Note on Chromosome Morphology in Picea rubens Sarg. and Picea mariana (Mill.) B.S.P.

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Cytogenetic studies in the genus Picea L. have progressed little beyond the stage of chromosome counts. Examination of sixteen species indicated that the haploid chromosome number is twelve (3, 7, 8), and little doubt remains that this number prevails in normally developed individuals throughout the genus. Chromosome morphology, thus being of greater interest than chromosome number, has been dealt with in only a small number of species. The studies of all species investigated agree that nine chromosomes have median and three submedian centromeres. Secondary constrictions were noted in two species, namely three constrictions in P. smithiana (Wallich) Boiss. (3) and two in P. jezoensis var. hondoensis (Mayr) Rehder (7). Detailed species comparisons, based on carefully drawn idiograms, are still lacking for this genus. As a result existence and nature of interspecific differences in chromosome morphology still require comprehensive investigations.

For a study of chromosome morphology in P. rubens and P. mariana, seed from two sources of each species was supplied by the Glendon Hall Laboratory of the University of Toronto. P. mariana came from the Longlac and the North Bay area of Ontario, and P. rubens from the Valcartier Forest Experiment Station, Quebec, and the Haliburton area of Ontario. Seedling root tips were pretreated in 0.1% colchicine for 20 hours, fixed in 3:1 alcohol-acetic acid for 30 minutes, stained according to the Feulgen procedure, and squashed in acetic acid. Slides were made permanent according to the dry ice method (1).

Analysis began with the preparation of camera lucida drawings of three metaphase plates of each species at a magnification of 5000. Length of chromosome arms was measured and summed within each plate to obtain "total diploid complement length" (TDCL). The contribution of each individual chromosome to the plate total could then be expressed as TDCL %. This term, being a measure of chromosome length in relative terms, permits the comparison of chromosomes from plates with different degrees of contraction (6). Next, arm ratios were obtained by dividing the length of the short arm by that of the long arm. On the basis of relative length and arm ratios, chromosomes were then paired to obtain the haploid set which was arranged in order of increasing length.

The resuling chromosome series showed few distinguishing characteristics. In both species the twelve chromosome pairs differed merely quantitatively from one another, i.e. in length and arm ratio, showing a lack of easily recognizable qualitative features such as secondary constrictions and satellites. Although observed, secondary constrictions could not be consistently identified. Especially difficult was their separation from other achromatic regions. Similar conditions have recently been described from a study of Pinus (9).

The exclusive presence of quantitative differences demanded a cautious interpretation of the data (5). Attention was focussed on distinguishable chromosome groups rather than on individual chromosomes because of optical limitations and random variation within the populations.

No clear-cut differences between species could be determined and for both species the chromosomes of each plate could be separated into three groups based on length and arm ratio. These groups, based on one plate of each species, are shown in Figure 1. Group I consists of one short pair with submedian centromere. Group 2 comprises three medium-sized pairs with one median and two submedian centromeres. Group 3 includes eight long pairs with more or less median centromeres.

The single pair in group 1 can always be easily identified but several individual pairs within groups 2 and 3 cannot. In group 2 the pair with median centromere (pair 2) can be distinguished from chromosomes in group 3, which also have median centromeres, by its much smaller size. But the pairs with submedian centromeres (pairs 3 and 4) are so close in length and arm ratio that their separation is rather difficult and probably not always reliable. In group 3 conditions are similar and only the...
differences in chromosome morphology is also in agreement with the hypothesis that in most conifer genera interspecific differences are generally small, in consequence of evolutionary divergence by gene mutations rather than by structural rearrangements (3,8). In the genus *Picea* this hypothesis still needs to be tested further by detailed studies of the many cytologically unknown species.

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**Literature Cited**


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**Viable Pine Pollen Stored 15 Years Produces Unsound Seed**

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Controlled pollination in 1960 with viable and non-viable samples of stored pine pollen produced only hollow seeds. The samples were from pollen used for a previous study which tested germination in vitro of pollen of seven species of pine.1) These pollens had been stored 15 years at 0° C. and 5° C. and at relative humidities of 10, 25, 50, and 75 percent. Only pollen stored at 10 percent relative humidity germinated, and germination in *Pinus ponderosa* was as high as 77 percent. Using samples of viable and non-viable *P. ponderosa* pollen, we made several crosses on three *P. ponderosa* seed trees. Only two crosses on one tree set cones.

One cross used pollen stored at 5° C. and 10 percent relative humidity. This pollen, which had 58 percent germination of the grains in vitro, produced 65 hollow seeds. The other cross used pollen that had been stored at 5° C. and 50 percent relative humidity and that had not germinated in vitro. From this cross only 11 hollow seeds were produced.

We found that:

1. Tube formation by pine pollen in vitro does not necessarily indicate ability to grow for a year through the nucellus and produce viable sperm nuclei;

2. Stored pollen that did not germinate in vitro was capable of inducing cone maturation, but incapable of producing sound seeds; and

3. Pollen that germinated in vitro produced more, though likewise unsound, seeds than did the non-germinating pollen.

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