**Supplementary Table1:** Observation of single dye degradation rate of methylene green (MG), acid blue (AB), and basic violet (BV) dyes at 614 nm, 620 nm and 590 nm respectively by on LB liquid media after 96 hours.

|  |  |  |  |
| --- | --- | --- | --- |
| Name of dyes /Isolates | Degradation rate of Methylene green (MG) | Degradation rate of Acid blue (AB) | Degradation rate of Basic violet (BV) |
| S-1 | 81% | 75% | 66% |
| S-2 | 79% | 79% | 77% |
| S-3 | 84% | 67% | 69% |
| S-5 | 89% | 70% | 65% |
| S-9 | 89% | 70% | 81% |
| S-11 | 94% | 88% | 81% |
| S-15 | 91% | 82% | 80% |
| S-17 | 88% | 61% | 72% |

**Supplementary Table 2:** The degradation rate of mixed dyes as MG+BV, MG+AB, AB+BV and MG+BV+AB have showed in below\_\_

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name of dyes/ Isolates | Degradation rate of MG+BV | Degradation rate of MG+AB | Degradation rate of AB+BV | Degradation rate of MG+BV+AB |
| S-11 | 74% | 75% | 73% | 80% |
| S-15 | 75% | 82% | 73% | 82% |

**Supplementary Table 3**. The results of morphological and biochemical test of *Bacillus psudomycoides* and *Acinetobacter haemolyticus*.

|  |  |  |  |
| --- | --- | --- | --- |
| **Serial No.** | **Test name** | **Results** | |
| **Isolate S-11** | **Isolate S-15** |
| 01. | Gram staining test | Gram-positive | Gram-negative |
| 02. | Motility test | + | \_ |
| 03. | Methyl Red test | + | \_ |
| 04. | Catalase test | \_ | + |
| 05. | MacConkey test | \_ | \_ |
| 06. | Mannitol salt test | \_ | + |
| 07. | Urea Hydrolysis test | + | + |
| 08. | Starch Hydrolysis test | + | \_ |
| 09. | Triple Sugar Iron(TSI) test | H2S+,gas- | H2S+,gas- |
| 10. | Simmon Citrate test | \_ | + |
| 11. | Bismuth Sulfate Agar(BSA) test | \_ | \_ |
| 12. | Eosin Methylene Blue(EMB) agar test | \_ | + |
| 13. | Oxidase test | \_ | \_ |

**Supplementary Table 4:** List of the antibiotic disks containing different concentration used in the antibiotic sensitivity test

|  |  |  |
| --- | --- | --- |
| Antibiotics | Symbol | Concentration |
| Penicillin | P | 10 units/disc |
| Amoxicillin | AXM | 30 mcg/disc |
| Gentamycin | GEM | 10 mcg/disc |
| Tetracycline | TE | 30 mcg/disc |
| Ciprofloxacin | CIP | 5 mcg/disc |
| Cefuroxime | CXM | 30 mcg/disc |
| Cefixime | CFM | 10 mcg/disc |
| Ampicillin | AMP | 25 mcg/disc |
| Erythromycin | E | 15 mcg/disc |
| Kanamycin | K | 30 mcg/disc |
| Ceftazidime | CAZ | 30 mcg/disc |
| Doxycycline | DO | 30 mcg/disc |

**Supplementary Table 5:** Comparison of different dye degrading bacteria with the isolated bacteria of the current study.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **S. No.** | **Textile dyes** | **Bacteria** | **Decolorization efficiency (%)** | **Reference** |
| **1.** | Crystal violet | *Pseudomonas aeruginosa, Clostridium perfringens, Bacillus subtilis, Enterobacter sp. , Laccase* | 75% | Kochher & Kumer -2011,  Ali-2014,  Hemapriya & J. -2014,  Li Z et al. -2020 |
| **2.** | Reactive red 4E8Y5 | *Bacillus spp., Aeromonas hydrophila* | 60.2% | Gudmalwar Rajesh et al.,  Hsueh et al. -2009 |
| **3.** | Reactive blue 19, Dark green dye | *Enterococcus sp. & Klebsiella sp., Coriolus versicolor laccase* | 45.7-88.2% | Gulati & Jha-2014,  Yuan H et al. -2020 |
| **4.** | Mordant Yellow | Mixed bacterial culture | 50% | Haug et al. -1991 |
| **5.** | Reactive black-5, Direct red-81, Acid red-88 | *Shewanella sp*. Strain IFN4, Aeromonas hydrophila | 60.2 & 80.9% | Imran et al.-2014,  Hsueh et al. -2009 |
| **6.** | Remazol orange | *Pseudomonas aeruginosa* | 94% | Sarayu & Sardhya -2010 |
| **7.** | Methylene Green | *B. pseudomycoides, A. haemolyticus* | 94% & 91% | Present study |
| **8.** | Acid Blue | *B. pseudomycoides, A. haemolyticus* | 88% & 82% | Present study |
| **9.** | Basic Violet | *B. pseudomycoides, A. haemolyticus* | 81% & 80% | Present study |

**Supplementary Table 6: The 16s rDNA sequence of isolate S-11**

CGNTGCTATACATGCAAGTCGAGCGAACCGATTAAGAGCTTGCTCTTAAGAAGTTAGCGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGATAACATTTTGCACCGCATGGTGCGAAATTGAAAGGCGGCTTCGGCTGTCACTTACAGATGGACCTGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGCGATGAAGGCCTTCGGGTCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGCAACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTCTGACAACCCTAGAGATAGGGCTTCCCCTTCGGGGGCAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCATCATTAAGTTGGGCACTCTAAGTGACTGCCGGTGACAACCGGAGGAAGGTGGGGATGACGTCAATCATCATGCCCCTTATGACCTGGGCTACCACGTGCTACATGGACGGTC

**Supplementary Table 7: The 16s rDNA sequence of isolate S-15**

TAGGNAGCTTACCATGCAAGTCGAGCGGGGAAGTGTAGCTTGCTACATTACCTAGCGGCGGACGGGTGAGTAATGCTTAGGAATCTGCCTATTAGTGGGGGACAACATTCCGAAAGGAATGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGATCTTCGGACCTTGCGCTAATAGATGAGCCTAAGTCGGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGGCGACGATCTGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGGAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCGAGGAGGAGGCTACTCTAGTTAATACCTAGAGATAGTGGACGTTACTCGCAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCGAGCGTTAATCGGATTTACTGGGCGTAAAGCGTGCGTAGGCGGCTGATTAAGTCGGATGTGAAATCCCTGAGCTTAACTTAGGAATTGCATTCGATACTGGTCAGCTAGAGTATGGGAGAGGATGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCCTAATACTGACGCTGAGGTACGAAAGCATGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCATGCCGTAAACGATGTCTACTAGCCGTTGGGGCCTTTGAGGCTTTAGTGGCGCAGCTAACGCGATAAGTAGACCGCCTGGGGAGTACGGTCGCAAGACTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATAGTAAGAACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTTACATACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTTTCCTTATTTGCCAGCGGGTTAGACCGGGAACTTTAAGGNTACTGCCAGTGACAACTGGAGGAAGGCGGGACAACTCAAGTCATNTGGCCCTTACAACAGGGCTACCCCCTGGCTACATGGTCGGACAAAGGGTGCTACTAGC

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