Data Article

Data on molecular identification, phylogeny and in vitro characterization of bacteria isolated from maize rhizosphere in Cameroon

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A R T I C L E   I N F O

Article history:
Received 10 May 2018
Received in revised form 16 May 2018
Accepted 5 June 2018
Available online 11 June 2018

Keywords:
Bacteria
Maize rhizosphere
Taxonomical affiliation
Functional traits
Growth promotion

A B S T R A C T

Bacteria, which establish positive interactions with plant roots, play a key role in agricultural environments and are promising for their potential use in sustainable agriculture. Many of these mutualistic bacteria provide benefits to plant hosts by facilitating soil mineral nutrient uptake, protecting plants from biotic and abiotic stresses and producing substances that promote growth.

The dataset presented here, is related to the publication entitled “Community structure and plant growth-promoting potential of cultivable bacteria isolated from Cameroon soil” (Tchuisseu et al., 2018) [1]. The data provide an extended analysis of the occurrence, taxonomical affiliation and functional traits of bacterial groups isolated from the rhizosphere of maize in Cameroon at different taxonomical levels, using a combination of molecular/bioinformatics tools and in vitro studies. Bacteria were isolated from maize rhizosphere soil. Isolated bacteria were identified using the 16s rRNA gene sequencing and phylogenetic analyses. All strains were...
characterized for their potential of salinity tolerance and growth promotion (phosphate solubilization, \textit{nifH} gene presence and siderophore production) in order to select efficient bacterial strains for designing biological fertilizer exploitable for agriculture under specific stress conditions of the country. The data will be valuable for further studies on plant associated bacteria in Cameroon, which are still largely unexplored.

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**Specifications Table**

| Subject area                  | Biology                                      |
|-------------------------------|----------------------------------------------|
| More specific subject area    | Microbiology, Biotechnology                  |
| Type of data                  | Table, Figure                                |
| How data was acquired         | Isolation of bacteria from rhizosphere soil of maize field. Molecular identification of isolates and phylogenetic analyses. In vitro screening of bacterial group based on their different functional traits. |
| Data format                   | Raw, Analyzed                                |
| Experimental factors          | DNA extraction of all isolates, determination of DNA concentration and quality check. 16S rDNA sequences were analyzed an edited using NCBI and Ribosomal Database Project (RDP), assembled using Muscle and the phylogenetic analysis was proceeded using Mega 7 version 7.0.21. Biochemical test to evaluate all bacterial strains for their salt tolerance, phosphate solubilization, \textit{nifH} gene possession and siderophore production potential. |
| Experimental features         | Isolation of bacterial isolates, followed by the identification using the 16S rRNA gene sequences, and then, the \textit{in vitro} characterization for the different functional traits tested. |
| Data source location          | Soil samples were collected in Ngaoundal locality (6° 30′ North, 13° 16′ East), Cameroon. |
| Data accessibility            | Data are presented in this article.          |

**Value of the data**

- Like in many sub-Sahara African countries, studies on plant growth-promoting bacteria (PGPB) are still largely untapped in Cameroon. This data provides the first collection of bacteria associated with maize in Cameroon and therefore is valuable for further studies of microbial communities associated with plants in the country.
- The different traits tested give insight into the functional difference between bacterial groups found in the maize rhizosphere and can be useful to understand the ecological role of newly isolated bacteria in their specific environment.
- The knowledge about the bacterial groups and their functional traits may contribute to improve management practices regarding plant resistance to salinity and plant nutrition.
- This data may contribute in promoting microbial bio-fertilizers based on native rhizobacteria in sub-Saharan Africa and enhancing sustainable crop production systems.
1. Data

The study of plant-associated microorganisms is of great importance for biotechnological applications, for example, resistance to abiotic and biotic stresses, plant growth-promotion, or isolation of active compounds [2]. The benefit that PGP bacteria exert to plant growth and yield is well known. However, the growth-promoting effect depends mainly on native biotic and abiotic factors including bacterial species and the soil types [1]. Therefore, knowledge about the native bacterial populations, their identification and their implications for plant physiology, is required for improving management practices regarding plant nutrition and resistance to abiotic stresses [3]. The dataset of this article provides information on the community and functional difference of different groups of bacteria isolated from maize rhizosphere soil in Cameroon. Phylogenetic analysis was used to cluster isolates to their closely related species (Fig. 1) where, the branch lengths displayed represent substitutions per site. Table 1 presents the ability of different bacterial groups to tolerate increasing concentration of sodium chloride (NaCl) at genus, family and phylum level. Table 2 shows the characterization of bacterial strains to solubilize seven different compounds of inorganic phosphate: tricalcium-

Fig. 1. Phylogenetic tree based on 16S rDNA sequences revealing phylogenetic classification of the 143 isolates. The Maximum Likelihood tree was structured using the Tamura 3-parameter model and the neighbor joining method. Methanococcus ssp. was used as outgroup. The isolates between sequences are represented in bold.
phosphate, hydroxyapatite, Malian rock phosphate (RP), Cameroonian RP, Algerian RP, Mexican RP, Moroccan RP at genus, family and phylum level. Table 3 shows the ability of bacterial groups to possess \textit{nifH} gene, responsible for nitrogen fixation and to produce siderophore at genus, family and phylum level.

2. Materials and methods

2.1. Isolation, molecular identification and phylogenetic analysis of bacterial isolates

Soil samples were collected in May 2015 from maize rhizospheres at a farm in the Ngaoundal locality. The isolation of microorganisms was assessed in non-selective nutrient agar (NA) medium (Standard nutrient agar I, Carl Roth, Germany) containing 6 g NaCl, 3 g yeast extract, 15 g peptone, 1 g glucose, 12 g agar-agar L$^{-1}$, pH 7. Bacterial colonies were selected based on their morphological characteristics [4] and purified. Genomic DNA was extracted from overnight pure bacterial culture grown in nutrient broth (Standard nutrient broth I, Carl Roth, Germany) at 28 °C was performed using
Table 2
Occurrence and characterization of bacterial strains to solubilize different types of inorganic phosphate source at genus, family and phylum level.

| Characterization level | Number of isolates | Chemical inorganic phosphate | Rock phosphate (RP) | Total P solubilizing isolates |
|------------------------|--------------------|-------------------------------|---------------------|-------------------------------|
|                        |                    | Tricalcium Phosphate | Hydroxyapatite | Malian RP | Cameroonian RP | Algerian RP | Mexican RP | Moroccan RP |
| Genera                 |                    |                               |                     | 0         | 0            | 0           | 0           | 0           |
|                        |                    |                               |                     | 0         | 0            | 0           | 0           | 0           |
| Aerococcus             | 1                   | 0                             | 0                   | 0         | 0            | 0           | 0           | 0           |
| Amycolatopsis          | 2                   | 1                             | 1                   | 1         | 0            | 1           | 0           | 1           |
| Arthrobacter           | 25                  | 19                            | 14                  | 18        | 10           | 15          | 12          | 2           |
| Bacillus               | 45                  | 18                            | 14                  | 17        | 13           | 11          | 12          | 2           |
| Burkholderia           | 3                   | 0                             | 0                   | 0         | 0            | 0           | 0           | 0           |
| Domibacillus           | 1                   | 0                             | 0                   | 0         | 0            | 0           | 0           | 0           |
| Kitasatospora          | 1                   | 0                             | 0                   | 0         | 1            | 0           | 0           | 0           |
| Leifsonia              | 8                   | 3                             | 2                   | 3         | 2            | 1           | 1           | 0           |
| Lysinibacillus         | 3                   | 0                             | 0                   | 0         | 0            | 0           | 0           | 0           |
| Microbacterium         | 1                   | 1                             | 1                   | 1         | 1            | 1           | 1           | 0           |
| Micrococcus            | 4                   | 3                             | 2                   | 3         | 3            | 2           | 2           | 0           |
| Mycobacterium          | 1                   | 0                             | 0                   | 0         | 0            | 0           | 0           | 0           |
| Paeenibacillus         | 7                   | 5                             | 5                   | 3         | 2            | 4           | 4           | 0           |
| Roseomonas             | 1                   | 0                             | 0                   | 1         | 1            | 0           | 0           | 0           |
| Sinononas              | 19                  | 12                            | 1                   | 11        | 6            | 3           | 2           | 0           |
| Solibacillus           | 4                   | 0                             | 0                   | 0         | 0            | 0           | 0           | 0           |
| Staphylococcus         | 11                  | 3                             | 1                   | 3         | 2            | 1           | 1           | 0           |
| Streptomyces           | 3                   | 1                             | 1                   | 1         | 1            | 1           | 0           | 0           |
| Unclassified           | 2                   | 0                             | 0                   | 0         | 0            | 0           | 0           | 0           |
| Unclassified Intrasporangiaceae |        |                               |                     | 0         | 0            | 0           | 0           | 0           |
| Unclassified Planococcaceae |        |                               |                     | 0         | 0            | 0           | 0           | 0           |

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| Total Families | Acetobacteraceae | Aerococcaceae | Bacillaceae | Burkholderiaceae | Intrasporangiaceae | Microbacteriaceae | Micrococcaceae | Mycobacteriaceae | Paenibacillaceae | Planococcaceae | Pseudonocardiaceae | Staphylococcaceae | Streptomycetaceae | Total Phyla | Actinobacteria | Firmicutes | Proteobacteria | Total |
|----------------|------------------|---------------|------------|------------------|-------------------|------------------|-----------------|----------------|----------------|-------------|------------------|-----------------|----------------|--------------|---------------|--------------|----------------|--------|
| 20             | 1                | 0             | 0          | 1                | 1                 | 0                | 0               | 0              | 0              | 1           | 0                | 3               | 1             | 3            | 66            | 73            | 4              | 143   |
| 20             | 1                | 0             | 0          | 0                | 0                 | 0                | 0               | 0              | 0              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 49               | 18            | 14         | 17               | 13                | 11               | 12              | 2              | 20             | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 3                | 0             | 0          | 0                | 0                 | 0                | 0               | 0              | 0              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 2                | 0             | 0          | 0                | 0                 | 0                | 0               | 0              | 0              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 9                | 4             | 3          | 4                | 3                 | 2                | 2               | 0              | 0              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 48               | 34            | 17         | 32               | 19                | 20               | 16              | 2              | 34             | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 1                | 0             | 0          | 0                | 0                 | 0                | 0               | 0              | 0              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 7                | 5             | 5          | 3                | 2                 | 4                | 4               | 0              | 7              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 5                | 0             | 0          | 0                | 0                 | 0                | 0               | 0              | 0              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 2                | 1             | 1          | 1                | 0                 | 0                | 1               | 0              | 1              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 11               | 3             | 1          | 3                | 2                 | 1                | 1               | 0              | 3              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 20             | 4                | 1             | 1          | 1                | 2                 | 1                | 0               | 0              | 0              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 13             | 66               | 40            | 22         | 38               | 24                | 23               | 19              | 2              | 41             | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 13             | 73               | 26            | 20         | 23               | 17                | 16               | 17              | 2              | 30             | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| 13             | 4                | 0             | 0          | 1                | 1                 | 0                | 0               | 0              | 1              | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
| Total          | 143              | 66            | 42         | 62               | 42                | 39               | 36              | 4              | 72             | 0           | 0                | 0               | 0             | 0            | 0             | 0             | 0              | 0      |
the DNeasy Plant Mini kit (QIAGEN, Germany) by following the manufacturer’s instructions. The genomic DNA extracted from all isolates was used for partial 16S rRNA gene amplification using two 16S rDNA sequencing universal primers: 9bfm (5’-GAGTTTGATYHTGGCTCAG-3’) and 1512R (5’-ACGGHTACCTTGTTACGACTT-3’) [5]. All PCR amplicons were confirmed by electrophoresis, purified and sequenced. The bacterial 16S rDNA nucleotide sequences were aligned with known sequences in the NCBI (http://blast.ncbi.nlm.nih.gov) and Ribosomal Database Project (RDP) databases using BLASTn. Multiple sequence alignments with the most closely related bacterial sequences were performed using Muscle (https://www.ebi.ac.uk/Tools/msa/muscle/) and phylogeny was inferred by the Maximum Likelihood approach based on the Tamura 3-parameter model and the neighbor-joining method [6], using Mega 7 version 7.0.21 (http://www.megasoftware.net/).

Table 3
Occurrence and characterization of bacterial strains for nifH gene presence and siderophore production at genus, family and phylum level.

| Characterization level | Number of isolates | nifH gene | Siderophore production |
|------------------------|--------------------|-----------|------------------------|
| Genera                 |                    |           |                        |
| Aerococcus             | 1                  | 0         | 0                      |
| Amycolatopsis          | 2                  | 0         | 0                      |
| Arthrobacter           | 25                 | 7         | 2                      |
| Bacillus               | 45                 | 3         | 13                     |
| Burkholderia           | 3                  | 0         | 1                      |
| Domibacillus           | 1                  | 0         | 0                      |
| Kitasatospora          | 1                  | 0         | 1                      |
| Leifsonia              | 8                  | 1         | 1                      |
| Lysinibacillus         | 3                  | 1         | 0                      |
| Microbacterium         | 1                  | 0         | 0                      |
| Micrococcus            | 4                  | 0         | 1                      |
| Mycobacterium          | 1                  | 0         | 1                      |
| Paenibacillus          | 7                  | 2         | 1                      |
| Roseomonas             | 1                  | 0         | 1                      |
| Sinomonas              | 19                 | 0         | 0                      |
| Solibacillus           | 4                  | 0         | 0                      |
| Staphylococcus         | 11                 | 1         | 5                      |
| Streptomyces           | 3                  | 0         | 0                      |
| Unclassified           | 2                  | 0         | 1                      |
| Intrasporangiaceae     |                    |           |                        |
| Unclassified           |                    |           |                        |
| Total Genera           | 20                 |           |                        |
| Families               |                    |           |                        |
| Acetobacteraceae       | 1                  | 0         | 1                      |
| Aerococcaceae          | 1                  | 0         | 0                      |
| Bacillaceae            | 49                 | 4         | 13                     |
| Burkholderiaceae       | 3                  | 0         | 1                      |
| Intrasporangiaceae     | 2                  | 0         | 1                      |
| Microbacteriaceae      | 9                  | 1         | 1                      |
| Micrococaceae          | 48                 | 7         | 3                      |
| Mycobacteriaceae       | 1                  | 0         | 1                      |
| Paenibacillaceae       | 7                  | 2         | 1                      |
| Planococaceae          | 5                  | 0         | 0                      |
| Pseudonocardiacae      | 2                  | 0         | 0                      |
| Staphylococaceae       | 11                 | 1         | 5                      |
| Streptomyctaceae       | 4                  | 0         | 1                      |
| Total Families         | 13                 |           |                        |
| Phyla                  |                    |           |                        |
| Actinobacteria         | 66                 | 8         | 7                      |
| Firmicutes             | 73                 | 7         | 19                     |
| Proteobacteria         | 4                  | 0         | 2                      |
| Total Phyla            | 3                  | 143       | 15                     | 28                     |
2.2. In vitro characterization of bacterial isolates

All identified bacterial strains were characterized in vitro by the salt tolerance, phosphate solubilization, nifH gene presence and siderophore production capacity. The salinity tolerance potential was evaluated by observing the growth on Standard I Nutrient agar (Carl Roth, Germany) amended with various concentrations of NaCl (2%, 4%, 6%, and 8% w-v) [7]. The ability of isolates to solubilize seven different inorganic phosphate sources (tricalcium phosphate, hydroxyapatite, Malian rock phosphate (RP), Cameroonian RP, Algerian RP, Mexican RP, Moroccan RP) was assessed on plates filled with the National Botanical Research Institute’s Phosphate growth medium (NBRIP) [8]. Potential nitrogen-fixing bacteria were determined by searching for the presence of the nifH gene, the marker gene for biological nitrogen fixation ability using the universal primers 19F (5’-GCIWTY-TAYGGIAARGGIGG-3’) and 366R (5’-AAICCRCCRCAIACIACRTC-3’) [9]. Siderophore production by bacterial isolates was determined following the universal assay of Schwyn and Neilands using CAS-blue plates [10].

Acknowledgements

This work was supported by the German Academic Exchange Service (Research Grants–Bilaterally supervised Doctoral Degrees, 2015/16, grant number: 57129430) and the Leibniz Institute of Vegetable and Ornamental Crops Großbeeren/Erfurt e.V.

Transparency document. Supplementary material

Transparency document associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.06.003.

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