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10. Supported by PHS grant HD-01236 from the National Institute of Child Health and Human Development. This paper is No. 31 in a series on the biochemistry of amphibian metamorphosis from this laboratory. Partial support for G.F. was provided by the Instituto Nacional de la Investigación Científica, Mexico 1, D.F.

19 September 1967

Avena magna: An Important New Tetraploid Species of Oats

Abstract. Avena magna *is a new tetraploid species morphologically similar to the hexaploid* A. sterilis, *having a high concentration of protein, large caryopses, and outstanding resistance to crown rust. One genome in* A. magna *appears homologous to the A_s genome present in hexaploid, tetraploid, and one group of diploid species.* Avena magna *is a possible ancestor of cultivated oats.*

We found a new tetraploid [2*n* (diploid number) = 28] species of *Avena* among collections obtained from the Mediterranean region by Rajhathy, Zillinsky, and Hayes (*1*). This species may have been significant in the evolution of hexaploid *Avena*. It is also of special interest because it has large caryopses (groats) with high protein content, outstanding resistance to crown rust, and thick culm wall.

The hexaploid (2*n* = 42) species *A. sterilis* L. is indigenous to the Mediterranean region. Murphy and co-workers (*2*) and Zillinsky and Murphy (*3*) have recently reported finding resistance to the major oat diseases among collections of *A. sterilis* obtained from Israel (*2*) and other Mediterranean countries (*1*).

While screening collections of *A. sterilis* for protein content at Beltsville, Maryland, we discovered that CW-525, C.I. 8330 (accession numbers of Canadian Department of Agriculture and U.S. Department of Agriculture, respectively) possessed unusually large caryopses with high protein content. The percentage of protein ranged from 23.4 to 30.0 percent, depending on the environment in which the plants were grown. The percentages of protein among cultivars of *A. sativa* L. ranged from 15 to 21. When CW-525 was grown in irrigated fields at Aberdeen, Idaho, in 1967, the weight of 100 caryopses was 3.5 g compared to 2.8 g for the cultivar Garland, C.I. 7453, and 0.9 to 2.4 g for several hundred lines of *A. sterilis* entries. The seedlings of CW-525 were resistant to race 264 of crown rust at Beltsville, Maryland, and Ottawa, Ontario; adults were resistant to race 264 in the cooperative oat-rust nursery in Puerto Rico (see *4*).

We crossed CW-525 with *A. sativa* and *A. sterilis* as a part of our inheritance and breeding studies. Reciprocal crosses between CW-525 and *A. sativa* and *A. sterilis* were obtained, but all F_1 plants were sterile. As a result of the unexpected sterility, we studied the taxonomy and chromosome number of several plants from the collection CW-525. All of the plants sampled were tetraploid.

Although CW-525 resembles *A. sterilis* more than it does any other species, it is markedly different in several characters. Like *A. sterilis*, its spikelets articulate only at the base of the lowest floret, leaving a dissemination unit of three tightly attached florets (Fig. 1). We believe that morphological and chromosomal differences in CW-525 favor its recognition as a new species. The herbaria of the U.S. National Museum, Smithsonian Institution, Washington, D.C., and Royal Botanic Gardens, Kew, England, were searched unsuccessfully for previous collections resembling CW-525.

AVENA MAGNA Murphy *et* Terrell, new species

Avenae sterili *affinis, internodorum parietibus incrassatis, florum characteribus, chromosomatum numero differt.*

Rachillae segmentum infimum latum compressum. Articuli cicatrix 3.3 ad 4.0 mm longa, 1.5 ad 2.0 mm lata. Lemmatum I et II partes inferiores ⅔ ad ⅚ densissime longo-villosae, pilis usque ad 8 mm longis; lemmatum partes superiores ⅙ ad ⅓ pilis usque ad 1 mm longis indutæ; lemmatum apices obtusi vel truncati, bidentati. Lemma III dense villosum. Aristarum segmenti basales densissime pilis circa 1 mm (raro 2 mm) longi armati. Paleae praecipue apices versus pubescentes. Chromosomatum numerus: 2n = 28.

Type: Plants grown in greenhouse (Beltsville, Maryland, U.S., August 1967) from seeds collected by F. J. Zillinsky from a roadside population in the Rabat region of western Morocco between villages Oulmes and Tiflet (approximately 30 km southeast of Tiflet) at an elevation between 1000 and 1300 m, 27 May 1964 (holotype K; isotopes NA, US). (Sixty plants of *A. magna* grown under field conditions at Aberdeen, Idaho, in 1967, were identical for all taxonomic characteristics and chromosome number with the plants grown in the greenhouse.)

In contrast, *A. sterilis* has a hollow peduncle; lowest rachilla segments are rounded; articulation scars are usually about 2 mm long and 1 mm wide; and the lower two-thirds of lemmas of first and second florets are rather densely long-villous with hairs up to 7 mm long (hairs not concealing the lemma surface in contrast with *A. magna*). The upper one-third of lemmas are glabrate to short-pubescent; lemma apices are long-attenuate to acute and bidentate (lemma width just below apices is less than 1 mm, but that of *A. magna* is 1 to 2 mm); and lemmas of tertiary florets are glabrous to sparsely villous. Basal segments of awns are glabrous or in subspecies *macrocarpa*, pubescent with hairs up to 1 mm long; paleae are glabrous and ciliolate. The somatic chromosome number is 42.

In addition, *A. magna* has slightly larger florets and caryopses, slightly thicker awns, and slightly longer pedicels. Glumes are about as large as the largest ones in *A. sterilis*. Density of lemma hairs is perhaps twice that in *A. sterilis*. Hairs in *A. magna* are either dark brown or whitish. In making comparisons between CW-525 and *A. sterilis* sens. lat., we took into account the hairiest extremes, particularly *A. sterilis* subsp. *macrocarpa* var. *setosissima* Malzew subvar. *maxima* (Perez-Lara) Malzew as illustrated by Malzew (*5*) in his Plate 87. Other differences include the internode walls, especially of the upper part of culms, which are much thicker in CW-525 than is usual in *A. sterilis*. Presumably, this characteristic may be of agronomic benefit in preventing breakage of culms. Finally, our plants of CW-525 have a

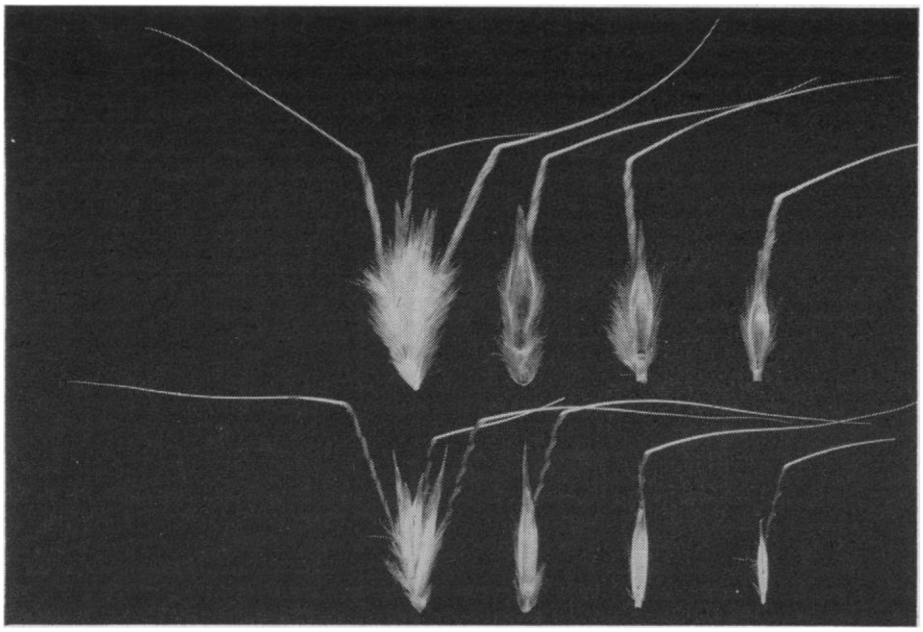

Fig. 1. (Left to right) Spikelets and primary, secondary, and tertiary florets of *Avena magna* (above) and *A. sterilis* (below).

more spreading habit and more pendulous panicles.

Since *A. magna* is a tetraploid with characteristics more extreme than those of *A. sterilis*, it could be an ancestor of *A. sterilis*, which in turn is supposed to have participated in the formation of the group comprising *A. sativa* L., *A. fatua* L., and *A. byzantina* K. Koch. Hence, *A. magna* may be an ancestor of cultivated oats.

Reciprocal crosses between *A. magna* and species representing the tetraploid, diploid, and hexaploid groups of *Avena* have resulted in viable F_0 seeds without requiring embryo culture. We have made successful crosses between *A. magna* and *A. sativa* and *A. sterilis* among the hexaploid group; *A. barbata* Pott ex Link and *A. abyssinica* Hochst. ex A. Rich. among the tetraploid group; and *A. strigosa* Schreb., *A. hirtula* Lag., *A. wiestii* Steud., and *A. longiglumis* Dur. among the diploid group.

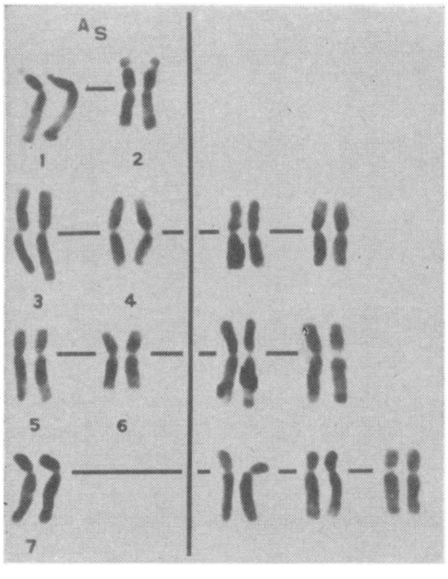

Fig. 2. Karyotype of *Avena magna*. Chromosomes 1 and 2 (satellited), 3 and 4 (median), 5 and 6 (submedian), and 7 (subterminal) appear similar to A_s genome (*6*).

We have prepared a karyotype of *A. magna* (Fig. 2). Pairs of chromosomes that might belong to the A_s genome (*A. strigosa*) are arranged and numbered from 1 to 7. The A_s genome is present in the diploid species *A. brevis* Roth, *A. hirtula*, and *A. wiestii;* in the tetraploid species *A. abyssinica*, *A. barbata*, and *A. vaviloviana* Malz. ex Mordv., and in the hexaploid species *A. sativa, A. fatua*, and *A. sterilis* (*6*). The second genome B, reported only in the tetraploid species, consists of four chromosomes with median or near median centromeres, two long chromosomes with submedian centromeres, and one short chromosome with a submedian centromere (*6*). The second genome in *A. magna* differs from the B genome and includes three chromosomes with subterminal centromeres not found in the aforementioned tetraploid species, but found in the hexaploid species.

The analysis of the karyotype of *A. magna* was supplemented with information on pairing behavior in an interspecific hybrid of *A. magna* and *A. sativa*. Meiosis in *A. magna* is normal with 14 bivalents. In the hybrid, an average of 14.2 univalents, 6.9 bivalents, 2.1 trivalents, and 0.1 quadrivalents per pollen mother cell (PMC) indicates that one genome, probably A, is common to both species. Furthermore, trivalents and higher associations observed in 96 percent of the 140 PMC's analyzed point to several possible hypotheses: (i) partial homology of the chromosomes of the second genome of *A. magna* to the A genome of *A. sativa*, (ii) partial homology of the A genome of *A. magna* to either the C or D of *A. sativa*, (iii) homoeology of the chromosomes of the two genomes in *A. magna*, or (iv) partial homology of several chromosomes of either the C or D of *A. sativa*. Under the third hypothesis, the assumption is that homoeologous chromosomes pair only in the absence of their homologue.

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29 September 1967