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Section 1. Agricultural sciences

PRODUCTION AND STUDY OF THREE-COMPONENT MIXTURES OF PHOSPHO-POLYMER COMPLEXES

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Abstract

The article is based on the preparation of a three-component composite mixture (TCCM) based on phosphogypsum, an interpolymer complex and humus and its study. It is known that phosphogypsum is a waste of the chemical industry.. The results of scientific research and practical experience have convincingly proved the technical feasibility and expediency of using phosphogypsum in the national economy instead of traditional types of natural raw materials. A brief description of phosphogypsum, promising directions of its processing and some statistical data are presented.

The use of TCCM based on phosphogypsum for effective fertilizing in various soil and climatic zones for cereals, vegetables, industrial and other agricultural crops, to improve the structure of the soil. That the application of TCCM as a chemical structure of soil formers gives an improvement in the chemical, physical and water-physical properties of saline soils.

Keywords: *interpolymer complex, phosphogypsum, humus, soil structure, chemical reclamation, salinization, gypsum, calcium dihydrate, calcium semi-hydrate, composite complex*

Introduction

The rapid pace of development of industry, energy, metallurgy, metalworking, chemical, petrochemical and other industries, as well as areas of engineering, construction and household activities entail the inevitable formation and accumulation of industrial waste on a global scale. And one of the mass types of waste is waste from the chemical industry. Currently the Republic of Belarus is solving the problem of processing a by-product — phosphonyls, formed in the process of phosphoric acid production. The issue of utilization of phosphonyls is becoming more and more relevant, and there are several reasons for this: transportation of phosphonyls to dumps and its storage require large capital investments and operating costs; when

creating phosphonyls dumps, it is necessary to alienate large areas, sometimes even cultivated land; storage of this material in dumps, even with the neutralization of soluble impurities and with the observance of dump operational rules causes irreparable harm to the environment. There are known studies of scientists on the use of phosphonyls for road construction as a binder for strengthening soils, foundations and repair work. The paper presents the results of experiments on obtaining road-building materials from this waste without converting it into a binder. Based on the research, a technology for the preparation of asphalt concrete mixtures with the use of mineral powder in the form of phosphonyls dihydrate has been developed (Kovalev Ya. N., 2021).

Thus, in the production of mineral fertilizers, various types of waste are formed, among which phosphonyls is the waste from the production of phosphorus fertilizers (Komilov K. U., 2005). It should be noted that at present, in general, there is a significant layer of agroecological problems associated primarily with extensive forms of environmental management, environmental degradation for various reasons. The shortcomings of common equipment for utilization of phosphonyls when processing it into semi-aqueous gypsum have been analyzed. Specific energy consumption per ton of produced construction gypsum in different equipment is shown. Calcination duration is compared. The reasons for the uncompetitively of the process of production of construction gypsum compared to the production of natural gypsum stone are analyzed. Two problems are considered. The first — common equipment for burning construction gypsum is energy-intensive. The second is the established practice of washing impurities in phosphonyls with water. At the same time, energy consumption increases several times due to the need for energy consumption for moisture evaporation. It is theoretically reasonable to carry out the firing in a suspended state. The firing time is a few seconds. The experimental studies show the possibility of producing construction gypsum by firing in a suspended state (Veshcheryakov Yu. G., 2007), including the irrational management of many branches of environmental management. The production of phosphoric acid from natural phosphate rock by the wet process gives rise to an industrial by-product called phosphonyls (PG). About 5 tons of PG are generated per ton of phosphoric acid production, and worldwide PG generation is estimated to be around 100––280 Mt per year. This by-product is mostly disposed of without any treatment, usually by dumping in large stockpiles. These are generally located in coastal areas close to phosphoric acid plants, where they occupy large land areas and cause serious environmental damage. PG is mainly composed of gypsum but also contains a high level of impurities such as phosphates, fluorides and sulphates, naturally occurring radionuclides, heavy metals, and other trace elements (Tayibi H., 2009).

Currently, there are more than 60 million tons of phosphonyls in the dumps of JSC Ammo Phos-Maxam and its quantity continues to increase annually (in terms of calcium dihydrate). There are a number of factors that an operator should consider before pursuing wet or dry stacking of the phosphonyls by-product from a phosphoric acid plant. In addition to process considerations, important factors include the climatologic regime, water balance considerations, hydrogeology, topography, capital cost, operating cost (and maintenance), closure costs (and handling of drainable pore water), availability (or scarcity) of a fresh water source, distance from the plant to the disposal site (and viability of dry versus wet transport methods), P_2O_5 recovery, impacts on the environment (from leakage, dusting, accidental spills, etc.) and applicable regulations (Nadim F., 2021). Monitoring studies of the phosphonyls dump located on the territory of the Almalyk chemical plant of mineral fertilizers of JSC Ammo Phos-Maxam showed that the stale phosphonyls has an identical chemical and phase composition. Phosphonyls stand for the chemical origin gypsum generated in fertilizers production, in which phosphate rock is attacked by sulfuric acid resulting in phosphoric acid (H_3PO_4) and phosphate fertilizers. Phosphonyls is not a commercial product and it is stocked in large open areas or accumulated in lakes inducing to a major environmental problem due to the presence of toxic and radioactive elements. The increasing world agricultural demand is the real responsible for the severity of this environmental problem. Nevertheless, there

are some possibilities for the application of this reject material, such as civil construction, waste water treatment, and in cultivated lands, etc. In the agriculture the phosphonyls is commonly used as a nutrient source due to its large amounts of phosphorus, calcium and sulfur. (Gennari R. F., 2011). Phosphonyls contains mainly oxides of calcium, sulfur and silicon with an admixture of oxides of iron, aluminum, magnesium, phosphorus, sodium and others. As can be seen from the table, the mass fraction of the main substance (CaSO4 * 2H2O) in terms of dry dihydrate is 97% (Larionov M. V., 2015), the mass fraction of hygroscopic moisture is 16.4%, the content of water–soluble fluoride compounds in terms of fluorine is 0.12%. No impurities of toxic compounds of cadmium, arsenic, mercury, lead were found in the composition of phosphonyls (Kurbanova A. Dj., 2021).

Table 1. *Results of chemical analysis of phosphonyls samples of JSC "Ammo Phos-Maxam" Almalyk, Uzbekistan*

Name of indicators	Phosphonyls (stale), dump of Almalyk-Maxam OJSC	
	density g/cm³–2.3	density g/cm³–2.4
1. $P_2O_{5\ common}$	2.00	1.39
2. SO_3	44.33	44.95
3. CaO	29.81	31.33
4. Fe_2O_3	0.29	0.64
5. F_{common}	0.42	0.39
6. SiO_2	13.75	12.44
7. Al_2O_3	0.31	0.58
8. Fe_2O_3	0.29	0.64
9. MgO	traces	0.5
Insoluble residue	9.09	7.78

The specific effective activity of natural radionuclides was determined for the samples of stale phosphonyls (waste of JSC Ammo Phos-Maxam), on the basis of which a sanitary and epidemiological conclusion was given that the samples of phosphonyls correspond to SP No. 202 of 03.02.2012. "Sanitary and epidemiological requirements for radiation safety" and phosphonyls can be used in economic activities without restrictions. Toxicological parameters were determined for phosphonyls samples, which showed that the toxicity of phosphonyls aqueous filtrate in an experiment on laboratory animals (white mice) corresponds to the 4th hazard class. The total toxicity index of the phosphonyls sample is 7.53 units, which according to GOST 30774–2001 refers this waste to hazard class 5 (not dangerous).

The total area of saline soils in the Republic of Uzbekistan is more than 2 million hectares, of which about 50% of the irrigated lands of Khorezm and the Republic of Karakalpakstan have undergone salinization and loss of nutrient reserves. For this reason, the yield of agricultural crops on these lands has decreased by almost 2 times.

To increase the yield of agricultural crops on saline and saline soils, it is necessary to increase calcium reserves in them by introducing calcium-containing chemical mixtures (gypsum, phosphonyls). In the conditions of the higher given areas, the most effective chemical mixture is phosphonyls, obtained as an industrial waste of phosphorus production (Kendivan O. D.-S., 2021). Today, a huge amount (more than 60 million) has accumulated at the Ammo Phos-Maxam plant (Almalyk, Uzbekistan). tons) phosphonyls, which consists mainly of calcium sulfate dihydrate (CaSO4 * 2H2O), phosphonyls also includes phosphates (1.3–2.9%) (Komilov K. U., 2021).

It should be noted that our country traditionally occupies one of the leading places in the Central Asian market of phosphate raw materials (Allayev J., 2021). In Uzbekistan, the largest enterprises in the mineral fertilizers industry are "Ammo Phos-Maxam" (Eshmatov A. M., 2021).

The problem of using phosphonyls as a secondary raw material for the production of liquid products has been relevant since the 60 s of the XX century (Temirov G. B., 2021). The results of numerous studies and practice have convincingly proved the technical feasibility and expediency of using phosphonyls in the national economy instead of traditional types of natural raw materials. This is due to the content of 80 to 98% gypsum in phosphonyls, which allows it to be attributed to gypsum raw materials. Here it should be noted the most promising areas of use of phosphonyls as a valuable large-tonnage secondary resource:

- in agriculture for chemical reclamation of acidic and saline soils and composting with organic fertilizers;
- in the cement industry as a mineralizer — an additive to the raw mixture and as a setting speed regulator — instead of natural gypsum;
- for the production of gypsum binders and products, filler in the production of plastics, glass;
- in the construction of highways, construction of buildings and structures;
- in the development of marine and coastal zones;
- for the production of sulfuric acid, etc.

Research methods

Thermal analysis. Phosphonyls, one of the components of a three-component mixture, was heated to 300 degrees Celsius and subjected to heat treatment.

Quantitative analysis. A 0.1 m/l solution of an interpolymer complex (obtained on the basis of 1:1 oligomeric urea formaldehyde and carboxyl methylcellulose) was prepared and mixed with spraying to the resulting phosphonyls mass.

Discussion

Humus was introduced into the resulting phosphonyls mass (phosphonyls-humus 5:1)

and formed a three-component composite mixture.

To improve the structure of the soil, it is desirable to include various structural formations in its composition. For this purpose, we have developed and carried out laboratory treatment of a three-component composite mixture that positively changes the structure of the soil.

Phosphonyls is used for: cleavage, soil salinization and reclamation of salt pans. Phosphonyls is effectively used on soils with a high sodium content. Mixed with lime for reclamation of acidic soils. As fertilizer ameliorants (1 ton of phosphonyls contains about 10 kg of phosphorite). For composting with biological products and organic fertilizers.

We have obtained a three-component composite mixture taking into account some of the above features.

The efficiency of using phosphonyls in heat treatment will be relatively higher compared to the fact that it dies only by itself as an improver of soil stricture, which we came to on the basis of our research.

Results and discussion. In connection with the above, laboratory and field studies were carried out using a three-component composite mixture (TCCS) as soil structurers. TKCC is introduced into the soil together with plowing, in which trace elements, Ca, S, are introduced into the soil, a water-saving process with an interpolymer complex occurs, and the intake of humus leads to an increase in soil fertility.

Conclusion

According to forecasts, the amount of waste may double by 2040. The question of bringing phosphonyls to such a state that it is possible to use it entirely and it is cost-effective, or assimilate waste in the natural environment without compromising its natural state is more relevant than ever.

Thus, modern problems of environmental management and waste generation are interrelated, which requires a step-by-step and at the same time a comprehensive solution.

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Section 2. Biology

UNMASKING GENETIC VULNERABILITIES IN BREAST CANCER THROUGH SNP ANALYSIS

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Abstract

Breast cancer is a prevalent and severe malignancy with significant morbidity and mortality rates worldwide. This investigation sought to elucidate the relationship between single nucleotide polymorphisms (SNPs) and breast cancer. Genome-wide sequencing data from the Sequence Read Archive were harnessed, and comprehensive pipelines were developed to align sequences against chromosome 10 in a cohort of individuals with a history of breast cancer. The study found that while the PTEN gene exhibited just a single unique SNP, suggesting its genetic resilience, other genes presented with a notably higher number of SNPs. Specifically, genes without a defined function harbored the most significant number of unique SNPs. Prior research has underscored its role as a tumor suppressor and its critical association with various malignancies, including breast cancer. These insights offer a deeper understanding of the genomic intricacies of breast cancer, revealing potential genetic vulnerabilities and emphasizing the significance of particular genes and SNP contributions to the disease.

Keywords: *breast cancer, single nucleotide polymorphisms (SNPs), PTEN*

Introduction

Breast Cancer

Breast cancer, a prevalent and life-threatening disease, is characterized by the uncontrolled growth of cells in the breast tissue, leading to the formation of abnormal masses or lumps (Wilkinson & Gathani, 2022). These growths can often be detected through palpable breast lumps or thickening, which feel distinguishable from the surrounding tissue. Breast cancer can manifest in both women and men, although the incidence is significantly higher in women. In the United States, approximately 264.000 cases of breast cancer are diagnosed annually in women, along with approximately 2.400 cases in men (Centers for Disease Control and Prevention, n.d.). Breast cancer remains a major public health concern globally, with a staggering 685,000 reported deaths in 2020 (World Health Organization, n.d.).

Stages

Breast cancer is classified into distinct stages, illustrated in Figure 1, that denotes its progression and severity, offering crucial insights for diagnosis and therapeutic strategies. Starting with stage 0, or ductal carcinoma *in situ* (DCIS), the cancer remains non-invasive, localized within the breast's ductal structures, yet, around 40% of DCIS cases can evolve into invasive forms (Trayes & Co-

kenakes, 2021). Stage I marks the onset of invasive breast cancer, subdivided into stages IA and IB. Specifically, stage IA pertains to tumors up to 2 cm contained within the breast and lacking lymph node involvement. Conversely, stage IB is characterized by the absence of a primary breast tumor but features small cancer cell clusters (0.2 mm to 2 mm) in the lymph nodes (*Breast Cancer Stages*, 2019).

Figure 1. *Stages of Breast Cancer*
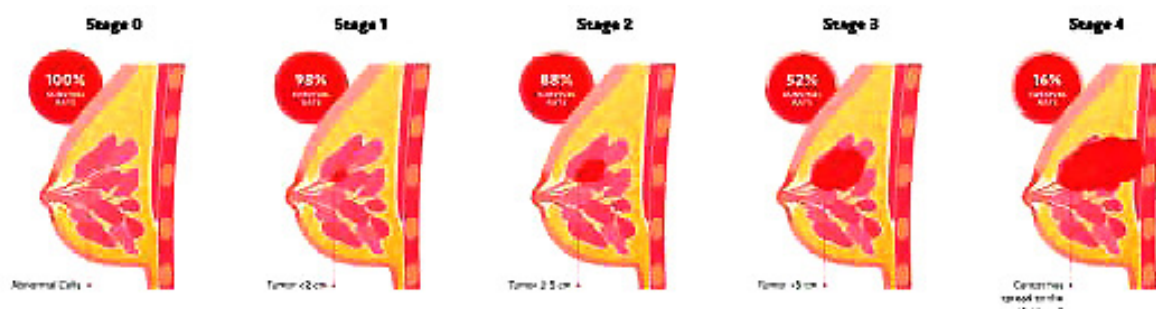
The stages of breast cancer range from 0 to IV numerically. Stage 0 denotes a cancer-free breast clear of any cancerous migration of abnormal cells. This stage demonstrates that the cancer is *in situ*, or present where it first appeared. The strength of the tumor's development increases from stages I through IV. Stage IV indicates that the cancer has progressed to nearby or distant body organs (Coughlin, 2019).

Stage II of breast cancer is categorized into two distinct sub-stages: IIA and IIB. In stage IIA, the tumor exceeds 2 mm but not 5cm in size and involves one to three axillary lymph nodes near the breast bone. Stage IIB is characterized by a tumor either more prominent than 5cm or 2 cm — 5cm with involvement of four to nine axillary lymph nodes, signifying a more extensive spread (Giammarile *et al.*, 2022). Stage III, on the other hand, indicates a more advanced stage where cancer has invaded the skin of the breast or the chest wall, exceeding 5cm in size, with the possible involvement of ten or more axillary lymph nodes or lymph nodes above or below the collarbone. The severity and spread continue to escalate through stages I to IV (*Breast Cancer Treatment*, 2021). Stage IV, known as metastatic breast cancer, marks the progression where the cancer cells have metastasized beyond the breast to distant organs such as the lungs, liver,

or brain. This pattern of progression illustrates the systematic manner in which breast cancer evolves and expands, with each stage signifying a more complex and extensive spread of the disease (*Breast Cancer Treatment*, 2021).

Treatments

The treatment paradigms for breast cancer are stratified based on the stage and molecular characteristics of the malignancy. In cases of DCIS, management options may include lumpectomy followed by radiation therapy or mastectomy, with additional endocrine therapy if the lesion is estrogen receptor-positive (*Breast Cancer Treatment*, 2021). For early invasive stages (Stages I, II a, II b) and locally advanced stages (Stages III a, III b, III c) that are nonmetastatic, a three-phase approach is typically employed. The preoperative phase may involve systemic therapies such as endocrine or immunotherapies, contingent on the expression of estrogen, progesterone, or ERBB2 receptors (Kerr *et al.*, 2022). Conversely, preoperative chemotherapy is indicated for tumors lacking these receptors. Surgical intervention may encompass a lumpectomy, accompanied by radiation if complete excision with satisfactory cosmetic outcomes is achievable, or a mastectomy otherwise. The postoperative phase integrates a multidisciplinary approach, consisting of radiation, endocrine therapy, immunotherapy, and chemotherapy,

tailored to the tumor's unique molecular profile and clinical context (*Breast Cancer Treatment*, 2021).

These therapeutic interventions, each with its unique pharmacological mechanisms, carry distinct adverse effects that vary in severity and manifestation. Immunotherapy may lead to fatigue and nausea, but can also result in more critical complications such as left heart dysfunction and myelosuppression (Fisusi & Akala, 2019). Chemotherapy, targeting rapidly dividing cells, can induce a broad spectrum of side effects ranging from bone marrow suppression, electrolyte abnormalities, gastrointestinal distress, alopecia, and myelosuppression to acute and delayed cardiotoxicity and peripheral neuropathy (Rossi *et al.*, 2019). Endocrine therapy, which modulates hormonal pathways, may be associated with hot flashes, an elevated risk of thromboembolism and uterine cancer, myalgias, and osteoporosis-related bone fractures. Additionally, agents that modify bone metabolism can induce fatigue, heartburn, gastrointestinal symptoms, peripheral edema, hypophosphatemia, and osteonecrosis of the jaw. The diverse nature of these side effects underscores the complexity of cancer treatment and necessitates a personalized, multidisciplinary approach to manage and mitigate these challenges (Rossi *et al.*, 2019).

Gene

The phosphatase and tensin homolog (PTEN) gene, situated on chromosome 10q23.31, has been the focus of our investigation for its relationship with breast cancer (Yehia *et al.*, 2020). PTEN, under normal physiological conditions, functions as a tumor suppressor by controlling cellular proliferation (see Figure 2). Its germline mutations are implicated in Cowden syndrome, a rare disorder characterized by an increased predisposition to both malignant and benign tumors in multiple organs, including breasts, digestive tract, thyroid, uterus, and ovaries. In a separate investigation conducted by a different laboratory, (Zhang *et al.*, 2013), PTEN expression was detected in 57.5% of patients diagnosed with breast carcinoma. Their analysis revealed a low occurrence of PTEN mutations, with only one instance identified among 45 sporadic breast cancer cases. The researchers in that study postulated that PTEN promoter methylation might have been the primary mechanism contributing to the decreased expression of PTEN. The findings from this distinct study further reinforce the critical role that PTEN plays in the tumorigenesis, progression, and prognostic evaluation of breast cancer, and provide additional insights into the complex genetic landscape of this disease (Alvarez-Garcia *et al.*, 2019).

Figure 2. *Detailed schematic of PTEN lipid phosphatase activity*
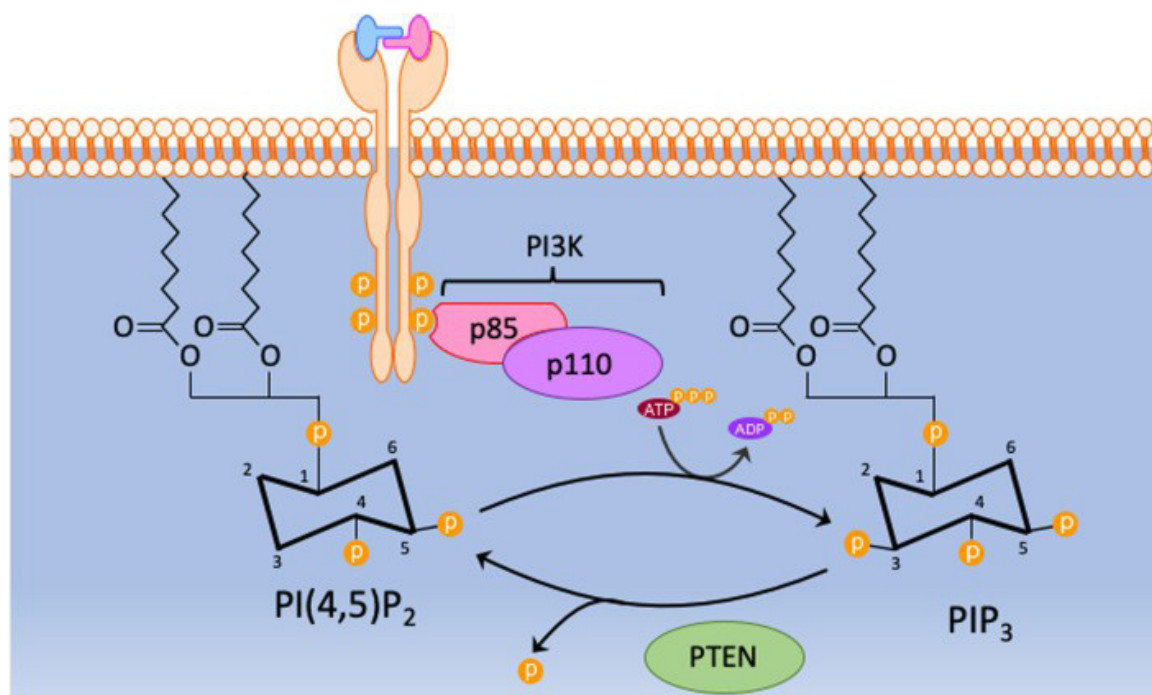
PTEN, a critical tumor suppressor protein, functions by selectively targeting the inositol ring at the 3rd position of phosphatidylinositol-(3,4,5)-triphosphate (PIP3). Through its enzymatic action, PTEN dephosphorylates PIP3, effectively converting it into

phosphatidylinositol-4,5-bisphosphate (PI(4,5) P2). This activity serves as a crucial regulatory mechanism in cellular pathways, especially those related to cell growth and survival (Chow & Salmena, 2020).

SNPs

Single Nucleotide Polymorphisms (SNPs) represent individual positions in the human genome where the nucleotide varies across different individuals, constituting the most prevalent form of genetic variation. In the context of non-familial breast cancer, SNPs are significant contributors, accounting for approximately 16% of genetic risk (He *et al.*, 2019). Specific to SNP18, its potential as a predictive marker for breast cancer (including invasive and ductal carcinoma *in situ*) was investigated in a cohort of 9363 women (mean age of 59, ranging from 46 to 73 years), (Su *et al.,* 2021) Among these women, 466 were diagnosed with breast cancer (271 prevalent; 195 incidents). The predictive power of SNP18 remained consistent whether unadjusted or adjusted for mammographic density and traditional risk factors, with odds ratios per interquartile range of 1.56 (95% CI, 1.38–1.77) and 1.53 (95% CI, 1.35–1.74), respectively.

Importantly, the observed risks are closely aligned with expected values, as indicated by an adjusted observed-to-expected odds ratio of 0.98 (95% CI, 0.69–1.28) (Roberts *et al.*, 2023).

The continued study and identification of SNPs may revolutionize personalized care in breast cancer management. This offers a further refinement of risk classification and holds the potential to integrate seamlessly with established risk-assessment strategies such as family history and phenotypic evaluations (Fagny *et al.*, 2020). SNP analysis is especially pertinent for women at high risk, who may seek genetic information to inform their choices about preventive or risk-reducing interventions. This approach to personalized risk assessment opens new avenues in breast cancer care, harnessing genetic in-

sights to augment clinical decision-making, particularly among those most vulnerable to the disease (Howe *et al.*, 2014).

Methods

The human genome reference sequence is an invaluable asset for contemporary genomics research, allowing for the examination of genetic polymorphisms across different individuals. In the present study, sequence reads from both BRCA patients and healthy controls were analyzed. The human reference genome, specifically chromosome 12 from Ensembl Release 104, was downloaded to facilitate the comparison of genetic variants relevant to our study (Cunningham *et al.*, 2021).

The Sequence Read Archive (SRA) sequences (PRJNA933635) were selected, adhering to the library strategy and comprehensive study design. The files were acquired using the fastq-dump tool from the SRA Toolkit (v2.10.7) (NCBI, 2021) and processed using terminal commands. The quality of the sequence reads was scrutinized with the FastQC tool (v0.11.9) to ensure the robustness of our analysis (Andrews, 2010). Following this, the sequences were refined using Trimmomatic (v0.39), and regions with poor base quality (Phred quality score < 33) were identified and addressed (Bolger *et al.*, 2014).

For alignment with the human reference genome, Bowtie2 (v2.4.2) was employed, followed by indexing of the reads (Langmead and Salzberg, 2012). The output in SAM format was then converted into a more succinct Binary Alignment/Map (BAM) file using SAMtools (v1.11) (Li *et al.*, 2009). Subsequent sorting and read coverage calculations enabled the assessment of coverage depth and identification of regions with potential genetic polymorphisms. Single nucleotide polymorphisms (SNPs) were discerned utilizing the BCF tools from the SAMtools suite, with subsequent filtering for high-quality variants through BCFTools (v1.11).

Statistical associations between variants in the BRCA cohort and the control cohort were appraised via RStudio, utilizing chi-square tests for categorical variables evaluation. The contingencies were structured, and chi-square statistics and p-values were calculated to quantify discrepancies and ascertain

statistical significance. A significant association ($p < 0.05$) emerged between the variants and the BRCA cohort, furnishing substantial evidence to refute the null hypothesis.

In RStudio, necessary libraries were loaded, and the datasets for both cohorts were prepared and merged for statistical testing. Specific code implementation details are described, including the condition check for saving significant association data to a file named "significant_association.csv".

To correlate SNP accession numbers with genetic consequences, Ensembl was accessed via a Python script. SNP information was retrieved from the BCF file and cross-referenced with Ensembl REST API, including attributes such as genomic location, alleles, and potential consequences. The process was automated using Python, ensuring efficiency and accuracy, and the results were integrated into a tab-separated file for further inquiry.

All Python scripts, including those employed for sequence read analysis and Ensembl access, are publicly hosted on GitHub (https://github.com/crisprmax/SNP-identifier-Python), complete with documentation and execution instructions.

Results

SNP Distribution Across Genetic Variants

Upon analysis of the SNP distribution (Figure 3), it is evident that the highest prevalence of SNPs is associated with unknown variants. This is succeeded by the missense variant in terms of SNP frequency. Interestingly, the intergenic variant demonstrated the minimal number of SNPs. While intergenic variants are typically common, the observed low SNP count could be an outcome of stochastic variation or may warrant further investigation into the sampling or sequencing processes.

Figure 3. *Distribution of SNPs across distinct genetic variants. The data reveals a predominant occurrence of SNPs in unknown variants, succeeded by missense variants, with the intergenic variants exhibiting the lowest frequency*
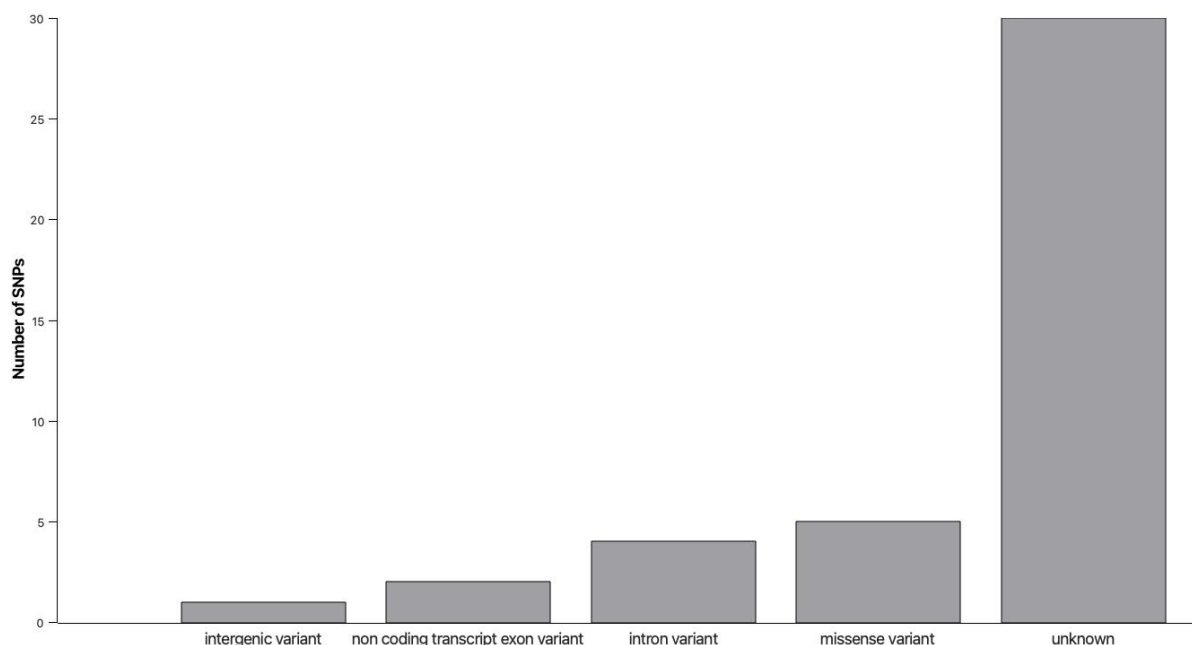
Characterization of Genetic Variants

Four principal genetic variants were delineated in this study:

1. Intergenic Variant: This variant represents sequence variations situated between genes within the intergenic regions.

2. Non-coding Transcript Exon Variant: Predominantly, these variations arise due to exon skipping events at either the first or last exon, potentially leading to the absence of start or stop codons.

3. Intron Variant: Introns play a pivotal role in diversifying the proteins produced from a gene's mRNA molecules. They can give rise to non-coding RNA and enable a plethora of protein varieties or differential protein levels specific to a cell type. Their

presence augments the evolutionary rate, facilitating the genesis of novel genes via exon duplication.

4. Missense Variant: Missense mutations can modulate DNA-transcription factor interactions, subsequently altering protein expression patterns.

Analysis of Unique SNPs in Genes

From the comprehensive analysis delineated in Table 1, it becomes evident that a significant portion of the unique SNPs, amounting to 127, are linked with genes that remain uncharacterized or have not been extensively studied in the current genetic landscape. This highlights a vast realm of the genome that warrants further investigation for its potential roles in various biological processes. In stark contrast, the PTEN gene, a pivotal regulator integral to numerous cellular pathways including cell growth, division, and apoptosis, showcased a mere single unique SNP. The limited genetic variability within PTEN is indicative of its conserved nature through evolutionary timelines. Such conservation suggests that any perturbation or mutation within this gene could lead to significant cellular anomalies, reinforcing its indispensable role in maintaining cellular homeostasis and integrity.

Table 1. *Distribution of unique SNPs across various genes. Notably, the PTEN gene exhibits a single unique SNP, while a significant fraction of SNPs are associated with genes that remain uncharacterized*

Gene Name	Gene Function	Total Unique SNPs
none	none	127
none	novel transcript	50
none	general transcription factor IIi (GTF2I) pseudogene	42
MTPAP	mitochondrial poly(A) polymerase	27
none	zinc finger protein pseudogene	24
SGMS1-AS1	SGMS1 antisense RNA 1	22
C10orf143	chromosome 10 open reading frame 143	20
BMS1	BMS1 ribosome biogenesis factor	18
AGGF1P2	angiogenic factor with G-patch and FHA domains 1 pseudogene 2	17
IMPDH1P5	inosine monophosphate dehydrogenase 1 pseudogene 5	13
GOLGA2P6	GOLGA2 pseudogene 6	13
OLMALINC	oligodendrocyte maturation-associated long intergenic non-coding RNA	13
CTNNA3	catenin alpha 3	10
LRRC37A6P	leucine rich repeat containing 37 member A6, pseudogene	9
ACTA2	actin alpha 2, smooth muscle	8
PTEN	phosphatase and tensin homolog	1

Discussion:

The exploration into various genetic variants and their influence on breast cancer provides critical insights into the intricate dynamics of the genome. Genetic variants, as showcased by this study, can have multifaceted consequences such as altering protein function.

Variants and Their Implications

- **Intergenic Variants**: The observed reduced number of SNPs in intergenic regions, as delineated from Figure 3, raises intriguing possibilities specific to breast cancer genetics. Given that these regions might be evolutionarily conserved, alterations within them could be indicative of crucial regulatory or structural roles that, when disrupted, may predispose individuals to breast cancer. Alternatively, changes in these regions might not manifest

immediately in the breast tissue phenotype, thereby evading early detection and potentially allowing for unnoticed progression of the disease.

- **Non-Coding Transcript Exon Variants**: In the context of breast cancer, potential alterations, such as the loss of start or stop codons, can lead to aberrant protein synthesis. These truncated or elongated proteins may disrupt normal cellular pathways, potentially driving oncogenesis or promoting tumor progression. Recognizing these variants is vital as they could be linked to specific breast cancer subtypes or influence responsiveness to treatments.

- **Intron Variants**: Introns, given their role as recombination hotspots, can be instrumental in breast cancer's genetic landscape. Their capacity to enable new exon combinations suggests they might contribute to the genetic heterogeneity observed in breast tumors. Such diversity can impact treatment outcomes, where certain combinations could confer resistance to standard therapies or lead to more aggressive disease forms;

- **Missense Variants**: These variants hold particular importance. A single amino acid change, especially in genes pivotal to breast cell regulation, can profoundly influence the cell's behavior. Whether it leads to loss of tumor suppressor functions, enhancement of oncogenic pathways, or introduces novel, detrimental functionalities, understanding these missense mutations becomes paramount. Their study can not only aid in early diagnosis but also in tailoring treatments specific to the genetic makeup of the tumor.

Insights from SNP Distribution

The SNP distribution across various genes offers some intriguing observations. The observation that PTEN, a gene integral to many cellular functions, exhibited just a single unique SNP suggests its genetic resilience. This limited variability further underscores the likely catastrophic consequences mutations in this gene could precipitate. On the other hand, genes with a higher number of SNPs could either be mutating rapidly or have regions that don't impact their function significantly when altered.

Limitations and Future Directions

While this study has provided valuable insights, it is essential to acknowledge its limitations. For instance, the number of SNPs in a gene does not necessarily correlate with its importance or functionality. Additionally, the effects of these SNPs at a phenotypic level were not explored. Future studies could delve deeper into the functional implications of these SNPs, especially in genes with high SNP counts. It would also be worthwhile to investigate the broader evolutionary significance of these variants and their role in species adaptation and survival.

As advancements in technology continue to drive down the costs of DNA sequencing, it is anticipated that an increasing number of individuals will have access to detailed genetic profiling, enabling the identification of specific SNPs. If their genetic profiles exhibit SNPs aligned with those identified in this study as predisposing factors for breast cancer, these individuals could benefit from more frequent screenings, enhancing early detection and diagnosis. Empowered with this knowledge, they can proactively adopt lifestyle modifications, such as tailored exercise regimens and dietary changes, to mitigate risks and potentially prevent the onset of breast cancer.

Investigating these genetic variants holds significant importance in the realm of medical science. Such variants can equip clinicians with the tools to detect breast cancer at earlier stages, given that genetic modifications can predispose cells to aberrant growth patterns that culminate in malignancies. It is noteworthy that most DNA alterations precipitating cancer manifest within genes. These genes harbor essential instructions for the synthesis of proteins or specialized RNA entities, such as microRNA, underscoring their pivotal role in cellular function and integrity.

Conclusion:

This investigation offers an in-depth exploration of the genomic nuances linked to breast cancer, elucidating the roles of distinct genetic variants in both the initiation and advancement of the disease. The pronounced

SNP patterns in genes, particularly in the likes of PTEN, delineate potential genomic regions of vulnerability and stability pertinent to breast cancer. The observed constrained genetic variability in pivotal genes accentuates the profound impact that even subtle genomic alterations can exert on breast cancer susceptibility and its subsequent trajectory. These genetic variations transcend mere random genomic aberrations; they serve as central determinants in the breast cancer continuum, shaping individual predisposition, disease progression, and therapeutic responsiveness. As we progressively decode the multifaceted breast cancer genomic landscape, we edge closer to tailored diagnostic and treatment modalities, envisioning a future where breast cancer's predictability and management are significantly enhanced, if not its outright prevention.

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Section 3. Chemistry

METHODS OF EXTRACTING OIL CONTAMINANTS FROM ABSHERON SOIL

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Abstract

The detrimental impact of heavy oil fractions is attributed to the formation of a mechanical barrier between seeds, the root system, and the surrounding environment, hindering water-air and nutrient regimes. Soil biota also experiences significant suppression. Oil-contaminated soils undergo various transformations depending on the composition and duration of pollutant exposure, leading to changes in soil structure and even the compositional makeup of oil. This study presents the results of soil samples with high concentrations of oil fractions. It is established that oil-contaminated soils undergo substantial structural changes under environmental influence, including agglomeration with the formation of long hydrocarbon chains and difficult-to-break complexes. This should be considered in the development of soil remediation methods for oil contamination. Additionally, this factor serves as a continuous source of hydrocarbon pollution in the atmosphere. A mechanism for the action of this phenomenon is proposed.

Keywords: *oil-contaminated soil, oil hydrocarbons, solvent, volatile components, chromatography*

Introduction

The oil industry is recognized as a polluter of the natural environment, causing damage to the biosphere. Specific areas, due to oil spills, approach ecological disaster zones. There is a threat of sustainable, often irreversible, transformation of natural environment components when ecosystems' normal functioning is disrupted, affecting the life processes of plants, animals, and humans. Oil pollution is accompanied by changes in the physical, chemical, and biological properties of soils. Natural soil self-purification from oil contamination can take decades. Traditional methods of restoring oil-contaminated soils (burning, burying) are not only inefficient but also environmentally harmful (Babaev, E. R., 2018).

Burning oil products affect vegetation and animal populations; pyrolysis of oil and its components results in toxic polycyclic aromatic hydrocarbons. Covering oil spots sharply reduces the speed of oil destruction, creates an unfavourable anaerobic environment, and so on. Therefore, finding environmentally and human-friendly means and methods of bioremediation for oil-contaminated soils becomes particularly relevant. Changes in soil properties due to oil pollution and the speed of oil destruction are determined not only by the pollutant dose but also significantly by the initial microbiological activity of the soil (Macaulay, B. M., & Rees, D., 2014).

Soil pollution with oil leads to a sharp change in its properties: the soil becomes hydrophobic, causing a sudden change in its agrophysical and especially hydro-physical properties (Rakhmanova, G. F., Sharonova, N. L., & Degtyareva, I. A., 2016). The carbon-to-nitrogen ratio is severely disrupted, and the content of plant-available nutrients (nitrate nitrogen, mobile phosphorus, exchangeable potassium) decreases. These changes, along with the direct toxic impact of pollutants on plants, are the cause of death and reduced productivity of agricultural crops on contaminated soils. Light fractions of oil, in particular, exhibit strong phytotoxic effects (Pikovsky, Y. I., Ismailov, N. M., & Dorokhova, M. F., 2015).

The harmful impact of heavy oil fractions is caused by the formation of a mechanical barrier between seeds, root systems, and the surrounding environment, hindering water-air and nutrient regimes. Soil biota also experiences significant suppression. The effect of oil on soil organisms is largely determined by its concentration. In low concentrations, oil has a stimulating effect on soil biota as it serves as an energy substrate for a large group of microorganisms and contains substances that stimulate plant growth and development. Severe soil oil pollution is accompanied by acute toxic effects on living organisms, especially in the initial period after contamination (Orudzhev, E. F., Avdotin, V. P., & Bryanskaya, I. P., 2018).

The soil cover, a fundamental element of the landscape, is the first to bear the "ecological impact". Developing a methodology to combat soil pollution with oil and oil products

is an extremely complex matter (Theoharides, K. A., & Suberg, M., 2019). Soil reactions to oil pollution and their sensitivity to these pollutants differ in various soil zones and within associated landscapes. The main factors include the chemical composition of the contaminant, soil properties and composition, and the physico-geographical conditions of the area.

Soil is a challenging object of analysis, and its organic part is complex and diverse in composition. Any soil contains 1 to 15% organic matter depending on the soil type. Humus constitutes 85–90% of the total organic matter in the soil. Additionally, soils contain nonspecific substances such as fats, carbohydrates (cellulose, pectins, pectosans, mannans, etc.), proteins, amino acids, amides, lignins, tannins, terpenes, resins, etc. (Zhang, J., Fan, S., Yang, J., Du, X., Li, F., & Hou, H., 2014). Therefore, when choosing a solvent, the complex chemical composition of both the determined substance (oil product) and the investigated object (soil) must be taken into account.

The impregnation of soil mass with oil leads to changes in the chemical composition, properties, and structure of the soil. This primarily affects the humus horizon, where the carbon content sharply increases, but the soil's properties as a nutrient substrate for plants deteriorate. Oil products cause the formation of a stable hydrophobic film, thereby disrupting the recirculation and exchange of nutrients through the soil. In the soil profile, changes in redox conditions are possible, an increase in the mobility of humic components, and certain trace elements (Barrosa, F. C. de F., Vasconcellos, L. C. G., Carvalhoc, T. V., & Nascimento, R. F., 2014). Volatile components of oil (substances with a boiling point up to 200 °C) hold a significant place among petroleum-derived substances polluting natural objects. These compounds constitute a substantial portion (20–30%) of the oil composition and are the primary components of many widely used petroleum products (gasoline, diesel fuel, etc.). These compounds are highly toxic and relatively resistant to biodegradation, making them more migratory within landscapes compared to other oil hydrocarbons.

However, the mechanisms of redistribution of a broad spectrum of individual volatile organic substances from oil remain poorly researched in ecosystems. It is believed that the

self-cleaning rate of soils from volatile hydrocarbons (VHC) through physical evaporation is sufficiently high, and their study is generally not given due attention (Zhang J., Fan S., Yang J., Du X., Li F., Hou H., 2014). Most commonly used methods for assessing oil pollution do not involve determining the composition and content of volatile components, as they include analytical operations such as soil drying and solvent evaporation after oil product extraction. Currently, there is insufficient data on the composition and content of light oil components in soils and adjacent environments.

The content of VHC in oil-contaminated soils is influenced by various processes, such as physical evaporation, radial and vertical migration, biodegradation, and may be associated with differences in the redistribution and transformation of volatile hydrocarbons on different elements of the meso relief (Francisco Cláudio de Freitas Barrosa, Luiz Constantino Grombone Vasconcellosb, Técia Vieira Carvalhoc, Ronaldo Ferreira do Nascimentoa Removal 2014). The high mobility of volatile oil products can increase the risk of secondary contamination of water bodies through transport with surface and soil waters from adjacent areas. When entering rivers and lakes, oil products can concentrate at the interface between the water and bottom sediments and in the bottom sediments. Consequently, a high content of soluble and hard-to-oxidise oil hydrocarbons in the water may be sustained for a long time due to the influx from bottom deposits.

Research method

In the scope of investigating the long-term negative impact of oil pollution on soil ecosystems, we conducted laboratory studies on the specific composition and concentration of petroleum products. These studies were based on chemical methods: extraction using organic solvents, ignition to determine volatile components, and gas-liquid chromatography.We took samples from two oil-contaminated soils of different degrees from the "Balahanyneft" field. The samples were collected from the well area at two different locations on April 4, 2023.

We studied the processes of extracting petroleum products from the samples using various solvents: benzene, n-hexane, and toluene. For this, we took samples 1 and 2, placed them in a flask, added one of the solvents, stirred in a flask with a reflux condenser for 3 hours at a temperature of 21–22 °C. The extraction for each sample was repeated three times. Then, the extracts were combined and the solvent was evaporated.

Table 1. *Amount of Extracted Petroleum Products by Extraction Method from Oil-Contaminated Samples,%*

Solvents	Samples	
	1	2
Benzene	0.48%	0.12%
Hexane	0.47%	0.11%
Toluene	0.65%	0.18%

The obtained samples of petroleum products after extraction were analysed using gas-liquid chromatography. Among the currently available monitoring methods, the most promising one with simultaneous decryption of the chemical composition is gas chromatography with flame ionisation, allowing the determination of individual components in a mixture of petroleum products, making this analysis method indispensable. Therefore, the samples of extracted petroleum products were analysed using the mentioned method.

Analysis of results

Despite the potentially high self-cleaning rate of contaminated soils from volatile hydrocarbons through physical evaporation in the climatic conditions of our region, and considering the limited data on the composition and content of light components in soils and similar environments at the moment, we decided to determine the composition and content of volatile components. The content of these components is significant, reaching up to 0.56%, and these compounds are char-

acterized by high toxicity, relative resistance to biodegradation, and migratory capability in the soil compared to other hydrocarbons. The mechanisms of their distribution in ecosystems remain poorly studied.

For a qualitative and quantitative characterization of the degree of contamination of samples with light-volatile hydrocarbons, we conducted the following studies. We took 5 portions of each sample, placed them in porcelain crucibles, and subjected them to ignition at 100, 200, 300, 400, and 500 °C. Initially, we obtained data on the moisture content of these soil samples, followed by the evaporation of hydrocarbons with different boiling temperatures. Essentially, we studied the content of light-volatile components. The data are presented in Tables 2 and 3.
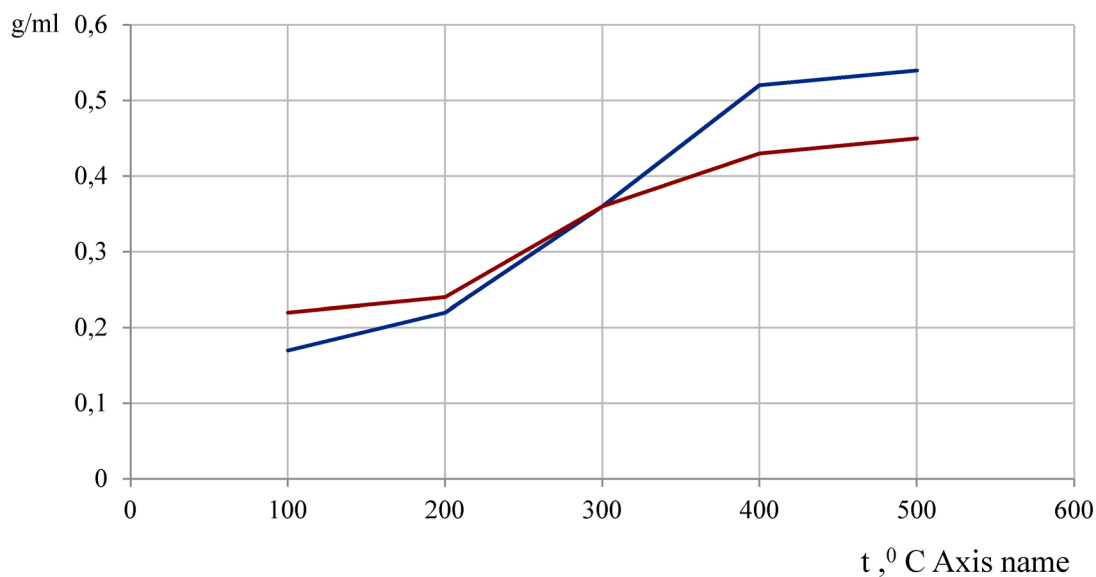
Table 2. *Content of Volatile Components in the Sample, g/ml*

Samples	Temperature, ^{0} C				
	100	200	300	400	500
A_1	0.17	0.19	0.38	0.52	0.55
B_1	0.19	0.24	0.40	0.51	0.53
C_1	0.16	0.23	0.38	0.53	0.55
D_1	0.17	0.23	0.22	0.4	0.51
E_1	0.18	0.20	0.42	0.55	0.56

Table 3. *Content of Volatile Components in the Sample, g/ml*

Samples	Temperature, ^{0} C				
	100	200	300	400	500
A_2	0.22	0.24	0.34	0.49	0.53
B_2	0.24	0.25	0.39	0.48	0.50
C_2	0.20	0.22	0.35	0.43	0.44
D_2	0.21	0.24	0.38	0.41	0.43
E_2	0.22	0.23	0.32	0.34	0.36

Figure 1. *Content of Volatile Components*

Conclusion

The research findings revealed that the content and composition of volatile compo- nents significantly vary depending on the sampling location of soils and the duration of contamination. Alongside heavy hydrocar-

bon fractions, the taken samples contain a certain amount of moisture and volatile toxic hydrocarbons (ranging from 0.17 to 0.56%).

Despite the existence of various methods for cleaning oil-contaminated soils, extraction remains the most effective physico-chemical method to date. In the future, we plan to enhance its efficiency through additives. In this study, organic solvents were applied as extractants, extracting petroleum products up to 0.65%. The extracted petroleum products can undergo additional industrial processing.

Even if land plots containing a large amount of petroleum products do not occupy extensive areas in a territorial context, they serve as constant sources of environmental pollution. Oil-contaminated soil mixtures with a high coefficient have the ability to form stable complexes, which, due to the gradual decay of heavy hydrocarbons over an extended period, become sources of hydrocarbon emissions. Considering that these sources of environmental pollution are located in densely populated areas of the Absheron Peninsula, eliminating these sources makes their urgency even more acute.

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Section 4. Food processing industry

OXIDATIVE TRANSFORMATIONS IN MEAT LIPIDS OF A NITRITE-FREE HAM, DRIED AND AGED IN NATURAL DRYING-AIR CONDITIONS

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Abstract

Raw dry-cured hams are highly valued and sought-after foods, the gastronomical identity of which is closely correlated to the climatic and geographical characteristics of the region of their production. The goal of the present study is to observe over time the oxidative transformations in the meat lipids of nitrite-free raw dry-cured pork leg during drying and maturing for 8, 18 and 36 months in natural drying-air conditions.

Prolonged maturation and drying of hams resulted in statistically meaningful differences in the ratios of PUFA and MUFA compared to SFA in meat lipids, which differences was observed to be more significant between samples aged 8 and 18 months, compared to the differences between samples aged 18 and 36 months. As drying and maturation progresses, the values of TBARs demonstrate tendency to go down and this tendency is more pronounced during the period 18÷36 months ($p < 0.05$). The complex analysis of the obtained results for the oxidative changes in the lipid fraction of the hams and their sensory perception shows that the duration of maturation over 18 months has a negative impact on the development of the aromatic and flavor properties as well as the sensory perceived value of these products.

Keywords: *dry meat products, lipid oxidation, PUFA, MUFA, SFA, organoleptic quality*

ОКИСЛИТЕЛЬНЫЕ ПРЕВРАЩЕНИЯ В ЛИПИДАХ МЯСА БЕЗНИТРИТНОЙ ВЕТЧИНЫ, ВЫСУШЕННОЙ И ВЫДЕРЖАННОЙ В ЕСТЕСТВЕННЫХ СУШИЛЬНО-ВОЗДУШНЫХ УСЛОВИЯХ

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Аннотация

Сыровяленые окорока являются высоко ценимыми и востребованными продуктами, своеобразие которых тесно связано с климатическими и географическими особенностями региона их производства. Цель данной работы – отследить окислительные превращения в мясных липидах безнитриного сыровяленого свиного окорока при вялении и созревании в течение 8, 18 и 36 месяцев в *natural drying-air conditions.*

Увеличение срока созревания и сушки ветчины водит к статистически значимым различиям в соотношении PUFA и MUFA по сравнению с SFA в мясных липидах, что было более существенным между образцами в возрасте от 8 до 18 месяцев по сравнению с образцами в возрасте от 18 до *36 месяцев*. По мере прогрессирования сушки и созревания значения *TBARs* показывают тенденцию к снижению, причём эта тенденция более выражена в период 18÷36 месяцев (p < 0,05). Комплексный анализ полученных результатов об окислительных изменениях липидной фракции ветчины и их сенсорном восприятии показал, что продолжительность созревания более 18 месяцев негативно влияет на развитие аромато-вкусовых свойств и сенсорную оценку этих продуктов.

Ключевые слова: *сухие мясные продукты, окисление липидов, ПНЖК, MUFA, SFA, органолептические качества*

Введение

Сыровяленая ветчина это высоко ценимые и востребованные продукты, идентичность которых тесно связана с климатом и географическими особенностями региона их производства (Toldrá, 2004).

В формировании сенсорного качества сыровяленой ветчины важную роль играют протекающие липолитические и окислительные процессы во внутримышечных липидах (Harkouss et al., 2015; Salazar et al., 2013; Salazar et al., 2016; Wei et al., 2023). Полученные гидролизом липидов ненасыщенные свободные жирные кислоты являются лёгким субстратом для окисления в мясной системе. В технологическом аспекте протекание реакций окисления липидов играет важную роль не только для органолептических качеств, но и для питательного и здорового образа этих сыровяленых мясных продуктов. Нитриты и/или нитраты используются по многим технологическим причинам при произ-водстве мясных продуктов, включая их антиоксидантный потенциал (Honikel, 2008). Вопреки этому, в некоторых традиционных ветчинах, таких как ветчина Парма, их не добавляют в солящую смесь, что влияет не только на цветовую характеристику, но и на окислительную стабильность липидов мяса (Ferrari et al., 2007; Wakamatsu, 2022).

В недостаточной степени изучено образование и накопление первичных и вторичных окислённых продуктов в ходе длительного процесса вяления и созревания свиных окороков, производимых без добавления нитратов и нитритов, и использование традиционных натуральных сушилок.

Вот почему фокусом данной работы является отслеживание окислительных трансформаций в мясных липидах безнитритного сыровяленого свиного окорока при сушке и созревании в течение 8, 18 и 36 месяцев в natural drying-air conditions.

Материалы и методы

Исследования проведены с традиционной для Еленского Балкана болгарской сыровяленой ветчиной, которая произведена без добавления нитритов и нитратов и высушена при natural air-drying conditions. Образцы сыровяленой ветчины «Еленски бут» получены от свиней, забитых в 12-месячном возрасте, выращенных в свиноводческом комплексе АО «Терахиб» – с. Никола Козлево, Болгария. От сырых свиных ножек отделяют тазовую кость, оставляя с голенью лишь небольшую часть тазового крыла (2–3 см). С внешней стороны кожа сохраняется, а с внутренней стороны удаляются мягкий и тазовый жир. Полученные окорока – со средним весом 10,595 ± 0,093 кг и pH, измеренным в *m Semimembranosus* – 5,86 ± ± 0,05. Окорока натирают по всей поверхности хлористым натрием и оставляют для посола и дозревания в камере при температуре 3 °C и относительной влажности воздуха 80–90% сроком на 45 дней. По окончании посола они очищаются от налипшей по поверхности солевой смеси, промываются чистой питьевой водой и после слива поступают в помещение, позволяющее дозревать и сушиться при естественных air-drying conditions в г. Елена (рис. 1). Размещение сыровяленых окороков в это помещение происходит в конце месяца Март, характеризующегося прохладным и сухим воздухом, при среднесуточных температурах от 2–5 °C до плюс 10–12 °C.

Для проведения анализов взяты образцы ветчины „Еленски бут" в возрасте 8, 18 и 36 месяцев сушки и созревания, причём исследуемые образцы содержали *m. Semimembranosus и m. Biceps femoris*. Образцы были доставлены в лаборатории УХТ-Пловдива в вакуумной упаковке и при холодильных условиях (<4 °C), а затем проанализированы в течение 24 часов. По каждому показателю проведено не менее пяти повторений измерений для образца.

Экстракция липидной фракции из исследуемых образцов проведена методом Bligh & Dyer, (1959). Определение жирнокислотного состава липидов проведено методом газовой хроматографии после предварительной этерификации высших жирных кислот низшими спиртами, метанолом, с целью получения в условиях анализа более летучих метиловых эфиров жирных кислот (ISO 5508). Индивидуальный состав идентифицирован с помощью свидетелей и, по относительному времени сдерживания, подведён к 100% (ISO 5508).

Исследование окислительных изменений липидной фракции проведено по показателям – пероксидному числу и вторичным окислённым продуктам путём определения тиобарбитуровых кислых реактивных соединений (TBARS).

Пероксидное число устанавливалось спектрофотомертично на основе окисления Fe^{2+} до Fe^{3+} в присутствии гидропероксидов и образования цветового комплекса между полученными Fe^{3+} ионами и SCN (тиоцианат), следуя рекомендациям Hornero-Méndez et al. (2001).

Тиобарбитуровокиселинные реактивоспособные соединения определены по методу, описанному Sörensen & Jörgensen, (1996).

Сенсорный анализ проведён дегустационной комиссией из 9 человек, включающей экспертов из области мяса. В ней основные показатели оценки делятся на 4 основные категории: 1. внешний вид и разрезанная поверхность; 2. цвет и стабильность цвета; 3. консистенция; 4. аромат и вкус. Продукт оценивается баллами от 1 до 5, максимальная оценка по каждому критерию – 5. В зависимости от критерия она умножается на фактор тяжести – для внешнего вида и разрезанной поверхности – x 1; для цвета и стабильности цвета – x 3; для консистенции – x 2; для аромата и вкуса – x 4. Сумма мультиплицированных оценок по отдельным показателям суммируется и делится на 10. Полученное таким образом значение даёт общую сенсорную оценку исследуемого продукта.

Статистическая обработка полученных данных осуществлена с помощью программного продукта «STATGRAFICS XVI». Проведён однофакторный дисперсионный анализ для оценки влияния продолжительности созревания (фактор I) на пероксидное число и тиобарбитуровокислые реактивноспособные соединения, а также в отношении показателей

сенсорного анализа. Расчёты проводились на уровне доверия α = 0,05 с использованием теста множественных сравнений Дункана. Эксперименты проведены с пятикратной повторяемостью, причём данные в таблицах и графиках среднеарифметические ± стандартное отклонение (SD).

Рисунок 1. *Помещение для natural drying-air conditons*

Результаты и обсуждение

В зависимости от длительности созревания и сушки изменения липидной фракции исследуемых сыровяленых ветчин представлены на (рис. 2 и в табл. 1 и 2).

Продление созревания и сушки сыровяленой ветчины при естественных воздушных условиях привело к статистически значимым различиям в соотношениях поли- и мононенасыщенных жирных кислот по сравнению с насыщенными жирными кислотами в липидах мяса (рис. 2 и табл. 1). Эти различия в процентном содержании ненасыщенных жирных кислот более существенны между образцами в возрасте 8 и 18 месяцев по сравнению с таковыми между образцами в возрасте 18 и 36 месяцев (табл. 1). Вероятно, более высокое содержание воды в образцах в возрасте 8 и 18 месяцев является причиной более интенсивных реакций окисления ненасыщенных жирных кислот, высвобождающихся при липолизе липидов мяса, что водит к слабому, но статистически значимому снижению ненасыщенных жирных кислот в общем жирнокислотном составе липидов мяса (p<0,05) (табл. 1). Доля жирных кислот C16:0, C16:1 и C18:0 несколько растёт с увеличением срока созревания, тогда как количество C17:0, C18:1 и C20:1 уменьшается. Изменения других жирных кислот не являются статистически значимыми (p>0,05). Доля полиненасыщенных жирных кислот в 18-месячных образцах статистически значимо снижается по сравнению с 8-месячными образцами (p<0,05), после чего остаётся неотличимой от определяемой в 36-месячных образцах (p>0,05), (табл. 1). В отличие от них количество мононенасыщенной олеиновой жирной кислоты (C18:1) уменьшается едва только в образцах, зревших в течение 36 месяцев.

Изменения количества первичных продуктов окисления липидов, определяемые по показателю пероксидного числа, показывают, что между образцами различной продолжительности созревания и сушки статистически значимых различий в содержании гидроперокси-

дов не выявлено (p > 0,05) (табл. 2). Об выравнивании скорости процесса образования окислённых пероксидов и их расщеплении и/или вступлении в реакции с другими веществами мясной матрицы сообщают и другие авторы (Andres et al., 2004).

Рисунок 2. *Жирнокислотный профиль образцов „Еленски бут“ в зависимости от продолжительности сушки и созревания*
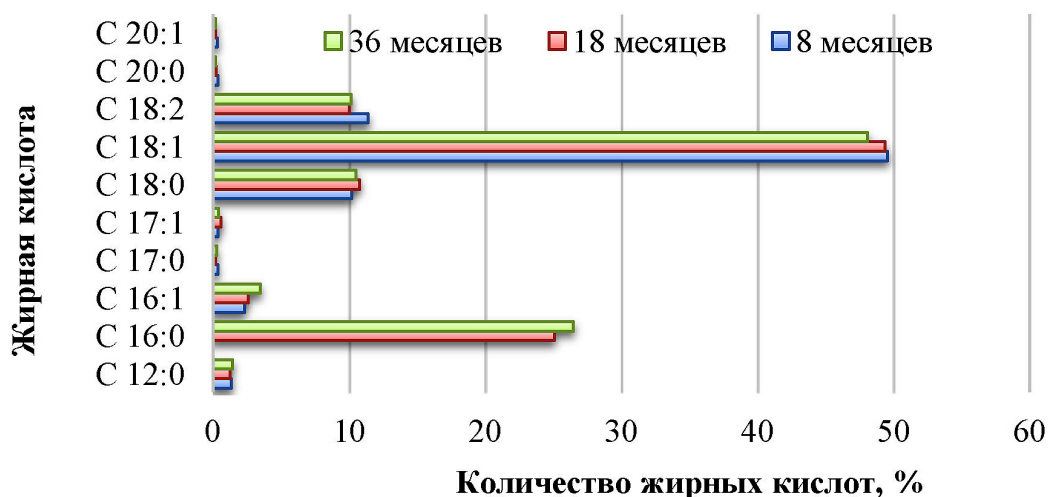
Таблица 1. *Изменения жирнокислотного профиля экстрагированных липидов из исследуемых образцов „Еленски бут“ с увеличением продолжительности сушки и созревания*

Показатель	Образец		
	8 месяцев	18 месяцев	36 месяцев
Насыщенные жирные кислоты НЖК,%	$37,16 \pm 0,63^a$	$37,37 \pm 0,29^a$	$38,75 \pm 0,5^b$
Ненасыщенные жирные кислоты, ННЖК,%	$63,84 \pm 0,37^b$	$62,63 \pm 0,3^a$	$62,17 \pm 0,42^a$
Мононенасыщенные жирные кислоты, МНЖК,%	$52,46 \pm 0,17^{a, b}$	$52,65 \pm 0,39^b$	$52,04 \pm 0,08^a$
Полиненасыщенные жирные кислоты, ПНЖК,%	$11,38 \pm 0,21^b$	$9,98 \pm 0,10^a$	$10,14 \pm 0,35^a$
Соотношение ННЖК/НЖК	$1,72 \pm 0,02^c$	$1,68 \pm 0,02^b$	$1,6 \pm 0,01^a$
Соотношение ПНЖК/НЖК	$0,31 \pm 0^c$	$0,27 \pm 0^b$	$0,26 \pm 0,01^a$

Примечание: Результаты в таблице представлены в виде относительных процентов площади соответствующих пиков, которые получены на хроматограмме, по отношению к общему количеству экстрагированных липидов; [a-c] *– значения в столбцах с одинаковыми буквенными обозначениями статистически неразличимы (p > 0,05).*

По сравнению с данными о пероксидном числе, данные TBARs показывают тенденцию к снижению по мере прогрессирования сушки и созревания, причём эта тенденция более выражена в течение периода 18÷36 месяцев (p < 0,05). За аналогичным уменьшением количества малонового альдегида, определенного через TBA, наблюдают и другие авторы, такие как Andrés *et al.,* (2004) исследовавшие сыровяленую иберийскую ветчину, а также Jin *et al.* (2012) в отношении сыровяленого свиного бекона.

Таблица 2. *Окислительные изменения липидной фракции исследуемых образцов „Еленски бут“ в зависимости от продолжительности сушки и созревания*

ОБРАЗЕЦ	ПОКАЗАТЕЛЬ	
	Пероксидное число meq O$_2$ /kg жир	TBARs Mmol TBA. kg-1 сухого вещества
8 месяцев	0,72 ± 0,34[a]	1,73 ± 0,54[b]
18 месяцев	0,62 ± 0,84[a]	1,29 ± 0,34[b]
36 месяцев	0,53 ± 0,95[a]	0,67 ± 0,11[a]

[a-c] *– значения в столбцах с одинаковыми буквенными обозначениями статистически неразличимы (p > 0,05).*

Снижение значений TBAR во время длительного периода созревания и сушки предположительно связано с тем, что альдегиды, которые нестабильны, могут расщепляться до летучих соединений (Jin et al., 2012). Другая гипотеза состоит в вероятности того, что они вступают в реакцию со свободными аминокислотными группами белков, в результате чего образуются новые соединения, такие как флуоресцентные Schiff базы (Gatellier et al., 2007). Таким образом предотвращается реакция альдегидов с ТВА, используемой в анализе (Harkouss et al., 2015).

Сенсорная оценка

Продление созревания с 8 до 18 месяцев в сушилках при естественных климатических условиях приводит к получению более высоких и статистически различимых оценок аромата и вкуса сыровяле-

ной ветчины (фиг. 3). В отличие от них, у образцов в возрасте 36 месяцев наблюдается снижение этих оценок, которые статистически значимо ниже, чем у двух других образцов. Основными недостатками, приводящими к снижению оценок, учитываются более жирный и горький вкус и более прогорклый запах, вероятно, из-за протекания в них более интенсивных окислительных и протеолитических реакций. Что касается цвета, то наблюдается тенденция к снижению оценок по мере увеличения времени созревания, причём самое низкое сенсорное восприятие цвета снова регистрируется в образцах в возрасте 36 месяцев. Образцы с продолжительностью созревания 18 месяцев получили самую высокую оценку за их внешний вид, но эта оценка статистически неотличима от той же оценки образцов возрастом 8 месяцев (p > 0,05).

Рисунок 3. *Органолептическая характеристика исследуемых образцов «Еленски бут» в зависимости от продолжительности сушки и созревания*
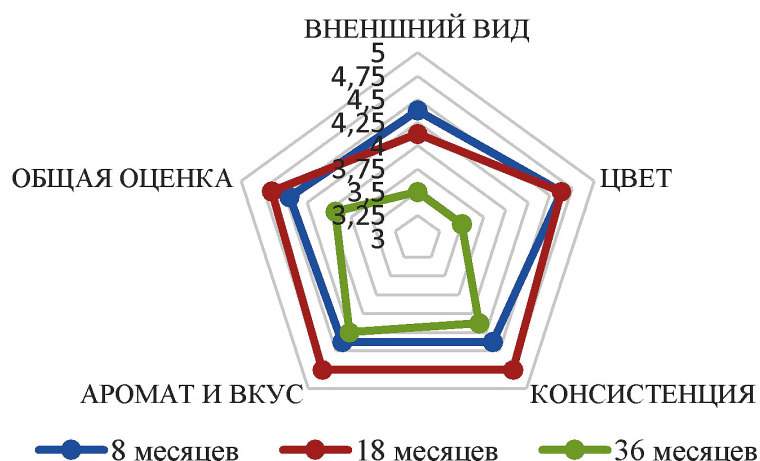
Заключение

Комплексный анализ полученных результатов об окислительных изменениях липидной фракции ветчины и её сенсорном восприятии показывает, что продолжительность созревания 18 месяцев в естественных климатических условиях может удовлетворить потребительский спрос на высококачественную сыровяленую ветчину с традиционным аспектом её производства. Продление созревания в этих условиях неоправданно и оказывает негативное влияние на развитие аромато-вкусовых свойств и сенсорную оценку этих продуктов.

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