

Preface

The second Italian Proteome Society (IPSo) congress has been held at the Università della Tuscia in Viterbo, Italy from 29 May to 1 June, 2005. *Lello Zolla* and *Alessio Valentini* were the organizers. The opening ceremony took place on Sunday afternoon in an old theatre (Fig. 1), built in the mid-19th century. It is a charming bombonnière of a building in which one would have expected one of those sparkling overtures of Rossini, the “Gazza Ladra” or the “William Tell”, had we been in Pesaro. The opening lectures started with *Peter Roepstorff* (Odense, Denmark) who spoke on “Proteomics why, how and when”, followed by *Joël Vandekerckhove* (Ghent, Belgium) “Peptide Centric Proteomics: A challenge for Protein Chemistry, Chromatography, Robotics, Mass Spectrometry and Bioinformatics” and closed with *Michele Morgante* (Udine, Italy) “From genomics to breeding in plants”.

At the end, a party was held in the foyer with prosciutto crudo sliced on the spot, whose fragrance slowly permeated and saturated the atmosphere.

The marathon began on Monday morning, in a brand new lecture room opened just for the occasion of the Viterbo meeting, in what had once been the storeroom of an old monastery, and that was later transformed into a jail. One had the impression of penetrating an ancient forest, as the panelling emanated a woody effluvium. The atmosphere warmed up quickly and in fact soon became overheated. This was not so much due to the excellent lecture topics, as they had not yet begun, but because the air conditioning had broken down and the heat quickly became unbearable. There was one hour of panic, trying to repair the system; then, as the air cooled down and the recalcitrant congress attendees filled the room, the official program could begin. The atmosphere was decidedly better during the poster sessions. First of all, the air was cool and pleasant, as the posters (no less than 140 of them) gently wound around the quadrilateral of an ancient cloister (Fig. 2), under the curious gaze of a renaissance bell tower. Secondly, because lunch breaks took place in this cloister, and good food and wine made science more palatable.

Following the scientific meetings was not an easy task, mind you. No matter how good the sessions were, science had to compete with the charms of Viterbo, an enticing medieval town, so rich in history and gothic architecture. Perhaps not so many of us knew that prior to their exile in Avignon, France (1309–1376), the popes had moved their court to Viterbo, where the pope’s

palace was erected during 1255–1267 on a hilltop overlooking the valley in the direction of Rome (Fig. 3). It was inaugurated in a most curious way: upon the death of Clemente IV, who lived there, a Conclave took place to elect the new pope; the most difficult election ever held in the Catholic Church. It continued for no less than 3 years, from 1268 until 1271. Confusion and chaos ensued in the entire Christian world, and there seemed to be no end to it. Finally, it was ended by the inhabitants of Viterbo, who – truly upset by this long inter-reign, and disgusted with having to maintain the large popish court – removed the palace roof. Rain and snow generously pouring down from the heavens quickly drove the conclave to an end. Trying to terminate an endless meeting this way might be prohibitively costly, indeed, so a new rule was introduced for all future Conclaves: the cardinals were imprisoned in the room (the Sistine Chapel, in general) until the election took place. That is the meaning of Conclave (*cum clavis*, i.e. locked in), by the way. Should we also lock any guest speaker who refuses to terminate his lecture in a cabinet? Well, it might be an option worth discussing.

More than 300 participants attended the meeting. A total of 142 posters and 46 lectures, a heavy program indeed for the two and a half days of the meeting. During the Second IPSo Congress “Proteomics and Genomics” particular focus was given on genome-based proteomics with an emphasis on the various technology platforms to allow such studies. Taking full advantage of the information encoded in the genomes and proteomes of cells could provide predictive models for how the cellular constituents interact to produce cellular phenotypes. During the meeting some spokesman illustrated recent advances in the discipline that convince us that this is not unjustifiable hubris, but rather a rational although ambitious vision of the near future of protein characterization. This new experimental technology has led protein biochemists to change how we think about biological problems. Instead of spending months to characterize a given protein, we aspire to characterize all of the proteins expressed by the genome under a given set of biological conditions. Impressive was the lecture given by *A. Butterfield* from the University of Kentucky, Lexington, USA on the use of redox proteomics to identify the oxidatively modified proteins in Alzheimer’s disease, found in the inferior parietal lobule and hippocampus. Interesting as well was the data shown by *W. Gruissem* from the Genomic Center of Zurich on the mechanisms that regulate the



Fig. 1. The Union Theatre.



Fig. 3. The Pope's Palace.



Fig. 2. The Cloister of Tuscia University Rectorate.

differentiation processes of progenitor plastids into functionally specialized organelles. The proteomics weapons to manage the diagnosis and treatment of systematic *Candida albicans* infection were presented by *C. Gil*, from the University of Madrid. *A. Bonin* from the Université Joseph Fourier, Grenoble, France, presented an interesting and not-so-politically-correct lecture on genotyping errors. *M.A. Beaumont* from the University of Reading, UK, presented a novel method to discover selection signatures by a population genomic approach. A spectacular overview of the post-genomic technologies that have played a key role in the discovery process of new vaccines was given by *G. Grandi* from Chiron vaccines. New methodologies were presented on the determination of single nucleotides polymorphism (SNP) by MALDI mass spectrometry by *F. Kirpekar*, and highly selective enrichment of phosphorylated peptides from complex mixtures using titanium dioxide microcolumns to reveal protein phosphorylation by *M. Larsen*. Proteomics analysis of protein glycation for diabetes diagnosis as well as the identification of tumor associated antigens or therapeutical studies by chemicals were reported.

Rewards were also generously offered for the best posters, which made for fierce competition among the young scientists. We are happy to note the winners here:

First poster prize (1000 Euros): Dr. *Andrea Totolo* from the University of Verona;

Second poster prize (600 Euros): Dr. *Davide Ticozzi Valerio* from the University of Milano-Bicocca and Dr. *Pavone Barbara* from the University of Chieti;

Third poster prize (300 Euros): Dr. *Elena López-Villar* from the University of Madrid.

We would also like to acknowledge the team of Prof. Zolla, without whose work and dedication this meeting would have not succeeded: Drs *Anna Maria Timperio*, *Sara Rinalducci*, *Gian Maria D'Amici*, *Corrado Ciambella* and *Marco Fagioni*.

As we close the curtains on the Viterbo meeting, we are sad to say that there will not be a follow-up: our beloved IPSo society, that seemed to be born to immortality, is indeed ceasing to exist in its infancy. Since we have two proteomic societies in Italy, and, by the laws of the newly created EuPA (European Proteomic Association), only one society per nation can be affiliated, it was wisely decided to merge these two societies into one. The merger (and the foundation of the new society, IPA, Italian Proteomic Association) will take place in Pisa, on July 2–4, 2006. We are glad to invite all of you there and hope that we will not have to end that meeting (it might take years here as well to implement the birth of the new society) by crashing the Leaning Tower down onto the meeting building.

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