*Keywords Z*hambyl region, anthrax, epidemiological situation, the epidemic situation, the road, "Western Europe - Western China".

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Shadenova E.A., Zhumabekov E.Zh., Sembekov M.T.

RGE "The institute of General genetics and cytology" CS MES RK

THE STUDY OF THE POLYMORPHISM OF THE KIND OF BETULA L.

Annotation

This paper presents the results of a study of polymorphism of six species of Betula L. growing in Kazakhstan.. Relationship between clones and their parental form set by comparing the profiles of amplified PCR products. Synthesized in the research process Semi-RAPD primers can be recommended for genotyping isolated and identified clones.

Keywords: Birch, identification, DNA extraction, PCR analysis.

Introduction

The previously genetic variety of birches and questions of their differentiated use by creating the plantation cultivations of raw designation in Kazakhstan were not examined.

Kind of Betula L. it is represented by the large number of forms interesting in the selective- genetic plan, which present forestry, decorative, and also practical value as the raw material for the production of thermal energy

It is known that the molecular markers, based on the application of PCR, are most actively utilized in view of simplicity and cheapness of method. One of the most common methods is RAPD (random of amplified of polymorphic DNA). In different sources use the terms “polyspecifical markers” or semi-RAPD, it adapts in studies of the field and vegetable cultures. Study issues of Molecular Systematics birches and practical application of molecular marking (certification) collection of clones of birch trees, held in Kazakhstan for the first time. The great significance the methods, based on the polymorphism DNA, acquired together with the traditional methods of studying the wood plants in genetic and selective studies. This method is widely used in eco - and phytosanitary certification of trees, identification of wood (tree species or geographical origin) [1,4].

The initial stage of these methods is the extraction of DNA. Note, however, in most cases, research linked using DNA isolated from leaves work with the release of DNA from the timber few. The latter is explained given, that in the wood are substances those impeding isolation and conducting the DNA analysis [2].

To date, the following parameters potentially affecting the quality of the DNA isolated directly from wood: a) the nature of the tissue (from crust to core); b) drying and storage conditions (indoor or outdoor); c) the nature of the genome (chloroplast, mitochondrial or nuclear); d) the size and number of amplified DNA fragments.

As a result conducting studies by scientists from Belarus' it is established that the best results are obtained with the isolation DNA from the cambium or the alburnum of the freshlyed-select wood of oak. However, rapid oxidation leads to the degradation and the disintegration DNA in these cloths, while DNA, isolated from the core of tree preserves its properties [1,3].

For studying the population gene pools widely are used different molecular- genetic methods, which make it possible to estimate the level of genetic variety, the degree of differentiation, to determine the genetic structure of the populations of wood plants.

The comparison of the sequences of homologous genes or fragments of DNA in the genome of plants is the most reliable, but expensive method. A large number of sequenced

genes and DNA sequences available in GenBank. But the analysis of genetic distances between plants, conducted on sequences of different genes, often gives divergent results.

The aim of this study is to: study of intraspecific polymorphism and improved methods of using molecular markers based on the use of genotype-specific PCR products and develop a method of molecular identification of birches. In connection with the stated goal is determined the task, whose essence consists into identification of the forms of birches being investigated and isolation of source material (population of the model forms of birches) for the introduction into the culture in vitro.

Material and methods

The sprouts and leaves of the following forms of the birches were used as the objects for the molecular- genetic identification: *Betula pendula var. Carelica., Betula pendula, Betula daurica, Betula turcestanica, Betula papyrifera, Betula pubescens,* leaves of clones obtained by direct regeneration and their parental form, presenting forestry and decorative value growing in the Issyk forest nursery.

Clean, intact leaves were used for the analysis of the genetic polymorphism DNA of the investigated forms of birches. Isolation DNA was conducted with the use CTAB buffer, which can be used both for the analytical isolation for the screening of a large quantity of material and for the preparative isolation of genomic DNA from the plant material. The analysis of polymorphism DNA is carried out in 600 tests by means of the polymerase chain reaction with the use RAPD - method.

The results of studies

Among the molecular markers, which have plural localization in the genome, the Semi-RAPD- markers are most common. The technique allows the PCR to amplify DNA from any part of the genome, including DNA fragments of unknown (Anonymous) a nucleotide sequence [5].

For molecular genetic analysis of important qualitative and quantitative characteristics of the DNA. The isolated DNA samples were tested by agarose gel electrophoresis and DNA concentration was measured using a spectrophotometer Digital Spect ND.

Semi-RAPD-procedure based on the use of the 10-nucleotide random sequence primers to amplify DNA fragments [6]. With the isolations of DNA was used CTAB buffer, concentration DNA varied from 150 to 400 ng/mkl.

The obtained in vitro clones in essence are the forms, which have normal phenotype and development, the preserving specific for the initial genotype special features of increase and development.

It was discovered, that the models of DNA contain a large quantity of admixtures of RNA. For the removal RNA, the models were subjected to repeated cleaning with the use of a ferment of RNAse, which catalyzes degradation the RNA. We have found that the number of generated DNA markers in the studied six shapes, lines and clones of birch with Semi-RAPD-marker can get the results that are characterized by a high level of standardization as a set of markers, and technology implementation analysisa. This form of analysis is possible for the use as the measures for the restoration of the natural of valuable population, so during the identification of wood plants.

Consideration of the results

For a detailed study of phylogenetic relationships effectively use sequences specific to the taxon. This will reliably locate certain types of clusters, but also track the relationships of species within the clusters. Can also be used to determine the type (population) of the founder of the cluster. In the future, we have studied the approach may be of value for a detailed study of evolutionary aromorphoses (shifts).

Conclusions

When analyzing samples birches shows that each of them has a characteristic only for a set of markers. However, some are common to investigate the shape of the birches.

Relationship between the clones and their parent form was established by comparing the profiles of the amplified PCR products. The results of the work is really regenerated clones derived from the original tree species studied and can be used for mass replication.

Synthesized in the research process Semi-RAPD primers can be recommended for genotyping isolated and identified clones. In the course of the work produced genetically diverse collection of clones of the six species of the genus Betula L. The most valuable genotypes will be used as the starting material for the creation of polyclonal plantation forestry purposes.

Methods of molecular marking and genotyping will be used in the certification of breeding materials with high growth characteristics and stability needed to sustain a population-genetic structure of plant communities, i.e., conservation of forest genetic resources.

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Шаденова Е.А., Жұмабеков Е.Ж., Сембеков М.Т.

BETULA L. ТҮРЛЕРІНІҢ ПОЛИМОРФИЗІН ЗЕРТТЕУ

Осы ғылыми жұмыста Қазақстанда өсетін Betula L. алты түрінің полиморфизмдерін зерттеу нәтижелері келтірілген. Олардың туыстық және ата-аналық түрі, амплификиялық ПТР-талдау нәтижелерін салыстыру арқылы тағайындалды. Зерттеу үрдісінде синтезделген Semi-RAPD праймерлерді генотиптеу және идентификация жасауға ұсынуға болады.

Шаденова Е.А., Жумабеков Е.Ж., Сембеков М.Т.

ИЗУЧЕНИЯ ПОЛИМОРФИЗМА РОДА BETULA L.

В данной работе приводятся результаты изучения полиморфизма шести видов Betula L. произрастающих в Казахстане. Родство между клонами и их родительской

формой устанавливали путем сравнения профилей амплифицированных ПЦР-продуктов. Синтезированные в процессе исследования Semi-RAPD праймеры могут быть рекомендованы для генотипирования выделенных и идентифицированных клонов.

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Шалгынбаев Э.К., Коспанова М. Н., Рябинникова А.И., Омарова З.Д., Орынбаев М.Б.

РГП «Научно-исследовательский институт проблем биологической безопасности» КН МОН РК

МОНИТОРИНГ, ВЫДЕЛЕНИЕ, ИДЕНТИФИКАЦИЯ И КУЛЬТИВИРОВАНИЕ ГЕРПЕСВИРУСА ЛОШАДЕЙ НА ТЕРРИТОРИИ РЕСПУБЛИКИ КАЗАХСТАН

Аннотация

В работе представлены результаты исследований биологических проб, отобранных от больных лошадей с признаками респираторного заболевания, а так же результаты выделения герпесвируса лошадей и изучения культуральных свойств выделенного вируса. Установлено, что заболевание животных в хозяйствах Т. Рыскуловского и Кордайского районов Жамбылской области вызвано герпесвирусом лошадей. Выделен эпидемиологически актуальный для территории РК изолят герпесвируса лошадей 4 серотипа. Отработаны оптимальные условия культивирования герпесвируса лошадей 4 серотипа, позволяющие нарабатывать вирусную массу для приготовления диагностических и профилактических препаратов.

Ключевые слова: ринопневмония, мониторинг, серотип, культивирования, цитопатическое действие, электронная микроскопия.

Введение

К одним из широко распространенных вирусных заболеваний относятся герпесвирусные инфекции лошадей. В настоящее время известны герпесвирусы лошадей 9 типов, представленные альфа – и гаммагерпевирусами. Из герпесвирусных болезней лошадей наибольшее экономическое значение имеют инфекции, возбудителями которых являются ВГЛ-1, вызывающий массовые аборты у кобыл, патологию органов дыхания у жеребят, спорадические случаи миелоэнцефалопатии у лошадей, независимо от возраста и физиологических особенностей; ВГЛ-4 – возбудитель ринопневмонии и спорадических абортов; ВГЛ-3 – возбудитель коитальной экзантемы лошадей, острого контагиозного заболевания, при котором поражается эпителий влагалища у кобыл и полового члена у жеребцов; ВГЛ-9 – возбудитель миелоэнцефалопатии лошадей и других гетерогенных хозяев: газелей, зебр, антилоп - часто с летальным исходом. Вирусы 2 и 5 типов (гаммагерпесвирусы) вызывают латентную инфекцию, а также участвуют в развитии респираторных поражений у жеребят. Наиболее значимые для коневодства заболевания вызывают вирусы 1-го (вирусный аборт) и 4-го (ринопневмония) типов [1, 2].

Ринопневмония - это вирусная инфекция лошадей, которая может проявляться поражением органов дыхания, абортами, пневмонией новорожденных жеребят или миелоэнцефалитами. Ранее заболевание было описано разными названиями: вирусный аборт кобыл, половая экзантема лошадей, катаральная инфлюэнца, герпес, ринотрахеит лошадей [1-3].