Preface

The phenomenon of seed development remains an intriguing problem and much effort has been directed toward its understanding. In this thesis, particular attention is drawn to early seed development and the process that lead up to the phase of storage product accumulation in barley by an integrative approach including genomics, biochemistry, physiology and histology. In addition, close inspection of early seed development in the *seg8* mutant of barley, which is defective in endosperm development, is carried out by genomic studies to understand the importance and complexity of maternal and filial tissue interactions during early caryopses development. By using the EST-array resources generated in this project we conducted gene expression analysis in foxtail millet cultivars differing in salt sensitivity by cross-hybridization experiments. The foxtail millet experimental system has been chosen because of the availability of two different genotypes differing in their sensitivity to salinity, which is absent in barley.

The thesis is comprised of four chapters. Chapter-1 is dealing with a general introduction of the main technology used; macroarrays based on expressed sequence tags (ESTs). A results and discussion section deals with construction and employment of an EST-based macroarray and its quality control. Chapter-2 consists of early seed development studies in the cultivar Barke of barley. Chapter-3 deals with early seed development in the *seg8* mutant of barley and chapter-4 with gene expression during salinity stress in foxtail millet. Each chapter (2, 3 and 4) starts with an introduction into the specific research area, describes the obtained results and discusses the relevant problems. To avoid repetitions Materials and Methods adopted are described in one section at the end of the thesis.

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