

Review

A review of chromosome cytology in Hyacinthaceae subfamilies Urgineoideae and Hyacinthoideae (tribes Hyacintheae, Massonieae, Pseudoprosperae) in sub-Saharan Africa

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Received 13 March 2012; received in revised form 11 July 2012; accepted 23 July 2012

Available online 13 September 2012

Abstract

The chromosome cytology of subfamilies Hyacinthoideae and Urgineoideae of the monocot family Hyacinthaceae are reviewed for their centres of diversity in sub-Saharan Africa within the framework of a recent molecular-based classification. We also provide some new chromosome counts for genera or species that are unknown or poorly known cytologically. We conclude that the ancestral basic chromosome number for Hyacinthoideae is $x=10$ but tribe Pseudoprosperae evidently has $x=9$, the most likely base in Hyacintheae. Tribe Massonieae has five of the nine (out of 10) genera counted apparently ancestrally tetraploid with $2n=40$ and we infer a basic chromosome number for the tribe of $x=10$ based on patterns within the tribe and by outgroup comparison. An extensive descending dysploid series is present in *Lachenalia*, ranging from a possible ancestral base of $x=10$ to $n=5$, and several species are polyploid or have diploid and polyploid populations. Basic number in Urgineoideae is also $x=10$ and the subfamily exhibits little divergence from that base among sub-Saharan species. Polyploidy at species rank is relatively rare among the sub-Saharan members of both subfamilies. Based on available data just 7% of species of Urgineoideae and 15% of sub-Saharan Hyacinthoideae are species level polyploids but several more have diploid and polyploid populations. This conforms to the pattern of low level of polyploidy in subfamily Ornithogaloideae of Hyacinthaceae and other sub-Saharan families of geophytic plants.

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Keywords: Africa; Base numbers; Chromosome cytology; Hyacinthaceae; Hyacintheae; Hyacinthoideae; Massonieae; Pseudoprosperae; Urgineoideae

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1. Introduction

Recent, molecular-based classifications of Hyacinthaceae recognize four subfamilies: the monogeneric South American Oziroëoideae and the three much larger Old World Hyacinthoideae, Ornithogaloideae and Urgineoideae (Manning et al., 2004). Subfamily Hyacinthoideae is subdivided into three tribes, the species-rich Eurasian Hyacintheae, the monospecific southern African Pseudoprosperae, and the predominantly sub-Saharan African Massonieae with 10 genera and ± 104 species in Africa and southern Asia. Urgineoideae are largely sub-Saharan African with several species in Eurasia as far east as India. Massonieae has a similar distribution but with a marked secondary radiation in Eurasia. This review complements the similar study in Ornithogaloideae (Goldblatt and Manning, 2011) and completes our cytological review for the family in sub-Saharan Africa.

Chromosome counts for Hyacinthoideae and Urgineoideae are widely scattered in the literature, many of them published under genera and species that are now relegated to synonymy. We assemble here all published counts for the two subfamilies excluding Hyacintheae (none of which occur in sub-Saharan Africa), under their current names and arranged according to the most recent infrafamilial classification (Manning et al., 2004). We also provide some new chromosome counts for genera and species uncounted or poorly known. We analyze the patterns of variation in chromosome number in relation to the molecular phylogeny, infer basic numbers for genera and sections, and highlight important gaps in our knowledge of the cytology of the subfamilies. These gaps limit a deeper understanding of the chromosomal evolution in some lineages of Hyacinthoideae but we infer an ancestral base for both Hyacinthoideae and Urgineoideae of $x=10$, which we also identified as the likely base number in the sister clade Ornithogaloideae (Goldblatt and Manning, 2011).

2. Materials and methods

2.1. Published counts

Data on chromosome number in genera of Hyacinthoideae and Urgineoideae were extracted from indexes to plant chromosome numbers covering the years since chromosome numbers were first made available in accessible compilations (Bolkhovskikh, 1969; Goldblatt, 1981; Goldblatt and Johnson, 1990; Moore, 1973, 1974, 1977, etc.; see Tables 2 and 3). We tabulate counts according to the current subfamilial classification, with species names corrected to reflect current nomenclature and taxonomy (Manning et al., 2004). Original sources were consulted for most

counts, especially those we had reason to question. We had hoped to check voucher specimens for questionable counts but those for the important contribution by De Wet (1957) could not be located at PRE where they had been deposited (C. Archer pers. comm. 2009). Most papers published before the 1980s do not list voucher specimens. There is no precedent for ignoring chromosome counts not linked to voucher specimens and we see no reason to do so here. Examples of doubtful identification are discussed in the text and noted in Table 3.

Patterns of change in chromosome number and karyotype are inferred using established hypotheses for these phenomena (Jones, 1970; Raven, 1975; Stebbins, 1950, 1971). Polyploid sequences are interpreted as proceeding from lower to higher numbers by doubling. Dysploid (aneuploid) sequences, i.e. stepwise changes rather than doubling of base numbers, are widely believed to be largely descending in a process involving translocation of chromosome material to a second chromosome and loss of a centromere plus those genes associated with cell division. Descending dysploid reduction frequently results in translocation of a long arm of an acrocentric chromosome to the short arm of another and loss of the centromere of the donor chromosome, resulting in a large metacentric chromosome (and lower base number), a process often called chromosome fusion or Robertsonian translocation.

We do not list authorities for species in the text as these are included in Tables 2 and 3.

2.2. Original counts

Material for the original counts reported here (Fig. 2; Table 1) was prepared according to the protocol described by Goldblatt and Takei (1993). The vouchers are housed at the Missouri Botanical Garden Herbarium (MO) and Compton Herbarium (NBG). Counts are based on samples of three to four individuals and are assumed to represent entire populations, following widespread practice in plant cytology.

Table 1

New chromosome counts in Massonieae and Urgineae. Vouchers are housed at the Missouri Botanical Garden (MO) and Compton (NBG) Herbaria.

Species	Diploid number, $2n$	Voucher data
<i>Daubenya aurea</i>	32	South Africa, N Cape, Roggeveld Plateau west of Sutherland, Hall 3269 (NBG)
<i>Drimia capensis</i>	60	South Africa, N Cape, Nieuwoudtville, Goldblatt 6537 (MO)
<i>Massonia depressa</i>	18	South Africa, N Cape, Nieuwoudtville, Goldblatt 6097 (MO)
<i>M. echinata</i>	22	South Africa, N Cape, Bushmanland, Goldblatt & Manning 13042 (MO)

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