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Stenotrophomonas maltophilia, A Commensal of Importance to Biotechnology

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***Stenotrophomonas maltophilia* (Sm) is endowed with immense prowess that can be exploited beneficially in Agriculture, Nutrition, Medicine, Biodegradation, Bioremediation and Phytoremediation. The bacterium possesses multitudinous extracellular proteins and enzymes lined by inherent and acquired mechanisms and/or genes which are primarily responsible for adaptation and survival in its niche. Accessibility to the versatility and synthetic dynasty embedded in the bacterium is however threatened by ease of contamination with toxic product(s) of the same bacterium and the bacterial implication in life threatening multidrug resistant infections promoted by the presence of resistance genes. High level technology and expertise, with collaboration by scientists from all wards of life is advocated to safely harness the biotechnological potentials of the organism at an economically viable magnitude.**

KeyWords: *Stenotrophomonas maltophilia*, Biotechnology,
Agriculture, resistance genes, commensal.

Stenotrophomonas maltophilia is a common ubiquitous commensal[1] that is readily isolated from water, soil, sewage and regularly on plant or within plant's rhizosphere where they play key roles in biogeochemical cycling of nitrogen, sulphur and other important elements. Though it has been implicated as opportunistic pathogens[2,3] and as true pathogens[4-6] due to their roles as aetiologies of life threatening infections[7,8], yet their beneficial roles in their niche vis-a-vis their importance in biotechnological advancement cannot be underestimated[9-11]. This article reviews the potentials of *S. maltophilia* in their niche and in biotechnological advancement, the inherent genes predicating the bacterium's attributes including antibiotic resistance genes and other selective properties.

Stenotrophomonas maltophilia (Sm) in an Ecological Niche: Adaptability and Resilience

Stenotrophomonas maltophilia is a Gram negative commensal bacterium found in myriads of habitats where it occupies a vital niche ranging from terrestrial to aquatic habitats[12] including the irrigation solutions used in hospitals[13]. While attempting to assess the safety of drinking water in the process of treatment until delivery, Newcombe *et al*. [14] detected *Stenotrophomonas maltophilia* among other opportunistic pathogens in International Space Station by qPCR. Some other studies have revealed that the bacterium is notable among the rhizosphere bacterial inhabitants[15-17]. Its fitness in this domain is dependent on the environment. A peculiarly related example is the

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resistant mutants of the bacterium that produce the multidrug efflux pump SmeDEF excessively[18,19] but less competitive in a slime mold infection model. Meanwhile, *Stenotrophomonas maltophilia* generally has immense adaptability to its natural environment, even in the face of unsuitable stress or at conditions below optimal. As already known, plants secrete a diverse class of polyphenolic compounds called flavonoids to ascertain interaction between microorganisms and the plant[20]. This compounds poses a challenge for less adaptable bacteria as they have been proven to have antimicrobial activities against extended spectrum beta lactamase producers[21-24], thus creating additional stress for rhizospheric bacteria including *Stenotrophomonas maltophilia* to combat. *Stenotrophomonas maltophilia* however withstands this stress and stands among the most successful rhizosphere bacteria.

It has been equally reported that the development of association with plants built up by *Stenotrophomonas maltophilia* encourages their abilities to survive in soils that are deplete of nutrients[15]. This association is facilitated by a number of anatomical structures like flagella[25] with which the bacteria moves in response to chemo-attraction from the root; pilli, fimbriae and biofilm for adhesion and adaptation against adverse chemicals and ions[26]. The bacterium obtains nutriment and shelter in this mutual association just as its extracellular proteins (enzymes) expel or exhibit lethal effect e.g. lipases, chitinases, nucleases, elastases and proteases[27], exterminating the root borers within the rhizosphere and leave the plants protected. Extracellular polymers produced by *Stenotrophomonas maltophilia* therefore appears to have potentials as possible source of antibiotics, even if it demands the incorporation of halogen moieties to reduce toxicity and enhance potency as does fluorine in fluoroquinolone[28].

Worth noting also is the resilience of this Gram negative rod, that resulted in its adaptation in diverse habitats and biomes across the globe[29]. Botes *et al*. [30] reported the survival of *Stenotrophomonas maltophilia* in South African antimony mine which is an environment that had been heavily impacted with high dosage of arsenic occasioned by refining activities. The resilience to withstand the effect of this supposedly adverse chemical in large concentrations (10 mmol l^{-1} arsenite and 20 mmol l^{-1} arsenate) might have informed the authors' reference to the observation as "hyper-resistance to arsenic". This adaptation extends to human and non human animals as a habitat for *Stenotrophomonas maltophilia*. For instance, Bollet *et al*. [1] noted that in France, the frequency of isolating *Stenotrophomonas maltophilia* from clinical samples has been on the increase since 1987, at time of the emergence of imipenem, the parenteral carbapenem with high pharmacokinetic profile. This adaptive attribute is due to its high resistance profile and unique physio-pathological attributes with which it avoids the non specific anatomical barrier of the immune system[31]. Also, *Stenotrophomonas maltophilia* exhibits mono-cultural growth and multiplies widely utilizing the accessible nutrients in the phyllosphere environment. To achieve this, it alters the cuticle of leaf surface to which it attaches e.g. in *Hedera helix* and *Prunus laurocerasus*[32] to increase the availability of water and dissolved compounds. *Stenotrophomonas maltophilia* also maintains good ecological relationships with other phyllospheric bacteria. Its effective alteration of plants cuticle is benefited to the epiphytic bacteria in the environment[33]. Previous study also revealed that *Stenotrophomonas maltophilia* strain BP1 and *Pseudomonas syringae* TLP2dell jointly exhibit a high level of coexistence with "respect" for each other, despite the seeming preponderance of *Stenotrophomonas maltophilia*[34].

Biotechnological Importance of *Stenotrophomonas maltophilia*

Stenotrophomonas maltophilia as agent in biological control

Another dimension to the importance of *Stenotrophomonas maltophilia* is its role in biological control. An example of such role is found in the biological control of *Bipolaris sorokiniana* on Tall Fescue by *Stenotrophomonas maltophilia* Strain C3[35]. In Zhang-Yuen's research, strain C3 was observed in growth chamber experiment to prevent the germination of conidial on the surfaces of leaves. When compared with non-treated control, noticeable reduction in lesion and infected area by *B. sorokiniana* was observed by Zhang and Yuen[35] which was proportional to the dosage used. This has been explained to have been predicated by the production of chitinase which prevent the conidial germination[9]. The lytic activity affected by the enzymes produced by this bacterium is a notable mechanism the organism explores for biocontrol[10,36]. Enzyme system that brought about the lytic activities have caught the attention of researchers on biocontrol agents especially those that are active in disrupting fungi cell wall e.g. chitinase[9]. Hence, *Stenotrophomonas maltophilia* is an important rhizosphere bacteria which can be explored for agricultural improvement against fungal infection[37].

Attributes of *Stenotrophomonas maltophilia* that can be explored in biocontrol arsenal include ease of colonization of rhizosphere, production of antimicrobial compounds and extracellular proteins (enzymes) [9,38,39], some of which have been discussed earlier in this review. Notable examples in this respect are four isolates designated as PD3531, PD3532, PD3533 and PD3534 which suppressed potato brown rot caused by *Ralstonia solanacearum* in Egyptian clay soil[37] and the *Stenotrophomonas maltophilia* strain 34S1 that was identified as a biocontrol against the fungus *Magnaporthe poae* which is an agent for patch disease of Kentucky bluegrass (*Poa pratensis*)[40,41], though more research input is advocated in this biocontrol activities to further define the roles of the participating agents.

Stenotrophomonas maltophilia in biogeochemical cycling

Stenotrophomonas maltophilia has been implicated in the biogeochemical cycling of vital elements like Nitrogen, Sulphur, Phosphorus and a number of others. Dungan *et al.*[42] reported the transformation of selenate and selenite by the bacterium; the attribute which made the author suggests the role of this bacterium in entire biogeochemical cycling. Since their research focussed on Agricultural pond sediment containing selenium, their conclusion affirmed the bacterium's importance, not only for nutrient cycling, but also in bioremediation[42]. In the meantime, the roles of the bacterium amidst other bacteria in nitrogen fixation have been observed by Park *et al.* [43] in Korea. The study was conducted in high inorganic fertilizer impacted soil within the rhizospheres of rice, maize and wheat, and the bacterium was observed to exhibit appreciable potentials for nitrogen fixation. Other studies have also confirmed *Stenotrophomonas maltophilia* as a good solubilizers of phosphate and phytate, and as biological fertilizer[44-46]. Mineralization of phytate in the biosphere with phytases produced by the soil microorganisms including *Stenotrophomonas maltophilia* stands as a formidable process of phosphorus recycling[46]. This attribute is of particular interest to crop breeders and soil scientists as the bacterial solubilisation will not only recycle nutrients but also convert them from various forms (e.g. tricalcium phosphate in phosphate min)[47] into utilizable form by plants.

The phytases produced by *Stenotrophomonas maltophilia* which are important in phosphate conversion have other numerous biotechnological applications. They reduce phytate contents in animal feed as well as human food and improve phosphorus' availability[48,49]. The enzymes are peculiarly incorporated into feeds of farm animals including poultry, swine, and fish diets, amino acids, and energy. *Stenotrophomonas maltophilia* ability to produce this enzyme in large deposit can serve as additional benefit similar to the cases of *Bacillus* sp. [50], *Raoultella* sp. [51], *Citrobacter braakii*[52].

Stenotrophomonas maltophilia in Biodegradation and Bioremediation

The impacts of *Stenotrophomonas maltophilia* in various forms of degradation processes stand as an indispensable prowess in nature's self cleansing dynamics[11]. Recalcitrants of various forms with tendency to choke up some low forms of life in various habitats are easily degraded by *Stenotrophomonas maltophilia*. Studies in laboratory scale and their subsequent applications in larger scales showed these remarkable decomposition properties. These attributes have been utilized in many quarters of human endeavour and may be applied in the removal of clogging that obstruct water filtrations in water treatment plants[53]. Biofilm produced by *Stenotrophomonas maltophilia* has been employed to biodegrade branched anionic surfactants from activated sludge by Farzaneh *et al.*[1] just as the bacterium has equally been recognized as a potent agent in bioremediation. Aromatic industrial emissions like toluene, xylene, benzene and ethylbenzene have been degraded using the *Stenotrophomonas maltophilia* strain T3-c[53-55]. *Stenotrophomonas maltophilia* strain M1 degrades methomyl, an oxime carbamates which though used extensively for the control of insects and nematode, is a toxic xenobiotics that disrupt the balance in the ecosystem killing vital primary consumers[56]. According to Mohammed[56], this plasmid based degradation exhibited by this organism was discovered through multiphase-coupled mass spectrometry, and this bioremediation potential promises to be of colossal advantage as one or more pesticides often detected in 95% of surface water systems' samples in USA could be treated with *Stenotrophomonas maltophilia*. Guan *et al*.[57] observed the degradation of aflatoxin B1 by *Stenotrophomonas maltophilia* 35-3 with highest degradation index of 0.84 at slightly alkaline pH (pH of 8). This enzymatic degradation has great industrial application. Also, many studies have reported the degrading potentials of various strains of *Stenotrophomonas maltophilia* with huge successes[16,58-60].

In the same vein, this important role in bioremediation encompasses heavy metals removal and phyto-remediation. Vallini *et al*.[61] reported selenium precipitation by *Bacillus mycoides* and *Stenotrophomonas maltophilia*. Antonioli *et al*.[62] report also confirmed this, as the researchers observed that *Stenotrophomonas maltophilia* strain SeITE02 can detoxify a selenite contaminated environmental matrix aerobically, reducing selenite to selenium. This attribute is also true for other heavy metals. Non-viable cells of *Stenotrophomonas maltophilia* can be utilized with higher effectiveness to remove Cu (II) from aqueous solutions than a viable one[63]. This makes *Stenotrophomonas maltophilia* a rear bacterium that is beneficial both as viable cell culture as well as its cell-free extracts or non viable cells. The use of non viable cells can stand as a unique dimension with less demand for cell maintenance in the management of wastewater to eliminate or at least, reduce the heavy metals especially discharged copper wastewater in the environment. Also, *Stenotrophomonas maltophilia* have been observed to play active roles in phyto-remediation of crude oil impacted soil. This attribute was closely connected with their nitrogen fixing potentials as all the bacteria isolated from the plants rhizosphere and used for the study were equally phyllospheric nitrogen-fixing (diazotrophic) bacteria, *Stenotrophomonas maltophilia* inclusive[64].

Genetic basis for the attributes of *Stenotrophomonas maltophilia*

Observed beneficial attributes of *Stenotrophomonas maltophilia* are orchestrated by inherent and acquired repository of genes[18,41,60], of which phenotypic expressions are primarily important for the survival of the bacterium in the natural environment. In terms of relatedness of some strains expressing these "wonders", Rocco *et al*.[65], observed that the chromosomes of *Stenotrophomonas maltophilia* K279a and R551-3 strains bear same GC content (67%), but different in length, i.e. K279a DNA has the length 4,851,126 bp while R551-3 DNA has 4,573,969 bp. This author further reported higher potential gene products in K279a than in R551-3. Meanwhile, the clusters of type I pili genome are distributed in a unique manner throughout the bacterial gene sequence. This may be interpreted as similar colonization strategies by *Stenotrophomonas maltophilia* in plants and animals. *Stenotrophomonas maltophilia* carries a number of biosynthetic genes for lipopolysaccharide and/or exopolysaccharide which include rmlA, rmlC and xanB[66]. The phenotypic expression of the genes in producing lipopolysaccharide, of course is imperative in cell function, cell integrity and bacterial adaptation, bringing about resistance to antibiotics and neutral detergents[67,68]. Some clusters of these genes (including the antimicrobial resistant genes) might have been transferred from other bacteria, even those belonging to distant species[18]. This is possible as many *Stenotrophomonas maltophilia* strains have been found to have identical BOX-PCR patterns with some endophytic isolates and acquire gene for the earlier observed beneficial attributes by horizontal transfer (HGT). A good example is trans-conjugation that has been observed in *Stenotrophomonas maltophilia* and *Enterobacter* sp[17].

With regards to antibiotic resistance genes, Alonso *et al*.[18] showed that a *Stenotrophomonas maltophilia* strain acquired a cluster of genes coding for antibiotic and heavy metal resistance from Gram positive bacteria. This was equally observed by Ojo *et al*.[69] in *Stenotrophomonas maltophilia* and two other Gram negative rod bacteria. *Stenotrophomonas maltophilia* is equally viewed as a reservoir for disseminating the resistance gene to other Gram negative rods. For example, Gordon and Wareham[70] following their observation of considerable diversity within plasmid-borne quinolone resistance gene, Smqnr alleles in *Stenotrophomonas maltophilia*, suggested that the bacterium might be a reservoir for the spread of quinolone resistant factor to the Enterobacteriacea family. Some schools of thought believe that commensal bacteria including *Stenotrophomonas maltophilia* are reservoir of antibiotic resistance genes[19,71], out of which some which are antibiotic producers are "developers" of antibiotic resistance and transfer same to pathogenic species by HGT. The presence of such large antibiotic resistance determinants and/or genes in soil actinomycetes was quoted as evidence to support their assertions[72,73].

For quinolone resistance, Hernandez *et al*.[74] noted that quite a number of "contributors" include protein protecting target sites, enzymes that modify fluoroquinolone and efflux pumps contribute immensely. Zhao and Drlica[75] and Drlica[76] showed mutation as the applicable yardstick to determine quinolone resistance measure. Quinolone resistance can be transferable being plasmid-borne. Fear correlation exists between the plasmid-borne quinolone resistance gene, Smqnr allele and quinolones resistance phenotype among the *Stenotrophomonas maltophilia* isolates[19,77]. Hence, the reservoir for quinolone-resistance genes and the risk of patients' compliance to antibiotics regimen in inducible antibiotic resistance in non-clinical environments is of immense interest to the clinical epidemiologist.

CONCLUSION

A careful consideration of the adaptation, 'prowess' and multitudinous applications of this bacterium reveal the inherent benefits and challenges. The attending challenges like concomitant production of toxic products and growing trend of pathogenicity should be tackled through a multidisciplinary approach. This step becomes imperative due to the active role the organism plays in nitrogen fixation, biodegradation, biological control, bioremediation and high potentials for use as a source of novel enzymatic activities in biotechnology. Also, how widespread the role of the bacterium is with regards to acting as reservoir of antibiotic resistance genes especially in underdeveloped countries should be of interest and is a subject of on-going investigation in our group.

REFERENCES

1. Bollet, C., Davin-Regli, A., De-Micco, P. A. Simple Method for Selective Isolation of *Stenotrophomonas maltophilia* from Environmental Samples. *Appl Environ Microbiol*., 1995; **61**(4): 1653–1654.
2. Mendoza, D.L., Darin, M., Waterer, G. W., Wunderink, R. G. Update on *Stenotrophomonas maltophilia* Infection in the ICU. *Clin Pulm Med*. 2007; **14**(1): 17-22.
3. Gnanasekaran, S., Bajaj, R. *Stenotrophomonas maltophilia* bacteremia in end-stage renal disease patients receiving maintenance hemodialysis. *Dial. Transpl*., 2009; **38**(1): 30–32.
4. Kim, J., Kim, S., Kang, H., Bae, G., Park, J., Nam, E., Kang, Y., Lee, J., Kim, N. Two Episodes of *Stenotrophomonas maltophilia* Endocarditis of Prosthetic Mitral Valve: Report of a Case and Review of the Literature. *J Kor Med Sci*., 2002; **17**: 263-5.
5. Pruvost C, May L, Davous N, *et al*.. Plantar pyoderma due to *Stenotrophomonas maltophilia*. Ann. Dermatol. Venereol., 2002; **129**: 886-887.
6. Talib, W.H., Mahasneh, A.M. Antimicrobial, Cytotoxicity and Phytochemical Screening of Jordanian Plants Used in Traditional Medicine. *Mol*, 2010; **15,** 1811-1824.
7. Gales, AC, Jones, RN, Forward, KR, Linares, J, Sader, HS, Verhoef, J. Emerging importance of multidrug-resistant *Acinetobacter* species and *Stenotrophomonas maltophilia* as pathogens in seriously ill patients: geographic patterns, epidemiological features, and trends in SENTRY antimicrobial surveillance program (1997–1999). *Clin Infect Dis*., 2001; 32: Suppl. 2, S104–S113.
8. Pathmanathan, A., Waterer, G.W. Significance of positive *Stenotrophomonas maltophilia* culture in acute respiratory tract infection. *Eur Respir J*. 2005; **25:** 911–914.
9. Zhang Z., Yuen G.Y. The Role of Chitinase Production by *Stenotrophomonas maltophilia* Strain C3 in Biological Control of *Bipolaris sorokiniana*. Papers in Plant Pathology. http://digitalcommons.unl.edu/plantpathpapers/191; 2000.
10. Idris H.A., Labuschagne N., Korsten, L. Screening rhizobacteria for biological control of Fusarium root and crown rot of sorghum in

Ethiopia. *Biol Contr*., 2007; **40**(1):97-106

11. Farzaneh, H., Fereidon, M., Noor, A., Naser, G. Biodegradation of dodecylbenzene solfonate sodium by *Stenotrophomonas maltophilia* Biofilm. *Afr J. Biotech*., 2010; **9**(1): 055-062
12. Borner, D., Marsch, W.C., Fischer, M. Necrotizing otitis externa caused by *Stenotrophomonas maltophilia*. *Hautarzt*. 2003; **54:** 1080-2.
13. Minkwitz, A., Berg, G., Comparison of antifungal activities and 16S ribisomal DNA sequences of clinical and environmental isolates of *Stenotrophomonas maltophilia*. *J Clin Microbiol*., 2001; 39, 139-145.
14. Newcombe, D., Stuecker, T., Duc, M. L., Venkateswaran, K. QPCR Based Bioburden Assessment of Drinking Water Throughout Treatment and Delivery to the International Space Station. *SAE Intern*., 2004; 051CES-57:1-11
15. Hartmann, A., Schmid, M., Van-Tuinen, D., Berg, G. Plant-driven selection of microbes. *Plant Soil* DOI 10.1007/s11104-008-9814-y; 2008; 1-24.
16. Ryan, R.P., Monchy, S., Cardinale, M., Taghavi, S., Crossman, L., Avison, M.B., Berg, G., van der Lelie, D., Dow, J.M. The versatility and adaptation of bacteria from the genus Stenotrophomonas. *Nat Rev Microbiol*., 2009; 7: 514–525.
17. Taghavi, S., Barac, T., Greenberg, B., Borremans, B., Vangronsveld, J., van der Lelie, D. Horizontal Gene Transfer to Endogenous Endophytic Bacteria from Poplar Improves Phytoremediation of Toluene. *Appl Environ Microbiol*., 2005; **71**(12): 8500-8505.
18. Alonso, A., Sanchez, P., Martínez, J.L. *Stenotrophomonas maltophilia* D457R Contains a Cluster of Genes from Gram-Positive Bacteria Involved in Antibiotic and Heavy Metal Resistance. *Antimicrob Agents Chemother*., 2000; 44(7): 1778–1782.
19. Sanchez , M.B., Hernandez , A. and Martinez, J.L. , Martinez-Martínez, L., Martinez, J. L. Predictive analysis of transmissible quinolone resistance indicates *Stenotrophomonas maltophilia* as a potential source of a novel family of Qnr determinants. *BMC Microbiol*., 2008, 8:148 doi:10.1186/1471-2180-8-148.
20. Shaw, L.J., Morris, P., Hooker, J.E. Perception and modification of plant flavonoid signals by rhizosphere microorganisms. Environ Microbiol., 2006; 8: 1867–1880.
21. Ozcelik, B., Orhan, D.D., Ozgen, S., Ergun, F. Antimicrobial Activity of Flavonoids against Extended-Spectrum -Lactamases (ESBLs)-Producing *Klebsiella pneumonia*. *Trop. J.Pharm Res*., 2008; 7 (4): 1151-1157.
22. Adegoke, A.A., Adebayo-tayo, B.C. Antibacterial activity and phytochemical analysis of leaf extracts of *Lasienthera africanum*. *Afric J Biotech*., 2009; 8 (1): 077-080.
24. Siddiqi, R,. Naz S. Ahmad, S., Sayeed, S. A. Antimicrobial activity of the polyphenolic fractions derived from *Grewia asiatica, Eugenia jambolana* and *Carissa carandas*. *Int. J.Food Sc Tech*., 2011; 46, 250–256.
25. Krzewinski JW, Nguyen CD, Foster JM, *et al*. Use of random amplified polymorphic DNA PCR to examine the epidemiology of *Stenotrophomonas maltophilia* and A*chromobacter* (Alcaligenes) *xylosoxidans* from patients with cystic fibrosis. *J Clin Microbiol*., 2001; 39:3597–3602.
26. Elvers K.T., Leeming K., Lappin-Scott H.M. Binary culture biofilm formation by *Stenotrophomonas maltophilia* and *Fusarium oxysporum*. *J. Ind. Microbiol. Biotechnol*., 2001; 26:178–183.
27. Du Z., Huang X., Wang K., Deng Y., Chen D., Geng Y., Su Pathology of extracellular protease of *Stenotrophomonas maltophilia* isolated from channel catfish (*Ictalunes punctatus*) to mice. *African J. Biotech*., 2011; **10**(10): 1953-1958.
28. Robinson, M. J., Martin, B. A., Gootz, T.D., Mcguirk, P.R., Osheroff, N. Effects of Novel Fluoroquinolones on the Catalytic Activities of Eukaryotic Topoisomerase II: Influence of the C-8 Fluorine Group. *Antimicrob Agents Chemotherap*., 1992; **36**(4): 751-756.
29. Harris, N. B., Rogers, D. G. Septicemia associated with *Stenotrophomonas maltophilia* in a West African dwarf crocodile (*Osteolaemus tetraspis* subsp. tetraspis). *Vet Diagn Invest*., 2001; **13:** 255–258.
30. Botes E., Van-Heerden, E., Litthauer D. Hyper-resistance to arsenic in bacteria isolated from an antimony mine in South Africa. *S. Afr J Sc*., 2007; 103: 279-282.
31. Oliveira-Garcia D, Dall'Agnol M, Rosales M. Fimbriae and adherence of *Stenotrophomonas maltophilia* to epithelial cells and to abiotic surfaces. *Cell Microbiol*. 2003; 5: 625-36.
32. Schreiber, L., Krim, U., Knoll, D., Sayed, M., Auling, G., Kroppensteadt, R.M. Plant–microbe interactions: identification of epiphytic bacteria and their ability to alter leaf surface permeability. *New Phytol*. 2005; 166, 589–594.
33. Krimm, U., Abanda-Nkpwatt, D., Schwab, W., Schreiber, L. (2005). Epiphytic microorganisms on strawberry plants (*Fragaria ananassa* cv.

Elsanta): identification of bacterial isolates and analysis of their interaction with leaf surfaces. *FEMS Microbiol. Ecol*., 2005; 53(3): 483–492.

34. Wilson, M., Lindow, S.E. Coexistence among Epiphytic Bacterial Populations Mediated through Nutritional Resource Partitioning. Appl Environ Microbiol., 1994; **60**(12): 4468-4477.
35. Zhang Z., Yuen G.Y. Biological Control of Bipolaris sorokiniana on Tall Fescue by *Stenotrophomonas maltophilia* Strain C3. *The Am Phytopathol. Soc*., 1999; 89(9): 817-822.
36. Giesler, L.J. and Yuen, G.Y. (1998). Evaluation of *Stenotrophomonas maltophilia* strain C3 for biocontrol of brown patch disease. *Crop Protect*., 1998; **17**(6): 509-513.
37. Messiha, N. A. S., van Diepeningen, A. D. , Farag, N. S., Abdallah, S. A., Janse J. D., van-Bruggen, A. H. C. *Stenotrophomonas maltophilia*: a new potential biocontrol agent of Ralstonia solanacearum, causal agent of potato brown rot. *Eur J Plant Pathol.,* 2007; **118:** 211-225.
38. Zhang, Z., Yuen, G.Y., Sarath, G., Penheiter, A.R. Chitinases from the Plant Disease Biocontrol Agent, *Stenotrophomonas maltophilia* C3. *Phytopathol*., 2001; **91**(2): 204-211.
39. Jorquera, M., Martínez, O., Maruyama, F., Marschner, P., Mora, M.L. Current and future biotechnological applications of bacterial phytases and phytase–producing bacteria. *Microb Environ.,* 2008; **23:** 182–191.
40. Kobayashi, D. Y., Guglielmoni, M., Clarke, B. B.. Isolation of the chitinolytic bacteria *Xanthomonas maltophilia* and *Serratia marcescens* as biological control agents for summer patch disease of turfgrass. *Soil Biol. Biochem*., 1995; **27:** 1479–1487.
41. Kobayashi, D. Y., Reedy, R. M., Bick, J.A., Oudemans, P. V. Characterization of a Chitinase Gene from *Stenotrophomonas maltophilia* Strain 34S1 and Its Involvement in Biological Control. *Appl. Environ Microbiol.,* 2002; **68**(3): 1047–1054.
42. Dungan R.S., Yates S.R., Frankenberger W.T. Transformations of selenate and selenite by *Stenotrophomonas maltophilia* isolated from a seleniferous agricultural drainage pond sediment. *Environ Microb*., 2003; **5**(4), 287–295.
43. Park, M., Kim, C., Yang, J., Lee, H., Shin, W., Kim, S., Sa, T.M. Isolation and characterization of diazotrophic growth promoting bacteria from rhizosphere of agricultural crops of Korea. *Microbiol Res.,* 2005; **160:** 127–133.
44. Suckstorff, I., Berg G. Evidence for dose-dependent effects on plant growth by Stenotrophomonas strains from different origins. *J. Appl. Microbiol*., 2003; **95:** 656-663.
45. Vessey, J.K. Plant growth promoting rhizobacteria as biofertilizers, *Plant Soil*, 2003; **255:** 571–586.
46. Lim, B.L., Yeung, P., Cheng, C., Hill, J. E. Distribution and diversity of phytate-mineralizing bacteria. *The ISME Journal*, 2007; **40**(1): 321–330.
47. Xiao, C., Chi, R., He, H., Zhang, W. Characterization of tricalcium phosphate solubilization by *Stenotrophomonas maltophilia* YC isolated from phosphate mines. *J. Cent. South Univ. Technol.*, 2009; **16:** 0581-0587.
48. Valencia-Cantero, E., Hernández-Calderón, E., Velázquez-Becerra, C., López-Meza, J. E., Alfaro-Cuevas, R., López-Bucio, J. Role of dissimilatory fermentative iron-reducing bacteria in Fe uptake by common bean (*Phaseolus vulgaris L.*) plants grown in alkaline soil. *Plant Soil*, 2007; **291:** 263–273.
49. Oh, B.C., Choi, W.C., Park, S., Kim, Y.O., Oh, T.K. Biochemical properties and substrate specificities of alkaline and histidine acid phytases. *Appl Microbiol Biotechnol.,* 2004; **63:** 362–372.
50. Choi, Y.M., Suh, H.J., Kim J.M. Purification and properties of extracellular phytase from Bacillus sp. KHU-10. *J. Prot. Chem*., 2001; **20:** 287-292.
51. Sajidan, A., Farouk, A., Greiner, R., Jungblut, P., Müller, E.-C., Borriss, R., Molecular and physiological characterization of a 3-Phytase from the *Rhizobacterium Klebsiella pneumoniae* ASR1. *Appl. Microbiol. Biotechnol*., 2004; http://dx.doi.org/10.1007/s00253-003-1530-1
52. Kim, H.-W., Kim, Y.-O., Lee, J.-H., Kim, K.-K., Kim, Y.-J., Isolation and characterization of a phytase with improved properties from *Citrobacter braakii*. *Biotechnol. Lett*., 2003; **25:** 1231-1234.
53. Ryu, H.W., Kim, S.J., Cho, K., Lee, T.H. Toluene Degradation in a Polyurethane Biofilter at High Loading. *Biotech and Bioproc Eng*., 2008; **13:** 360-365.
54. Juhasz, A.L., Naidu, R. Bioremediation of high molecular weight polycyclic aromatic hydrocarbons: a review of the microbial degradation of benzo[a]pyrene. *Intern Biodeter & Biodeg*., 2000; **45:** 57-88.
55. Lee, SR, Park, HM, Lim, H, Kang, T, Li, X, Cho, WJ and Ha, CS. Microstructure, tensile properties and biodegradability of aliphatic polyester/clay nanocomposites. *Polymer,* 2002; **43:** 2495-2500.
56. Mohammed, M.S. Degradation of methomyl by the novel bacterial strain *Stenotrophomonas*

maltophilia M1. Electronic *J. Biotechnol.,* 2009; **12**(4): http://www.scielo.cl/pdf/ejb/v12n4/a06.pdf.

57. Guan, S., Ji, C., Zhou, T., Li, J., Ma, Q., Niu T. Aflatoxin B1 Degradation by *Stenotrophomonas maltophilia* and Other Microbes Selected Using Coumarin Medium. *Int J Mol Sci*. 2008; **9**(8): 1489-1503.
58. Gilliom, R., Barbash, J., Kolpin, D., Larson, S. Testing water quality for pesticide pollution. *Environ Sci Technol.,* 1999; **33:** 164–169.
59. Gren, I., Wojcieszynska, D., Guzik, U., Perkosz, M., Hupert-Kocurek, K. Enhanced biotransformation of mononitrophenols by *Stenotrophomonas maltophilia* KB2 in the presence of aromatic compounds of plant origin. *W. J Microbiol and Biotech*., 2010; 26(2): 289-295.
60. Zhao, X. H., He, X., Wang, J. H. Biodegradation of Swainsonine by *Stenotrophomonas maltophilia* Strain YLZZ-2 and its Isolation and Identification. *Adv Material Sci* 2011; 178: 59-64.
61. Vallini, G., Di Gregorio, S., Lampis, S. Rhizosphere-induced selenium precipitation for possible applications in phytoremediation of se polluted effluents. *Z Naturforsch C*. 2005; 60(3-4):349-56.
62. Antonioli, P., Lampis, S., Chesini, I., Vallini, G., Rinalducci, S., Zolla, L., Righetti, P.G. *Stenotrophomonas maltophilia* SeITE02: a new bacterial strain suitable for bioremediation of selenite-contaminated environmental matrices. *Appl. Environ. Microbiol.* 2007; doi:10.1128/AEM.00957-07
63. Ting A.S.Y. and Choong C.C. Utilization of Non-viable Cells Compared to Viable Cells of *Stenotrophomonas maltophilia* for Copper (Cu(ii)) Removal from Aqueous Solutions. *Adv. Environ. Biol*., 2009; 3(2): 204-209.
64. Al-Awadhi, H., El-Nemr, I., Mahmoud, H., Sorkhoh, N.A., Radwan, S.S. Plant- associated bacteria as tools for the phytoremediation of oily nitrogen-poor soils. *Intern. J. Phytoremed*., 2009; 11:11–27.
65. Roccoa, F., De-Gregorioa, E., Colonnab, B., Di Nocera, P. P. *Stenotrophomonas maltophilia* genomes: A start-up comparison. *Intern J Med Microb*., 2009; **299**(8): 535-546.
66. Huang, T.P., Somers, E.B., Wong, A.C.L. Differential biofilm formation and motility associated with lipopolysaccharide/exopolysaccharide-coupled biosynthetic genes in *Stenotrophomonas maltophilia*. *J. Bacteriol*., 2006; 188, 3116–3120.
67. Michel, G., Ball, G., Goldberg, J. B., Lazdunski, A. Alteration of the lipo-polysaccharide structure affects the functioning of the Xcp secretory system in *Pseudomonas aeruginosa*. *J. Bacteriol.* 2000; 182: 696–703.
68. Poole, K. Outer membranes and efflux: the path to multidrug resistance. in gram-negative bacteria. *Curr. Pharm. Biotechnol*., 2002; **3:** 77–98.
69. Ojo, K. K., Ruehlen, N.L., Close, N.S., Luis, H., Bernardo, M., Leitao, J., Robert, M.C. The presence of a conjugative Gram-positive Tn2009 in Gram-negative commensal bacteria. *J. Antimicrob Chemother.*, 2006; **57:** 1065–1069.
70. Gordon, N. C., Wareham, D. W. Novel variants of the Smqnr family of quinolone resistance genes in clinical isolates of *Stenotrophomonas maltophilia*. *J Antimicrob Chemother.,* 2010; **65:** 483–489
71. Knezevic, P., Petrovica, O. Antibiotic resistance of commensal *Escherichia coli* of food-producing animals from three Vojvodinian farms, Serbia. *Inter J. Antimicrob Agts*., 2008; **34**(8): 360-363.
72. D’Costa, V. M., McGrann, K. M., Hughes, D. W., Wright, G. D. Sampling the antibiotic resistome. *Sc*., 2006; **311:** 374–377.
73. Wright, G. D. The antibiotic resistome: the nexus of chemical and genetic diversity. *Nat. Rev. Microbiol*., 2007; **5:** 175–186.
74. Hernández, A., Sánchez, M.B., Martínez, J.L. Quinolone resistance: much more than predicted. Frontier in Antimicrob Res and Chemotherap. 2011. http://www.frontiersin.org/antimicrobials,resistance_and_chemotherapy/10.3389/fmicb.2011.00022/full.
75. Zhao, X., Drlica, K. Restricting the selection of antibiotic-resistant mutants: a general strategy derived from fluoroquinolone studies. *Clin. Inf. Dis*., 2001; **33**(Suppl. 3): S146-S157.
76. Drlica, K. The mutant selection window and antimicrobial resistance. *J. Antimicrob. Chemother.*, 2003; **52:** 11-17
77. Sanchez , M.B., Hernandez , A., Martinez, J.L. *Stenotrophomonas maltophilia* drug resistance. *Fut Microbiol*., 2009; **4**(6): 655-660.