



Università degli Studi di Verona

Scuola di Dottorato di Scienze Ingegneria Medicina

Ca' Vignal 2  
Strada le Grazie 15  
37134 Verona - Italia  
Tel. +39 045 802 7026  
Fax +39 045 802 7068

PhD Program in Applied Biotechnologies

## **“Evolution of diverse inflorescence architectures”**

**February 25, 2013 - h. 15:30**

**Prof. Ronald Koes**

Dept of Molecular Cell Biology, VU-University  
Amsterdam, The Netherlands

### **Abstract:**

A major challenge in biology is to understand the molecular basis of the evolution of the enormous morphological diversity seen among animal and plant species. Higher plants are particularly useful for such "evo-devo" studies as they evolved a wide variation in architectures in relatively short time and because many plant species are, in contrast to animals, amenable to genetic analyses. Angiosperms, for example, diverged widely with regard to flowering time and inflorescence architecture. In racemose inflorescences, like that of *Arabidopsis*, the apical meristem is indeterminate and flowers derive from lateral meristems, resulting in single (monopodial) axis bearing many lateral flowers. In cymose inflorescences, however, the apical meristem terminates development by forming a flower and growth continues via a lateral (sympodial) meristem. The reiteration of this patterns results in a zigzag-shaped 'truss' consisting of serial sympodial units that each terminate with a flower. By forward genetics we identified several genes that specify the architecture of the cymose *petunia* inflorescence. Their orthologs in *Arabidopsis* and *Antirrhinum*, which bear racemose inflorescences, encode functionally similar proteins but have different functions, which is in most cases due to changes in gene expression patterns.

The picture that emerges is that architectural diversity is associated with an extensive rewiring of the regulatory network that determines when (flowering time) and where (architecture) flowers are formed, which is at least in part due to changes in cis-regulatory gene elements that control transcription.

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The lecture will take place in the **room Verde** of **Cà Vignal - Strada Le Grazie, 15 - Verona**

Local organization and contact:

Giambattista Tornielli  
[giovannibattista.tornielli@univr.it](mailto:giovannibattista.tornielli@univr.it)

The seminar is compulsory for students of the PhD Program in Applied Biotechnologies

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