of antibiotics and have had a significant role in the discovery and development of commercially successful drugs of all classes. Over 75% of the antibacterial new chemical entities (NCEs) introduced worldwide between 1981 and 2002 were based on natural products. The unmatched chemical diversity and complexity of natural products is one reason for their success over those obtained by pure chemical synthesis. Another reason for their superiority can be explained by the fact that their synthesis evolved naturally in response to needs and challenges of the natural environment generating compounds which are pre-selected for activity. Despite these facts, natural product research has recently gone through a phase of reduced interest. Big pharmaceutical companies in particular have downgraded or even stopped this kind of research. The reasons for this development may be that natural products are often produced in low quantities and as mixtures of similar compounds, the rediscovery of known compounds and the challenge of natural product derivatisation using classical chemical means.
The past few years have witnessed major developments in the use of innovative natural product related technologies, such as fermentation optimisation, separation, structure elucidation and dereplication allowing much faster access to sufficient quantities of pure natural compounds. The application of modern medicinal chemistry adapted to the special needs of natural products is also an efficient way to revisit and recycle old antibiotic classes. The use of modern Genome-based technologies, established in the past few years, offers the opportunity to increase the attractiveness of natural products. Genome-based screening technologies provide fast access to the enormous genetic potential of Actinomycetes, soil bacteria known to represent one of the most important sources for bioactive metabolites. Additionally, genetic engineering technologies will help to overcome two of the main hurdles connected to natural products, the difficulty in derivatising complex structures and the quantitative improvement of the production yield.
By focussing on examples in the field of genome based screening and genetic engineering this presentation will give an overview of major improvements that may lead to a rediscovery of natural product based drugs to meet the urgent need for new antibiotics.

Respiratory pathogens and vaccination

O348 Clinical evaluation of a new ID-Tag RVP assay for the detection of 20 respiratory viruses

J. Mahony, S. Chong (Hamilton, CA)

Objectives: To evaluate the performance of the ID-Tag RVP test for the detection of respiratory viruses.
Methods: NP specimens [N = 227] were collected from symptomatic patients under ERB approval and were tested by the ID-Tag RVP test (TmBioscience Corp'n, Toronto, Canada) and conventional DFA plus culture. The RVP test is a new test for the detection of 20 respiratory viruses that uses multiplex PCR, a Universal Array of oligonucleotides (TmBioscience), and a fluidic microbead array (Luminex X-Map). The test detects Influenza A (subtypes H1, H3, and H5 Asian lineage), Influenza B, Parainfluenza types 1, 2, 3, 4, RSV types A and B, Adenovirus, Metapneumovirus, Rhinovirus/Enterovirus, Coronavirus 229E, OC43, NL63, HKU1, and (SARS-CoV). The ID-Tag RVP test was performed according to manufacturer's instructions. Briefly, viral nucleic acid was amplified by a multiplex PCR followed a multiplex Target Specific Primer Extension (TSPE) reaction and sorting of TSPE products using the Luminex X-Map system. DFA and culture were performed using MCabs and R-Mix shell vials (Diagnostic Hybrids Inc.). For discordants and RVP positives where the targets were not tested by DFA/culture, a second PCR (unique primers) and sequencing was performed as the comparator test.
Results: Twenty-two of 227 specimens (9.7%) failed to give a signal for the internal control indicating extraction failure or was called equivocal for at least one target. Of the 206 specimens analysed, 135 were RVP+ DFA/culture+ and 37 were RVP– DFA/culture– concordant. There were 7 RVP– DFA/culture+ and 27 RVP+ DFA/culture– discordants. After resolution of discordants RVP had a sensitivity of 95.8% (138/144) compared with 93.7% (135/144) for DFA/culture. RVP detected an additional 26 confirmed positives including 22 Rhino/Entero, 1 NL63, and 3 HKU1 that are not routinely tested by DFA or culture and 4 additional Flu B positives that were missed by DFA/culture.
Conclusion: The ID-Tag RVP test is more sensitive than DFA/culture and detects a number of respiratory viruses not routinely tested for. Overall 22.5% additional positive specimens were detected that were either missed by DFA/culture or not tested for. The ID-Tag RVP test should improve the ability of hospital and public health laboratories to diagnose viral RTIs in a hospital or community outbreak situation.

O349 Molecular epidemiology, genotypes and recombination of coronavirus HKU1, a novel human coronavirus associated with respiratory tract infections

P.C.Y. Woo, S.K.P. Lau, C.C.Y. Yip, Y. Huang, H.W. Tsoi, R.W.S. Poon, B.H.L. Wong, K.H. Chan, K.Y. Yuen (Hong Kong, HK)

Objectives: Recently, we described the discovery of a novel group 2 coronavirus, coronavirus HKU1 (CoV-HKU1), from a patient with pneumonia. In this study, we examined the molecular epidemiology, genotype distribution and recombination in CoV-HKU1.
Methods: We collected nasopharyngeal aspirates of patients with respiratory tract infections over a two-year period. The complete genomes of a total of 22 strains of CoV-HKU1 were sequenced and compared. Genotypes and possible sites of recombination were determined.
Results: Phylogenetic analysis of 24 putative proteins and polypeptides showed that the 22 CoV-HKU1 strains fell into three clusters (genotype A, 13 strains; genotype B, three strains and genotype C, six strains). However, different phylogenetic relationships among the three clusters were observed in different regions of their genomes. From nsp4 to nsp6, the genotype A strains were clustered with the genotype B strains. For nsp7 and nsp8, and from nsp10 to nsp16, the genotype A strains were clustered with the genotype C strains. From hemagglutinin esterase (HE) to nucleocapsid (N), the genotype B strains were clustered closely with the genotype C strains. Bootscan analysis showed possible recombination between genotypes B and C from nucleotide positions 11500 to 13000, corresponding to the nsp6/nsp7 junction, giving rise to genotype A; and between genotypes A and B from nucleotide positions 21500 to 22500, corresponding to the nsp16/HE junction, giving rise to genotype C. Multiple alignments further narrowed the sites of cross-over to a 143-bp region between nucleotide positions 11750 and 11892, and a 29-bp region between nucleotide positions 21502 and 21530. Genome analysis also revealed variable numbers of tandem copies of a perfect 30-base acidic tandem repeat which encodes NDDEDVVTGD and variable numbers and sequences of imperfect repeats in the N-terminal of nsp3 inside the acidic domain upstream of papain-like protease 1 among the 22 genomes. All 10 CoV-HKU1 with incomplete imperfect repeats (1.4 and 4.4) belonged to genotype A.
Conclusions: Three genotypes, genotype A, genotype B and genotype C, exist in CoV-HKU1. Analysis of a single gene is not sufficient for genotyping of CoV-HKU1, but would require amplification and sequencing of at least two gene loci, one from nsp10 to nsp16 (e.g. pol or helicase) and another from HE to N (e.g. spike or N).

O350 Epidemiology and diagnosis of epidemic and avian influenza in Australia

C. Baleriola, S. Stelzer, R. Escott, P. Kirkland, P. Robertson, W. Rawlinson (Randwick, North Ryde, Candem, AU)

Influenza activity in temperate regions of Australia typically occurs between May and September, whereas in tropical regions influenza can occur any time throughout the year.
The main purpose of this presentation is to outline the epidemiology of human influenza during 2001–2006 in NSW. The second purpose is to report a quality assurance programme for laboratory diagnosis of influenza throughout Australia, including avian influenza.