

Possibilities for adaptation of *Alnus glutinosa* L. to changing environment

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The objective of the study was to assess the level of intra- and inter-population variation of adaptive traits (juvenile height growth, phenology, and frost resistance) of black alder (*Alnus glutinosa* L.) in different ecological conditions, to estimate its phenotypic plasticity and on this ground to evaluate the possibilities for adaptation to the changing environment in the course of global climate warming. Eighty-five open pollinated families from 17 Lithuanian populations were studied for 5 years in 3 progeny test plantations. Strong significant effects of site conditions found for most growth traits indicate a high phenotypic plasticity of black alder and show the ability of the species to a rapid response to changed environmental conditions. The family variance components in every single test plantation were significant and reached up to 38.3%. A significant additive variance found within populations suggests good prospects for genetic adaptation to changes of climate and environment via natural selection during the juvenile stage. The highest population variance component, which reached up to 35.3%, was found for bud flushing. A significant genotype \times environment interaction indicated existence of differences among families regarding their plastic response and presence of specific adaptation. However, the performance of families across trials was rather stabile: only 16.5% of the families contributed significantly to the $g \times e$ interaction for phenology and 24.7% for height, and their ecovalence estimates were low ($< 5.5\%$). The genetic variation found among families and among populations facilitates developing an efficient dynamic Multiple-Population joint gene conservation and tree breeding system (MPBS) for black alder in Lithuania.

Key words: *Alnus glutinosa*, genetic variation, phenotypic plasticity, adaptation

INTRODUCTION

Forest tree species have been exposed to significant changes in environmental conditions during the last millennia and have responded by migration and/or adaptation to the most suitable habitats [1]. Most of our forest tree species migrated to Lithuania after the last glaciation 6–9 thous. years ago from southern populations in refuges in the Balkans or the Apennines. For tree species, with their long ontogenesis, this period was too short to reach maximum adaptation in our temperate and boreal climate. The process of adaptation in forest tree species is slow, because the inter-population genetic variation is counteracted by a high gene flow, high plasticity, significant annual climate variations and tree ontogenesis. At present, populations of forest tree

species grow in very heterogeneous environments – in different eco-climatic conditions, forest communities, habitats, and sites, which are not always optimal for a species. Due to the global warming of the climate, more extreme temperatures and levels of precipitation are predicted to occur [2], thus increasing the environmental stress on trees. Moreover, increased temperature is expected to favour the epidemic spread of pathogens and parasites. Black alder (*Alnus glutinosa* L.), which is one of the most important forest tree species, grows on wet sites and is rather sensitive to changes of the water-table level. Seedlings and young trees are very sensitive to spring frosts, which currently become too frequent and too heavy. Mild winters and the early start of bud flushing increase the danger of spring frost damage even more. Due to this multitude of

reasons, the ability of this tree species to adapt to the direct and indirect consequences of quick global climate warming is very uncertain.

The possibilities of a species to cope with the consequences of global climate warming to a greatest extent will depend on phenotypic plasticity and the amount of genetic variation in populations. In a population having a considerable genetic variation, as the environment changes the population adapts when the best genotypes survive and reproduce, but maladapted genotypes disappear due to natural selection. Natural selection results in formation differences in allele- and genotype frequencies among populations [3]. When rapid adaptation is required or when genetic variation is lacking, plants respond to temporal or spatial fluctuations by modifying their phenotype [4]. This specific response to a certain range of conditions for a particular character or set of traits is called *phenotypic plasticity* [5]. Studies of plastic response along an environmental gradient [e.g., 6–8] indicate that reaction norms and responses to environment gradients vary significantly among the genotypes. One hypothesis suggests that genetic variation and plasticity represent alternative strategies for coping with environment heterogeneity [9, 10]. Other hypotheses consider genetic variations and phenotypic plasticity to be positively correlated [11]. Moreover, phenotypic plasticity is considered to be a trait in itself that is under genetic control [5, 12] and can evolve independently of the trait [13]. A phenotypic response can be adaptive when enhancing fitness in a changing environment [14], or non-adaptive when resulting in deterioration of individual fitness expressed in reduced growth, which reflects the inevitable metabolic or developmental response [15]. Adaptation in heterogeneous environments can be achieved by both phenotypic plasticity and stability. In the first case, populations may be subjected to selection resulting in specialized genotypes that perform better in local (optimal) environments than in non-local environments [16]. The phenotypic plasticity of such genotypes is high. The second case refers to situations when selection favours genotypes capable of buffering their phenotypes in changing environments. The phenotypic plasticity of such genotypes is low.

Black alder has a wide range of natural distribution, and natural populations of the species are found in different ecological conditions that might promote climatic or edaphic differentiation. Such a wide range of distribution combined with relatively small and isolated populations causes a high degree of variability [17]. The results of provenance research revealed very distinct genetic differences in phenological characteristics, such as budburst and vegetation time; survival, production, trunk shape, and root system features [18–23]. Geographical population

structuring within *A. glutinosa* and *A. cordata* species was also found in chloroplast DNA studies using the PCR-RFLP method and nuclear genome studies by ISSR analysis [24], however, the intra-population variation of DNA markers was much higher (43.65% against 6.15%). A significant intra-population genetic variation was found for growth and phenology traits of some broad-leaved tree species, including *A. glutinosa*, in Sweden [23]. Studies on the intra-population genetic variation and phenotypic plasticity of *A. glutinosa* in Continental Europe are scarce and provide no possibility to prognosticate the ability of the species to adapt and survive under global climate warming. Therefore, the objective of our study was to assess the level of intra- and inter-population variations of adaptive traits such as juvenile height growth, phenology and frost resistance of black alder in different ecological conditions, to estimate the phenotypic plasticity, and to evaluate its possibilities for survival and adaptation in changing environment.

MATERIALS AND METHODS

Eighty-five open pollinated families from 17 Lithuanian populations of black alder were studied for 5 years in 3 progeny test plantations established in 3 forest ecoclimatic regions of Lithuania on different sites: Kaunas, site Nc, index continentality (i.c.) 29; Īialiai, site Nd, i.c. 27; Īilutė, site Ld, i.c. 25. In each trial, all 17 populations were represented by 5–6 half-sib families in 5 randomised blocks, 10 tree-plots per family in each block. The spacing between trees was 2.0×1.5 m.

At 3 and 5 years of age the following traits that reflect adaptation were measured and analysed: height of tree, stem diameter, bud flushing stage, frost resistance, and resistance to diseases. The bud flushing stage was rated 1 to 5 (1 – dormant bud; 5 – leaves are spread), frost resistance was rated 1 to 4 (1 – stem and shoots dead; 4 – no visible injury), resistance to diseases was rated 0 to 1 (0 – dead from fungi; 1 – not damaged).

Variance analysis was done using the MIXED procedure in the SAS Software [24]. Mixed model equations (MME) and the restricted maximum likelihood (REML) method were used for computing variance components.

The following linear models were used for joint data analyses of the 3 progeny trials together and for separate analyses of individual treatments:

$$1) \text{ Joint: } y_{ijklmn} = \mu + b_i(t)_j + t_j + f_i(p)_m + p_m + ft_{ij} + pt_{mj} + \varepsilon_{ijklmn}$$

$$2) \text{ Separate: } y_{ilmn} = \mu + b_i + f_i(p)_m + p_m + \varepsilon_{ilmn}$$

where y_{ijklmn} and y_{ilmn} are the values of a single observation, μ – the grand mean, t_j – the fixed effect of

trial j , $b_i(t)_j$ – the fixed effect of block i within trial j , b_i – the fixed effect of block i , $f_l(p)_m$ – the random effect of family l within population m , p_m – the random effect of population m , f_{lj} – the random effect of interaction between family l and trial j , pt_{mj} – the fixed effect of interaction between population m and trial j , ε_{ijlmn} and ε_{ilmn} – random error terms.

The genetic parameters were estimated from model (2) separately for both each trial and individual population:

Additive genetic variance: $\sigma_A^2 = 4\sigma_f^2$

Additive genetic coefficients of variation:

$$CV_A = 100 \cdot \sqrt{4 \cdot \sigma_f^2 / \bar{X}}$$

Heritabilities (on individual tree base):

$$h_i^2 = \sigma_A^2 / (\sigma_A^2 + \sigma_E^2)$$

where σ_f^2 is the family variance component, \bar{X} – the phenotypic mean of the trait, σ_A^2 – the additive genetic variance, σ_E^2 – the environmental variance.

Two types of genetic correlations were calculated: among different traits within an individual trial (Type A) and between the same trait assessed in different trials (Type B; Burdon [25]). The Type B genetic correlations were calculated to evaluate the contribution of each pair of trial to the total *genotype* × *environment* interaction.

Phenotypic plasticity in individual families and populations was estimated using the Wricke [26] ecovalences derived from the breeding values (obtained from the MIXED procedure of the SAS) across 3 trials. The ecovalence indicated the contribution (expressed per cent) of each family (or population) to the total family (or population) interaction with trial variance. The Shukla's stability variances were computed and the significance of the ecovalences was tested using the method developed by Shukla [27].

RESULTS

Strongly significant trial and block effects (among environment variation) evaluating the phenotypic

plasticity of progenies were found for most growth, phenology, and resistance traits (Table 1).

Throughout the 3 test plantations, the family variance component was relatively low, varying from 0 to 3.1% (Table 1). The family effects in every single test plantation were often significant for most of traits, with high variance components reaching up to 38.3% (Table 2). The heritabilities and CV_A for growth and phenology traits were generally higher than for other traits, however, they varied from site to site. The CV_A in individual populations was very different and changed from site to site (Table 3).

The family × environment interaction, which characterises differences in the type of phenotypic plasticity, was significant. The family × environment interaction variance component was rather small, however, larger than the family variance component (Table 1). Fourteen families (16.5% of the total number of families tested) contributed significantly to the $g \times e$ interaction for phenology and 21 families (24.7%) for height growth with generally low estimates of the ecovalence values (< 5.5%). Within individual progeny trials, a significant genetic correlation was found between height growth and frost resistance ($r = 0.42$ – 0.68); the highest families were less damaged. However, no significant genetic correlation was found between bud flushing stage and height growth or frost resistance.

Over the entire experiment, a significant variance component of the population effect was found only for bud flushing, reaching up to 8.4%. It is noteworthy that the population variance component was present in the absence of the family variance component. In each single trial the population variance component was higher than throughout the 3 test plantations and comprised 10.6% in the Āiauliai trial and 35.3% in the Āilutė trial. However, it was insignificant in the Kaunas trial. The Kazlė Rūda and Āakiai populations were the earliest flushing, while the K. Nerija and Āiauliai populations were among the last to flush (Table 3).

Table 1. Results from a joint mixed linear model (1) analysis of variance of data on *Alnus glutinosa* progeny growth in 3 trials: variance components for random effects as a percentage of the total random variation, and significance of fixed effects. σ_f^2 , σ_p^2 , σ_{fl}^2 and σ_{pt}^2 are the variance components for family, population, family × trial and population × trial interactions, respectively. Level of significance is indicated by: * – $0.05 > P > 0.01$, ** – $0.01 > P > 0.001$, *** – $P < 0.001$

Trait	Variance components of random effects, %				Significance of fixed effects	
	σ_f^2	σ_p^2	σ_{fl}^2	σ_{pt}^2	block	trial
Height	2.1	0	9.7***	0	***	
Stem diameter	3.1	0.0	4.3	0	***	***
Bud flushing stage	0	8.4*	5.6***	8.3***	***	*
Frost resistance	2.1*	0.6	4.8***	0.5	***	***
Resistance to diseases	0	0	1.0**	0.4		**

Table 2. Results from a mixed linear model (2) analysis of variance of data in individual trials: mean values, population variance component, family components, standard errors, individual habitabilities, and additive genetic coefficients of variation of different traits of *Alnus glutinosa* open-pollinated families for 3 trials

Trait	Trial	Mean	Variance components				Family additive	
			Population		Family		h ²	CV _A (%)
			%	± se	%	± se		
Height, cm	Kaunas	90.91	1.5	± 1.1	10.8	± 2.9	0.43	19.5
	Šiauliai	96.53	2.0	± 1.0	13.2	± 2.8	0.53	22.0
	Ėilutė	104.21	7.7	± 5.4	17.6	± 8.3	0.70	20.6
Stem diameter, mm	Kaunas	20.20	0.8	± 0.8	7.0	± 2.2	0.28	14.1
	Šiauliai	–	–	–	–	–	–	–
	Ėilutė	21.39	8.6	± 5.5	12.7	± 7.0	0.51	17.3
Bud flushing stage, class	Kaunas	3.42	1.6	± 1.1	7.4	± 2.4	0.30	20.8
	Šiauliai	3.37	10.6	± 4.1	17.9	± 3.5	0.72	24.5
	Ėilutė	3.45	35.3	± 14.8	38.3	± 11.4	1.53	45.3
Frost resistance, class	Kaunas	3.14	1.2	± 0.9	9.2	± 2.6	0.37	7.5
	Šiauliai	3.13	3.1	± 1.4	10.3	± 2.3	0.41	9.1
	Ėilutė	3.05	0	± 0	0.9	± 4.8	0.04	1.5
Resistance to diseases, class	Kaunas	0.93	1.7	± 1.1	5.2	± 2.0	0.21	12.6
	Šiauliai	0.90	0.6	± 0.6	2.3	± 1.1	0.09	10.1
	Ėilutė	0.91	0.6	± 4.4	0	± 0	0	0

Table 3. Population mean values of bud flushing and height growth and additive genetic coefficients of variation (CV_A, %) within populations of *Alnus glutinosa* in individual trials (Kaunas, Šiauliai, and Ėilutė)

Population	Bud flushing						Height					
	Means in trials, pt			CV _A in trials, %			Means in trials, cm			CV _A in trials, %		
	Kaunas	Šiauliai	Ėilutė	Kaunas	Šiauliai	Ėilutė	Kaunas	Šiauliai	Ėilutė	Kaunas	Šiauliai	Ėilutė
Kaišiadorys	3.62	3.61	4.26	17.0	5.3	0	95.2	92.8	111.9	0	30.4	0
Panevėpys	3.49	3.12	4.00	8.8	24.2	0	82.3	95.0	100.0	0	27.5	23.3
Prienai	3.29	3.93	4.50	0	18.8	18.1	89.6	83.9	85.0	33.3	26.2	16.5
Tauragė	3.50	3.39	2.50	26.4	12.9	69.3	79.0	96.6	100.1	0	13.3	22.4
Šiauliai	3.08	3.10	4.00	17.1	20.0	0	97.4	97.2	80.0	36.8	27.2	0
Dzūkija NP	3.58	3.59	2.40	18.6	11.2	0	98.8	92.3	94.6	0	14.5	24.9
Marijampolė	3.49	3.34	3.86	43.5	11.2	0	92.3	96.6	99.1	19.7	24.0	0
Šakiai	3.76	3.39	4.49	23.9	9.6	16.0	94.4	100.3	115.6	22.9	6.0	0
Kurs. Ner. NP	3.05	2.88	2.51	12.8	30.9	0	91.1	91.4	97.8	20.8	29.2	34.1
Plungė	3.39	2.53	2.21	28.9	8.6	51.5	92.0	108.9	107.7	36.5	28.0	45.6
Jonava	3.58	3.65	3.67	0	22.5	0	85.5	95.8	96.7	34.7	17.6	66.1
Kaėerginė	3.41	3.49	3.94	32.3	0	0	85.0	99.0	111.1	1.3	0	64.5
Kazlė Rūda	3.81	3.70	4.40	26.9	16.1	0	92.7	100.2	92.3	21.9	5.7	20.3
Kurėėnai	3.33	3.05	2.98	21.9	9.1	35.3	89.8	92.6	104.8	0	29.8	0
Pajiesys	3.00	3.53	3.92	0	28.8	61.8	81.8	98.0	115.6	13.7	0	0
Ėilėnai	3.38	3.49	4.47	32.2	8.4	19.2	93.6	94.7	84.5	23.3	21.8	50.8

The variance component of population × environment interaction was significant for bud flushing only, however, it was of the same small scale as the population variance component and comprised up to 8.3%. Many populations changed their behaviour ac-

ross the 3 test plantations, however, only the Prienai and Plungė populations had high and significant Wricke's ecovalences (19.1 and 22.1%). The most stable time of bud flushing was found for the Kazlė Rūda, Kaišiadorys and Kurėė Neringa NP populations.

DISCUSSION AND CONCLUSIONS

Strongly significant effects of site conditions in the variation of height growth and bud flushing of progenies among trials with different environments reflect the reaction of trees to the combined effects of edaphic site and climatic conditions in a trial and the climatic conditions of the eco-climatic region. This variation indicates a high phenotypic plasticity of Lithuanian black alder populations and families, showing the ability of individual trees in populations in a short term to respond to environmental changes and cope with some of the foreseen consequences of global climate warming. However, the question remains whether this response is adaptive, enhancing plant fitness, or non-adaptive, deteriorating plant fitness. Eriksson [28] emphasizes that a high phenotypic plasticity in adaptive traits may be useful under changing conditions in a short-time period but may be detrimental in a long-term perspective, since natural selection is misguided and cannot be fully efficient. Strongly significant effects of the site conditions in variation and frost resistance did not give an indication of the existence of general plastic response but rather reflected the rate of negative consequences of unfavourable local climatic factors in some of the locations where progeny trials were established.

Throughout the three test plantations studied, the family variance component was relatively low because of strong genotype \times trial interactions and disturbances in the growth of progenies induced by severe frost damage. However, in every test plantation the family variance component was often significant and high. Even if the growth data of the 3 trials did not differ much (Table 2), the individual populations differed in CV_A for height, diameter and other traits (Table 3), showing that individual populations had a different potential for future adaptation. The CV_A in our study was similar to those estimated for other broadleaf tree species [23, 29–31, etc.]. The presence of sufficient additive variance in traits of adaptive significance is of greatest value for the long-term gene conservation and tree breeding [28, 32–35, etc.]. A high additive variance within populations suggests that black alder has a potential for adaptation via natural selection during the juvenile stage if environmental conditions change. The presence of genetic variation in frost resistance found in the study shows the possibility of the species to cope with a higher frequency and rate of spring frosts, which are predicted as one of the many consequences of global climate warming. However, a negative consequence of this adaptation can be a significant loss of genetic variation in traits of both resistance and growth. The significant ge-

netic correlation found between height growth and frost resistance within individual progeny trials indicated that frost negatively influenced the growth. Fast-growing families can better survive and adapt, because they more quickly pass the stage when trees are most sensitive to spring frosts. The negative impact of frost damage on survival and growth is expected to increase in the course of global climate warming. This problem might be even more pronounced in reforestation of clear-cut areas and abandoned agricultural lands. Due to the fact that spring frost occurred very late and severely damaged the whole stem increment in all our trials when trees had already passed all bud-flushing stages, we did not find any significant genetic correlation between the bud-flushing stage and height growth or frost resistance which are present in other broadleaved tree species [23, 31].

The fact that population variance components for most adaptive traits, except bud flushing over the 3 progeny trials were low or absent could be explained by presence of population \times environment interaction, by a low population differentiation, or/and by the small number of families per population included into the study. For height growth, only some fastest growing populations (the Marijampolė and Ėakiai populations in the Kaunas trial and the Plungė, Ėakiai, Kazlė Rūda, and Kaėerginė populations in the Ėiauliai trial) significantly differed from populations that performed most poorly. Recent studies of *A. sinuata* also showed the absence of significant inter-population variations in spring frost hardiness [36], however, indicated their presence in winter frost hardiness and biomass production. Comparative studies of some broadleaf tree species [23] indicate that both inter- and intra-population genetic variation in phenology and height growth were lower in *A. glutinosa* than in *Acer platanoides* or *Fraxinus excelsior*. Rather high population variance components for bud flushing within individual trials found in our study show presence of clear differences in phenology among populations and indicate the existence of population structuring of black alder in Lithuania.

The importance of using black alder autochthonous provenances well adapted to habitats has been emphasized earlier [17, 37 etc.]. Recent studies of *A. rubra* show that provenances from locations close to test plantations had superior performance in growth and survival, suggesting the adaptation of the species to local environments [38]. However, we did not find a clear trend that local populations of black alder performed better in trials established in the neighbourhood of their origin. Progeny from only some single populations originating near the trial areas performed better than average, e.g., the Ėiauliai and Plungė populations in the Ėiauliai trial or

the Marijampolė and Kaišiadorys populations in the Kaunas trial. Considering growth as an indicator of adaptation, the Āakiai and Plungė populations could be defined as populations of general adaptation, because they exhibit high growth in all trials (Table 3). The Prienai, Kurėėnai and Āilėnai populations are of low general adaptability. Variation in adaptive traits among populations in our study shows a possibility for genetic gain in selection of the best populations and is positive for developing an efficient long-term dynamic gene conservation and tree breeding program of black alder based on the Multiple-Population Breeding System (MPBS) concept developed by Namkoong [7].

The family \times environment interaction variance component in the variation of height growth and phenology and the absence of a significant genetic correlation among trials indicate the presence of differences among families in their plastic response and some specific adaptation. However, in general the performance of the families across environments was rather stable. Only 16.5% of the families tested contributed significantly to the $g \times e$ interaction for phenology and 24.7% of families for height growth, and their estimates of ecovalence values were generally low (< 5.5%). The reaction norms and growth of families were not always interrelated. The largest differences between families in response to the range of environments were within the Plungė and Marijampolė populations, which were the most productive. A significant genotype \times environment interaction for height growth at the population and family levels was also found in recent studies of *Alnus rubra* [38]. Due to presence of $g \times e$ interaction, under diverse selective pressures from negative factors caused by global climate warming (*e. g.*, rate of spring frosts), stands of different genotypic structure can arise in natural regeneration under the shelter and in reforestation of large clear-cut areas or abandoned agricultural lands. Differences in plasticity and adaptability should be considered in order to maximise the genetic gain in breeding of black alder. If some of the best performing families are adapted specifically to certain environments, then family selection should be made on an ecological basis, *i.e.* adequate families should be selected for specific ecological conditions of a given provenance region or even site type (in terms of microclimate or edaphic conditions).

The significant variance component of population \times environment interaction in variation of bud flushing, which characterises differences in the type of phenotypic plasticity of populations, indicates the possible presence of specific adaptation in phenology on the population level. However, only two populations (Prienai and Plungė) had significant and

high ecovalence estimates. Populations that were the most distinctive in bud flushing preserved similar phenological behaviour over different test plantations. Based on studies of responses of *A. glutinosa* and other broadleaf populations to climate change by simulating transfers of populations, it was concluded [39] that local adaptation would probably not be a serious constraint in predicting the phenological responses to global warming. Absence of specific adaptedness in growth or frost resistance was indicated by the lack of a significant population \times environment interaction for these traits. Nevertheless, the populations differ in response to the environmental gradient over trials. The Āiauliai, Āilėnai, Dzūkija NP, and Marijampolė populations were the most responsive to height growth. This variation among populations in adaptive traits is positive for developing an efficient joint breeding and gene conservation system for black alder, based on the Multiple-Population Breeding System. Most suitable are populations showing a high adaptability, wide intrapopulation genetic variations, low phenotypic plasticity for the countrywide use or high plasticity for the use in specific regions. The results of our studies give main indications on target populations that can be included into the national network of multiple-population gene conservation and the tree breeding system which is under development [39] for black alder.

Received 3 October 2002

Accepted 12 November 2003

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ALNUS GLUTINOSA L. GEBĖJIMAI PRISITAIKYTI PRIE KINTANĖIOS APLINKOS

S a n t r a u k a

Tiriant juodalksnio (*Alnus glutinosa* L.) 17-os Lietuvos populiacijø 85 motinmedþiø palikuoniø ðeimø adaptacijos poþymius – augimo spartos, fenologijos ir atsparumo ðalnoms – kaità skirtingomis ekologinėmis sąlygomis trijuose bandomuosiuose þeldiniuose nustatyta, kad jauni palikuonys pasiþymėjo dideliu fenotipiniu plastiškumu ir nemaþa tarp-populiacine bei tarpþeimynine genetine variacija (variacijos komponentai siekė atitinkamai iki 35,3 ir 38,3%). Nustatyta esminė genotipo ir aplinkos sąveika ($g \times e$), rodanti skirtumus tarp ðeimø pagal adaptyvumo laipsnà ir reakcijos normas, taèiau ðeimø rodikliai skirtingomis bandymø sąlygomis buvo palyginti stabilūs – tik nedidelà dalà ðeimø ið esmės paveikė genotipo ir aplinkos sąveika (16,5% ðeimø pagal fenologinius poþymius ir 24,7% ðeimø pagal augimo poþymius), o jø ekvalentingumo koeficientai siekė tik iki 5,5%. Nustatytas didelis juodalksnio fenotipinis plastiškumas indikuoja rûðies gebėjimą fiziologiškai prisitaikyti pakitus aplinkos sąlygoms. Nustatyta adityvinė genetinė variacija rodo, kad jaunam amþiui juodalksnis pasiþymi gera genetinė adaptacija prie klimato ir aplinkos pokyèiø vykstant natūraliai atrankai, todėl galima sukurti efektyvià dinaminà daugiapopuliacinà juodalksnio genetiniø iðtekliø iðsaugojimo ir selekcijos sistemà Lietuvoje.