The ABCDE model and formation of flower outer whorls.

Vsevolod Filaretov
Institute for Information Transmission Problems; Voronezh State University
vsfilaretov@gmail.com

Abstract

MADS-box proteins are a family of transcription factors controlling a variety of organ development processes in plants, in particular - flower development. We analyze the distribution of transcription factors regulating the development of the outer whorls in the genomes of plants with unusual flower structure.

1. Introduction

The acronym MADS box is derived from the initials of four loci, MCMI of Saccharomyces cerevisiae, AG of Arabidopsis thaliana, DEF of Antirrhinum majus and SRF of Homo sapiens. All these proteins contain the MADS-box domain, a conserved protein domain of approximate length of 58 amino acids [1].

MADS-box genes encode a family of transcription factors which control a variety of organ development processes in plants. Although thoroughly researched, this gene family still leaves a lot of questions, especially in the area of flower development.

The floral homeotic genes activity is described by the ABCDE functional model [2]. Most of genes involved are MADS-box genes from various functional classes with the characteristic MIKC-type structure. The only exception is the B-group formed of AP2 genes neither MIKC-structured, nor MADS-box containing. A peculiar feature of these genes are two DNA-binding AP2 domains. Other functional classes of the ABCDE model are A-class (AP1/SQUA-like proteins), already mentioned B-class (AP3/DEF-like and PI/GLO-like proteins), C-class (AG-like proteins), D-class (STK-like) and E-class (SEP-like proteins). Proteins of these classes form homo- and heterodimers that recognize the conserved nucleotide CC(A/T)_{3}GG DNA sequences, which are known as the CArG boxes [3]. These dimers group further forming functionally active “floral quartets”, which specifically regulate corresponding differentiation of an exact flower whorl (according to the traditional Arabidopsis-derived scheme): A+E group complexes control the outer (or sepal) whorl formation, A+B+E, the second (or petal) whorl formation, B+C+E, the stamen whorl, C+E, the carpel formation and D+E, the ovule formation, respectively [4]. Here we discuss the A, B and E-group, the proteins involved in the outer whorls formation.

2. Data and methods

Amino acid sequences containing floral homeotic proteins were extracted for the 13 plants having large-scale sequence projects completed and in-progress. BLAST similarity search in the UniProt and NCBI protein databases was used to obtain respective sequences using Arabidopsis thaliana and the corresponding plant proteins as queries (UniProt: default settings; NCBI blastp: expect threshold 1e-7, proteins matching with the reference in the key regions were chosen). BLAST search in UniProt was performed to retrieve a sample of flower homeotic proteins AP1/SQUA-like, AP2-like, AP3/DEF-like, PI/GLO-like, SEP-like (500 hits, identity 90%), based on Arabidopsis thaliana proteins APETALA1-3, PISTILLATA, SEPALLATA, respectively.

3. Discussion

One of unresolved questions of the flower development analysis is the place of B-functional group in the ABCDE model. They mediate the outer whorls formation dependent on a plant clade, and the aspects of such a fact remain unclear despite a row of hypotheses: “sliding” hypothesis [5], “fading borders” hypothesis [6], correlations between variation in gene expression patterns and “complexity” in petal morphology hypothesis [7], hypothesis of AP3 and PI specifying regional domains in the flower rather than organ identity [8]. To address this problem using computational methods, we plan to analyze the distribution of
proteins regulating floral development in genomes of plants with unusual flower structures (e.g. tepaloid flowers instead of common petal-sepal ones), such as buckwheat.

References