

SEED PROTEINS, PT. 1

江南大学



SEED PROTEINS

Edited by

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and

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Seed Proteins

Peter F. Slattery and Rod Casey (Eds.)

The volume is the most comprehensive and detailed account of seed proteins ever published and the first dedicated volume for a number of years. It covers the major storage protein groups (prolamins, 2S albumins, 7S globulins and 11S globulins) focusing on those present in crops. It also covers other widely distributed groups of proteins including protease inhibitors, antifungal proteins, thionins and oil body protein. The breadth of coverage of the proteins include including their structures and properties, evolutionary relationships, classical and molecular genetics and mechanisms of synthesis, trafficking and deposition within the cells.

It should therefore become a standard source book for all seed scientists as well as for higher level teaching.

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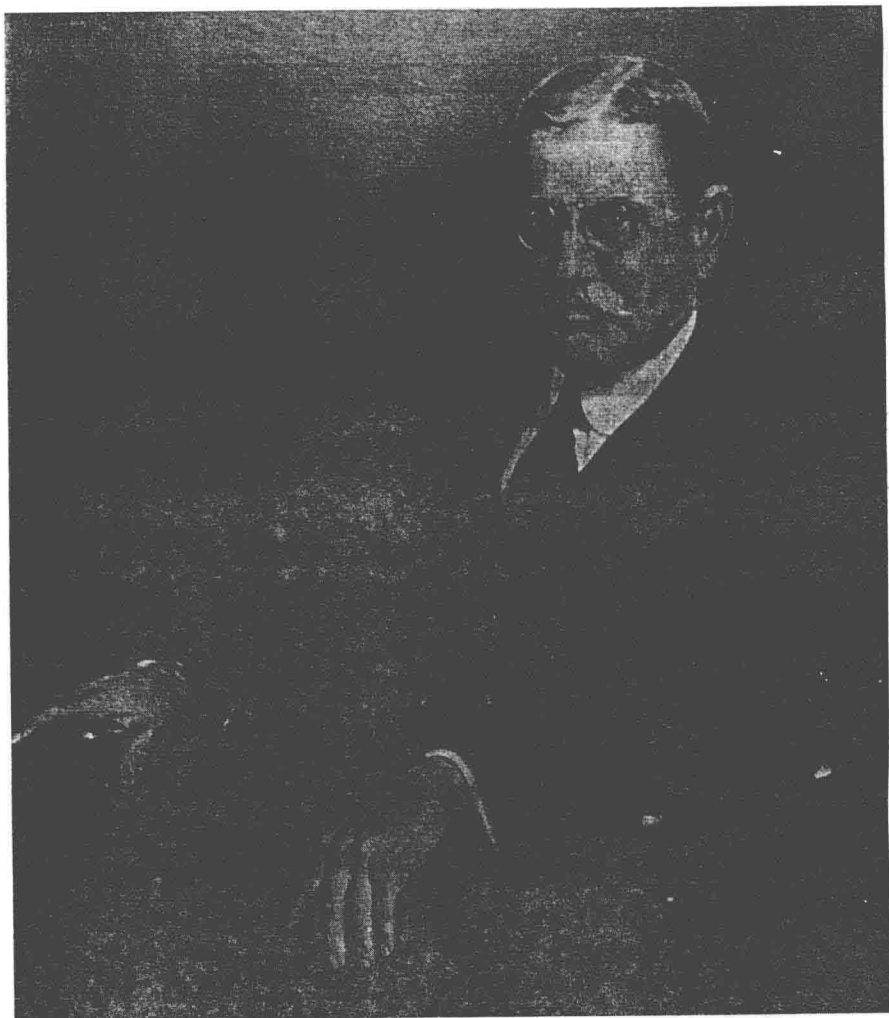
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FRONTISPIECE

Thomas Burr Osborne (1859-1929) was one of the founding fathers of protein chemistry. He worked at the Connecticut Agricultural Experiment Station from 1886 till 1928, publishing some 250 papers including studies of seed proteins from 32 plant species. Oil portrait provided by the Connecticut Agricultural Experiment Station.



FOREWORD

Seeds provide more than half of the world's intake of dietary protein and energy and thus are of immense economic, cultural and nutritional importance. Proteins can account for up to 40% of the dry weight of various types of seeds, thereby making a large contribution to the nutritional quality and processing properties of seeds. It is, therefore, not surprising that seed proteins were among the first plant components to be systematically studied, some 250 years ago, and have been a major focus of research over the past 100 years. The properties and behaviour of seed proteins pervade modern life in numerous ways. For example, legume and cereal proteins are used in the production of a wide range of meat-free foods; the process of bread-making is dependent on the physical chemical properties of wheat seed proteins; and in developed, as well as developing, countries, nutritional deficiencies among vegetarian diets are avoided through balancing legume and cereal seeds as sources of dietary proteins. Understanding seed proteins, in order to improve their composition and properties and to increase their concentrations, will thus continue to be an important research objective for the future.

The present volume represents the culmination of a long-discussed plan of the editors, to bring together the best international authorities in order to compile a definitive monograph on biological, biochemical, molecular and genetic aspects of seed proteins. The aim has been to include not only the major crop species, but also a wider spectrum of plants of biological and evolutionary interest. Similarly, although there is an emphasis on the storage proteins which have the greatest impact on seed utilization, a range of other proteins are covered including many which may contribute to the protection of the seed against pests and pathogens.

An enormous amount of work has gone into the individual chapters and we are grateful to the authors of these for all their efforts. In addition, we are indebted to our colleagues at IACR-Long Ashton and the John Innes Centre for their assistance, particularly Mrs. Valerie Topps, Mrs. Pat Baldwin (IACR-Long Ashton) and Miss Tarn Dalzell (John Innes Centre) for skilled secretarial help. Finally, we wish to thank Mr. Ken Williams (IACR-Long Ashton) for photographs including the front cover of the volume.

Peter R. Shewry and Rod Casey

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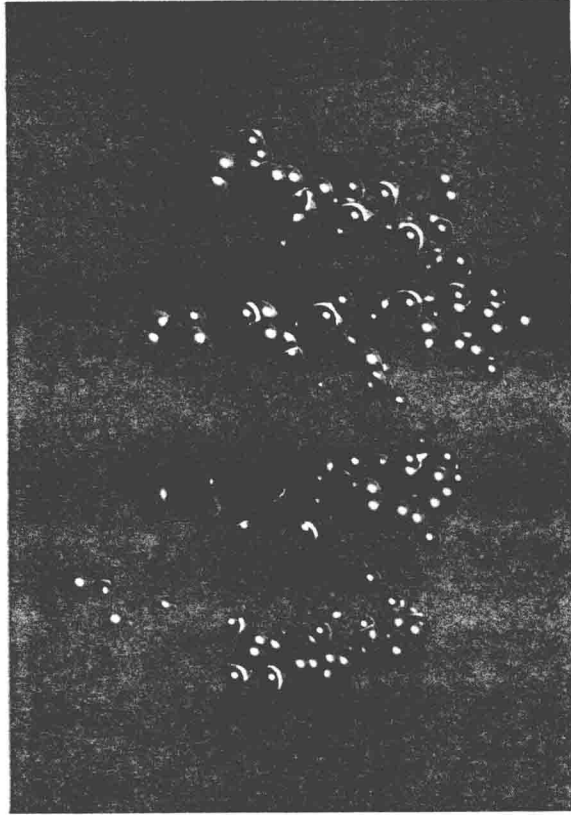
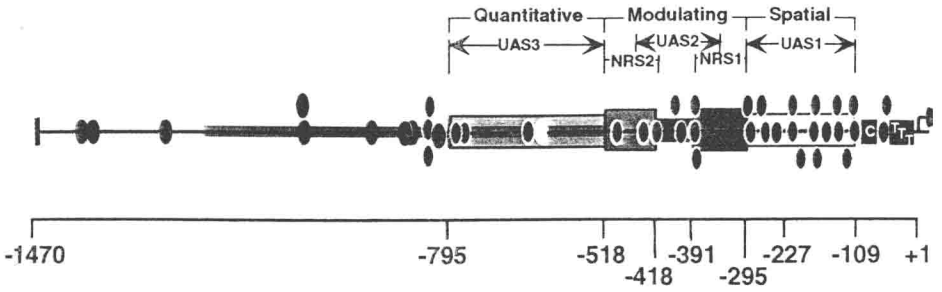


Plate 1 Molecular modelling of the β -spiral structure formed by the repetitive sequences present in the HMW subunits of glutenin. The figure was kindly provided by Dr. O. Parchment and Dr. D. Osguthorpe of the University of Bath, UK.

A.



B.

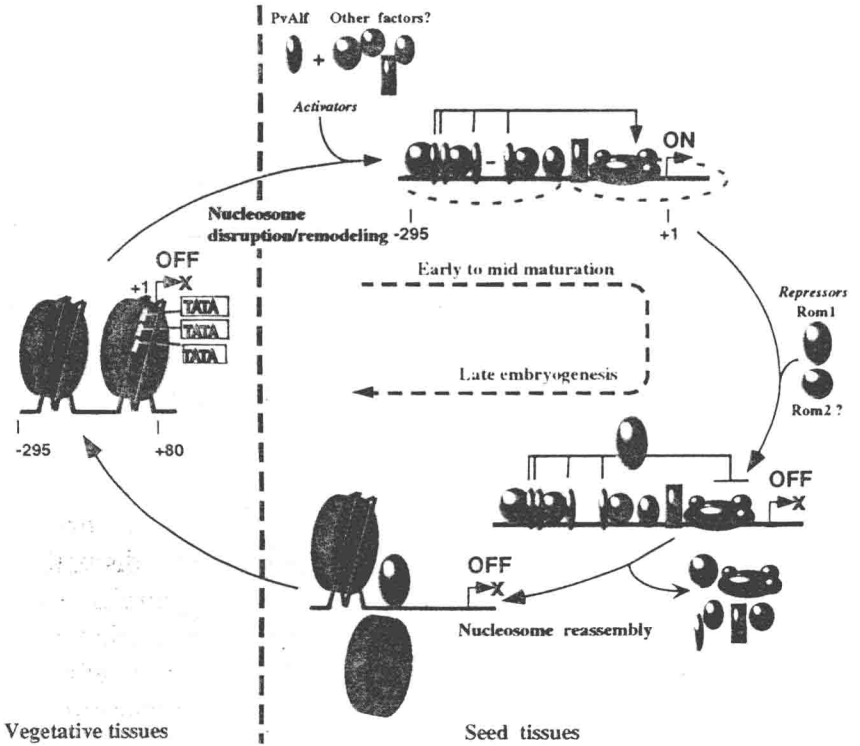


Plate 2 Regulatory elements in the phaseolin (*phas*) promoter and their assembly into chromatin. A. Diagram of the various regions of the *phas* promoter discussed in the text. UAS1, UAS2 and UAS3 are upstream activating sequences; NRS1 and NRS2 are negative regulatory sequences. UAS1 includes three domains: a seed specific enhancer (SSE), a minimal seed specificity element (MSS) and a minimal promoter (MP). The orange bar denotes the 5' matrix attachment region. There are three TATA-regions (T) and one CAAT-like element (C). Each of the colored ovals represents a consensus *cis*-element: blue, RY elements (CATGCAC/A); green, E sites (CANNTG); yellow, pollen box (GAATTTGTGA); red, various other *trans*-acting factor binding elements predicted on the basis of sequence comparison. B. Model for the involvement of chromatin in regulation of expression from the *phas* promoter. In vegetative tissues, the TATA regions are rendered inaccessible to TATA-binding protein by a rotationally and translationally-positioned nucleosome. Nucleosome disruption (by remodeling or displacement) during embryogenesis permits access by transcriptional activators and assembly of the basal transcription apparatus. Reassembly of the nucleosome, perhaps assisted by regulation of maturation (Rom) factors, occurs late in embryogenesis, terminating transcription. For details, see text.

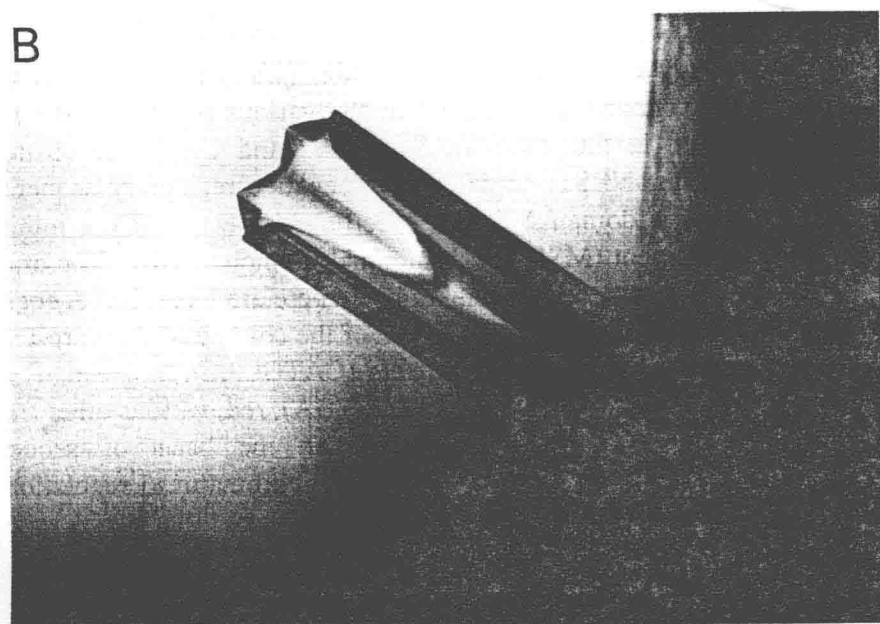
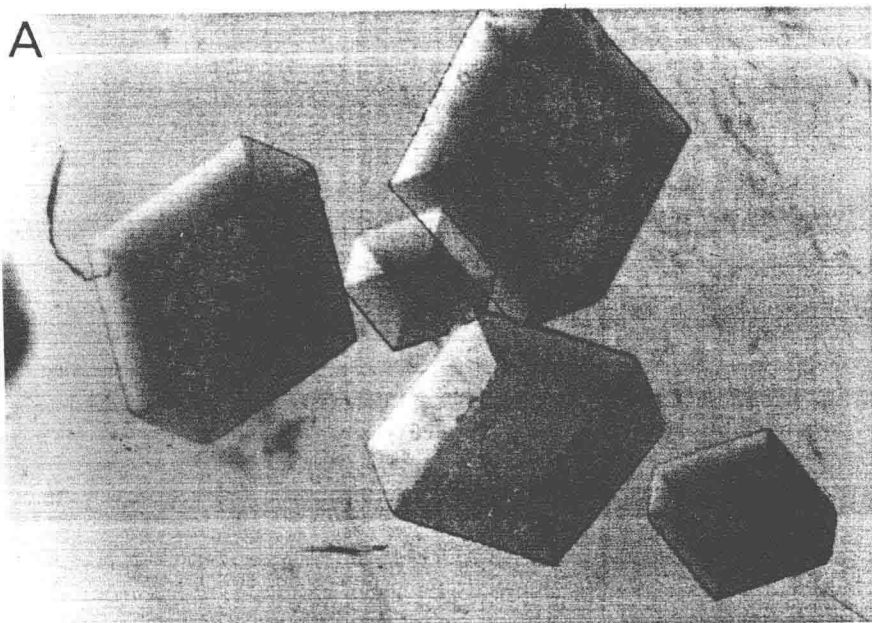


Plate 3 A are rhombohedral crystals of canavalin like those grown by Sumner and Howell (1936). It is the most common crystal form. B is a single crystal of the hexagonal modification of the canavalin crystals, and the form from which the structure of canavalin was first elucidated by X-ray diffraction analysis. Unlike the crystals first grown by Sumner and Howell, these particular crystals were not grown on earth but on the U.S. Space Shuttle in the course of macromolecular crystallization experiments in microgravity, in space.