

solution of coumarin and paradichlorobenzene, with 0.1%, 0.2% and 1.0% aqueous solution of colchicine were tried out. It was found that after the pretreatment with 0.2% aqueous solution of colchicine for 5 hours at +20° to +26° C, the contraction of the chromosomes was the most suitable to distinguish satisfactorily the details of chromosome morphology of Norway spruce.

The following techniques were applied:

1. *Germination*: Seeds were germinated on a moist filter paper in a petri dish at the temperature of +26° C.
2. *Colchicine pretreatment*: When the roots of germinating seeds had reached a length of 0.5 to 0.7 cm, the seeds were transferred to another petri dish containing the filter paper

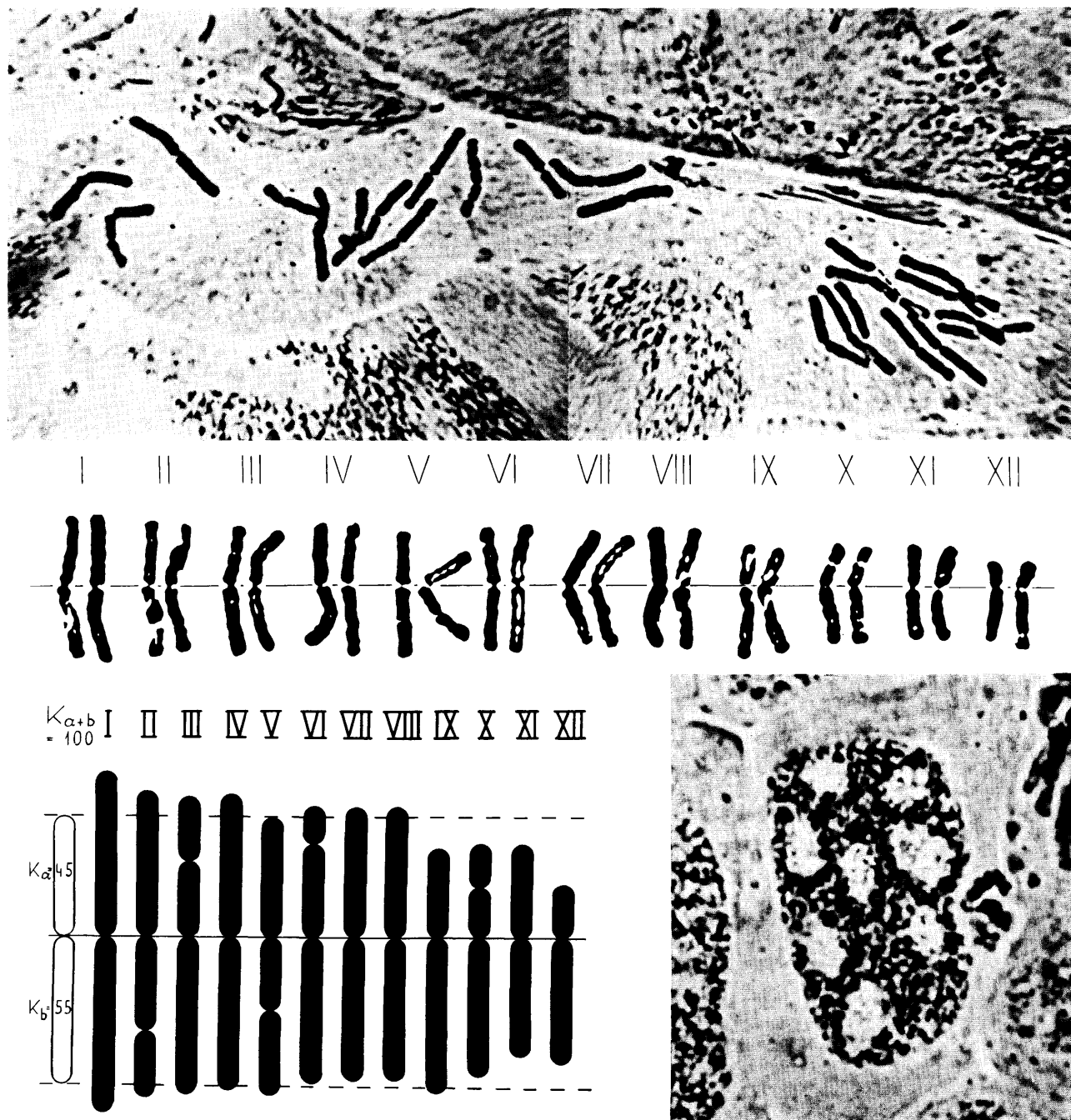
moistened with 0.2% colchicine solution and germination continued there for another 5 hours.

3. *Fixing*: After the pretreatment the root tips were fixed in alcohol-acetic acid (3 : 1) for 0.5 to 2 hours.

4. *Hydrolysis and staining*: Root tips were stained at first in a mixture of 2% aceto-orcein and NHCl (9 : 1) for 30 minutes at +60° C and in addition to this for 30 to 45 minutes in the same mixture at room temperature.

Then squash preparations were made.

The length of the chromosomes was measured from camera lucida drawings (×2100) with dividers and engineer's ruler to the nearest 0.2 mm. All the chromosomes in a plate (2n = 24) were measured. The regions of centromeres and secondary constrictions were omitted from



Figures 1-4: — Fig. 1 (above). Metaphase chromosomes (2n = 24) of *Picea abies* (×1440). One chromosome has broken from centromere region on squashing. — Fig. 2 (midst). Karyotype on the ground of the same metaphase plate as fig. 1 (×1800). — Fig. 3 (below left). Idiogram of *Picea abies*. — Fig. 4 (below right). An interphase nucleus with 8 nucleoli (×2000).

measurements. Then the absolute values of chromosome length were put in relation to the average chromosome (= 100 units) of the plate as it was earlier done by SIMAK (1962; 1964; 1966). Only such plates were selected for the measurements on which the spiralization index of chromosomes was approximately of the same value. The spiralization index was calculated as the ratio (in percentages) of the sum of the length of the two smallest chromosomes to the sum of the length of the two biggest one. This method of determining the spiralization index of the chromosomes was according to the idea of SASAKI (1961) successfully used in karyological investigations with mitotic chromosomes in man (GINDILIS, 1966) as well as with plant chromosomes in *Allium* species (PAVULSONE *et al.*, 1970).

For each chromosome, too, was determined the arm index as the ratio of the longer arm to the shorter one.

Results and Discussion

The haploid chromosome number of the genus *Picea* showed earlier, is $n = 12$ (SAX and SAX, 1933; KIELLANDER, 1950; MEHRA and KHOSHOO, 1956 a; SANTAMOUR, 1960; MORGENSTERN, 1962; BURLEY, 1965).

The present investigation also shows $n = 12$ chromosomes of which 10 are with centromere in the median region (arm ratio 1.0 to 1.7) and 2 are with submedian centromere (arm ratio is 1.7 to 3.0) (Fig. 1 and 2). The centromeric position of the chromosomes was described on the ground of the nomenclature published by LEVAN *et al.* (1964).

On the basis of 35 measurements the haploid karyotype in the form of an idiogram was constructed. In the idiogram the chromosomes were placed in order of their total relative length, the longest chromosome first and the shortest one last, and were arranged with the short arm directed upwards (Fig. 3).

Table 1. — Relative length and arm ratio of the chromosomes.

Chromosome Nos.	Relative length	Arm ratio
I	126.4 ± 0.5	1.07 ± 0.01
II	114.3 ± 0.6	1.10 ± 0.01
III	111.3 ± 0.6	1.12 ± 0.01
IV	110.2 ± 0.6	1.07 ± 0.01
V	103.5 ± 0.6	1.32 ± 0.01
VI	103.4 ± 0.5	1.10 ± 0.01
VII	102.0 ± 0.4	1.10 ± 0.01
VIII		
IX	91.2 ± 0.7	1.73 ± 0.02
X	86.7 ± 0.6	1.47 ± 0.02
XI	79.1 ± 0.5	1.26 ± 0.01
XII	68.7 ± 0.3	2.12 ± 0.03

Table 1 shows the average relative length of each individual chromosome in relation to the mean chromosome length of the karyotype and the average value of the arm ratio.

5 of the chromosomes with the centromere in the median region show to have a secondary constriction: chromosomes II and V have a secondary constriction on the longer arm and chromosomes III, VI and X on the shorter one. But it should be mentioned that the secondary constrictions were not always apparent on all the 5 pairs of abovementioned chromosomes. In some cases only one of the homologous chromosomes of the pair indicated a secondary constriction.

Secondarily constricted chromosome pairs (II, III, V, VI and X) as well as chromosomes I, IX, XI and XII are quite easily identified on the plate. Chromosome IV, VII and VIII are more less easily identified whereas chromosomes VII and VIII are impossible to distinguish from each other.

At least 4 pairs of the secondarily constricted chromosomes appear to be capable of organizing the nucleoli, since it was possible to count 8 nucleoli in the interphase nuclei (Fig. 4). But in most of the nuclei there was observed a varying number of nucleoli (4 to 7). The low number of nucleoli may be due to the fusion of several nucleoli. Such an opinion was earlier calculated also by NATARAJAN *et al.* (1961) in the paper which deals with the chromosome morphology of *Pinus silvestris*.

Of the literature cited in this paper in connection of chromosome morphology studies of conifers, only SAX and SAX (1933) have published the idiogram of *Picea abies* observed in the early development of the endosperm. But the paper contains no direct data on the length of the chromosomes and data of this kind for the comparison with results of the present study can only be procured by measurement on the published idiogram and calculating likewise the absolute length of each chromosome in relation to the average one. The comparison is presented in the form of the table 2.

Only the longest chromosome (I) has a clearly different length. In the idiogram published by SAX and SAX, it is longer than on the ground of the present investigation. But in the idiogram of SAX and SAX there are 3 chromosomes with submedian centromere since in the present idiogram there are only 2 of this kind.

No considerations have been taken in the analysis of SAX and SAX as to the occurrence of secondary constrictions. Unlike the present described 5 chromosomes each having a secondary constriction in haploid karyotype, TOYAMA and KUROKI (1967) have mentioned that *Picea abies* has 4 pairs of secondary constrictions.

Summary

Solution of 0.2% colchicine was satisfactorily used for the pretreatment of root tips to determine the karyotype of Norway spruce. The results of the investigation were presented in the form of the idiogram and were compared with data of other authors.

Literature Cited

AASS, I.: En cytologisk analyse av Skjåkfurua. Det Norske Skogsforsøksvesen 14, 96—109 (1957). — BURLEY, J.: Karyotype analysis of Sitka spruce, *Picea sitchensis* (BONG.) Carr. Silvae Genetica 14, 127—132 (1965). — CHRISTIANSEN, H.: On the chromosomes of *Pseudo-*

Table 2. — Comparison of the karyotype of Norway spruce with results of the investigation of SAX and SAX.

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
SAX and SAX	146	114	108	107	105	101	99	93	86	85	85	73
Present study	126	114	111	110	104	103	102	102	91	87	79	69
Difference	+20	±0	—3	—3	+1	—2	—3	—9	—5	—2	+6	+4

tsuga macrocarpa and *Pseudotsuga menziesii*. *Silvae Genetica* 12, 124–127 (1963). — GINDILIS, V. M.: (The spiralization of mitotic chromosomes and karyogrammic analysis in man). *Cytologiya* 8, 144–157 (1966). (In Russian). — KEDHARNATH, S., and UPADHAYA, L. P.: Chromosome preparations from needle bases of Chir pine (*Pinus roxburghii* SARG.). *Indian For.* 91, 477–478 (1965). — KJELLANDER, C. L.: Polyploidy in *Picea abies*. *Hereditas* 36, 513–516 (1950). — KRUKLIS, M. V.: (A karyotypic analysis of *Larix dahurica* TURCZ. Materials of the Confer. on For. Genet., Selection and Seedage). Petrozavodsk, 1967, 25–28. (In Russian). — KUMAR, S., BANSAL, H. C., SINGH, D., and NATARAJAN, A. T.: Consistency of karyotypes and classification of chromosomes in the genus *Pinus*. *Indian J. Genet. and Plant Breed.* 26, 311–316 (1966). — LEVAN, A., FREDGA, K., and SANDBERG, A.: Nomenclature for centromeric position on chromosomes. *Hereditas* 52, 201–220 (1964). — MEHRA, P. N., and KHOSHOO, T. N.: Cytology of conifers. I. *J. Genet.* 54, 165–180 (1956 a). — MEHRA, P. N., and KHOSHOO, T. N.: Cytology of conifers. II. *J. Genet.* 54, 181–185 (1956 b). — MERGEN, F., and NOVOTNY, H. M.: Squash technique for chromosome studies in pine needles and root tips of Slash pine. *For. Sci.* 3, 56–60 (1957). — MERGEN, F., and BURLEY, J.: *Abies* karyotype analysis. *Silvae Genetica* 13, 63–68 (1964). — MORGENSTERN, E. K.: Note on chromosome morphology in *Picea rubens* SARG. and *Picea mariana* (MILL.) B.S.P. *Silvae Genetica* 11, 163–164 (1962). — NATARAJAN, A. T., OHBA, K., and SIMAK, M.: Karyotype analysis of *Pinus silvestris*. *Hereditas* 47, 379–382 (1961). — PAVULSONE, S. A., IORDANSKY, A. B., and GINDILIS, V. M.: (Comparative morphometrical analysis of chromosomes of *Allium cepa* L. and *Allium fistulosum* L.). *Genetika* 6, 40–56 (1970). (In Russian). — PEDERICK, L. A.: The structure and identification of the chromosomes of *Pinus radiata* D. DON. *Silvae Genetica* 16, 69–77 (1967). — PRAVDIN, L. F.: [Scots pine (*Pinus silvestris* L.). Variability, intraspecific taxonomy and selection.] Published by "Nauks". Moscow, 1964, 96–99. (In Russian).

— SANTAMOUR, F. S.: New chromosome counts in *Pinus* and *Picea*. *Silvae Genetica* 9, 87–88 (1960). — SASAKI, M.: Observations on the modification in size and shape of chromosomes due to technical procedure. *Chromosoma* (Berl.) 11, 514–522 (1961). — SAX, K., and SAX, H. J.: Chromosome number and morphology in the conifers. *J. Arnold Arbor.* 14, 356–375 (1933). — SAYLOR, L. C.: A karyotypic analysis of selected species of *Pinus*. *Silvae Genetica* 10, 77–84 (1961). — SAYLOR, L. C.: Karyotype analysis of *Pinus*-group laticiones. *Silvae Genetica* 13, 165–170 (1964). — SHISHNIASHVILI, R. M.: (A karyotypic analysis of *Pinus sosnowskyi* NAKAI). *Cytologiya* 10, 255–258 (1968). (In Russian). — SIMAK, M.: Karyotype analysis of *Larix decidua* MILL. from different provenances. *Medd. Sta. Skogsforskn. Inst.* 51, 3–22 (1962). — SIMAK, M.: Karyotype analysis of Siberian larch (*Larix sibirica* LEDB. and *Larix sukaczewii* DYL.). *Studia Forestalia Suecica*, Nr. 17, 15 pp. (1964). — SIMAK, M.: Karyotype analysis of *Larix griffithiana* CARR. *Hereditas* 56, 136–141 (1966). — SIMAK, M., and HAPPEL, C.: Vorbehandlung der Koniferensamen für Chromosomenuntersuchungen. *Silvae Genetica* 15, 38–41 (1966). — TARNAVSCHI, I. T., and CIOBANU, I.: Karyologische Untersuchungen an *Pinus nigra* ARN. Ssp. *Nigricans* HOST Var. *banatica* GEORG. et IONESCU im Vergleiche mit *Pinus nigra* ARN. Var. *austriaca* HOESS. *Rev. Roum. Biol. (Ser. Bot.)* 10, 371–375 (1965). — THOMAS, G., and CHING, K. K.: A comparative karyotype analysis of *Pseudotsuga menziesii* (MIRB.) FRANCO. and *Pseudotsuga wilsoniana* (HAYATA). *Silvae Genetica* 17, 138–143 (1968). — TOYAMA, S., and KUROKI, Y.: (Studies on the karyotypes of forest trees. III On the chromosomes of some species of the *Pinaceae*). *Rep. Kihara Inst. Biol. Res.* No. 19, 161–162 (1967). (In Japanese). — Plant Breed. Abstr. 39, 3501 (1969). — WINTON, L. L.: Cytotechniques for spruce chromosomes. *Minnesota For. Notes*, No. 146 (1964). — YIM, K. B.: Karyotype analysis of *Pinus rigida*. *Hereditas* 49, 274–276 (1963).

Inheritance and Correlation of Growth Characters in *Populus deltoides*

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Introduction

Since unrooted cuttings rather than seedlings of eastern cottonwood (*Populus deltoides* BARTR.) are usually planted for timber production in the Lower Mississippi Valley (McKNIGHT, 1970), replicated clonal tests are ideally suited for selecting superior genotypes for planting there. These tests cannot be adequately designed without phenotypic and genetic correlations between measurements made over time and estimates of total genetic variance and covariance. The few data published to date have been based on first- and second-year measurements (WILCOX and FARMER, 1967; FARMER and WILCOX, 1968). We report here figures gathered over six growing seasons in a replicated clonal test.

Materials and Methods

Clones were taken randomly from a natural stand of 2-year-old seedlings near Rosedale, Mississippi (Bolivar County). For the test, unrooted cuttings from these clones were planted at 9- by 9-foot spacing on a recently cleared site near Stoneville, Mississippi. The soil was a Sharkey clay, which BROADFOOT (1960) described as marginally suitable for cottonwood in the Mississippi alluvial plain. Details related to establishment were given by WILCOX and FARMER (1967).

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The test design was a randomized complete block with six replications, 49 clones, and single-tree plots. Data collected after 1 and 2 years were analyzed on the basis of this design and reported by WILCOX and FARMER (1967). Mortality and damage to trees by the end of six growing seasons led to the restriction of current analyses to 38 clones in five replications with no missing plots. The following variables were examined:

- 1–4. Total height after one, two, three, and five growing seasons.
- 5–6. Height growth in the second and third growing seasons.
- 7–11. Diameter at 1 foot after one and two growing seasons and at 4½ feet after three, five, and six growing seasons.
- 12–13. Diameter increment in the second and sixth growing seasons.

All heights were measured to the nearest 0.1 foot with the aid of a pole, and diameters were measured to the nearest 0.1 inch.

Following analysis of variance, the clone and error variance components were estimated from the mean square for all variables. Ratios of genetic to phenotypic variance (broad-sense heritability) and their confidence limits were calculated from two formulas:

$$H^2 = \frac{\sigma_c^2}{\sigma_c^2 + \sigma_e^2} \quad (1)$$

$$P [1 - K_{\alpha/2} \leq H^2 \leq 1 - K_{1-\alpha/2}] = 0.95 \quad (\text{BECKER, 1967}) \quad (2)$$

$$\text{where } K_x = \frac{r MS_2 F_x}{MS_1 + MS_2 (r-1) F_x}$$