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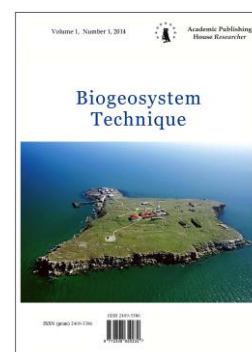
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Benzo(a)pyrene Uptake by Spring Barley Plants in Model Vegetation Experiment

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Abstract

Polycyclic aromatic hydrocarbons (PAHs) are common environmental pollutants. They are formed by incomplete combustion of organic materials (coal, wood, oil and petroleum products). The most dangerous compound among PAHs is benzo(a)pyrene (BaP), as it is a carcinogen and a class 1 mutagen and must be controlled in all natural environments. The aim of this study was to evaluate the accumulation of BaP in soil and plants under the conditions of a model vegetation experiment. The object of the study was spring barley, which was grown under the conditions of a model vegetation experiment, the soil of which was contaminated with various doses of BaP. The soil of the model experiment was incubated under conditions close to natural on the experimental site of the Southern Federal University (Russia, SFU) for 36 months. PAHs were extracted from soil samples using the ecologically clean express method of subcritical water extraction. The concentration of priority PAHs in soil samples was determined, and the concentration of BaP in the vegetative and root parts of barley plants was also determined. During 3 years of the experiment, there was a decrease in the concentration of PAHs in soil samples. The content of BaP in the soil and its accumulation in barley plants decreased during 3 years from the initial contamination.

Keywords: benzo(a)pyrene, PAHs, model experiment, soil contamination, spring barley, soil plant system, accumulation, migration, transformation, toxic effect.

1. Introduction

Long-term studies have made it possible to designate such a dangerous compound as benzo(a)pyrene (BaP), which requires measures for constant monitoring and regulation of its

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content in environmental objects, due to its extreme toxicity. (Tobiszewski, Namieśnik, 2012; Wenzl et al., 2006). Getting to the soil surface as a pollutant, BaP is included in the soil-plant system and migrates along the soil profile. Among the class of polycyclic aromatic hydrocarbons (PAHs), BaP is one of the most dangerous compounds, a carcinogen and a class I mutagen. The background values of the BaP content in ordinary chernozem and plants are 15-20 ng/g, which in turn is justified by the special physicochemical properties of organic substances in the chernozem, as well as by the specific composition of soil microorganisms (Kasimov et al., 2016; Sushkova et al., 2017). Polyaromatic hydrocarbons (PAHs) are usually present in water, air, soil, food and living organisms and persist in the environment for a long time (El-Shahawi et al., 2010). PAHs are relatively inert compounds that are resistant to various degradation processes, and therefore it is usually assumed that they are stable in the environment (Liu et al., 2005). Plants are an integral component of terrestrial ecosystems and are exposed to the entire group of pollutants, and almost 45% of all PAHs released into the environment end up in plants (Eisler, 1987; Huang et al., 2004). The complex of interaction of soils and plants is an important object of environmental pollution control by BaP. Since soils and plants function in close relationship with each other, a whole system arises that links the processes of accumulation and transformation of BaP in soils and plants (Yakovleva et al., 2008). Plants react very quickly to the presence of PAHs, as they influence primary and secondary processes (Tomar et al., 2004). The effect of each PAH can be specific for different plant species and even varieties (Simonich, Hites, 1995). The assimilating organs of plants are a regulatory link in the functioning of the whole organism; they are highly sensitive and stable in response to the action of external factors (Glinushkin, 2008). The carcinogenic effect of BaP consists in the interaction of its metabolites with proteins and nucleic acids, which causes disturbances leading to the transformation of normal cells into tumor cells (Kireeva et al., 2009). The ability of BaP to accumulate in plants and migrate in the soil depends mainly on the sorption properties of the soil matrix, as well as on its physicochemical properties, first of all, its water solubility and the ability to pass into the soil solution (Gennadiev, Tsibart, 2013; Belykh, 2009).

The aim of the study was to evaluate the benzo(a)pyrene uptake by spring barley plants the conditions of a model vegetation experiment.

2. Research objects

In the experiment, it was used soil and plant samples taken from the top soil layer of 0-20 cm in the virgin area of the Persianovskiy soil nature reserve. The studied soil is Haplic Chernozem with the following characteristics: physical clay content – 52%, silt – 30%, humus – 4.2%, pH_{water} – 7.5, CaCO_3 – 0.4%, CEC – 33.0 cmol (+)/kg. The enzymatic activity of the studied soil was determined: catalase – 4.0 ± 0.3 ml O_2 /g, urease – 5.6 ± 5.0 mg NH_4^+ /10 g, invertase – 1.45 ± 0.09 mg glucose/g. Respiration of soil – 0.11 mg CO_2 /g per day. The initial number of different groups of microorganisms in the soil, assessed by the method of seeding on selective media: heterotrophs – $3.7 \pm 0.5 \times 10^6$ /g; actinomycetes – $4.5 \pm 0.04 \times 10^5$ /g, micromycetes – $3.8 \pm 0.1 \times 10^4$ /g.

Conditions for the vegetation experiment. The studies were carried out under the conditions of a vegetation experiment. The soil was sifted through a sieve with a diameter of 1 mm and placed in 2 kg pots in 4l pots. A solution of BaP in acetonitrile was added to the soil surface based on the creation of a pollutant concentration in the soil of 20, 200, 400, and 800 $\mu\text{g}/\text{kg}$, which corresponds to 1, 10, 20, and 40 MPC. The initial soil and the soil supplemented with pure acetonitrile were used as controls. The experiment was repeated three times. The incubation of the soil in the vessels took place in conditions close to natural conditions, on the territory of a special experimental site of the Southern Federal University for 36 months. To maintain the optimal amount of moisture in the incubation vessels, the soil was watered with distilled water. 1 and 2 years after the start of incubation, the vessels were inoculated with a test culture of spring barley of the "Odessky-100" variety. After 12, 24 and 36 months, before sowing spring barley, a heart sample was taken after stirring it in vessels. In the samples of the initial and incubated soil, the content of BaP was determined at the indicated time by HPLC with preliminary sample preparation of soil samples by subcritical water extraction. Barley plants that were removed from the vessel were cleaned of soil particles, washed with water, dried, weighed, crushed, sieved through a sieve. 1 mm and used the middle sample for analysis. The content of BaP was determined in them by subcritical water extraction.

3. Materials and methods

Soil samples were taken annually and prepared for chemical analysis in accordance with the requirements (GOST, 1986; ISO, 2005). To extract BaP from soil and plant samples, we used the method of extraction with subcritical water (Lekar et al., 2014; Sushkova et al., 2014). Whole barley plants grown in the control background soil were used as a plant sample.

The sequence of the analysis. A weighed portion of a specially prepared soil or plant sample weighing 1 g, sifted through a 1 mm sieve, was placed in a stainless steel extraction cartridge (Sushkova et al., 2014) and hermetically tightened with bolts from both sides. The cartridge was installed in a thermostat and heated to 250°C and a pressure of 100 atm within 30 minutes. After cooling the system, the cartridge was unscrewed, the contents were filtered two or three times until the solution became clear. The resulting aqueous extract was mixed with 5 ml of n-hexane (analytical grade) and placed on a mechanical shaker for 15 minutes. Separation of layers was carried out on a 50 ml separating funnel sequentially in three stages with another portion of hexane. The combined hexane extract was passed through a funnel with anhydrous sodium sulfate into a clean dry round-bottom flask, evaporated on a rotary evaporator at a water bath temperature of 40°C to dry residue. The resulting dry residue was dissolved in 1 ml of acetonitrile with stirring for 30 minutes.

The quantitative determination of BaP in extracts was carried out by high performance liquid chromatography (HPLC) on an AGILENT 1260 instrument. The BaP peak in the chromatogram of the soil extract was identified by comparing the retention time of BaP in the analysis of the extract and the standard sample with simultaneous detection on two detectors. This makes it possible to identify the BaP peak with a sufficiently high degree of reliability and more accurately determine its concentration in the extract. The BaP content in the analyzed samples was calculated using the external standard method. The BaP content in the soil was calculated using the formula:

$$C_n = k \times S_i \times C_{st} \times V / (S_{st} \times m),$$

where C_n is the BaP content in the soil sample ($\mu\text{g}/\text{kg}$); k is the coefficient of extraction of BaP from the sample; S_i and S_{st} are the BaP peak areas of the standard solution and sample; C_{st} is the concentration of a standard BaP solution ($\mu\text{g}/\text{ml}$); V is the volume of the acetonitrile extract (ml); m is the mass of the sample (g).

4. Results and discussion

PAH content in soil and plants of a model vegetation experiment for 3 years

The concentration of priority PAHs in the soil of the model experiment was determined in the first year of the experiment (Figure 1), in the second year (Figure 2) and in the third year (Figure 3).

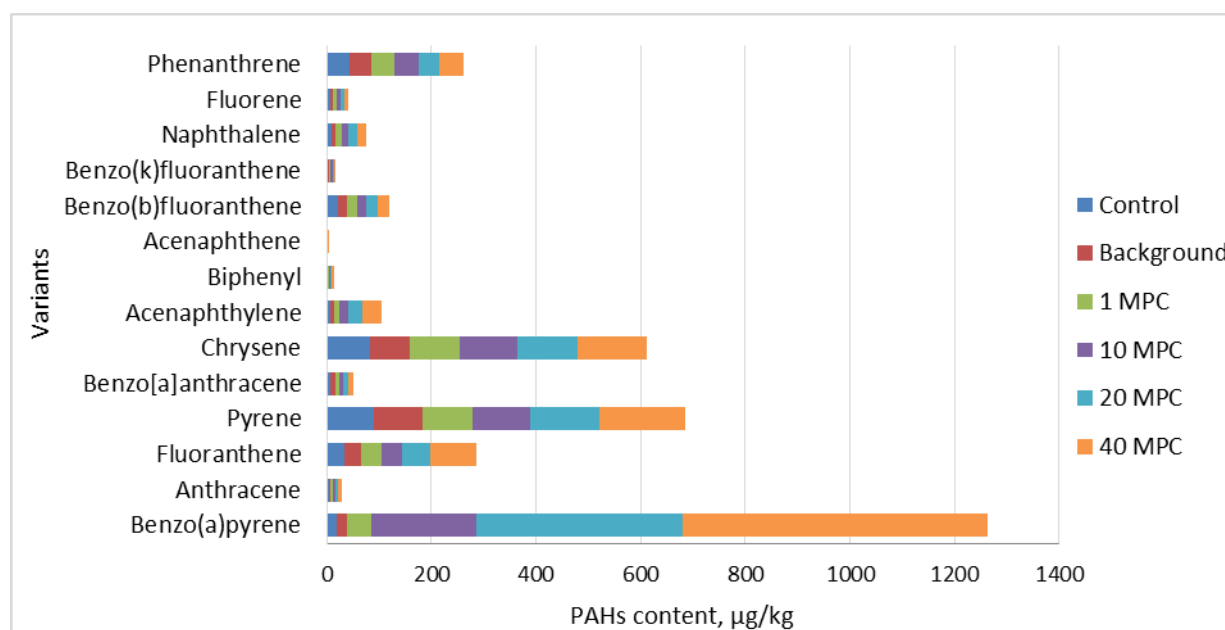


Fig. 1. The content of PAHs in the soil of the model experiment in the 1st year

The control sample and the background sample contained a small amount of such PAHs as phenanthrene, chrysene and pyrene in concentrations equal to 42.4-43.6; 76.3-82.1 and 90.1-92.3 $\mu\text{g}/\text{kg}$, respectively. In the sample with the introduction of 1 MPC BaP, only the concentration of BaP changed, the concentration of the remaining PAHs did not change relative to the control values. With the introduction of 10 MPC, the concentration of BaP in the sample increased, and the concentration of chrysene and pyrene also increased to 109 $\mu\text{g}/\text{kg}$ relative to the control. A similar increase in the concentration of chrysene and pyrene occurred in the samples with the addition of 20 and 40 MPC BaP, but with the introduction of 40 MPC, the concentration of fluoranthene increased up to 82 $\mu\text{g}/\text{kg}$ by 3 times relative to the control values.

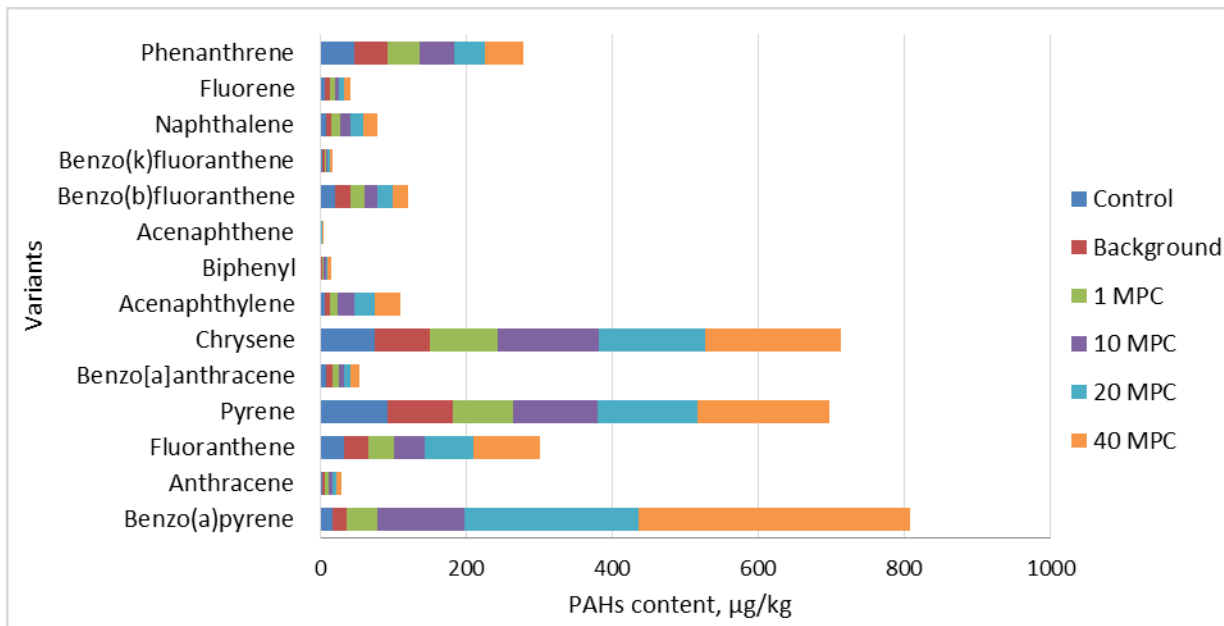


Fig. 2. PAH content in the soil of the model experiment in the 2nd year

In the second year of the experiment, the BaP was observed to decrease in content in relation to the first year of the study. In the sample with 1 MPC BaP, changes in the concentration of Other PAHs are not significant. However, in the samples with the introduction of 10, 20 and 40 MPC, with a decrease in the concentration of BaP, the concentration of chrysene increased by 26.9-40 % and the concentration of pyrene by 3-9 % relative to the first year, as well as in the sample with the introduction of 40 MPC of BaP, the concentration of fluoranthene increased by 6 %. In the control and background samples, no changes in the concentration of PAHs were observed.

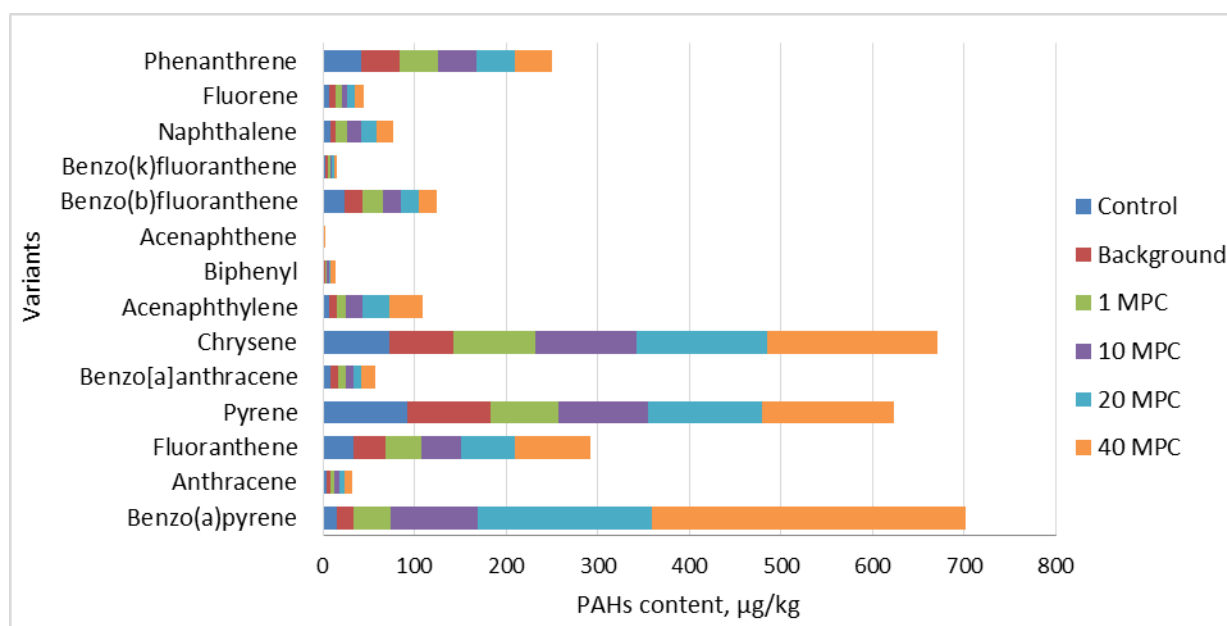


Fig. 3. PAH content in the soil of the model experiment in the 3rd year

In the third year of the experiment, similar to the second year, there was a decrease in the concentration of BaP in the samples, but in all samples there was a decrease in the concentration of the remaining PAHs, approximately to the level of concentration in the first year of the study.

The concentration of BaP in the soil of the model experiment was determined for three years (Figure 4).

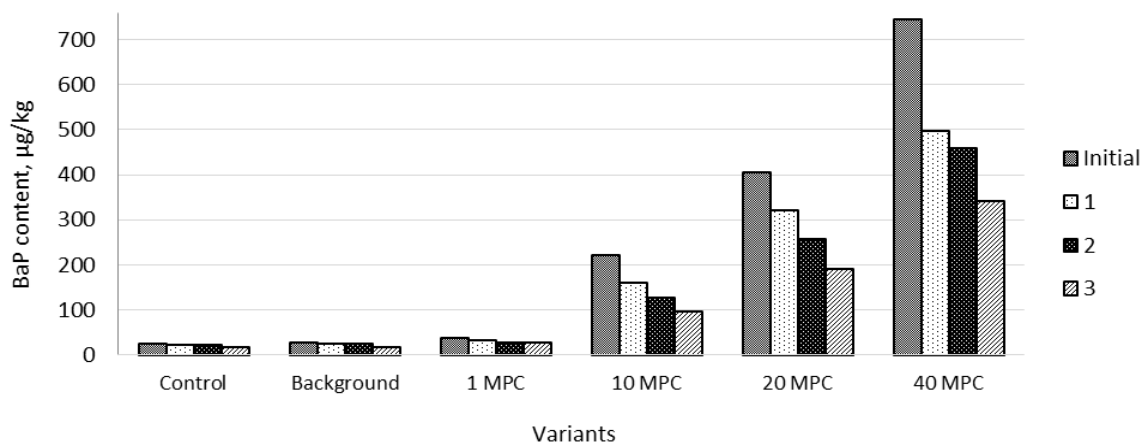


Fig. 4. Concentration of BaP in the soil of the model experiment for three years

In the initial soil in the control sample and with the addition of acetonitrile (background), the concentration of BaP was at the level of 24.3 and 27.2 µg/kg, respectively. With the introduction of 1 MPC BaP, the concentration increased to 45.4 µg/kg. In samples with 10, 20, and 40 MPC BaP, the concentration of the pollutant increased to 221, 406, and 743.4 µg/kg, respectively.

In the first year of the experiment, the concentration of BaP slightly decreased in the control and background samples to 21 µg/kg in the control and to 25 in the background. Also, a slight decrease in the concentration of BaP occurred in the sample with the addition of 1 MPC BaP up to 31 µg/kg. More significant reductions occurred in samples with 10, 20 and 40 MPC BaP to values equal to 159, 321, and 497 µg/kg, respectively.

In the second and third years, there was a gradual decrease in the concentration of BaP. During the second year of the experiment, a significant decrease in the concentration of BaP occurred in the samples with the introduction of 10, 20, and 40 MPCs of BaP to values of 127, 256,

and 458 $\mu\text{g}/\text{kg}$, respectively, and in the third year, the concentration of BaP in these samples decreased to 95, 190, and 342 $\mu\text{g}/\text{kg}$, respectively. In the second year of the experiment, no significant decrease in the concentration of BaP was found in the control and background samples, and in the third year, the values decreased to 15 $\mu\text{g}/\text{kg}$ in the control and 17 in the background samples. In the sample with the introduction of 1 MPC BaP, the concentration of BaP in the second year decreased to 27 and in the third year did not change and does not differ significantly.

We obtained data on the concentration of BaP in the roots (Figure 5) and vegetative part of the plants (Figure 6) for three years of the experiment. In the vegetative part, the concentration of BaP was lower than in the root part. The increase in the accumulation of BaP occurred in proportion to the increase in its concentration in the soil of the model experiment. The minimum accumulation of the pollutant in plant parts was observed in the control sample and reached values equal to 0.8 $\mu\text{g}/\text{kg}$ in the roots and 0.3 $\mu\text{g}/\text{kg}$ in the vegetative part, and the maximum in the sample with the introduction of 40 MPC BaP in the first year of the experiment and reached 23.4 $\mu\text{g}/\text{kg}$ in the root and 12.4 $\mu\text{g}/\text{kg}$ in the vegetative.

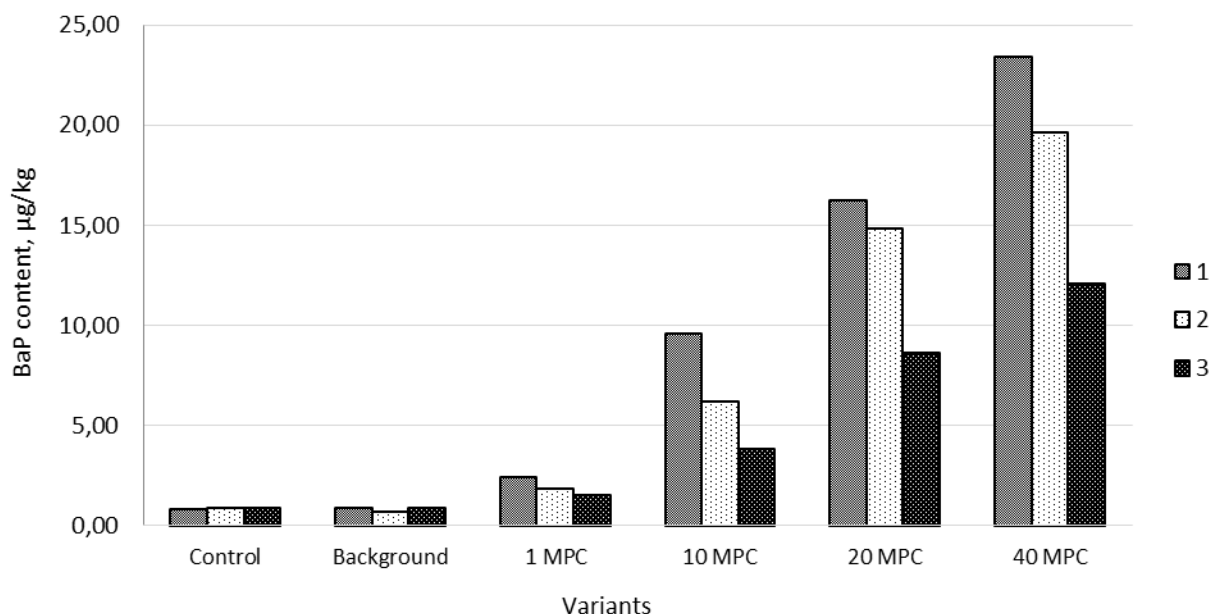


Fig. 5. Concentration of BaP in barley roots for three years

In the first year of the experiment, 0.8 and 0.9 $\mu\text{g}/\text{kg}$ BaP were found in the plant roots in the control sample and the sample with the addition of acetonitrile. When 1 MPC BaP was introduced into the soil, 2.4 $\mu\text{g}/\text{kg}$ BaP accumulated in the roots, which is higher than the control values. With an increase in the dose of introduced BaP to 10, 20 and 40 MPC, BaP accumulated in plant roots in values equal to 9.6, 16.2, and 23.4 $\mu\text{g}/\text{kg}$, these values are 12.20 and 29 times higher than the values obtained in the control sample.

In the second and third years of the experiment, the accumulation of BaP by the roots decreased. Thus, in the sample with the introduction of 1 MPC BaP in the second year, the accumulation in the roots decreased to 1.8 $\mu\text{g}/\text{kg}$ of BaP, and in the third to 1.5 $\mu\text{g}/\text{kg}$, which is comparable to the control. In samples with doses of BaP introduced at 10.20 and 40 MPC, the accumulation of BaP by plant roots decreased and reached values in the second year: 6.2; 14.8 and 19.6 $\mu\text{g}/\text{kg}$, and in the third year, values were obtained equal to 3.8; 8.6 and 12.1 $\mu\text{g}/\text{kg}$, respectively.

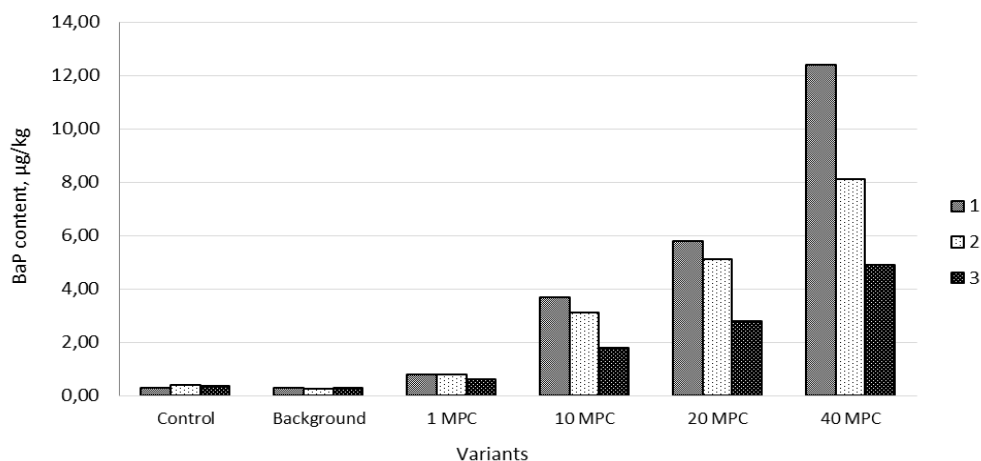


Fig. 6. Concentration of BaP in the vegetative part of barley for three years

In the first year of the experiment in the vegetative part of the plants in the control sample and with the addition of acetonitrile, the BaP content was 0.3 and 0.28 µg/kg, respectively. The accumulation of BaP in the vegetative part in the sample with the addition of 1 MPC BaP to 0.8 µg/kg slightly increased from the control. However, in the samples with the introduction of increased doses of BaP equal to 10, 20 and 40 MPC, the accumulation in the vegetative part of the plant reached values equal to 3.7; 5.8 and 12.4, which are 12, 19 and 41 times higher than the control values, respectively.

Thus, in the second and third years of the experiment, the values of BaP accumulation in the vegetative part of plants decreased in the samples with the addition of 10, 20, and 40 MPCs for BaP. In the second year, the values dropped to 3.1; 5.1 and 8.1 µg/kg, and in the third year up to 1.8; 2.8 and 4.9 µg/kg, respectively. In the control sample, in the sample with the addition of acetonitrile, and in the sample with the addition of 1 MPC of BaP, no significant differences were found in the accumulation of BaP in the vegetative part of the plants.

5. Conclusion

For the first time, the features of accumulation, migration and transformation of benzo(a)pyrene (BaP) in the soil-plant system were studied using original methods of analysis under the conditions of a unique model experiment with ordinary carbonate chernozem contaminated with BaP. This model can be used to predict the situation in different regions prone to contamination with such hazardous organic pollutants as PAHs, as well as to assess the likelihood of PAH accumulation in plants and their involvement in the food chain.

The concentration of priority PAHs in the soil of the model experiment was determined. During the three years of the experiment, the total concentration of PAHs in the soil in the control and with the addition of acetonitrile (background) was in the range of 382-327 and 379-322 µg/kg, respectively. In the sample with the introduction of 1 MPC BaP, the concentration of PAHs was 445-363 µg/kg, and with the introduction of large doses of PAHs, such as 10, 20 and 40 MPC, the concentration of PAHs was within the limits of 666-476, 920-658 and 1234-920 µg/kg, respectively.

6. Acknowledgements

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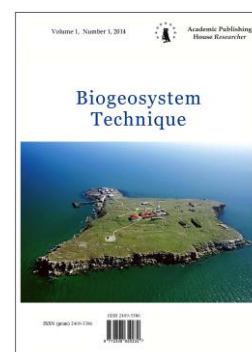
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Assessment of South Russia Arid Soils Resistance to Gasoline Contamination Using Biological Indicators

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Abstract

Arid ecosystems occupy a significant part of the world's ecosystems and play important role in the biodiversity and stability of natural ecosystems. At the same time, Soils of arid ecosystems significantly differ in their ecological and genetic properties, and, accordingly, in their resistance to chemical pollution. It has been established that the soil pollution of arid ecosystems by gasoline in Russia leads to decrease the biological activity: Inhibition of enzyme activity (activity of catalase and dehydrogenases), decrease the general number of bacteria in the soil, decrease the galore of bacteria of genus *Azotobacter* in the soil, phytotoxic properties, cellulolytic ability. In most cases, there is a significant decrease in all the studied parameters. The degree of decrease depends on the concentration of gasoline in the soil. The obtained sequence of arid soils resistance of the south of Russia to gasoline pollution: ordinary chernozem (haplic chernozem loamic) > chestnuts soils (haplic kastanozems chromic) > dark chestnuts soils (haplic kastanozems chromic) ≥ light chestnuts soils (haplic kastanozems chromic) ≥ sandy soils (calcaric arenosols) ≥ brown semi – desert soils (haplic calcisols) > solonetz medow (gleyic solonetz albic) > shor solonchaks (puffic solonchaks aridic).

Used in the study indicators of the soil biological state can be recommended for forecasting, assessment and control of chemical contamination of arid soils. Based on the assessment of soil ecological functions violation in oil industry, the quantitative regional standards landmarks were developed of the maximum permissible gasoline concentrations (MPC) in arid soil.

Keywords: arid soils, bio-testing, chestnut soil, sandy soil, gasoline, maximum permissible concentrations, pollution.

1. Introduction

High rate industrial activity increase demand for energy sources. This increases the oil extraction and production to meet the world energy needs. The number of cases The soil contamination with oil hydrocarbons is also growing (Engelking, 2000; Marinescu et al., 2010).

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During the oil extraction, transportation, distillation, and in result of accidents on pipelines, up to ten million tons of oil hydrocarbons are lost. The oil and oil products spill creates a constant threat for agriculture and forestry (Ogri, 2001; Agbogidi, 2003). Soil contamination by oil and oil products destroys the physical (Marin-Garcia et al., 2016; Gordon et al., 2018), chemical (Benka-Coker & Ekundayo, 1995) and biological (Agbogidi et al., 2003, 2007; Onwurah et al., 2007; Samedov et al., 2011; Singh et al., 2012; Golan et al., 2016; Girsowicz et al., 2018) soil properties, reduces fertility, and deteriorates the state of terrestrial ecosystems as a whole (Grechishcheva, Meshcheryakov, 2001; Ogri, 2001; Khalilova, 2015).

Unfortunately, soil pollution with oil and oil products, including gasoline, is common on the territory of the South Russia. Arid ecosystems have vast natural resources. Large reserves of hydrocarbons are located in the Volgograd, Astrakhan regions, in the Krasnodar Territory, Ingushetia Republic, and Chechen Republic. Oil production and supply increase can lead to soil pollution (Otchet o nauchno-proizvodstvennoi..., 2016). To maintain the biological diversity and stability of natural ecosystems, it is important to preserve the soil in the arid ecosystems (Zasolennye pochvy Rossii, 2006; Khalilova, 2015; Girsowicz et al., 2018).

On the territory of arid ecosystems in the South of Russia, there are zonal chestnut and brown semi-desert soils, as well as intrazonal sandy brown semi-arid soils (Natsional'nyi atlas..., 2011). The soils significantly differ in their ecological and genetic properties, and, respectively, in their resistance to pollution by gasoline (Kolesnikov et al., 2011).

Thus, the bio-testing of arid ecosystem soil resistance to gasoline pollution is highly relevant in order to predict the change of soil, as well as assess the condition of soil evolution.

2. Materials and methods

Contamination of the soil by gasoline was modeled in the laboratory conditions. The soils of arid ecosystems of the South Russia (dark chestnuts, chestnuts, light chestnuts, brown semi-desert, sandy soils, solonetz medow and shor solonchaks), as well as an ordinary chernozem, were the objects of study. For model experiments, soil samples were selected from the top 0-10 cm layer. In the non-arable soils, major amount of pollutants is accumulated in this surface layer.

The sample sites, the soil names and properties are presented in the Tables 1, 2.

Table 1. Soil sampling points

Name of soils	Ecosystem	Soil sampling point
Ordinary chernozem/Haplic Chernozem (Loamic)	typical steppe	Rostov region, Oktyabrskii district, Persianovskii village
Dark chestnut/Haplic Kastanozems Chromics	dry steppe	Rostov region, Orlovskii district, Maiorskii farm
Chestnut/Haplic Kastanozems Chromics	dry steppe	Rostov region, Remontnoe village
Light chestnut/Haplic Kastanozems Chromics	dry steppe	Republic of Kalmykia, Elista
Brown semidesert/Haplic Calcisols	semidesert	Republic of Kalmykia, Yashkulskii District, Khulkhuta Village
Sandy brown semidesert/Calcaric Arenosols	semidesert	Astrakhan region, Narimanovskii district, Novokucherganovka village
Solonetz medow/Gleyic Solonetz Albic	dry steppe	Republic of Kalmykia, Yashkul district, Gashun village
Shor Solonchaks/Puffic Solonchaks Aridic	the bottom of the dried estuary. rare halophytic vegetation	Astrakhan region, Narimanov district, with. Turkmen woman

Table 2. Soil properties

Name of soils	pH	Organic matter, %	Granulometric composition	Activity of catalase, ml O ₂ /g of the soil per 1 minute	Activity of dehydrogenases activity, mg triphenylformazan /g per 24 hours
Ordinary chernozem/Haplic Chernozem (Loamic)	7.6	4.6	heavy loam	15.8	28.9
Dark chestnut/Haplic Kastanozems Chromics	7.6	3.5	heavy loam	13.5	25.9
Chestnut/Haplic Kastanozems Chromics	7.8	2.8	heavy loam	11.4	23.0
Light chestnut/Haplic Kastanozems Chromics	8.1	1.4	medium loam	9.8	20.6
Brown semidesert/Haplic Calcisols	8.3	1.2	light loam	6.4	19.6
Sandy brown semidesert/Calcaric Arenosols	8.3	0.8	Sandy	3.3	17.4
Solonetzes meadow/Gleyic Solonetz Albic	8.4	1.3	medium loam	7.8	13.4
Shor Solonchaks / Puffic Solonchaks Aridic	7.8	0.7	heavy loam	5.8	15.5

On the territory of arid ecosystems in the Astrakhan region there is the largest gas condensate field in Europe. This deposit produces about 500 thousand tons of gasoline and the same amount of diesel fuel every year. Therefore the gasoline was chosen as a pollutant in our research. The production transportation, and processing of these substances ensures severe soil pollution.

In model experiment, the soil was incubated at a room temperature (20-22 °C) and the optimal moisturizing (60% of the field moisture capacity) in the vegetation vessels in three-fold repetitions.

Environment status of the soil was determined 30 days after pollution. To assess the soil chemical contamination effect, this duration is of most significance, since the biological indicators degradation degree is maximal (Kolesnikov et al., 2002). Laboratory analytical studies were performed using the conventional methods (Metody pochvennoi mikrobiologii i biokhimii, 1991; Kazeev et al., 2016). In this work, we determined in the soil the enzymatic activity (catalase and dehydrogenases), general number of bacteria, galore of bacteria of genus *Azotobacter*, cellulolytic ability, phytotoxic properties, and some other soil biological properties.

To combine a large number of indicators, a bio-testing method was developed of integral indicator of biological state of soil (IIBS) (Kazeev et al., 2016). The IIBS method allows to determine and evaluate the biological state of the soil as a whole.

3. Results and discussion

In this model experiment, it was shown that the introduction of gasoline into the arid ecosystem soils causes the reliable changes in soil biological parameters. (Figures 1-7). Studied parameters decreased significantly, namely the enzymatic activity (catalase and dehydrogenases), general number of bacteria in soil, galore of bacteria of genus *Azotobacter* in the soil, cellulolytic ability, and phytotoxic properties. These changes influenced the IIBS values.

The introduction of 1 % gasoline into the soil caused a significant decrease in the number of bacteria in ordinary chernozem by 29 %, in chestnut soil by 21 %, in brown semidesert by 37 %, in sandy brown semidesert and solonetzes meadow by 50 %, and by 59 % in shor solonchaks. The gasoline dose of 5 % reduced the number of bacteria in ordinary chernozem by 45 %, and in chestnut soil by 37 %, in brown semidesert by 45 %, in sandy brown semidesert and solonetzes meadow by 50 %, and by 59 % in shor solonchaks.

in chestnut soil by 46 %, in light chestnut soil by 53 %, in solonetztes meadow and shor solonchaks by 68 %, in brown semidesert by 75 %, and in sandy brown semidesert soil by 83 %. The gasoline dose of 10 % reduced the number of bacteria in ordinary chernozem by 41 %, in chestnut soil by 57 %, in brown semi-desert soil by 79 %, and in dark chestnut soil, in solonetztes meadow, and shor solonchaks by 20 % (Figure 1).

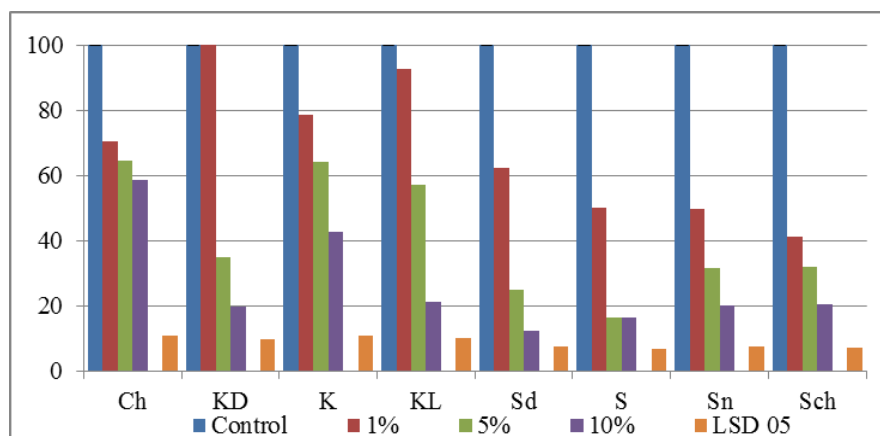


Fig. 1. Change in the total number of bacteria in the arid soil contaminated by gasoline. *Ch* – Ordinary chernozem/Haplic Chernozem (loamic), *KD* – Dark chestnut/Haplic Kastanozems Chromics, *K* – Chestnut/Haplic Kastanozems Chromics, *KL* – Light chestnut/Haplic Kastanozems Chromics, *Sd* – Brown semidesert/Haplic Calcisols, *S* – Sandy brown semidesert/Calcaric Arenosols, *Sn* – Solonetztes meadow/Gleyic Solonetz Albic, *Sch* – Shor solonchaks/Puffic Solonchaks Aridice

The abundance of bacteria of the genus *Azotobacter* did not significantly change in ordinary chernozem, dark chestnut soil and chestnut soil contaminated with gasoline at a concentration from 1-10 %. The introduction of gasoline at a dose of 1 %, a decrease in bacteria number was observed only in the solonetztes meadow by 25%, and in the shor solonchaks by 61 %. The addition to the soil of the gasoline 5 % caused a decrease in the number of *Azotobacter* bacteria in light chestnut soil and sandy brown semi-desert soil by 12 %, in brown semi-desert soil by 26 %, in solonetztes meadow by 53 %, and in shor solonchaks by 84 %. The 10 % concentration of gasoline in light chestnut soil reduced the abundance of *Azotobacter* by 33 %, in brown semi-desert soil by 41 %, in sandy brown semi-desert soil by 33 %, in Solonetztes meadow by 53 %, and in shor solonchaks by 83 % (Figure 2).

Catalase activity decreased with the introduction of 1 % gasoline in ordinary chernozem by 17 %, in dark chestnut soil by 40 %, in chestnut soil by 23 %, in light chestnut soil by 25 %, in brown semi-desert soil by 39 %, in sandy brown semi-desert soil by 32 %, in solonetztes meadow by 35 %, and in shor solonchaks by 52 %. When contaminated with 5 % gasoline, a decrease in catalase in ordinary chernozem was observed by 18 %, in dark chestnut soil by 48 %, in chestnut soil by 25 %, in light chestnut soil by 29 %, in brown semi-desert soil by 42 %, in sandy brown in semi-desert soil by 34 %, in solonetztes meadow by 67 %, and in shor solonchaks by 55 %. Contamination of 10 % of gasoline caused a decrease in catalase in ordinary chernozem by 21 %, in dark chestnut soil by 46 %, in chestnut soil by 26 %, in light chestnut soil by 30 %, in brown semi-desert soil by 46 %, in sandy brown semi-desert soil by 35 %, in solonetztes meadow by 19 %, and in shor solonchaks by 59 % (Figure 3).

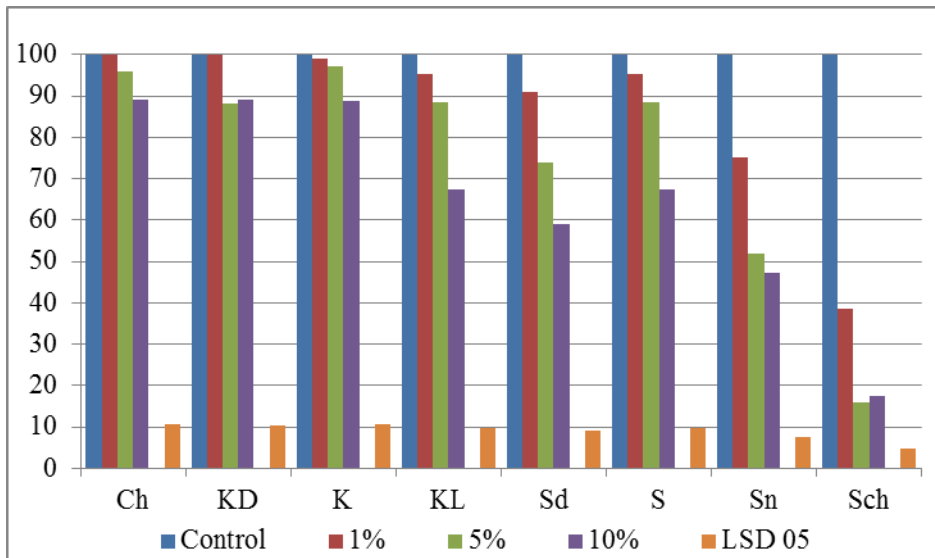


Fig. 2. Change in the abundance of bacteria of the genus *Azotobacter*, % of control when they contaminated by gasoline. Type codes: Ch – Ordinary chernozem/Haplic Chernozem (loamic), KD – Dark hestnut/Haplic Kastanozems Chromics, K – Chestnut/ Haplic Kastanozems Chromics, KL – Light chestnut/Haplic Kastanozems Chromics, Sd – Brown semidesert/Haplic Calcisols, S – Sandy brown semidesert/Calcaric Arenosols, Sn – Solonetztes medow/Gleyic Solonetz Albic, Sch – Shor solonchaks/Puffic Solonchaks Aridice

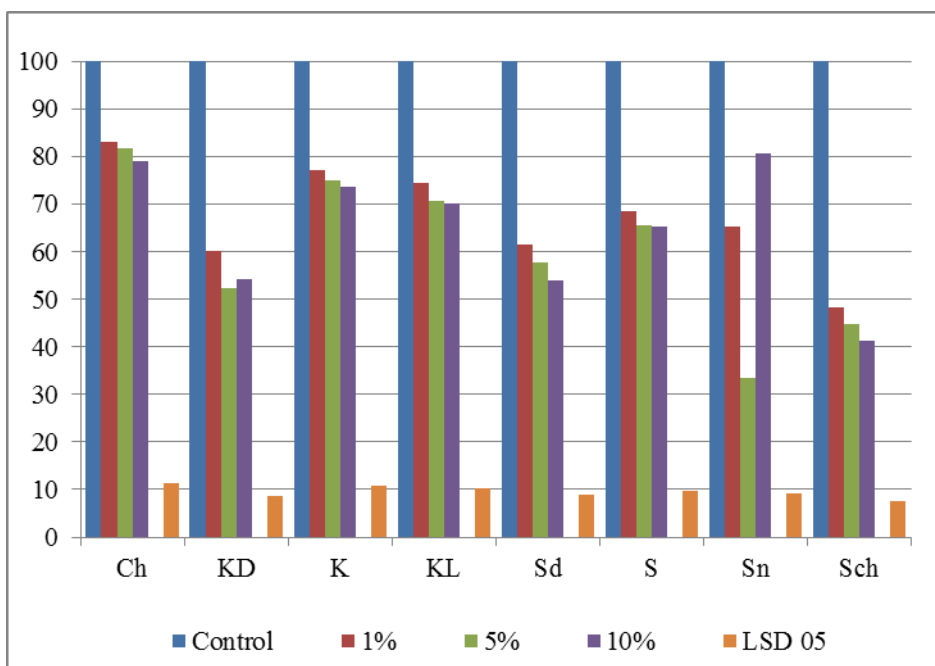


Fig. 3. Change in the catalase activity of arid soils when they contaminated by gasoline. Type codes: Ch – Ordinary chernozem/Haplic Chernozem (loamic), KD – Dark hestnut/Haplic Kastanozems Chromics, K – Chestnut/ Haplic Kastanozems Chromics, KL – Light chestnut/Haplic Kastanozems Chromics, Sd – Brown semidesert/Haplic Calcisols, S – Sandy brown semidesert/Calcaric Arenosols, Sn – Solonetztes medow/Gleyic Solonetz Albic, Sch – Shor solonchaks/Puffic Solonchaks Aridice

The activity of dehydrogenases decreased with the introduction of 1 % gasoline in ordinary chernozem by 37 %, in dark chestnut soil by 67 %, in chestnut soil by 26 %, in light chestnut soil by 52 %, in brown semi-desert soil by 31 %, in sandy brown semi-desert soil by 21 %, in a solonetztes medow by 24 %, and in shor solonchaks by 43 %. When contaminated with 5 % gasoline, a decrease

in dehydrogenases in ordinary chernozem was observed by 61 %, in dark chestnut soil by 69 %, in chestnut soil by 75%, in light chestnut soil by 66 %, in brown semi-desert soil by 27 %, in sandy brown semi-desert soil by 37 %, in solonetztes meadow by 28 %, and in shor solonchaks by 58 %. 10 % gasoline contamination caused a decrease in dehydrogenases in ordinary chernozem by 67 %, in dark chestnut soil by 72 %, in chestnut soil by 66 %, in light chestnut soil by 64 %, in brown semi-desert soil by 72 %, in sandy brown semi-desert soil by 46 %, in solonetztes meadow by 42 %, and in shor solonchaks by 74 % (Figure 4).

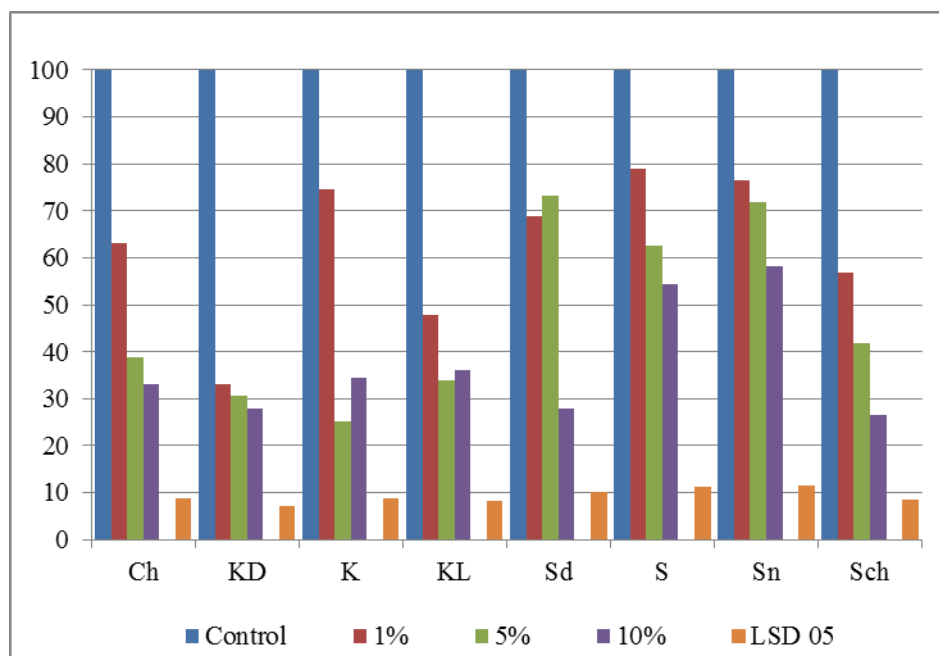


Fig. 4. Change in the dehydrogenases activity of arid soils when they contaminated by gasoline. Type codes: Ch – Ordinary chernozem/Haplic Chernozem (loamic), KD – Dark hestnut/Haplic Kastanozems Chromics, K – Chestnut/Haplic Kastanozems Chromics, KL – Light chestnut/Haplic Kastanozems Chromics, Sd – Brown semidesert/Haplic Calcisols, S – Sandy brown semidesert/Calcaric Arenosols, Sn – Solonetztes meadow/Gleyic Solonetz Albic, Sch – Shor solonchaks/Puffic Solonchaks Aridice

The soil cellulolytic activity when contaminated with gasoline at a dose of 10 % decreased to 0 in all variants of the experiment. With 1 % pollution, a significant decrease was recorded for chestnut soil (by 20 %), for light chestnut soil (by 68 %), for brown semi-desert soil (81 %), for sandy brown semi-desert soil (by 85 %), for solonetztes meadow (by 68 %), and for shor solonchaks (by 55 %). When contaminated with 5 % gasoline, a decrease in cellulolytic activity in ordinary chernozem was observed by 85 %, in dark chestnut and shor solonchaks by 93 %, in chestnut, light in chestnut and solonetztes meadow by 94 %, and in brown semidesert soil by 85 % (Figure 5).

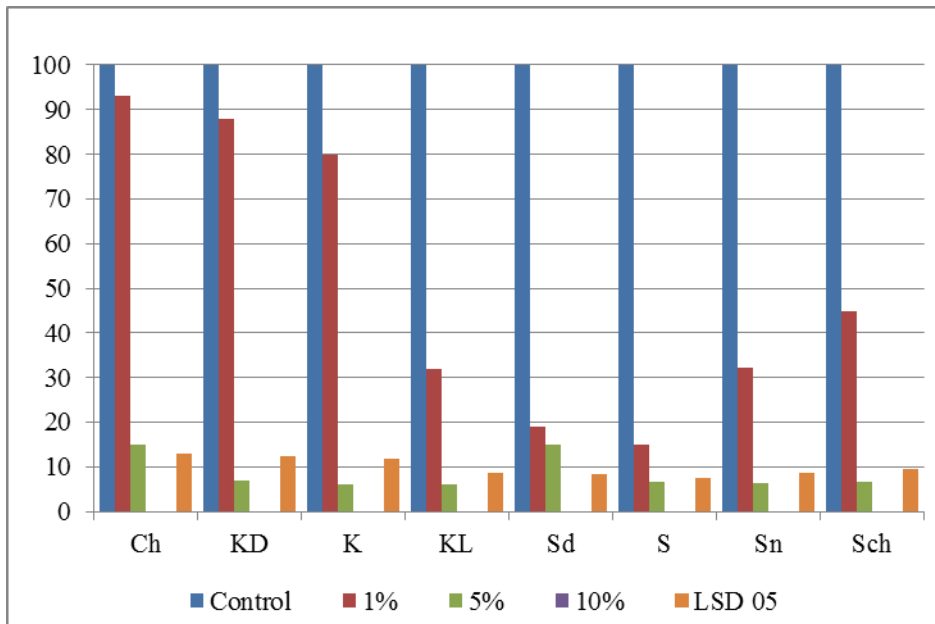


Fig. 5. Change in cellulolytic activity of arid soils when they contaminated by gasoline. Type codes: Ch – Ordinary chernozem/Haplic Chernozem (loamic), KD – Dark hestnut/Haplic Kastanozems Chromics, K – Chestnut/Haplic Kastanozems Chromics, KL – Light chestnut/Haplic Kastanozems Chromics, Sd – Brown semidesert/Haplic Calcisols, S – Sandy brown semidesert/Calcaric Arenosols, Sn – Solonetztes medow/Gleyic Solonetz Albic, Sch – Shor solonchaks/Puffic Solonchaks Aridice

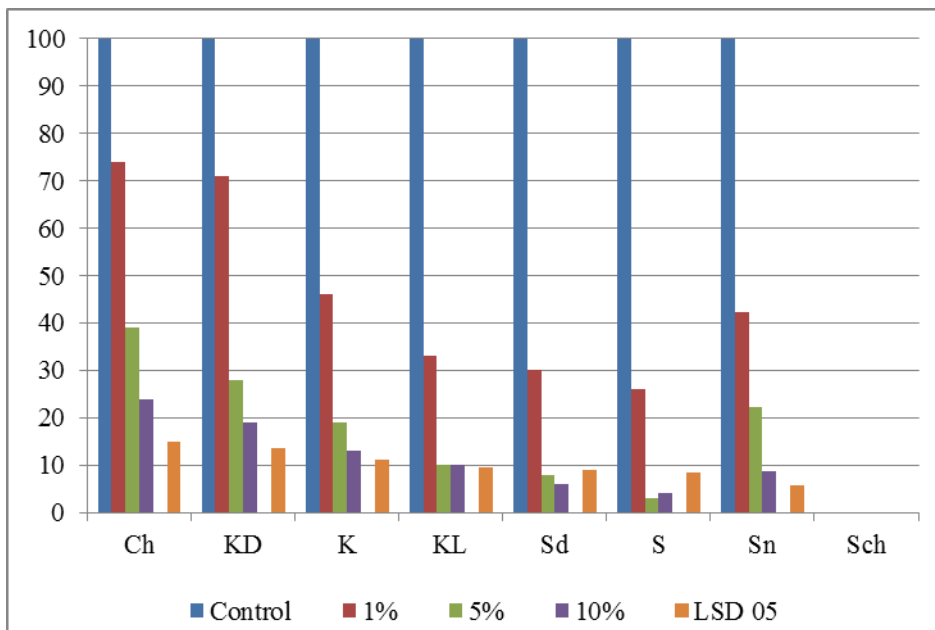


Fig. 6. Change in the length of the roots of radish of arid soils when they contaminated by gasoline. Type codes: Ch – Ordinary chernozem/Haplic Chernozem (loamic), KD – Dark hestnut/Haplic Kastanozems Chromics, K – Chestnut/Haplic Kastanozems Chromics, KL – Light chestnut/Haplic Kastanozems Chromics, Sd – Brown semidesert/Haplic Calcisols, S – Sandy brown semidesert/Calcaric Arenosols, Sn – Solonetztes medow/Gleyic Solonetz Albic, Sch – Shor solonchaks/Puffic Solonchaks Aridice

Contamination with gasoline at a concentration of 1, 5 and 10 % turned out to be toxic for the growth of radish on a shor solonchaks. The length of radish roots decreased when 1 % gasoline was added in ordinary chernozem by 26 %, in dark chestnut soil by 29 %, in chestnut soil by 54 %, in light chestnut soil by 67 %, in brown semidesert soil by 70 %, in sandy brown semidesert soil by 74 %, in solonetztes medow soil by 58 %, in shor solonchaks soil by 100 %.

in light chestnut soil by 67 %, in brown semi-desert soil by 70%, in sandy brown semi-desert soil by 74 %, and in solonetztes medow by 58 %. When contaminated with 5 % gasoline, a decrease in root length in ordinary chernozem was observed by 61 %, in dark chestnut soil by 72 %, in chestnut soil by 81 %, in light chestnut soil by 90 %, in brown semidesert soil by 92 %, in sandy soil. brown semi-desert soil by 97 %, and in solonetztes medow by 78 %. Contamination of 10% gasoline caused a decrease in the length of radish roots by 76 % in ordinary chernozem, in dark chestnut soil by 81 %, in chestnut soil by 87 %, in light chestnut soil by 90 %, in brown semi-desert soil by 94 %, in sandy brown semi-desert soil by 96 %, and in solonetztes medow by 91 % (Figure 6).

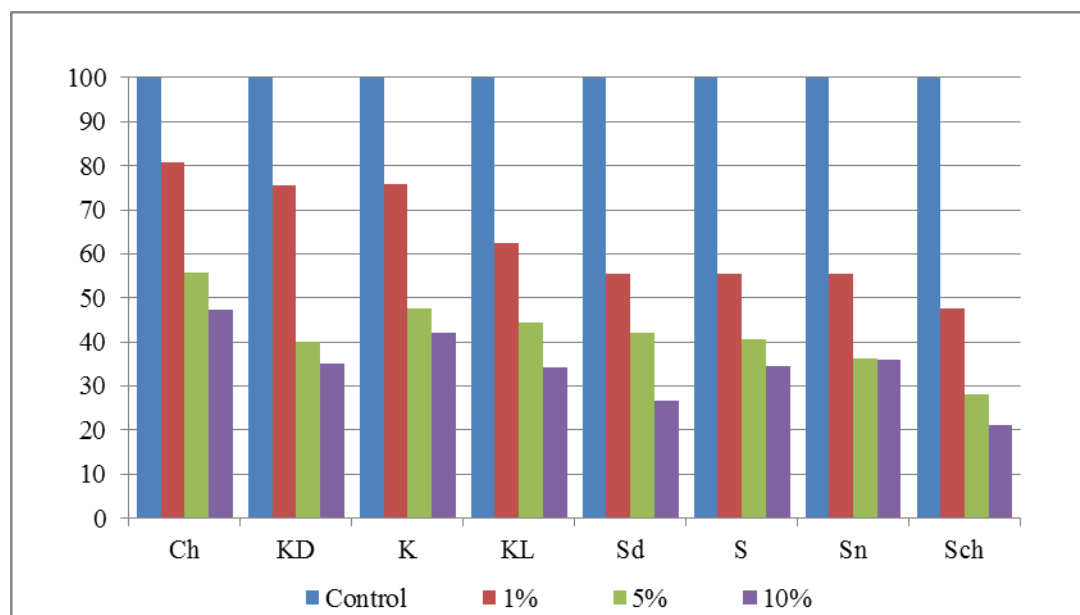


Fig. 7. Change in IBS of arid soils when they contaminated by gasoline. *Type codes: Ch – Ordinary chernozem/Haplic Chernozem (loamic), KD – Dark hestnut/Haplic Kastanozems Chromics, K – Chestnut/Haplic Kastanozems Chromics, KL – Light chestnut/Haplic Kastanozems Chromics, Sd – Brown semidesert/Haplic Calcisols, S – Sandy brown semidesert/Calcaric Arenosols, Sn – Solonetztes medow/Gleyic Solonetz Albic, Sch – Shor solonchaks/Puffic Solonchaks Aridice*

As a rule, extended soil biological indicators degradation in all studied is directly related to the concentration of pollutant in the soil. The obtained sequence of soil resistance of arid ecosystems in the South Russia to gasoline pollution is as follows: ordinary chernozem (haplic chernozem loamic) > chestnuts soils (haplic kastanozems chromic) > dark chestnuts soils (haplic kastanozems chromic) ≥ light chestnuts soils (haplic kastanozems chromic) ≥ sandy soils (calcaric arenosols) ≥ brown semi-desert soils (haplic calcisols) > solonetztes medow (gleyic solonetz albic) > shor solonchaks (puffic solonchaks aridic).

When gasoline penetrates the soil, it is divided to the free liquid, vapor, adsorbed on soil particles or dissolved in water phases. The texture of the soil, the porosity of the soil, and the duration of pollution affect the gasoline phases distribution. Although petroleum hydrocarbons are usually considered insoluble in water, the lighter hydrocarbons, such as benzene, are more soluble in water than polycyclic aromatic hydrocarbons, which are often components of diesel fuel (for example, naphthalene, anthracene, or pyrene) (Cole, 1994; Bennett, 1999). Due to the relatively high solubility in water, these compounds will, as a rule, will be dissolved in the aqueous phase or evaporated throughout internal air spaces of the soil. Because of relative hydrophilic nature, the compounds will not be held up by soil particles and therefor under certain conditions can move for the long distances (Shayler et al., 2009).

Based on the results of the study, the regression equations were developed, which reflect the relationship between the IBS values and the gasoline content in the soil. Using these equations, the concentrations of gasoline, that cause a violation of one or another group of soil eco-

functions, were calculated, and a scheme of ecological regulation of pollution of arid soils by gasoline was proposed (Table 3).

Table 3. Rationing of gasoline content in arid soils of South Russia by degree of ecological function violation (biogeoholistic)

Soil contamination	Not polluted	Slightly polluted	Medium-polluted	Heavy-polluted
IIBS ¹ change	< 5 %	5 – 10 %	10 – 25 %	> 25 %
impaired functions ²	–	informational	chemical, physico-chemical, biochemical; holistic	physical
Gasoline content in the soil, mg / kg				
Ordinary chernozem/Haplic Chernozem (Loamic)	< 0.19	0.19 – 0.26	0.26 – 0.81	> 0.81
Dark chestnut/Haplic Kastanozems Chromics	< 0.17	0.17 – 0.22	0.22 – 0.47	> 0.47
Chestnut/Haplic Kastanozems Chromics	< 0.17	0.17 – 0.22	0.22 – 0.58	> 0.58
Light chestnut/Haplic Kastanozems Chromics	< 0.13	0.13 – 0.17	0.17 – 0.39	> 0.39
Brown semidesert /Haplic Calcisols	< 0.12	0.12 – 0.15	0.15 – 0.33	> 0.33
Sandy brown semidesert/Calcaric Arenosols	< 0.11	0.11 – 0.14	0.14 – 0.32	> 0.32
Solonetzes meadow/Gleyic Solonetz Albic	< 0.11	0.11 – 0.14	0.14 – 0.31	> 0.31
Shor Solonchaks/Puffic Solonchaks Aridic	< 0.12	0.12 – 0.14	0.14 – 0.24	> 0.24

¹ Determination of the integral index according to (Kolesnikov et al., 2002).

² Classification of ecological functions according to (Dobrovolsky and Nikitin, 1990).

According to Table 3, when the content of gasoline in the dark chestnut soil is less than 0.17 %, the soil performs its functions normally. If the concentration of gasoline is from 0.17 to 0.22 %, there will be a violation of informational ecological functions of the soil, from 0.22 to 0.47 % – in addition to information, chemical, physicochemical, biochemical and integral functions will be violated, more than 0.47 % – there will be the soil physical functions breakdown. To ensuring soil fertility, it is impossible to allow violations of the chemical, physicochemical, biochemical, and most important integral functions of the soil. Consequently, the concentration of 0.22 % gasoline in soil should be considered the maximum permissible concentration (MPC) of gasoline for the soils of arid ecosystems in the South Russia. Basing on bio-testing study, we propose to use the above mentioned concentration as the regional MPC (r MPC).

4. Conclusion

The arid soil pollution by gasoline in the South Russia leads to decrease of the biological activity: enzymatic activity (catalase and dehydrogenases), the general number of bacteria in the soil, the galore of bacteria of genus *Azotobacter* in the soil, phytotoxic properties, cellulolyticability. In most cases, there is a significant decrease in all the studied parameters. The degree of decrease depends on the concentration of gasoline in the soil.

The sequence of the South of Russia arid ecosystem's soils resistance to gasoline pollution is as follows: ordinary chernozem (haplic chernozem loamic) > chestnuts soils (haplic kastanozems chromic) > dark chestnuts soils (haplic kastanozems chromic) ≥ light chestnuts soils (haplic kastanozems chromic) ≥ sandy soils (calcaric arenosols) ≥ brown semi – desert soils (haplic calcisols) > Solonetz medow (gleyic solonetz albic) > Shor Solonchaks (puffic solonchaks aridic).

We recommend the developed bio-testing indicators of the soil biological state for application in the forecasting, assessment, and control of chemical contamination of arid soils. Suggested quantitative landmarks will be useful to the development of regional standards for the maximum permissible concentrations of gasoline in arid soils based on the degree of violation of the soil ecological functions.

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Monitoring Soil Salinity and Recent Advances in Mechanism of Salinity Tolerance in Plants

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Abstract

Salt stress is the most prominent factor that has affected agriculture production, induced various problems, and a serious challenge to food security. Numerous adverse effect can be noticed during salt stress that is pretentious to their physiological, biochemical, molecular, and morphological functions. Plants develop a mechanism to subdue the problem that arises through salt stress via adoption or tolerance process but these mechanisms are not sustainable. It leads to a decline in the biomass of plants and overall crop productivity. For sustainable development of food security and overcome the looming endanger of salt stress in the reduction of food production and exponential population growth, novel and advanced technologies like plant breeding, biotechnology, nanotechnology can be explored and made to work for the development of salt tolerance of crop varieties.

Keywords: Salt stress, food security, physiological, molecular, plant breeding, biotechnology, nanotechnology.

1. Introduction

The world population is expected to reach 9.6 billion by the year 2050 and approximately 83 million people are being added to the world's population every year (UNFPA, 2014). To feed

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such a huge population, about 44 million metric tons of food crops will have to be produced every year to meet the demands of the increased population by 9.6 billion by 2050. However, the expansion of arable land has been limited due to climate change and global warming (FAO, 2012; Miah et al., 2013), the climatic change affected plant physiological, biochemical, and molecular functions known Abiotic stress, affected plant called abiotic stressors. Out of all abiotic stresses, salinity and drought are the two main abiotic stresses that impede large-scale world crop production (Munns, 2011). Soil is the blood of the earth, if blood is affected by various types of diseases then the body is not fit, similarly, if earth blood that is soil is affected by various types of problems such as salinity, nutrition, etc. then it can not produce healthy crops.

Globally, about 53 % in Asia and Australia, 13 % in Latin America, 13 % in Near East, 10 % in Europe, 9 % in Africa, and 2 % in North America lands are salt-affected. More than 30 % of the world's total irrigated lands are used to produce food crops. On the other hand, an estimated 20 % or more of irrigated lands are high saline, and 50 % of irrigated land is affected by medium or secondary salinity (Munns, 2002, Ruan et al., 2010). Data from all these salt-affected lands show that the saline situation in the land increased every year due to poor agricultural practices and climate change. The present review, focus special attention to all the aspects of soil salinity monitoring, crop improvement approaches, and stress tolerance mechanism in plants.

2. Results and discussion

GIS remote sensing for monitoring soil salinity

Remote sensing is a fundamental process that helps in monitoring crop health through analyzed soil, weather, temperature, humidity, this analyzed study beneficial for crop production (Wu et al., 2015). The working principle of GIS remote sensing is recording and measuring some components like electromagnetic radiation which is reflected by the earth's surface (Nezami et al., 2012). For monitoring the agricultural production GIS remote sensing are using several types of vegetation indices (VIs) tools like NDVI (Normalized Difference Vegetation), PVI (Perpendicular Vegetation Index), and SAVI (Soil Adjusted Vegetation Index) (Tucker et al., 1979; Rondeaux et al., 1996; Huete, 1988).

GIS remote sensing is useful for analysis of salty soil, salt-affected vegetation, saline water, pond water, and high water table area give a unique reflectance in comparison to other landscape features, for example, GIS remote sensing techniques are used to monitoring saline-sodic soil patches in the Machhlishahr of Jaunpur district of the Indian state of Uttar Pradesh, India (Figure 1).

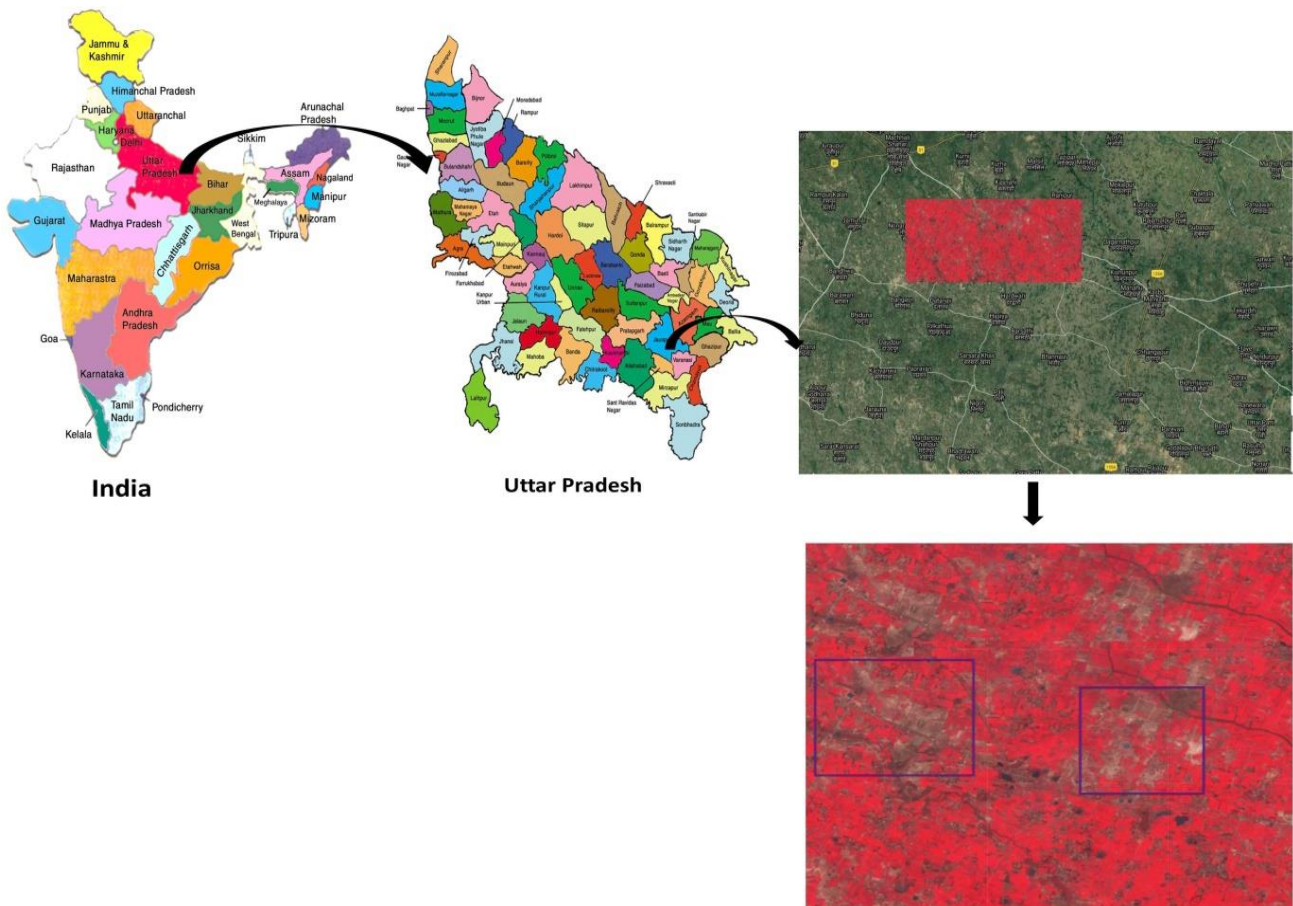


Fig. 1. GIS remote sensing monitoring of Saline-sodic soil land in the Machhlishahr of Jaunpur district of the Indian state of Uttar Pradesh, India

Remote sensing is an art of analysis which combined with science through it can elucidate the properties of the earth's surface by collecting the different types of earth surface data using various types of sensors. For the land survey, remote sensing techniques work on a range of wavelengths between 0.4 and 2.4 nm (Ojo, Ilunga, 2018). Salt patches present on terrain surface can be detected by remote sensing or directly on bare soils, with the help of salt efflorescence and crust. It can also be analyzed by the plants that are grown in a salt-affected area through GIS remote sensing base vegetation indices techniques (Mougenot et al., 1993). Regions in arid salt-affected land, the soil have a salt crust that is whitish in structure. White color have high reflectance that is easily being able to be detected by GIS remote sensing base vegetation indices.

Mechanism of plant responses and adaptation to soil salinity

Plants are divided into two classes based on their response to salt concentrations. In first-class comes “halophytes” plants: completed their life cycle in the salt environment thus they are native towards it. In the second class comes “glycophytes” plants: sensitive to a saline environment. At an above considerable concentration of salts glycophytes, plants are showing some physiological disorders like leaf discoloration, loss of biomass, and growth inhibition. Based on the growth response in salinity conditions. Halophytes and glycophytes are classified into the following groups:

Group I – In this group, those halophytes are come which continue to grow rapidly at 200-500 mM NaCl concentration (Greenway, Munns, 1980). Group I is further divided into Group I A and Group I B. In group IA which halophytes plants are come which continuously grown with Cl⁻ in 400 mM salt concentration, for example, *Suaeda maritime*, *Atriplex nummularia* (Greenway, Munns, 1980; Taiz, Zeiger, 2002). In group I B these halophytes are come which are salt tolerance but their growth is retarded, for example, *Atriplex hastata*, *Spartina townsendii*, and sugar beet (Greenway, Munns, 1980).

Group II – In group II halophytes plants are grow very slowly above than 200 mM NaCl concentration. Group II divided into following groups

(1) Tolerant: In this group salt tolerant halophytic monocotyledons without salt glands are come for example *Festuca rubra ssp. litoralis*, *Puccinellia peisonis*. Also some glycophytes or nonhalophytes also come under in this group like cotton and barley.

(2) Intermediate: Under this class, plants are come that partially affected by salt concentration, for example, tomato.

(3) Sensitive: In this group, plants are highly sensitive to salt concentration, for example, common beans and soybeans.

Group III – In this group glycophytes or non-halophytes come which are very salt-sensitive, even in low concentration of salt, for example, Fruit trees like citrus, avocado and stone fruit.

The primary response for the salinity level in the plant is slow growth rate of leaves (Kibria and Hoque, 2019) in salt stress shoot is much affected than root (Munns and Termaat, 1986), but when plant root is exposed to higher soil, salinity level then root growth is also effected (Koca et al., 2007; Tuna et al., 2008). Shabala, Babourina and Newman (2002) reported that due to salinity stress the new cell production rate reduced that inhibited the overall growth of plants. Due to alteration of plant cell wall structure induced by salinity stress, caused stiffness in cell wall which leads the reduction in dry weight of plant. Salinity stress in root zone is developed the osmotic stress, which caused disruption in cell ion homeostasis by inducing both the inhibition in uptake of essential nutrients like K^+ ions and increased accumulation of Na^+ and Cl^- ions (Paranychianakis and Chartzoulakis, 2005).

Under salt stress conditions, plants are increase the uptake of Na^+ ions that affected uptake of other ions like K^+ that leads to cause the K^+ deficiency resulting the lowering of K^+/Na^+ ratio (Kibria et al., 2017). Salt stress induced the significant changes in physiological and biochemical conditions in plant, for example. decrease in protein synthesis, lower level of leaf chlorophyll content, increased ROS accumulation, changes in antioxidant enzymatic activities, enhanced accumulation of compatible solutes such as proline, glycine betaine, sorbitol, mannitol, pinitol and sucrose (Figure 2) (Kibria, Hoque, 2019).

Effect of salinity on plant physiological and biochemical states

High salinity in soil effects plants at physio-biochemical and molecular levels by inducing oxidative stress, water stress, nutritional disorders, ion toxicity, alteration of metabolic processes, membrane disorganization, reduction in cell division and expansion, and genotoxicity (Carillo et al., 2011).

All these adverse physio-biochemical and molecular conditions simultaneously leads to inhibits plant growth, and its development (Table 1).

Table 1. Physio-biochemical effects of salt stress in plant

Physio-biochemical processes	Salt induced damage and symptoms	References
Photosynthesis	Salinity affects photosynthesis mainly through reduction in leaf area, chlorophyll content and stomatal conductance, and to lesser extent decrease in photosystem II efficiency	Netondo et al., 2004
Reproductive development	Salinity essentially affects plant reproductive development by inhabiting microsporogenesis and stamen filament elongation, which lead programmed cell death in some tissue. It also promote ovule abortion and senescence of fertilized embryos.	Shrivastava and kumar, 2014
Water transport	The initial stage of salt stress plants experiences water stress condition resulting in plant reduces leaf expansion.	Carillo et al., 2011

Osmotic regulation	Plants immediately experienced salt stress conditions cause osmotic stress. If plant continuous experience osmotic stress condition it inhibited cell expansion and cell division as well as stomatal closure.	Flowers, 2004, Munns, 2002
Ionic regulation	Long term exposure to salinity plant experience ionic stress, this ionic deregulation lead to premature senescence of adult leaves. Mature leaves also face senescence condition because of higher Na ⁺ accumulation which affected protein synthesis and enzymatic activity.	Cramer and Nowak, 1992; Carillo et al., 2011

Reduction of plant growth and development affected the production of grains, and to overcome this problem, research community use new tools and techniques for improvement of crops against the salinity stress but for this they required deep information related physiology, morphology, molecular and biochemical changes in plants due to salt stress.

Salinity effects on the physiological condition of plant

Salinity effects on plants photosynthesis and photosynthetic pigments

During salinity response, plants exhibits dramatic decrease in stomatal aperture number. Rajput et al. (2015) studied on stomatal density, area, and size of stomata opening that were highly affected by different salt concentrations, led to reduce evaporation. Quite a few studies also reveal that higher or moderate salinity level has affected the gas exchanges, decrease in photosynthetic rate, and these symptoms are completely analogous to drought stress (Bongi, Loreto, 1989; Loreto et al., 2003). Wang and Nil (2000) have reported that *Amaranthus tricolor* plants are adapted against salt stress conditions by deviating in its leaf growth and chemical composition, i.e., chlorophyll content, ribulose bisphosphate carboxylase-oxygenase (RuBisCO), and glycine, betaine as photosynthesis and transpiration rates were unaffected. Though in general, salt stress decreases the chlorophyll and total carotenoid contents of leaves that may impact photosynthetic rate (Parida, Das, 2005).

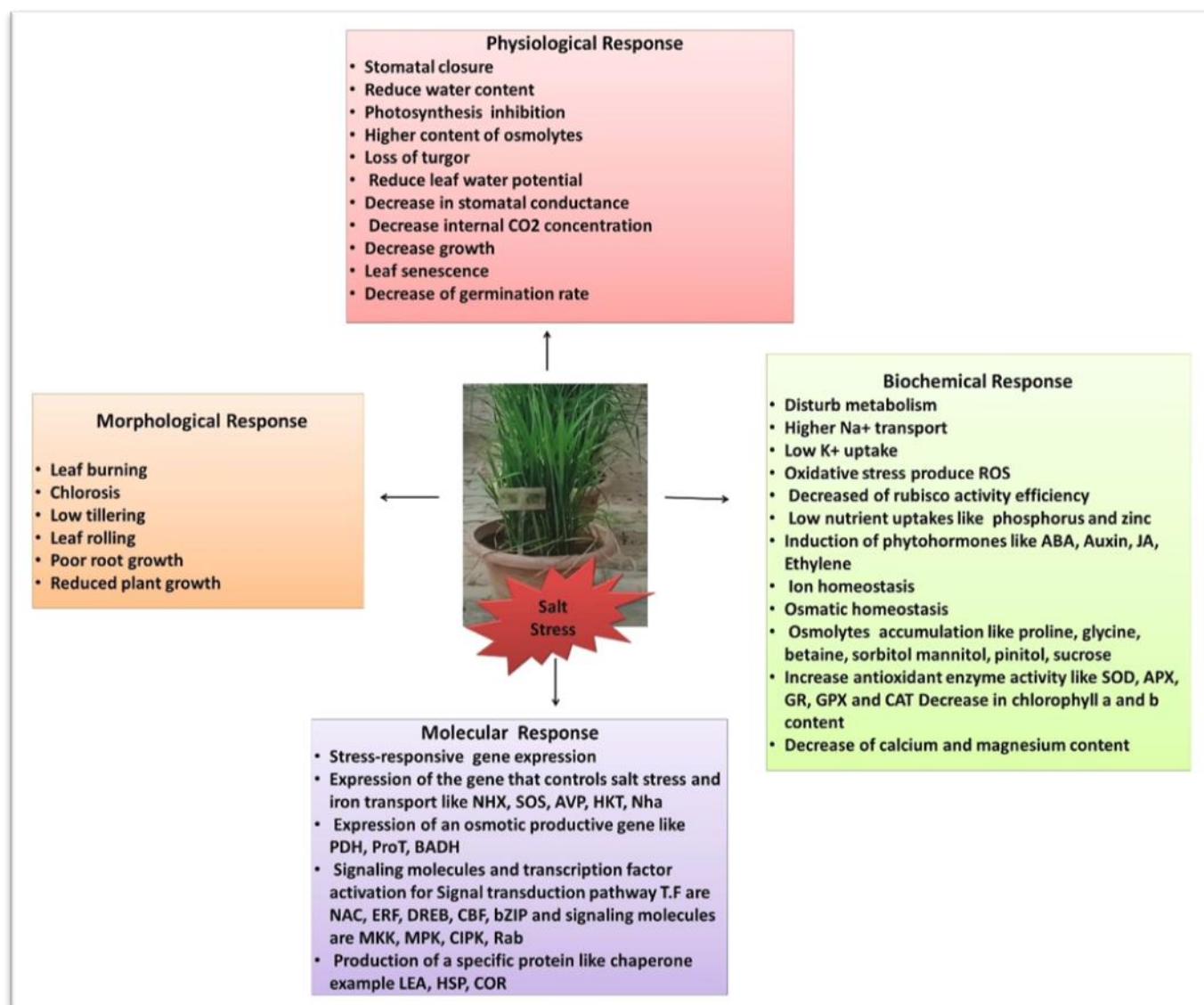


Fig.2. Overview of various types of plant response under the salt stress

During the NaCl stress in *Grevilea* plant, protochlorophyll, chlorophylls, and carotenoids have been largely reduced in comparison to Chl-a and carotenoids (Parida, Das, 2005). But on the other hand, other pigments like anthocyanin is significantly increased with increases in salt stress (Kennedy, De Fillippis, 1999). Alamgir and Ali (1999) revealed that under salt stress, leaf pigments in nine genotypes of rice were reduced in general, but relatively high pigment levels were found in other six genotypes, whereas, it was observed that some factors decreased the photosynthetic rate during the in-saline condition, i.e., high osmotic potential and reduced water availability to plants, ionic stress due to this toxicity of NaCl ions, the Cl⁻ ion inhibits photosynthetic rate, closure of stomata causing the reduction in CO₂ supply resulting carboxylation reaction-restriction, cytoplasmic structure and change in enzyme activities (Lyengar, Reddy, 1996; Rajput et al., 2016, 2017).

Effects of salinity on plant water relations

Water availability is the major factor in growth reduction in plants under salt stress condition but some plant grows easily with abundant water supplies even in saline environments such as mangroves (Taiz, Zeiger, 2002). Since mangroves adapted to the salt salinity of sea to obtain its water requirement and can adjust their osmotic conditions and water potential (Ψ_w). At water deficit conditions, plants cells can regulate their water potential (Ψ_w) in response to osmotic stress by lowering their solute potential (Ψ_s) (Taiz, Zeiger, 2002).

The solute potential (Ψ_s) is decreased by two intercellular processes, first by accumulation of ions in the vacuole and second by synthesis of compatible solutes in the cytosol (Taiz, Zeiger, 2002). It can be concluded that salt stress causes osmotic stress leads to water-deficit stress, reduced

water potential (Ψ_w) and turgor pressure in plant, that are enough to impinge on normal functions (de Oliveira et al., 2013). In water stress conditions, moderate loss of water can also leads to stomatal closure and limits exchange of gases. During low to moderate salinity and higher soil water potential, plant can maintain their water status through accumulation of compatible solutes and maintenance of influx of water and nutrient via potential gradient (Koyro, 2006; Shannon, 1997).

It was determined osmotic and ionic toxicity that caused reduction in germination of halophyte *Sueda* spp. and as salinity alleviated, germination improved and water loss controlled by regulation in transpiration or adjusting osmotic potential (Song et al., 2015). In sugar beet relative water content (RWC) decreased in salt conditions (Ghoulam et al., 2002) and decrease in RWC and loss of turgor could results in limited water availability for cell extension processes (Katerji et al., 1997). Informatirom drawn from conducted studies on salinity could led to conclusion that during higher salt concentration plant leaf cells accumulate more Na^+ and Cl^- than the normal situation. This causes lower osmotic potentials and more negative water potentials in leaf cells, reduction in root hydraulic conductance that directly influences the amount of water flow from the roots to the leaves resulting in water stress in the leaf tissues (Torabi et al., 2013).

Effects of salinity on plant ion levels and nutrient contents

Salinity stress causes double impact due to ionic toxicity and osmotic stress in plants that leads to nutritional disorder (Hasegawa et al., 2000; Zhu, 2003). In saline soil, the concentration and availability of Na^+ are higher than the concentration of K^+ (Tavakkoli et al., 2010). If NaCl concentration in the root zone of plants gets increased then Na^+ and Cl^- accumulation gets started in shoot tissue which leads to a decline in Ca^{2+} , K^+ , and Mg^{2+} levels (Bayuelo-Jimenez et al., 2003; Khan et al., 2000; Perez-Alfocea et al., 1996). When soil solution gets enriched with cations and anions then it moves towards plant cytoplasm. This movements of cations and anions are controlled by the permeability of cell membranes that contain protein transporters which facilitate the passage of ions (Jiménez-Casas, 2009). Under salt stress, salt-sensitive and salt-tolerant plants show differential responses towards K^+/Na^+ ions ratio in both root and shoot tissues (Zheng et al., 2012).

Some crops like potato showed a decrease in K^+/Na^+ ratio under salt stress that causes Na^+ toxicity leads to cellular damage whereas deficiency of K result decreases crop growth and productivity of plants (Daneshmand et al., 2009; Kibria, Hoque, 2019).

Effect of salinity on biochemical condition of plant

Salinity stress in plants causes certain biochemical changes in metabolic processes of protein, amino acid and carbohydrate. Based on the stress severity and duration, it directly inhibit the crop growth and productivity (Kibria and Hoque, 2019). Under the salt stress condition, proteins get starts accumulating that serve as a reservoir of energy or maybe adjuster of osmotic potential in plants (Ingram, Bartels, 1996; Mansour, 2000; Pessaraki, Tucker, 1985; Pessaraki, Huber, 1991). Ashraf and Harris (2004) demonstrated that some salt-tolerant cultivars of rice, barley, sunflower, finger millet have a higher amount of soluble proteins. Because of the salinity stress, soluble proteins level observed to decrease in leaves but at low to moderate salt stress concentration, soluble protein level start to increase.

Under the salt stress condition, plant accumulates various type of amino acids like proline, alanine, arginine, glycine, serine, leucine, valine and the non-protein amino acids i.e. citrulline and ornithine amides like glutamine and asparagines (Mansour, 2000). Amongst all these amino acids, proline accumulation is higher during salt stress condition in the plant cytosol due to an osmotic adjustment (Torabi et al., 2010; Abraham et al., 2003; Ketchum et al., 1991). Soluble carbohydrate in plants gets accumulated during the salt stress response and the CO_2 assimilation rate decreases significant (Murakezy et al., 2003). When glycophytes subjected to salt stress, they increase in soluble sugars up to 50% due to osmotic potential adjustments (Parvaiz, Satyawati, 2008). The building block of carbohydrates such as monosaccharides and disaccharides, i.e., glucose, fructose, sucrose, fructans and polysaccharides like starch accumulates under salt stress conditions and play a major role in osmoprotectant, osmotic adjustment, carbon storage, and radical scavenging (Parida et al., 2002).

Most prominent biochemical changes during abiotic stresses is observed, was ROS (reactive oxygen species) production (Apel et al., 2004). ROS are highly reactive agents which can cause serious disruption in metabolism through oxidative damage in cellular components like lipids, protein and nucleic acids (Arora et al., 2002). During salt stress, molecular oxygen (O_2) acts like as an electron acceptor due to which accumulation of ROS get enhanced (Gupta, Huang, 2014). ROS

include singlet oxygen ($^1\text{O}_2^*$), hydroxyl radical (OH^-), superoxide radical (O_2^-), and hydrogen peroxide (H_2O_2) are all strong oxidizing compounds that can damage the biological membranes of cell and cell organelles (Santos et al., 2018).

Overview of salt stress signaling

When plants are subjected to the salt stress conditions then the salt stress sensing signaling pathway gets activated and the $\text{Ca}^{2+}_{\text{cyto}}$ amount heightened that acts as a secondary messenger and initiates a series of reactions or signaling cascade. This signaling cascades modifies the expression of several genes responsive to salt stress. This signaling cascade also knows as salt stress signal transduction pathway is a complex mechanism that involves proteins, lipids, hormones, metabolites, Ca^{2+} and ROS.

This salt signal transduction pathway has mechanism constitutes of (i) SOS pathway; (ii) mitogenic activated protein kinases (MAPK) cascade; (iii) phospholipid dependent; (iv) phosphoprotein cascade; (v) calcium/ calmodulin-dependent; (vi) H_2O_2 activated; and (vii) acid abscisic (ABA) dependent (Taiz, Zeiger, 2002; Conde et al., 2011; Peng et al., 2014; Shinozaki et al., 2015).

(1) Osmotic signal transduction

Osmotic signal transduction-triggered genes are mainly regulated by ABA phytohormones, but not applicable for all osmotic genes that are involved in salt stress. It is regulated by ABA-dependent or independent regulatory pathway. Both these two signalling pathways are activated by the transcription factors that interact with the promoter region of specific salt induced responsive genes resulting in up or down-regulation of their expression (Figure 3).

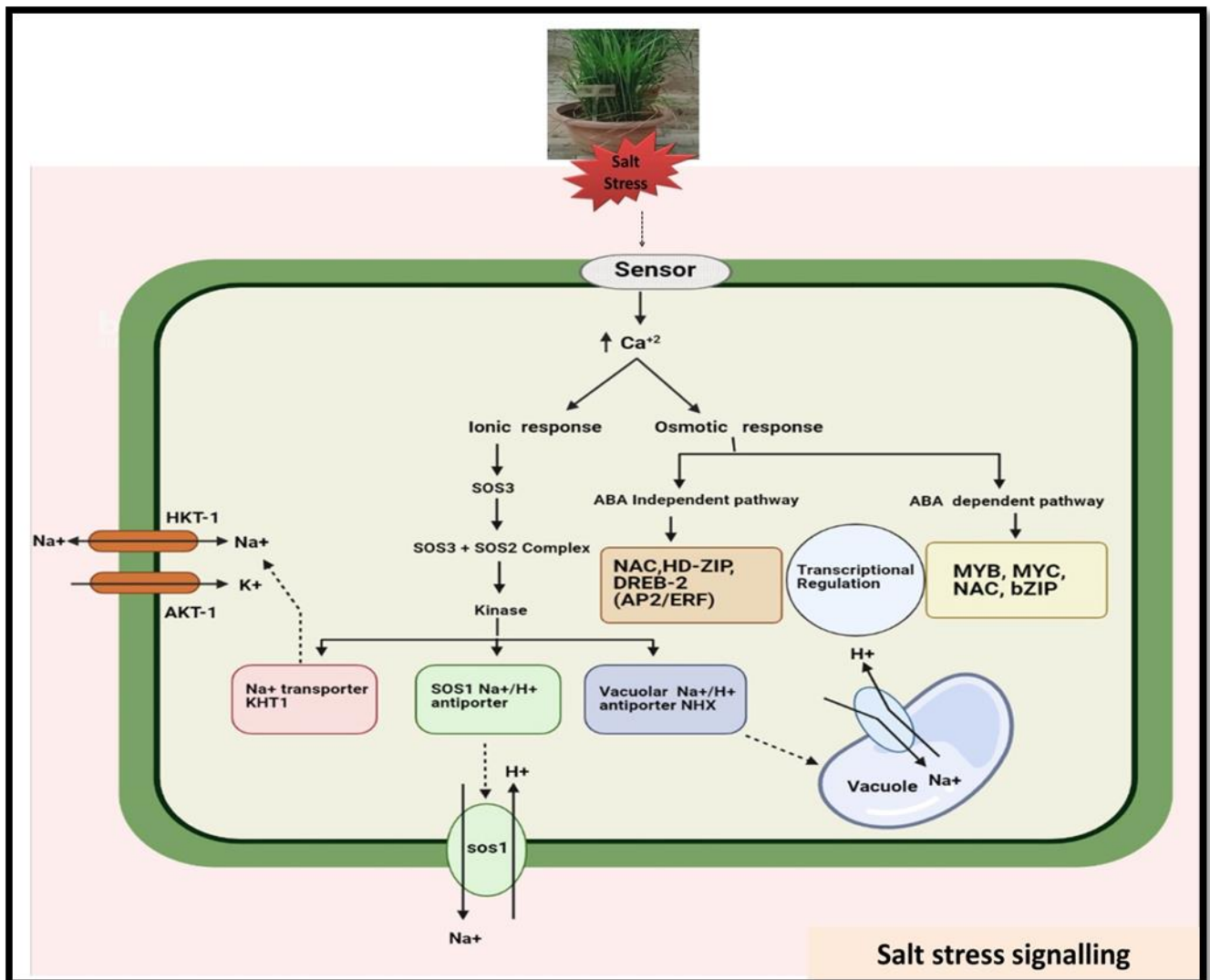


Fig. 3. Diagrammatic representation of salt stress signalling

(A) ABA-dependent signaling pathway

During the salt stress, ABA-dependent signalling pathway has ABA-regulated gene promoters that have six nucleotide sequence elements known as ABRE (ABA-responsive element). ABRE element is cis-acting regulatory protein that is required for expression and function of its own gene and also other cis-acting elements.

Under salinity stress, the lots of ABA signalling cascades functions., e.g., upstream of basic leucine zipper (bZIP) transcription factors, PYR1/PYLs/ RCARs receptors, PP2C phosphatases, and SnRK2 protein kinases (Shinozaki et al., 2015).

(B) ABA-independent signaling pathway

In the ABA-independent signalling pathway, osmotic stress-responsive genes are regulated by two signalling pathways. In one pathway, DREBP/CBF transcription factors binds to DRE (dehydration-responsive element)) elements in the promoter of osmotic stress-responsive gene and activates its function whereas in second pathway, ABA-independent osmotic stress-responsive genes are directly controlled by the MAP kinase signaling cascade of protein kinases or MAPK signaling pathway (Taiz and Zeiger, 2002).

(2) Ionic signal transduction

Ionic signal transduction pathways are involved in ion homeostasis that has been first characterized in Arabidopsis through the studies on mutant plants that are excessively sensitive to salt (SOS mutant). Early response to salt stress increased calcium (Ca^{2+}) level and this increment of calcium was attached by the calcium-binding protein SOS3 and undergoes conformation changes that facilitate its interaction with the kinase SOS2 a serine/threonine protein kinase.

The SOS2 have negative regulatory domain but its interaction with SOS3 leads the negative domain get autoinhibited and results in induced kinase activity. The SOS2 have a specific role in adaptation to high sodium and low potassium stress. The SOS3-SOS2 complex get phosphorylates and activates SOS1. SOS1 is a type of Na^+/H^+ antiporter of the plasma membrane of plant cell. Higher activity of SOS1 decreased the level of cytosolic Na^+ in saline conditions.

Morden crop improvement technology for development of salt resistance crops

Soil salinity is a major constraint to agriculture crop production, food and feed.

Various traits such as ion exclusion, osmotic tolerance and tissue tolerance can be integrated to improve salinity tolerance in crops. Several approaches has been made to improve salinity tolerance in crops such as genetic engineering, nanoparticales mediated crop improvements and marker assisted breeding.

Modern biotechnological methods (marker-assisted selection or genetic engineering) needs to be progressively exploited for introduction of the correct combination of genes into elite crop cultivars. In modern biotechnological methods, genetic engineering has been recognized as a revolutionary technique for generation of salt tolerant plants as one can transfer desired gene from any genetic resource to another and can alter the expression of existing gene(s) (Singh et al., 2021). Through the use of genetic engineering various crops have improved salinity tolerance (Nongpiur et al., 2016). Molecular markers associated with genes or quantitative trait loci (QTLs) affecting important traits are identified, and could be used as indirect selection criteria to improve breeding efficacy through marker-assisted selection (MAS). Numerous QTLs have been reported for salt tolerance in different crop species, however, MAS has been used in few commercial cultivars or breeding lines to improve salinity tolerance (Ashraf et al., 2012). Nanoparticles application has been found to be promising technique in agriculture to augment crop productivity under normal and harsh environmental conditions such as salt stress (Khan et al., 2020). Various evidences (Zulfiqar et al., 2021) have suggested that supplementation of nanoparticles to plants can significantly reduce the injurious effects caused by numerous harsh conditions including salt stress, and therefore can regulate adaptive mechanisms in plants. Various types of nanoparticles and nanofertilizers have shown a promising evidence regarding salt stress management.

In this section, the latest progress have made towards obtaining salt stress tolerance in crop plants utilizing genetic engineering, molecular marker and nanoparticles are explained.

Genetic engineering

Genetic engineering has been in the major attention of crop improvement for decades. This is mostly due to the several debates has been made up by the first generation of genetically engineered/genetically modified (GM). Transgenic plants displayed enhanced tolerance for high salt concentration and extreme temperature by expressing bacterial choline-oxidizing enzymes

(Sakamoto, Murata, 2001). Tarczynski et al. (1993) introduced a bacterial gene that encodes mannitol 1-phosphate dehydrogenase into tobacco plants, resulting in mannitol accumulation and enhanced tolerance to salinity. Transgenic tobacco plants carrying a cDNA encoding myo-inositol O-methyltransferase (IMT1) resulted in accumulation of D-ononitol, enhanced photosynthetic protection and enhanced recovery under drought and salt stress (Sheveleva et al., 1997).

SOS 1 gene in *A. thaliana* encode for plasma membrane Na^+/H^+ antiporter, was reported to be essential for salt tolerance (Shi et al., 2002) and recently Shi et al. (2003) stated that overexpression of SOS1 improves salt tolerance in transgenic *Arabidopsis*. Xu et al. (1996) described that the expression of HVA1, an LEA III family protein in barley, confers tolerance to water deficiency and salt stress in transgenic rice plants. Recently, biochemical analysis validated that SP1, which is a stress responsive gene and member of a novel protein family functions as a molecular chaperone in protecting and repairing various heat-labile enzymes (Wang et al., 2001, 2002b).

Preliminary results reported that elevated expression of SP1 have correlation with salt-stress tolerance (Wang et al., 2003; Barak, 2003). Lately, transgenic tobacco that were transformed with the animal cell death suppressors Bcl-xL and Ced-9 resulted in enhanced resistance to various stresses such as UV-B, paraquat, salt, cold and wounding stress (Mitsuhara et al., 1999; Qiao et al., 2002). Transgenic tobacco seedlings, grew significantly faster than control seedlings that were exposed to chilling or salt stress which were overexpressing cDNA which encodes an enzyme with both glutathione S-transferase (GST) and glutathione peroxidase (GPX) activity (Roxas et al., 1997). Transgenic tobacco (*Nicotiana tabacum*) overexpressing the p5cs gene that encodes P5CS produced 10- to 18-fold more proline showed better performance under salt stress (Kishor et al., 1995) because P5CS have role of rate-limiting enzyme in proline biosynthesis in plants, and is subject to feedback inhibition by proline, thus removal of the feedback inhibition can lead into a high level of proline accumulation in plants (Hong et al., 2000).

Transgenic plants overexpressing ADC (arginine decarboxylase) gene showed an increase in biomass and better performance toward salt stress conditions (Wang et al., 2011). In different conditions of environmental stresses there is the accumulation of LEA proteins, including several groups of high molecular weight proteins. It has been reported that plants expressing a wheat LEA group 2 protein (PMA80) and group 2 protein gene (PMA1959) resulted in increased tolerance to dehydration and salt stresses (Amudha et al., 2011). Transcription factors (TFs) exhibit higher correlation with salinity have roles in regulation and modification of different stress-responsive genes such as AP2/ERF, bZIP, NAC, MYB and WRKY inhibitor (Kumar et al., 2017).

Recently, it has been reported that the HDAC (histone deacetylase) inhibitor, suberoylanilide hydroxamic acid (SAHA) have role in enhancing tolerance to high salinity in cassava (Patanun et al., 2017). NHX genes from wheat have potential role in conferring salinity tolerance in *Arabidopsis*, tobacco, vegetable, and legume forage crops through the approach of genetic engineering (Yarra, 2019). Saxena (2020) reported that Cytosolic ascorbate peroxidase (Apx1) gene that was isolated from *Arabidopsis thaliana*, selected as the candidate gene for strengthening the antioxidative defense system of *Brassica juncea*. The transgenic plants performed well as compared to their non-transgenics under saline condition, exposed through greater proline accumulation, increased chlorophyll stability index, lower chlorophyll a/b ratio, and higher antioxidative enzyme activities.

Nanoparticles mediated crop improvement for salinity tolerance

Accumulation of excessive salt contents in the soil can inhibit plant growth and decreased crop production directly or indirectly. Salinity stress causes negative impact on the plants growth through the ROS generation and increased osmotic stress. Similarly, lowering of leaf water potential leads physiological and morphological changes and ion toxicity alters the biochemical processes (Rajput et al., 2015).

Recently, various nanoparticles are used for development of salt tolerance crops such as C, K, Ca, S, Ag, Cu, Fe, Zn, B, Si, Ti, and many others (Avestan et al., 2019; Abdoli et al., 2020; Alabdallah, Alzahrani, 2020; Khan et al., 2020; Ye et al., 2020). Zinc is supposed to have played various vital roles in plants particularly salinity stress (Sofy et al., 2020). Farouk and Al-Amri (2020) reported that Zn-NPs application to salt stressed canola (*Brassica napus*) plants upregulated the antioxidant system, osmolyte biosynthesis, and ionic regulation to lessen the

harmful effects of salinity. The Ag NPs identified for modulating numerous physio-biochemical traits in plants to improve multiple growth related features comprising germination and growth even under harsh condition including salinity (Soliman et al., 2020; Mohamed et al., 2017). Khan et al. (2020) reported that oxidative damage was reduced under saline condition when seeds of *Pennisetum glaucum* were primed with Ag nanoparticles due to enhanced antioxidant enzyme activities. Moreover, Ag nanoparticles suppressed Na^+/K^+ ratio thus increased flavonoids and phenolic contents in leaves (Khan et al., 2020). Mohamed et al. (2017) reported that when wheat seeds were treated with Ag nanoparticles before sowing showed improved growth, proline, soluble sugars, and peroxidase activity even in salt stress condition.

Silicon is not an integral plant nutrient but various reports have showed that application of Si can improve improved photosynthesis, vegetative growth, and dry matter production, as well as decreased shoot Na^+ and Cl^- deposition and improved K^+ accumulation under salt stress condition (Javaid et al., 2019; Abdelaal et al., 2020; Hurtado et al., 2020). Mushtaq et al. (2019) reported that treatment of nano- SiO_2 resulted in enhanced seed germination and growth on salt stressed wheat cultivars by improving leaf K^+ concentration, and levels/activities of biological antioxidants (Farhangi-Abriz, Torabian, 2018).

Copper metal-based micronutrient that influences numerous vital metabolic reactions in plants and can mediate photosynthesis in plants (Yamasaki et al., 2008). In tomato plants, application of Cu nanoparticles improves the growth performance and Na^+/K^+ ratio under salt stress condition (P´erez-Labrada, Lopez-Vargas, 2019). Hernandez-H et al. (2018) suggested that the application of Cu nanoparticles can enhance salt tolerance by activating the antioxidant defense mechanism and by the octadecanoid pathway of jasmonates. The effect of Fe_2O_3 nanoparticle on *Dracocephalum moldavica* plants showed enhanced growth and enzymatic activities under salinity stress (Moradbeygi et al., 2020). Abdoli et al. (2020) examined that the combined treatment of Fe_2O_3 nanoparticles alleviated salt stress via improving K^+/Na^+ ratio, Fe content, the activities of antioxidant machinery (SOD, CAT, POD, and polyphenol oxidase), endogenous salicylic acid, and some key osmolytes in *Trachyspermum ammi*.

Manganese is a crucial component of vital plant processes (Ye et al., 2019). *Vigna radiata* plants is reported to improve membrane stability index, chlorophyll content, and nitrate reductase activity under salt stress condition (Shahi, Srivastava, 2018). Application of Mn caused recovery from chlorosis and restricted growth due to saline stress in rice seedlings (Rahman et al., 2016). Application of carbon nanomaterials (CNMs) in agriculture has shown typical potential towards improving crop yield under nonstress and stress condition (Martínez-Ballesta et al., 2016; Baz et al., 2020). Nanoparticles (NPs) can alleviate unfavorable environmental conditions in plants predominantly salinity stress (Khan et al., 2017). Supplementation of multi-walled carbon nanotubes (MWCNTs) resulted in improved rate of photosynthesis and water uptake in broccoli under salt stress (Martínez-Ballesta et al., 2016). MWCNTs were reported to mediate salinity stress by improving aquaporin transduction, which resulted in enhanced water uptake (Martínez-Ballesta et al., 2016). Zhao et al. (2019) reported increase in nitrate reductase dependent NO biosynthesis, re-establishment of ion and redox imbalance demonstrated by the decrease in ROS overgeneration, reduction in thiobarbituric acid production, and decrease in Na^+/K^+ . He also provided molecular evidence of induced alteration in Na^+/H^+ exchanger 1 (NHX1) and K^+ transporter 1 (KT1) transcripts, antioxidant defense system genes, and salt overly sensitive 1 (SOS1) genes when treated with MWCNTs.

Spray of carbon nanohorns (CNHs) on *Sophora alopecuroides* seedlings showed improved the root fresh weight, leaf soluble sugar content, leaf and root total protein contents, leaf PSII activity and Cu contents (Wan et al., 2020). Through pyrolysis process of bioenergy and agricultural feedstocks, carbonaceous material generated that is Biochar (Lehmann et al., 2007). Spectroscopic analysis proved enhancement of soil P absorption when Mahmoud et al. (2020b) applied nanobiochar. Titanium dioxide (TiO_2) NPs can alter enzyme activities and improve chlorophyll pigments and photosynthesis in plant (Carbajal-Vázquez et al., 2020). Recently, it was shown improved growth and increase in activities of some key enzymes when they were treated with TiO_2 on *Dracocephalum moldavica* plants under salinity stress (Gohari et al., 2020a, 2020b). TiO_2 NPs in lowest concentration (0.01 %) can reinforce salt tolerance via enhancing enzymatic activities, amino acids, soluble sugars, and proline (Abdel Latef et al., 2018).

Under normal growth conditions Ce nanoparticles at low concentration can influence physio-biochemical characteristics in plants (Salehi et al., 2018). Abbas et al. (2020) reported that low levels of Ce NPs can enhance growth and photosynthesids in wheat. Potassium is vital for growth, metabolism, and unfavorable stress alleviation in plants (Jan et al., 2017). When crop plants were applied K exogenously under normal (non-stress) or stress conditions showed benefitted widely (Hatam et al., 2020; Xu et al., 2020). El-Sharkawy et al. (2017) reported the role of K_2SO_4 NPs on *Medicago sativa* L under salt stress condition altered the physiological characteristics via lowering the electrolyte leakage thus improved antioxidant enzymes and osmoprotectants activities.

Sulfur has been demonstrated as a necessary element for the growth and development processes of crop plants. Najafi et al. (2020) reported the effect of green synthesized sulfur nanoparticles on lettuce and reported enhanced osmoprotectants, total phenols, soluble sugars, flavonoids, anthocyanins, and tannin. The research on role of sulfur NPs under salt stress is rare and therefore, future studies should focus on application of sulfur NPs on salt stressed plants.

Marker-assisted breeding

In recent decades, DNA marker technology has reformed the genome research and breeding. Application of various available molecular markers and QTL mapping techniques that have contribution in various agronomically important traits such as resistance to biotic stresses, abiotic stresses tolerance, yield and nutritional quality in various crops (Xue et al., 2010; Ali et al., 2013) for the good knowledge of genetic bases of these stress related traits. A few salt stress related QTL detected by various molecular markers have been discussed in this section. *Kna1* has been reported in hexaploid bread wheat (*Triticum aestivum*) that regulate the transport of Na^+/K^+ from root to shoot precisely, by comprising a lower Na^+/K^+ ratio within the leaves (Gorham et al., 1987, 1990; Luo et al., 1996). In durum *Triticum turgidum* L. ssp. durum Desf. (wheat) discharge process of Na^+ is associated to *Nax1* (Na^+ exclusion 1; Huang et al., 2006, 2008), that might be related to the HKT8 (HKT1;5) and HKT7 (Na^+ transporters HKT1;4). It has been reported that *Nax1* loci efficiently reduce Na^+ passage to shoot from root, by keeping Na^+/K^+ balance by loading K^+ into and excluding Na^+ from, the xylem within the leaf of wheat plant (James et al., 2006). Yao et al. (2006) have identified two QTLs for root Na^+/K^+ ratio that were mapped to chromosomes 2 and 6 by using F₂ population of a hybrid within indica rice cultivar 'IR36' and japonica rice cultivar 'Jiucaiqing'. In rice different QTLs have been recognized for Salt tolerance which include those at chromosome number 1- *Saltol* QTL, *QNa*, and *SKC1/OsHKT8* along with, *QNa:K* on chromosome 4. *Saltol* states many changes for the uptake of ion during salinity stress (Bonilla et al., 2002; Gregorio et al., 2002). For highest Na^+ uptake *QNa* is QTL (Flowers et al., 2000) and for Na^+/K^+ , *QNa:K* is the corresponding QTL (Singh et al., 2001). *SKC1/OsHKT8* is the resultant QTL for K^+/Na^+ ratio regulation for homeostasis in salt stress tolerant indica cultivar 'Nona Bokra' (Lin et al., 2004; Ren et al., 2005). Many other QTLs are identified in the root for Na^+/K^+ ratio except chromosome 9 and for exchange of ion three QTLs on chromosomes 10 and 3 (Sabouri and Sabouri, 2008), for tissue Na^+/K^+ ratio four QTLs and each for Na^+ and K^+ uptake on various chromosomes one QTL (Lang et al., 2001). Consequently, 14 QTLs has been identified for shoot and root Na^+/K^+ ratio and Na^+ and K^+ content on different rice chromosomes (Ahmadi, Fotokian, 2011).

The *QKr1.2* was identified as one of the major QTL on chromosome 1 for root K^+ content, that explained around 30% of the variation of observed salt stress tolerance in rice. Moreover, two newly identified QTLs (*SalTol8-1* and *SalTol10-1*) on chromosome 8 and 10 based on an F₂ hybrid of a cross between a high salt stress tolerant line (IR61920-3B-22-2-1) and a medium salt stress tolerant line BRRI- dhan40 (Islam et al., 2011). Many studies have revealed QTLs for salt stress tolerance related phenotypes in *Hordeum vulgare* L. (barley). Lately, 30 QTLs were identified for 10 different traits, such as K^+ and shoot Na^+ content, yield-related traits, several growth and Na^+/K^+ ratio, in populations grown on normal soil and saline soil. In the three species of *Helianthus* sp. (sunflower) and *Helianthus paradoxus*, fourteen ion uptake QTLs were identified for QTL analysis from highly salt affected habitat and its salt sensitive ancestor *H. petiolaris* and *H. annuus* (Lexer et al., 2003).

Huyen et al. (2013) developed new rice lines with salinity tolerance and high yield by applying markers assisted selection (MAS). Q5DB/FL478 were investigated to evaluate the introgression of *Saltol* fragment into Q5DB cultivar and developed salt tolerant rice with high yield. In one of the study (D Leon TB et al., 2017), introgression lines (ILs) of a salt tolerant donor line 'Pokkali' developed in a susceptible high yielding rice cultivar 'Bengal' background was evaluated

for numerous morphological and physiological traits under salt stress. Both SSR and genotyping-by-sequencing (GBS) derived SNP markers were employed to characterize the ILs and identify QTLs for salinity tolerance trait. In recent study various efforts have been made to generate NILs of a popular rice genotype 'Improved White Ponni' displaying increased tolerance against salinity through marker assisted introgression of 'Saltol', which is a major QTL of FL478. IWP-*Satol* NILs exhibited enhanced tolerance against salinity under hydroponic conditions (Valarmathi et al., 2019).

Lately, Muthu et al. (2020) developed abiotic stress-tolerant rice genotypes in the genetic background of the popular rice variety Improved White Ponni (IWP) through a marker assisted backcross breeding approach by introgressing major effect quantitative trait loci (QTLs) conferring tolerance against drought (qDTY_{1.1}, qDTY_{2.1}), salinity (*Saltol*), and submergence (*Sub1*). Additional studies are required to decide the benefits of unreported QTLs for crop breeding to improve salt stress tolerance. As molecular marker techniques for breeding is economical and rapid. This technique is a very powerful method to enhance breeding programs to improve plant tolerance toward salinity.

Pond soil culture technology

In rural areas where there is a sodic-saline land for farming on these land, rural farmers use a method in which they use the dry fertile soil of the ponds and put it on sodic-saline land at a certain level, which makes that land fertile. Scientifically observed, the same amount of micros are found in the soil of the ponds, which make the soil of the pond more fertile and when these microbes reach the sodic-saline land slowly these lands are also made fertile, by which this land is ready to grow different crops (Figure 4).

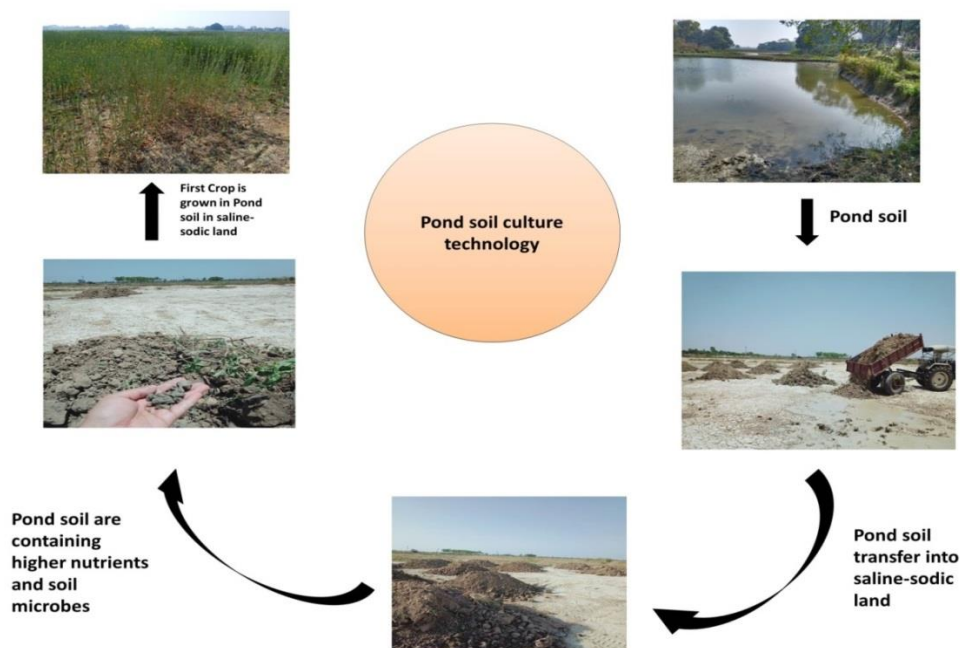


Fig. 4. Pond soil culture technology which mostly uses in East Uttar Pradesh where land is saline-sodic, these photographs are taken from a village of east Uttar Pradesh Machhlishahr of Jaunpur district name Pauha, India where this technology is used by progressive farmers

3. Conclusion

Soil salinity poses a serious threat to food security worldwide. To meet with food requirement of the ever-increasing population and shrinkage of cultivable land due to industrialization and urbanization has put the onus on the scientific community to develop sustainable agriculture practices and enhance food production, restore salt-affected soils, and its management through government policymaking, and contribution from all stakeholder provide potential hope of land expansion and production enhancement for future food security. Agricultural intensification through various methods like nanoparticles-based agro-practices, genetic engineering,

development of salt stress plants deemed indispensable and possibly leading to increased food production per unit area that paves the way to achieve food sustainability.

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