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Editorial

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It's barcoding Jim, but not as we know it

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It has long been the dream of many ecologists that one day it will be possible to use a hand-held machine to identify biological specimens in the field (e.g. Janzen 2004). An analogy has been made with the so-called "tricorder" from the popular science fiction televison series *Star Trek* (Savolainen et al. 2005). This idea has arisen largely from the DNA barcoding community, who promote the use of a single universal DNA sequence (usually the mitochondrial cytochrome oxidase I (COI) gene) for species identification (Hebert et al. 2003). Such a device is typically imagined as using DNA as the basis for species determination. However, critics of this idea (e.g. Cameron et al. 2006) have argued that a DNA-based device would be impractical as tissue samples would need to be obtained as a source of DNA, which would necessitate handling the specimen. This suggests that the tricorder may not be such a good analogy; whereas, in *Star Trek*, the crew of the *USS Enterprise* merely had to point their tricorders at the organism in question, in reality, field-workers using a DNA-based system would have to obtain a tissue sample and load it into the machine in order to identify their specimen (Cameron et al. 2006, p.844).

A report in this issue of *Zootaxa* (Rodríguez-Fernández et al. 2011) suggests a possible alternative to DNA as the basis for a hand-held field identification device. Instead of DNA, Rodríguez-Fernández et al. use near-infrared (NIR) spectroscopy to obtain physiochemical profiles of the phenotypes of nine species of flies from the genus *Neodexiopsis* (Diptera: Muscidae), and show that these profiles can be used to discriminate between these species with 100% accuracy. This method works by pointing beams of near infrared light, at monochromatic wavelengths, at a specimen and recording the reflected light to calculate the absorption spectrum. As different metabolites absorb light of different wavelengths, the reflected light contains information about the substances and structures of the insect, providing a fingerprint of the physiochemical state of the intact insect phenotype. No tissue samples are needed; indeed, it should even be possible to obtain in this way a profile of the dynamic metabolic stages over time from a live specimen.

Near-infrared technology is today widely used in the area of food and agriculture as a multi-meter to predict the chemical composition of foods such as wheat and barley by calibration with chemical analysis using soft (self-modeling) analytical models for multivariate data (chemometrics). A chemometric method, principal component analysis (PCA), was used by Rodríguez-Fernández et al. (2011) for classification of their insect spectra. It has been demonstrated in plant endosperm genotypes and mutants from barley that the fingerprint of a NIR spectrum from a unique barley endosperm individual represents a coarse-grained overview of the whole physiochemical composition of the "phenome" of this tissue (Munck et al. 2010). The method of scanning the specimen with a beam of light seems to be a much closer analogy to the concept of barcode scanning as used in shops and businesses, and to the notion of a hand-held tricorder as it was originally conceived. As the phenomic profile results from the sum total of all the metabolic processes occurring in the insect, it represents the combined effects of the entire genome, proteome and metabolome of all tissues (equal to the phenome) and is therefore likely to be as potentially representative of the unique autonomously developing individual as its total DNA sequence.

While the entomological application of these methods reported by Rodríguez-Fernández et al. consists of only a single case-study involving a small group of congeneric insects, it does represent an important proof-of-principle demonstration, sufficient to indicate that this technique is worthy of further investigation. Many questions remain; for example, can this method be generalized to other taxa? How big is the overlap between intra- and inter-specific variation? What do the metabolomic profiles of hybrids and individual mutants look like? What are the effects of

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