The history of cell wall studies can be traced back to the time of Nehemiah Grew and Marcello Malpighi, who gave their papers on microscopic investigations of plant tissues at the Royal Society of London in 1671 soon after the Restoration of Charles II. The two pioneers described plant organs as being composed of cells with rigid walls in the same way that a house is made up of bricks (Grew 1682). The static view of plant cells with rigid walls was extensively revised in the 19th century by Julius von Sachs and his contemporaries. They recognized the cell wall as a dynamic architecture responsible for regulation of growth and differentiation in plants (Sachs 1887).

The current view of the plant cell wall largely stems from the structural model based on the molecular dissection of sycon- more cell wall as pioneered by Albersheim’s school in the 1970s (Keegstra et al. 1973). This model envisaged xyloglu- can molecules to be bound to the surface of cellulose microfi- brils by hydrogen bondings. Some xyloglucan molecules are further linked covalently through certain cross-linking polysaccharides. Consequently, a cellulose microfibril coated with xyloglucan molecules is interconnected to two or more microfibrils, thereby forming a single supermolecular framework structure surrounding the cell. Whereas various significant findings have challenged the details of the original model, its essence has broadly speaking withstood the test of time. Curr- ently, it is widely accepted that the cellulose–xyloglucan framework constitutes the central underpinning of the cell wall, and that cell growth and differentiation are mediated by con- struction and restructuring processes of this framework.

It was not until the 1990s that a major breakthrough was achieved in elucidating proteins responsible for the construc- tion and modification of the cellulose–xyloglucan framework. These proteins include, chronologically, (1) xyloglucan endotransglucosylase/hydrolases (XTH) (Fry et al. 1992, Nishi- tani and Tominaga 1992, Okazawa et al. 1993), (2) expansins (McQueen-Mason et al. 1992, Shcherban et al. 1995), (3) cellu- lose synthases (Pear et al. 1996, Arioli et al. 1998, Taylor et al. 1999), (4) membrane-anchored endo-β-(1–4)-glucanases (Brum- mell et al. 1997, Nicol et al. 1998) and (5) yealdins (Okamoto- Nakazato et al. 2000, Okamoto-Nakazato et al. 2001). Com- plete genome sequences for Arabidopsis (Arabidopsis Genome Initiative 2000) and rice (Yu et al. 2002, Goff et al. 2002) have revealed that these classes of proteins are, without exception, encoded by fairly large multi-gene families. This means that comprehensive analyses of a whole complement of family members is required to clarify the whole picture of cell wall dynamics in plants. Thus, plant cell wall biology fields have entered the post-genomic era.

From the post-genomic point of view, this issue of PCP contains four review articles that deal with individual gene families committed to dynamics of basic architecture of the cell wall framework. While Höfte and his colleagues deal with role of membrane-bound endo-β-(1–4)-glucanases in cellulose bio- synthesis (Molhøj et al. 2002), Delmer and her colleagues sum- marize recent achievements in molecular dissection of the cen- tral machinery of cellulose biosynthesis (Doblin et al. 2002). In the third article, Rose and co-authors present current perspec- tives of the XTH genes, formerly termed EXGT and XET, and propose a new unifying nomenclature (Rose et al. 2002). Finally, Cosgrove and his colleagues summarize the growing world of the expansin gene family (Cosgrove et al. 2002).

References
