,30}=4.17$), N=32 ($F_{1,30}=4.17$), N=21 ($F_{1,19}=4.35$)); **c** – $F_{1,32}=27.616$, **f** – $F_{1,21}=24.192$, **i** – $F_{1,32}=19.136$ (exceed the value of the upper 5% F-distribution limit for N=34 ($F_{1,32}=4.17$), N=34 ($F_{1,32}=4.17$), N=23 ($F_{1,21}=4.32$)). These facts means the absence of linear dependence in the cases **a**, **d**, **g** and the presence of linear dependence in the cases **b**, **e**, **h**, **c**, **f**, **i.** A detailed description of this algorithm application is presented in the paper (Miryuta et al. 2019b).

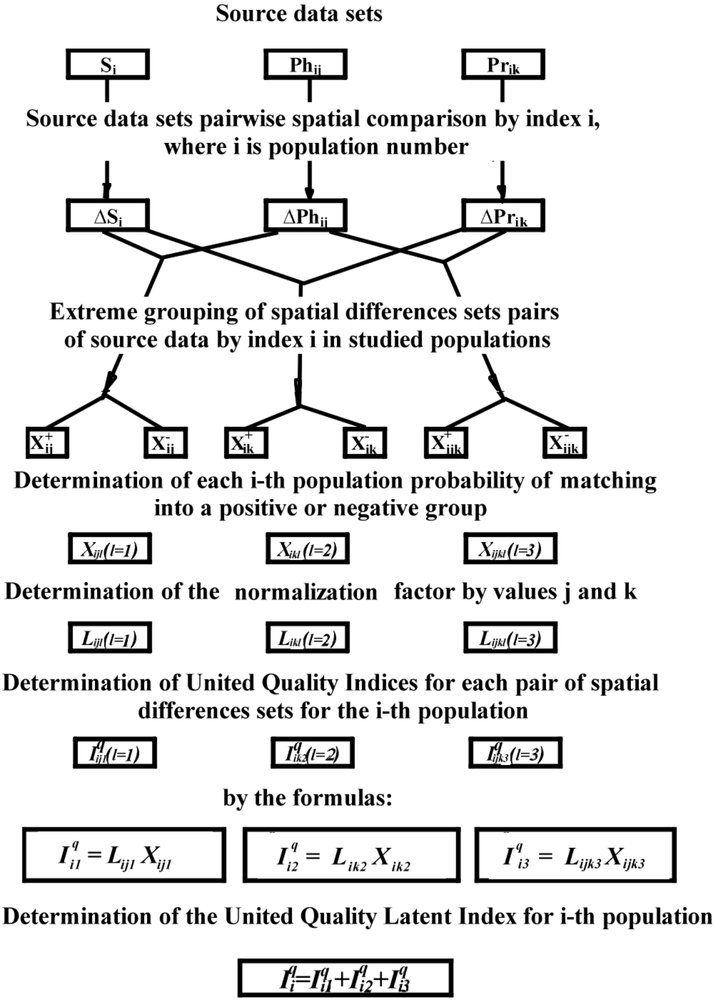

Fig. 2s. The algorithm for determination plant populations I^q_i by three indices under natural conditions, where

Notes to Fig. 2s, 3s :
S_i is plant number in *i*-th population;
Ph_{ij} were morphometric parameters, where j = 1,2,3,4 corresponded to the parameters, respectively: leaf length (dl), inflorescence length (dm), flower length (lower flower glume lenght, dk), number of flowers in the inflorescence (dn);
Pr_{ik} were the relative content of protective and reserve proteins in the seeds, where k = 1,2, ... 5 (6) (number of the fraction that correspond to: globulins with molecular mass more than 150, glutenins with mm from 94 to 145, sulfur-poor prolamins - from 45 to 80; sulfur-rich prolamins - from 20 to 40; part of sulfur-rich prolamins and probably IRIP protein - 27-31; not full formed prolamins and low molecular weight dehydrins - less than 20 kDa).
A detailed description of this algorithm application is presented in the paper (Miryuta et al. 2019a).

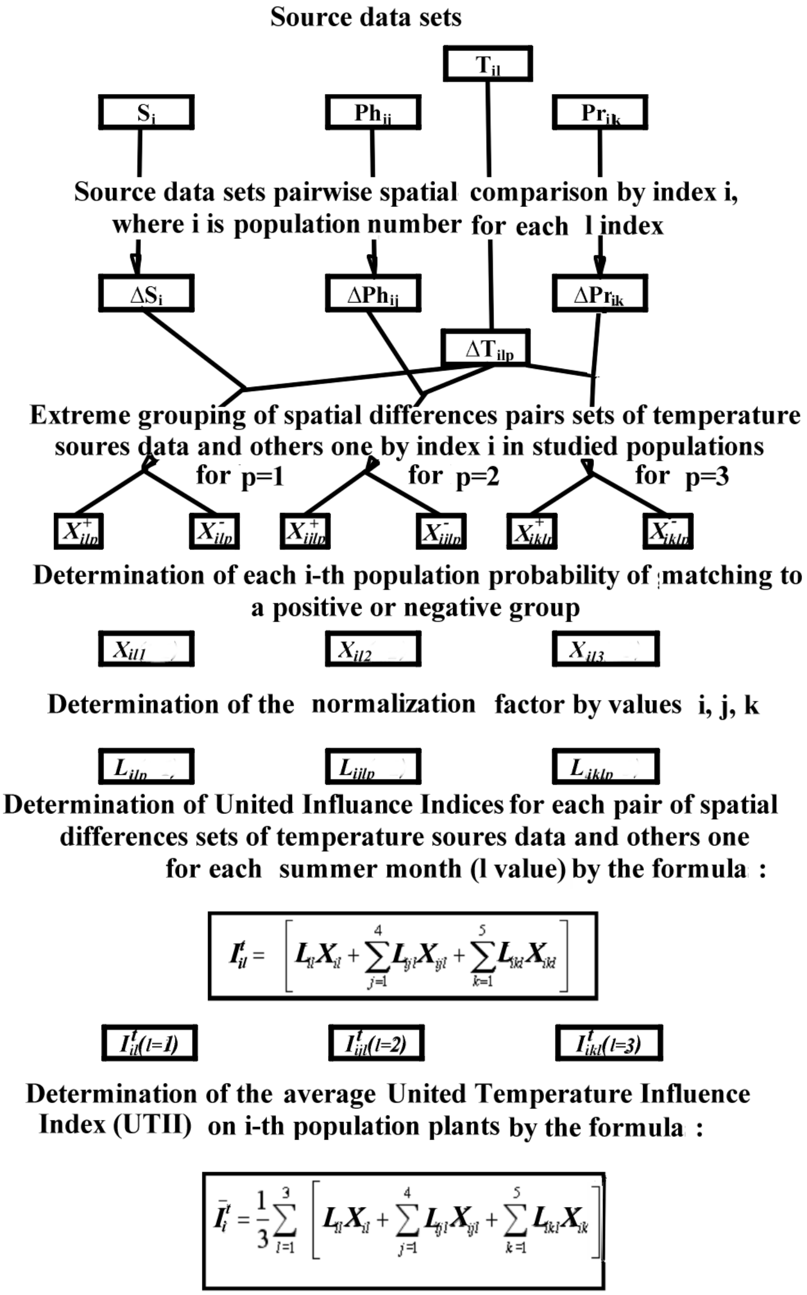

Fig. 3s. An example of an algorithm for I^{tk}_i determination for vascular plant populations, where

Notes to Fig. 3s:

T_{il} is the average monthly soil surface temperature near plants, where i = 1.2, ... 11 and runs around the values corresponding to the number of the studied site of the populations D_1 (D1), D_2 (D2), ... D_7 (D7), D_8 (D9) , ... D_{11} (D12), l = 1,2,3 corresponds to the month summer season number (T_{i1} - average temperature in December 2017, T_{i2} - in January 2018, T_{i3} - in February 2018).

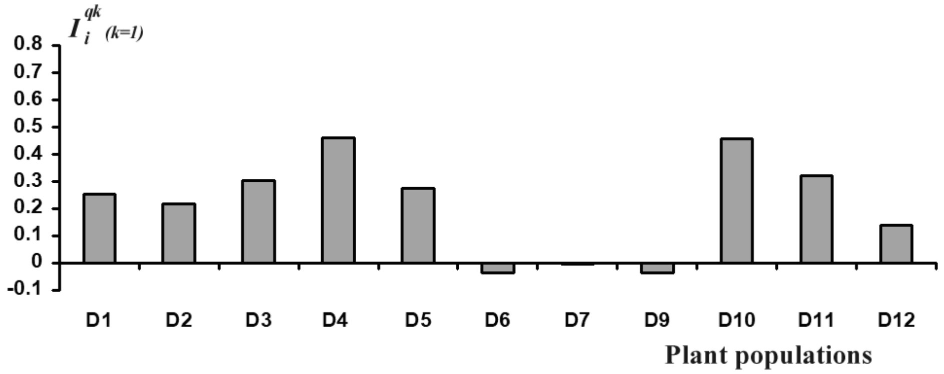

Fig. 4s. The United quality latent index of *D. antarctica* populations adaptability (I^{q1}_i) in different Galindez Island localities.

Notes to Fig. 2, Fig. 4 and Fig. 5: Positive value "+" is the plants portion in the population that are positively influenced by the individual rhizosphere bacteria i groups n the corresponding location, negative value "-" is the plants portion in the population that are not affected or negatively influenced by the individual bacteria groups.

Notes to Table 2: : I^{t1}_i is United temperature influence index on population adaptability indices, I^{rb1}_i is United rhizosphere bacterial community influence index and I^{rb1p}_i is a United individual rhizosphere bacteria groups influence index on population adaptability indices in the 2017/18 season; *i* – the population serial number in the metapopulation, *p* – the serial number of individual (p=1÷5) rhizosphere bacterial community, k=1 is season serial number correspomding to 2017/18 season, *n* – the number of studied populations with a significant correlation coefficient between I^{t1}_i and I^{rb1}_i or I^{rb1p}_i, respectively, R^2 – the square of the correlation coefficient, $F_{1,n-2}$ is the tesr value, $F_{1,n-2}$ (α=0.05) is the upper 5% limit of the F-distribution, R is the correlation coefficient.

Notes to Table 3: I^{q1}_i is United quality latent index of *D. antarctica* plant population adaptability, I^{rb1}_i is United rhizosphere bacterial community influence index and I^{rb1p}_i is a United individual rhizosphere bacteria groups influence index on population adaptability indices in the 2017/18 season, *i* – the population serial number in the metapopulation, *p* – the serial number of individual (p=1÷5) rhizosphere bacterial community, k=1 is season serial number correspomding to 2017/18 season, *n* – the number of studied populations with a significant correlation coefficient between I^{q1}_i and I^{rb1}_i or I^{rb1p}_i, respectively, R^2 – the square of the correlation coefficient, $F_{1,n-2}$ is the tesr value, $F_{1,n-2}$ (α=0.05) is the upper 5% limit of the F-distribution, R is the correlation coefficient.