IOCBI
2026
Conference

The 1st International Online Conference on Biology

10–12 February 2026 | Online

MDPI

Chromosome Number Determination and Karyotype Evolution in Different Species of the Tribe Naupactini (Coleoptera, Curculionidae)

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INTRODUCTION & AIM

The family Curculionidae shows a high incidence of parthenogenesis, particularly among broad-nosed weevils (subfamilies Entiminae and Cyclominae). Many parthenogenetic species are also polyploid, which may have important implications for their evolution and adaptation. The tribe Naupactini is a Neotropical group and one of the most diverse lineages within Curculionidae, including species of both ecological and agronomic relevance. However, cytogenetic studies of this tribe are scarce, and some reports of polyploidy remain uncertain or contradictory.

Thus, the determination of the modal chromosome number (i.e., characteristic of this taxon) is highly relevant for understanding both the evolutionary history and genetic diversity of these species.

The main objective of this study was to establish the chromosome number of different Naupactini species by analyzing spermatogonial meiosis, and subsequently to propose hypotheses on karyotype evolution.

Naupactus dissimulator

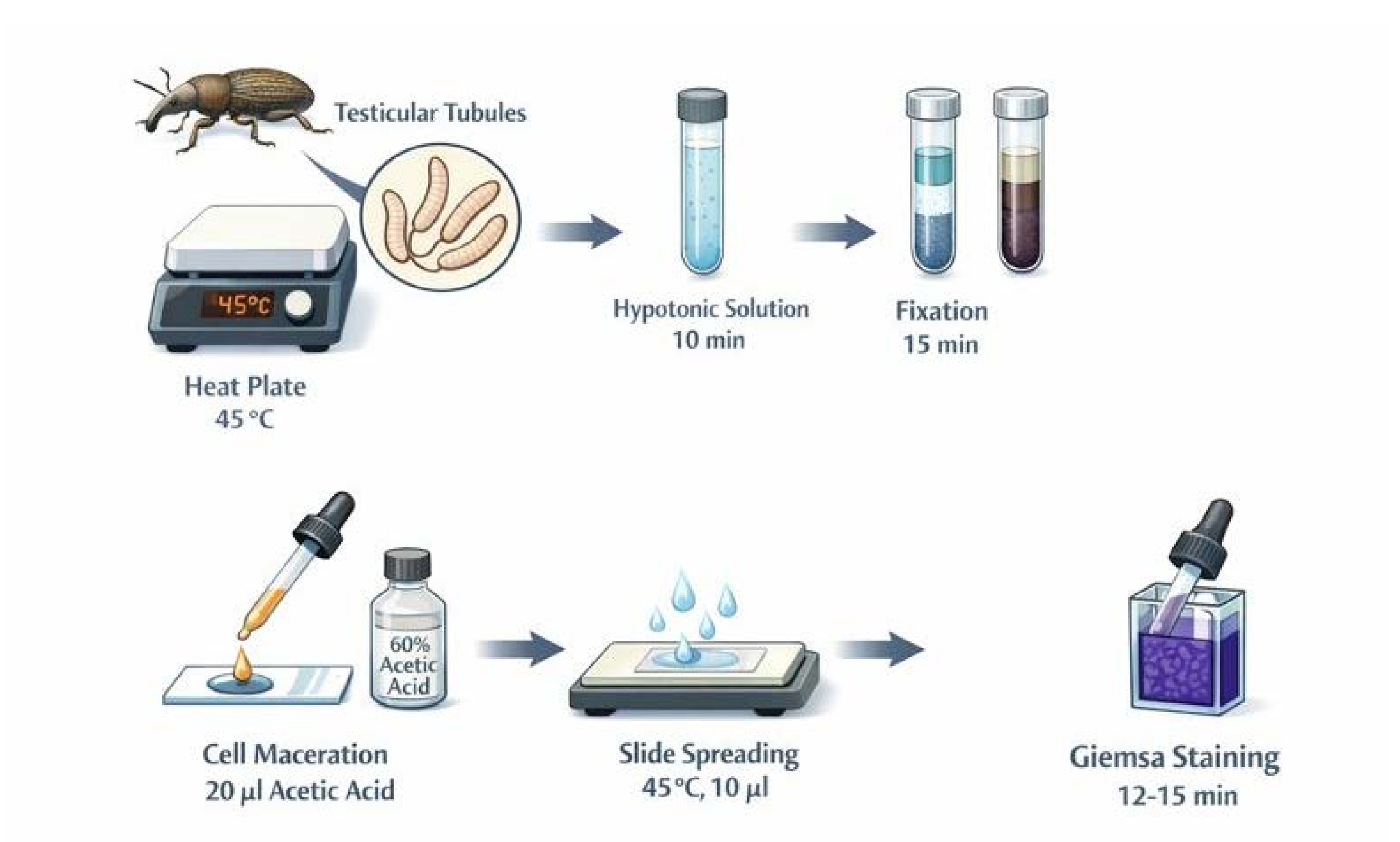
Naupactus xanthographus

Pantomorus postfasciatus

Species images were obtained from the website of Lanteri and del Río(1)

METHOD

Testicular tubules from adult weevils were dissected and processed for chromosome preparations. Samples were incubated in a hypotonic solution (0.075 M NaCl) for 10 min and fixed in ethanol:acetic acid (3:1) for 15 min. Cell suspensions were macerated in 60% acetic acid, dropped onto slides pre-heated at 45 °C, and spread on a hot plate. Preparations were then stained with 5% Giemsa for 12–15 min and analyzed under light microscopy.



Between 5 and 10 meiotic preparations were examined for *Naupactus dissimulator*, *Naupactus xanthographus*, and *Pantomorus postfasciatus*.

RESULTS & DISCUSSION

N. dissimulator and *N. xanthographus* showed 2n = 22, whereas *P. postfasciatus* had 2n = 26. 2n = 22 is prevalent and appears to be the ancestral chromosome number in Curculionidae species (2, 3). In this context, the most parsimonious explanation for the karyotype variation observed here is a chromosome fission event leading to 2n = 26 rather than multiple fusion events. In addition, centric fission has been described as an important mechanism in the karyotype evolution of several Curculionidae species, such as *Peritelus familiaris* (4), *Cirrorrhynchus kelecsenyi* (5), and three sibling species of the *Acalles echinatus* group (*A. echinatus*, *A. fallax* and *A. petryszaki*) (6), supporting chromosome fission as the most likely mechanism explaining the increase to 2n = 26 observed in this study.

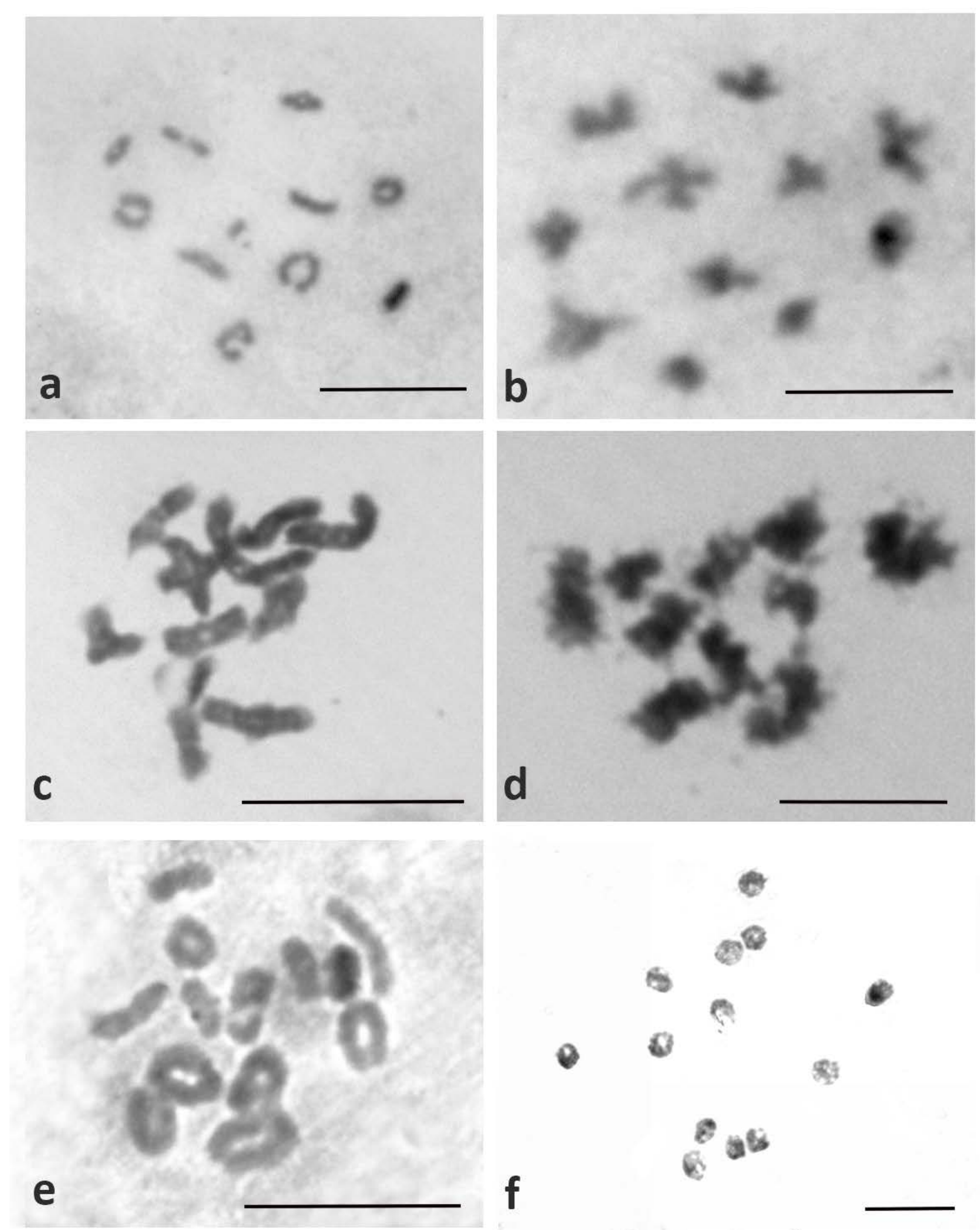


Figure 3. Meiotic chromosomes of *N. dissimulator* (a–b), *N. xanthographus* (c–d), and *P. postfasciatus* (e–f). a, c, e: diakinesis. b, d: metaphase I. f: metaphase II. Barra :10 um

CONCLUSION

Our results show that *N. dissimulator* and *N. xanthographus* share the modal and likely ancestral chromosome number for Curculionidae (2n = 22), whereas *P. postfasciatus* exhibits a derived karyotype with 2n = 26. The most parsimonious explanation for this difference is a chromosome fission event. These findings highlight the value of cytogenetic approaches for understanding chromosomal evolution in agronomically important weevil species.

FUTURE WORK / REFERENCES

These findings provide a foundation for future research on polyploidy and its evolutionary significance in parthenogenetic Curculionidae.

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