

Natural forest regeneration in spruce monocultures in the Ukrainian Beskids – prognosis by FORKOME model

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ABSTRACT: This paper presents the results of investigations on natural forest regeneration in Norway spruce (*Picea abies* L. Karst.) monocultures in the Ukrainian Beskids with the use of FORKOME model prognostic possibilities. Different variants of regeneration methods are presented. Selective cutting with planting was determined as the most effective: spruce selective cutting with simultaneous planting of target species: beech (*Fagus sylvatica* L.) and fir (*Abies alba* Mill.) with admixture of ash (*Fraxinus excelsior* L.). Beech and fir biomass increases rapidly over the first 20 years – then it stabilizes. After another 20–30 years the initial form of beech forest is recognizable and it is possible to speak about an increase of beech forest, which in the course of time achieves a higher degree of similarity to natural stand. In the Ukrainian Beskids the potential forest stand consists of beech and fir (*Dentario glandulosae-Fagetum*).

Keywords: Norway spruce; beech; computer model FORKOME; Ukrainian Beskids; spruce monocultures; forest management

Extensive Norway spruce (*Picea abies* L. Karst.) growing has been a characteristic method of forest management for Central Europe over the last two centuries. Norway spruce monocultures take up considerable areas in the Ukrainian Carpathians and in the Beskids. According to GOLUBETS (1978), their area increased during two centuries from initial 126 thousand hectares to 325 thousand hectares presently. Health and density of these forests are far from being satisfactory. The spruce increased proportion does not reflect the potential vegetation schemes in the Beskids. There arises a problem of natural forest regeneration in the spruce monocultures.

It is doubtless that the spruce forest area needs to be decreased. The current health state of Carpathian spruce forests documents it very clearly. The stands grown against the habitat requirements are weaker than natural forests. Consequently, a more frequent occurrence of pests and diseases threatens the surrounding forests seriously.

The paper presents several possibilities of remedying the situation. A complex approach to the issue of implementing natural (potential) forest species scheme on a research plot helps to rethink the forest management direction. The FORKOME computer model aids and facilitates the search for optimal methods of forest scheme change described by KOZAK et al. (2003).

MATERIALS AND METHOD

The specificity of regeneration is shown on an example of spruce forest research plots in the Ukrainian Beskids, located in the 3rd forest section, 10th forest subsection of Jablunec Forest Administration region of Borynsky Derzlishosp, Lviv Province. Spruce forest research plots are located on the northern slope of the mountain (inclination 6°–8°) at the altitude of 650–652 m a.s.l. Brown soils are characteristic of these plots. There are rich eutrophic conditions in this stand. The area of stands was 1 ha. The area

Supported by the Polish Committee for Scientific Research, Project No. N 6 P06L 042 21.

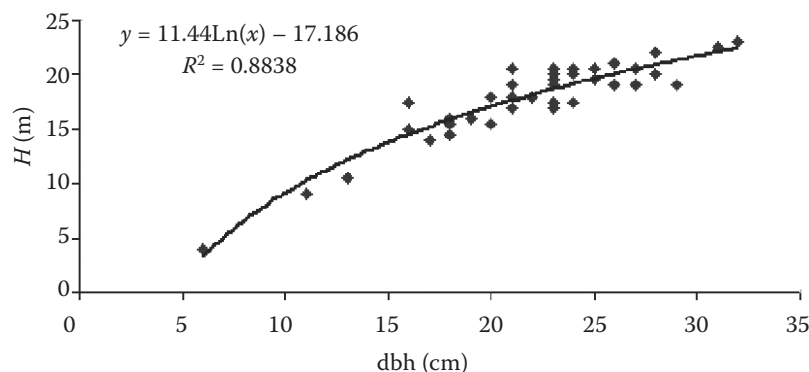


Fig. 1. N1 Norway spruce research plot: $\text{dbh}_{1.3}$, H relationship

affected by felling – 625 m². A near-by spruce stand dominates the tree species beech composition. The stand is characterized by the values of spruce (*Picea abies* L.) diameter ($\text{dbh}_{1.3}$) and height (H) (Fig. 1). Spruce stand density is low (Fig. 2). It is also a single species – only 1 fir per 38 spruce trees (Table 1). Data on dbh and H was put into FORKOME model. Prognoses were run with the use of FORKOME model. The results of regeneration are presented for N1 Norway spruce research plot. The FORKOME model was presented and analyzed in detail in previous publications (KOZAK et al. 2002, 2003), so only the general basis of the model is to be introduced in this paper. FORKOME model represents the patch model family used for simulating forest association succession allowing single tree research. Two types of analysis are possible to run with FORKOME. Statistical analysis includes the calculation of mean values and standard deviations, while sensitivity analysis concerns the calculation of auto- and cross-correlation functions. The model enables site, species, climate and felling parameters setting. The results are saved and additional analysis by other computer methods and programs is also possible.

Within certain scenarios (KOZAK, MENSHTUKIN 2001; KOZAK et al. 2003) the option of setting tree

felling mode, temperature and humidity conditions is available. Monte Carlo statistic method allows to simulate up to 200 variants of each scenario. The model returns average number and average biomass of trees with standard variation each year. To improve the sensitivity analysis of forest ecosystems auto- and cross-correlation functions are included. Tree biomass and number of trees are important parameters in the calculations. Various charts present relationships between these parameters for each species, whole association and two ecological factors (temperature and humidity).

Basic parameters for the FORKOME model are listed according to species in Table 2. There are adequate parameters with the proposed ones by BRZEZIECKI (1999). The FORKOME model simulates the dynamics of 5 chosen species that dominate on the investigated plots (more are available).

FORKOME is an object system with basic components: area – represents a current patch (gap), tree – represents a single tree. The area object has its characteristic properties: dimensions, habitat conditions, climate conditions, etc. The user's interface simplifies the modification of patch properties. The area object contains an almost unlimited amount of tree objects, being representatives of already existing trees.

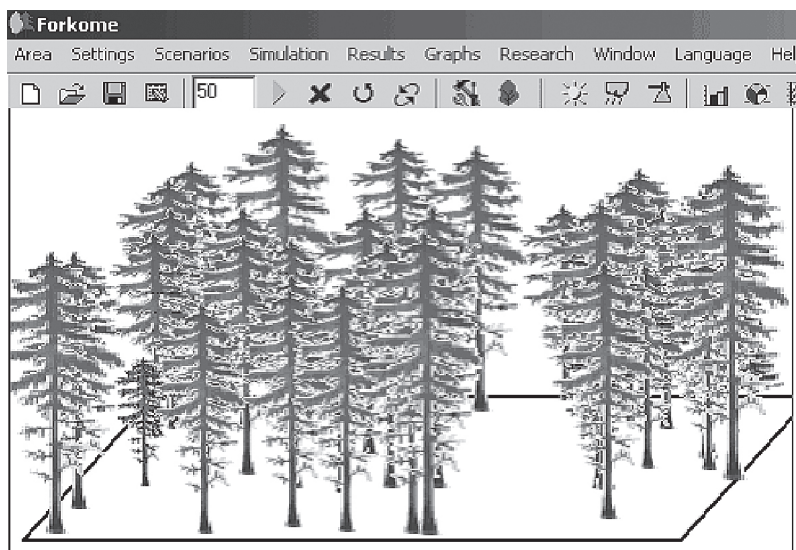


Fig. 2. N1 Norway spruce research plot: initial state in the FORKOME model

Table 1. N1 Norway spruce research plot (25 m × 25 m)

GP	Lp. tree	Sp (No.)	Species	dbh	H	Age	X	Y
1	1	2	<i>Picea abies</i>	23	20.5	47	1.3	24.2
1	2	2	<i>Picea abies</i>	27	19.0	52	4.6	24.6
1	3	2	<i>Picea abies</i>	21	19.0	45	7.8	31.2
1	4	2	<i>Picea abies</i>	26	21.0	55	12.5	22.5
1	5	2	<i>Picea abies</i>	18	14.5	42	11.6	19.1
1	6	2	<i>Picea abies</i>	23	17.5	50	18.6	23.0
1	7	2	<i>Picea abies</i>	23	19.0	50	18.6	20.7
1	8	2	<i>Picea abies</i>	21	20.5	44	20.4	19.2
1	9	2	<i>Picea abies</i>	17	14.0	42	23.0	18.8
1	10	2	<i>Picea abies</i>	19	16.0	44	21.0	12.5
1	11	2	<i>Picea abies</i>	27	20.5	54	22.9	14.2
1	12	2	<i>Picea abies</i>	13	10.5	34	19.9	9.2
1	13	2	<i>Picea abies</i>	29	19.0	56	20.0	8.8
1	14	2	<i>Picea abies</i>	32	23.0	60	24.5	10.5
1	15	2	<i>Picea abies</i>	25	19.5	50	21.2	3.8
1	16	2	<i>Picea abies</i>	23	20.0	48	1.0	21.2
1	17	2	<i>Picea abies</i>	21	17.0	45	1.5	19.3
1	18	2	<i>Picea abies</i>	19	16.0	44	1.2	17.9
1	19	2	<i>Picea abies</i>	21	18.0	44	4.3	19.2
1	20	2	<i>Picea abies</i>	18	16.0	42	6.3	18.5
1	21	2	<i>Picea abies</i>	11	9.0	34	2.5	9.5
1	22	2	<i>Picea abies</i>	25	20.5	50	0.6	5.3
1	23	2	<i>Picea abies</i>	23	17.0	47	5.8	11.5
1	24	2	<i>Picea abies</i>	24	20.0	50	9.8	14.9
1	25	2	<i>Picea abies</i>	16	15.0	42	4.9	9.0
1	26	2	<i>Picea abies</i>	28	20.0	54	0.5	1.2
1	27	2	<i>Picea abies</i>	20	18.0	44	8.2	9.2
1	28	2	<i>Picea abies</i>	16	17.5	40	10.2	8.1
1	29	2	<i>Picea abies</i>	24	20.5	50	11.8	9.0
1	30	2	<i>Picea abies</i>	28	22.0	54	13.5	9.1
1	31	2	<i>Picea abies</i>	22	18.0	47	6.4	1.0
1	32	2	<i>Picea abies</i>	23	19.5	50	9.4	2.4
1	33	2	<i>Picea abies</i>	26	19.0	50	14.2	1.1
1	34	2	<i>Picea abies</i>	24	17.5	50	11.6	1.5
1	35	2	<i>Picea abies</i>	31	22.5	60	14.8	0.9
1	36	1	<i>Abies alba</i>	6	4.0	20	22.8	25.3
1	37	2	<i>Picea abies</i>	18	15.5	42	15.5	24.5
1	38	2	<i>Picea abies</i>	20	15.5	44	23.4	12.2

GP – area number; Lp. tree – tree number; Sp (No.) – species code; species – tree species Latin name; dbh – diameter at breast height; H – height; age – tree age; X, Y – coordinates of the tree on the research plot

The area object is formed in the system imitating real world conditions (climate settings, tree felling). The area object affects its tree objects by transmit-

ting information about current conditions e.g. light availability to trees. This parameter is calculated for certain height values in the patch. On that basis

Table 2. Basic parameters of growth for the main tree species in the Beskids used in the FORKOME model

Tree species	H max. (cm)	D max. (cm)	Age (years)	B2	B3	G
<i>Fagus sylvatica</i> L.	4,500	150	300	58.26	0.194	290
<i>Abies alba</i> Mill.	6,000	150	400	78.26	0.261	200
<i>Picea abies</i> (L.) Karst.	5,500	150	400	71.60	0.239	370
<i>Acer pseudoplatanus</i> L.	4,000	150	300	51.60	0.172	160
<i>Betula pendula</i> Roth	3,500	100	100	67.40	0.337	540
<i>Fraxinus excelsior</i> L.	4,000	150	300	51.60	0.179	270

tree growth simulation runs with one-year interval. Within a single one-year simulation the area object exercises the following calculations for existing trees: input parameters (leaf area, moisture conditions); growth; mortality; felling; regeneration. The preceding year's final state becomes an input state for the following year.

In the FORKOME model the growth block describes tree growth on the current area for each year simulating the real world. Each tree has its genetically coded way of growth. Conditions the tree is exposed to also influence the growth process. FORKOME model's trees are also described by species-specific growth function, main parameters (dbh, H, age) and external conditions (described for each stand). Thanks to this solution, every Tree object possesses the function of height. Simulation of height imports itself to the creation of this function on every tree providing parameters of recent conditions in the given moment in a stand. The basic simulation part consists in tree diameter calculation. Annual diameter increment ranges from 0 (minimal value) to ideal conditions value (maximum for each species). The following equation is used:

$$\delta(D^2H) = rLa \left(1 - \frac{DH}{D_{\max}H_{\max}} \right)$$

- where: *r* – species constant describing assimilation apparatus photosynthetic productivity,
La – relative tree leaf area (m²/m²),
D – tree diameter measured at 1.30 m above the ground (cm),
H – tree height (cm),
*D*_{max} – species maximum diameter (cm),
*H*_{max} – species maximum height (cm),
 $\delta(D^2H)$ – tree volume increment (cm).

The influence of external conditions is taken into account in tree annual increment. Real tree increment $\delta(D^2H)_{\text{real}}$ is a result of optimal increase $\delta(D^2H)_{\text{opt}}$ and tree growth inhibiting conditions f_1, f_2, \dots, f_j , each value is ranged (0, 1).

$$\delta(D^2H)_{\text{real}} = \delta(D^2H)_{\text{opt}} \times f_1 \times f_2 \times \dots \times f_j$$

where: $\delta(D^2H)_{\text{real}}$ – real tree volume increment, after considering the influence of external conditions,

$\delta(D^2H)_{\text{opt}}$ – tree growth optimum conditions,

f_1, f_2, \dots, f_j – external conditions range (0, 1).

The equations are components of a multiplicative approach.

Tree height is calculated with the use of tree diameter;

$$H = 130 + b_2D - b_3D^2$$

where: b_2, b_3 – parameters of each species are calculated with the use of equations according to BORKIN et al. (1972):

$$b_2 = 2 \left(\frac{H_{\max} - 130}{D_{\max}} \right)$$

$$b_3 = \left(\frac{H_{\max} - 130}{D_{\max}^2} \right)$$

Light availability is the most important external factor that inhibits tree growth. The light amount available to each tree is calculated in FORKOME by considering the light radiation loss. The loss is caused by the sum of shading by the leaf area of higher trees. The radiation on each level of tree canopy is registered with the use of a professional tool for the patch.

The available light function describes the amount of light available for specific tree leaves and is calculated according to the equation:

$$Q(h) = Q_{\max} E^{-k \times LA(h)}$$

- where: $LA(h)$ – (Leaf Area) – leaf area above height *h*,
*Q*_{max} – solar radiation measured on the tree tops,
Q(*h*) – radiation measured at height *h*,
k – constant value – 0.25.

Trees are divided into 3 types depending on their light tolerance index: sun tolerant, medium, shadow tolerant.

The tree growth inhibiting light index is called light reaction function and is calculated in two different

ways depending on the tree light tolerating index. Light demanding and medium species have the same equations:

$$r = 2.24 (1 - e^{-1.136[Q(h) - 0.08]})$$

for shade-tolerant trees:

$$r = 1 - e^{-4.64[Q(h) - 0.05]}$$

where: r – light reaction function,
 $Q(h)$ – radiation at a given height.

Thermal conditions of the model are described by the annual sum of effective temperatures (higher than 5°). The temperature index inhibiting tree growth is calculated according to the equation below, according to BOTKIN (1993).

$$t = \frac{4(DGD - DGD_{\min})(DGD_{\max} - DGD)}{(DGD_{\max} - DGD_{\min})}$$

where: t – growth inhibiting index,
 DGD – sum of effective temperatures for a given association,
 DGD_{\min} – minimal sum of effective temperatures required by the species,
 DGD_{\max} – maximal sum of effective temperatures required by the species.

FORKOME model also takes into account leaf transpiration depending not only on meteorological conditions but also on tree species like in the other patch models. There are also relations between the tree species and groundwater level and between the tree growth rate and availability of groundwater implemented into the model structure. The block is created on the basic water balance equation.

$$W(t + 1) = W(t) + \text{Prec}(t) - \text{Trans}(t) - \text{Evapor}(t)$$

where: $W(t)$ – groundwater amount in the period of time t ,
 $\text{Prec}(t)$ – precipitation,
 $\text{Trans}(t)$ – transpiration,
 $\text{Evapor}(t)$ – soil surface water evaporation.

Another tree growth inhibiting index is called SITE INDEX. It describes the ratio of stem occupied area to maximal available area (BOTKIN 1993).

$$s = 1 - \frac{BAR}{SOILQ}$$

where: s – tree growth inhibition site index, depending on the already tree occupied area,
 BAR – total stem occupied area,
 $SOILQ$ – maximal stem area to be occupied on the patch.

There are two ways for a tree to die in the FORKOME model. First, if the tree does not reach the minimal diameter increment. Second, the tree dies randomly.

The model assumes that if during 10 consecutive years the tree does not increase its diameter, then there exists only a 1% chance that the tree will survive the decade. Annual tree death probability MORTAL is 0.386.

The FORKOME model studies if tree data get a minimum increase. If the minimum value is not exceeded, then random number (0.1) is taken, and if that value is greater than MORTAL parameter, the tree is removed.

Random tree mortality is based on an assumption that only a part of healthy trees succeed to live their maximal age. A FORKOME assumption is that 2% of the trees reach their maximum age and so inequality comes up described by BOTKIN (1993):

$$RND < \frac{4.0}{AGE_{\max}}$$

where: RND – random number ranged (0.1),
 AGE_{\max} – maximum tree species lifetime.

Trying to estimate the seed and sprout amount of some species one encounters several problems. Usually, the area all around the studied plot is unknown, therefore that makes the seed amount rather a guesstimate. That is the main reason for a stochastic approach to the seed and sapling problem in the model. Research was carried out and an empirical maximum amount of seeds and saplings was collected for each of the model species during one vegetation season. The amount is restricted by random and available light on the ground level. The amount of new saplings is generated separately for each type of light tolerance.

For the block of nutrients we used a polynomial function described by WEINSTEIN et al. (1982).

FORKOME model provides a possibility of defining felling scenarios. The interface supports determining the time of felling and diameters of tree species. The felling series can also be determined. The block construction of FORKOME model allows to use a wide range of climatic, soil and forest conditions. The species included in the model are both forest predominant species and admixed ones. The future extended use of the model is also possible for different scientific simulation experiments.

RESULTS AND DISCUSSION

There are two main variants of reaching the natural forest species composition. The first is a long-lasting one, assuming no anthropogenic interventions in natural succession mechanisms. The FORKOME prognosis reveals that the dominance of beech bio-

Fig. 3. N1 Norway spruce research plot: biomass change prognosis. Natural succession

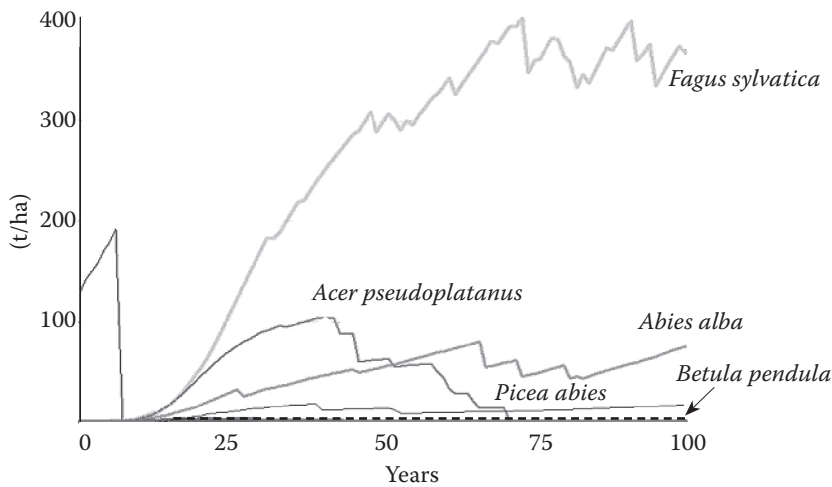
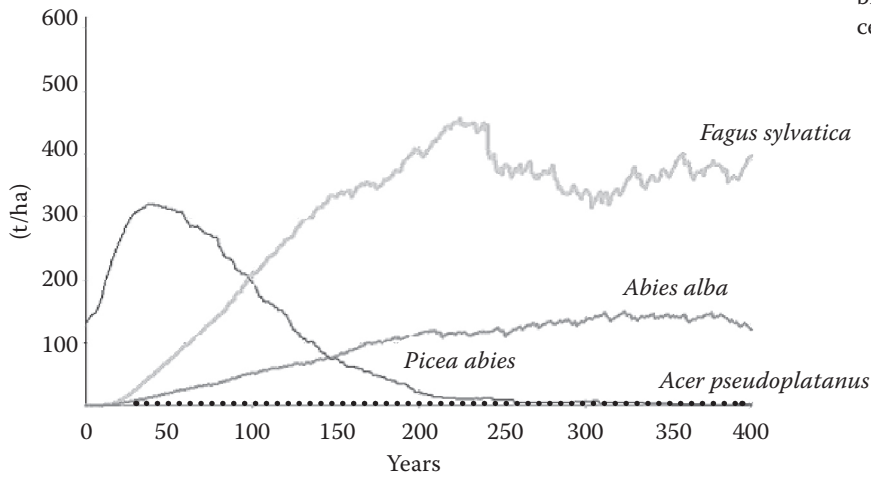


Fig. 4. N1 Norway spruce research plot: biomass change prognosis. Felling management method

mass over Norway spruce does not set over 100 years of simulation time (Fig. 3).

The other variant (quicker result) assumes anthropogenic interventions of various extent, such as felling or felling and planting.

The felling variant is characterized by a complete cutout of spruce trees with dbh more than 4 cm. This measure was performed in the 6th year of prognosis

with the FORKOME model. The results are as follows: beech biomass intensive increase to the level of 400 t/ha after 70 years of prognosis and spruce biomass almost completely decreasing (Fig. 4). Such a quick increase of beech biomass after 70 years in the felling variant depends on rich site conditions and on dominance of beech trees all around the spruce plot. The felling and planting variant is a selective method

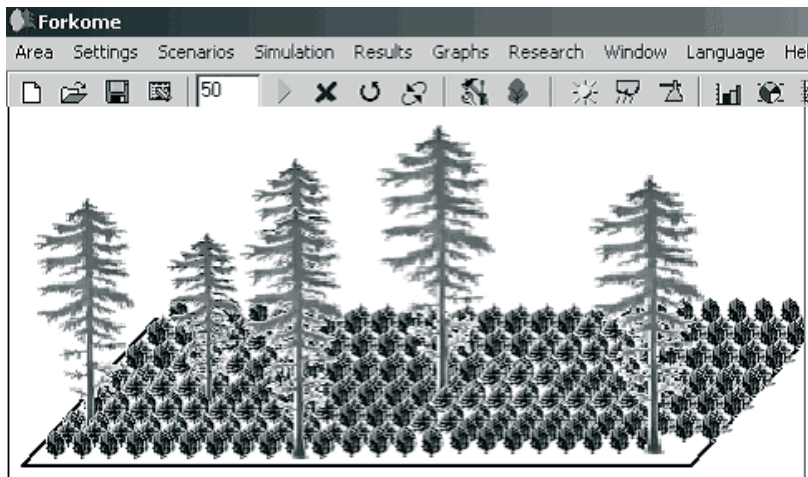


Fig. 5. N1 Norway spruce research plot: felling and planting management method. General visualization

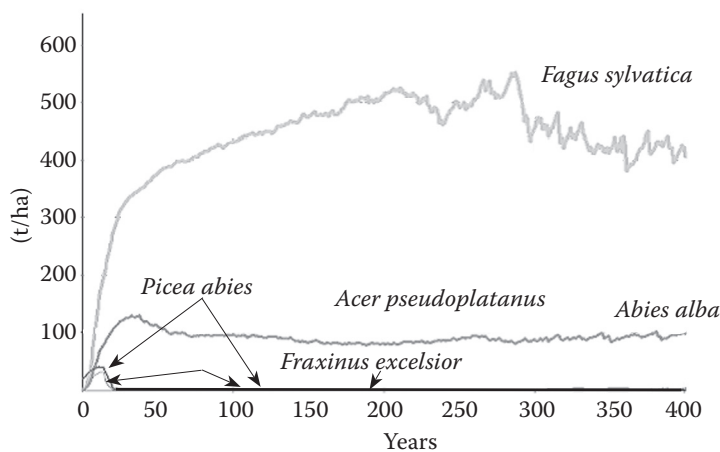


Fig. 6. N1 Norway spruce research plot: biomass change prognosis. Felling and planting management method

of cutting spruce trees out. The method allows to keep minimal shade, required by beech, fir (*Abies alba* Mill.) and ash (*Fraxinus excelsior* L.) saplings. Sapling density was assumed to be 6,000 specimen of beech, fir and ash per 1 hectare described in Zasady Hodowli Lasu... (2000). It is approximately 370 trees (beech – 127, fir – 117, ash – 120) per 25 m × 25 m research plot. The FORKOME model imperfect visualization (Fig. 5) poses several program problems, therefore the dimensions and bitmaps of saplings do not fully correspond with the real ones. These minor visual inconveniences do not affect the model working or prognosis results. Quick biomass increase is simulated for this option (Fig. 6).

Beech and fir biomass increases in the first 20 years of prognosis. Ash improves shaping the near-natural tree stand composition. It disappears just after 20 years, when beech and fir biomass stabilizes. Within 30–40 years beech biomass reaches 400 t/ha and holds the dominant position to the end of prognosis. Fir biomass does not exceed 100 t/ha.

Each variant solves the issue of replacing spruce stands with near-natural, habitat compatible forests. Felling and planting scenario is the most suitable one. There is often not enough time for natural succession mechanisms to work or on the other hand, the risk of a complete cutout is too great. Selective cutting and planting target species mixed with ash may be a solution uniting the advantages and decreasing the risks of former variants. After 40–50 years a young beech-fir forest is developed, its natural forest similarity approaching the potential (*Dentario glandulosae-Fagetum*) forest association in the Beskids Mts.

CONCLUSIONS

Presented results indicate high usefulness of the FORKOME model while investigating natural forest

regeneration in spruce monocultures. The prognosis indicates that the most effective method of regeneration is spruce selective cutting and planting target species of beech and fir with admixture of ash. Quick beech and fir biomass increase and beech forest development in the direction of natural (potential) forest are characteristic in the prognosis. The forest continually evolves into the potential Ukrainian Beskids beech-fir forest type.

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Received for publication April 4, 2006

Accepted after corrections October 9, 2006

Přirozená obnova lesa ve smrkových monokulturách ve Východních Beskydech – prognóza s využitím modelu FORKOME

ABSTRAKT: Příspěvek přináší výsledky výzkumu přirozené obnovy lesa ve smrkových monokulturách (*Picea abies* L. Karst.) Východních Beskyd s využitím prognostických možností modelu FORKOME. Byly předloženy různé varianty obnovních metod. Jako nejefektivnější se projevila selektivní těžba s výsadbou – selektivní těžba smrku se současnou výsadbou cílových dřevin: buku lesního (*Fagus sylvatica* L.) a jedle bělokoré (*Abies alba* Mill.) s dodáním jasanu ztepilého (*Fraxinus excelsior* L.). Biomasa buku a jedle rostla velmi rychle v prvních dvaceti letech, pak došlo k její stabilizaci. Po dalších 20–30 letech bylo již možné rozpoznat iniciální formu bukového lesa a stálý vývoj (potenciálně) přirozeného lesa. Potenciální (přirozené) lesní porosty Východních Beskyd se skládají z buku a jedle (*Dentario glandulosae-Fagetum*).

Klíčová slova: smrk ztepilý; buk lesní; počítačový model FORKOME; Východní Beskydy; smrkové monokultury; lesní hospodaření

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