Table 2 Effects of ANP and LPS on microvascular constrictive response. Values are mean [SEM]. *P<0.05, control+ANP vs LPS+ANP (arterioles). †P<0.05, control+ANP vs LPS+ANP (venules)

		10 min	60 min	120 min	180 min	240 min
		36.7 (5.8)		` ′		. ,
		33.3 (3)				
						5.1 (3.1)*
ANP	Venules	$2.3 (1.2)^{\dagger}$	13 (3.3)	3.2 (1.3)	2.3 (1.2)	0,

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Keywords: antigen, lipopolysaccharide; blood, plasma, atrial natriuretic peptide; cardiovascular system

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Categorization and significance of non-conformities in anaesthetic practice: pointers from the Lancaster anaesthetic expertise study

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Measuring the quality of anaesthetic care is difficult. Previous approaches have tended to focus on outcomes while process measures have received little attention. With this in mind, we analysed the transcripts from our observation of anaesthetists and other staff at work gathered as part of the Lancaster expertise study, which provided a large and unique repository of observations of 'everyday' anaesthetic practice. Aberrations in process, no matter how minor, were noted and categorized as below.

We had over 130 h of observation of anaesthetists at work. Whilst we witnessed no serious mishaps, we noted 103 'events', which were categorized as in Table 3. We also noted five instances of actions intended to reduce some of the above hazards.

Minor deviations from what might be called protocolized practice are very common in anaesthesia. There is thus a potential problem with what these events should be called. Possible terms include *variances*, *non-routine events*, *deviations*, and *non-conformities*, but the choice must be made carefully to avoid the implication that such events come about as a result of some failing on the anaesthetist's part. However, some unconventional events may actually make practice safer—rigid adherence to protocol may in some circumstances cause more problems. If, though, these events are preventable by a change of process (consistent with the Royal College of Anaesthetists' definition of a critical incident), further study and analysis of process measures such as these may be a fruitful approach to measuring the quality of anaesthetic care.

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Keywords: anaesthesia, professional expertise; anaesthesia, quality of care

Table 3 Categories and frequencies of events, with examples

Category	Example	n
'Lack of smoothness'	Cough on induction. Movement on incision	28
Procedural difficulty	Failed venous cannulation. Failed spinal	19
'Failure to follow protocol'	Inappropriate sharps disposal Re-use of i.v. fluid bag	18
Monitoring/equipment difficulties	Alarms sound inappropriately ECG electrode falls off Capnometer not functioning	15
Organizational/staff-related	No assistant available No handover in recovery room	14
Physical hazards	Trip over wires. I.V. cannula accidentally pulled out	5
Drug-related events	Near miss—i.v. connection of local anaesthetic infusion (averted)	4

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Advances in the genetic basis and diagnosis of susceptibility to malignant hyperthermia

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Malignant hyperthermia (MH) is an autosomal dominant disorder with estimated prevalence of 1 in 8500. For approximately 30 yr the only method of clinical diagnosis was by the invasive *in vitro* contracture test (IVCT). In the early 1990s the first MH susceptibility locus was identified, *RYR1* on chromosome 19q13.1. To date, it remains the major genetic locus for MH, although a further five susceptibility loci have been identified. In 2001 guidelines for genetic diagnosis of MH were published. Since 2000 the MH unit, in partnership with the Yorkshire Regional Genetics Service has been developing a DNA screen, which now benefits approximately 36% of families. A major research focus is to further increase the number of patients who may benefit from such testing. Here we report our progress with this research.

The MH Unit holds the National MH Register, which comprises nearly 700 families. The methods used include the following.

Genome wide approaches

- (i) Family linkage studies to estimate the proportion of families where there is chromosome 19, and therefore likely *RYR1* gene involvement.
- (ii) Association analyses to assess the involvement of multiple loci in MH susceptibility in single families, rather than a single susceptibility locus.

Gene-specific analysis

- (i) Mutation scanning of functionally relevant regions of *RYR1*, and whole gene sequencing to identify mutations associated with MH susceptibility.
- (ii) Mutation frequency assessment in the UK MH population to assess the potential benefit for use in a DNA test.
- (iii) Functional characterization of mutations identified by *in vitro* assessment.

Our linkage results indicate that *RYR1* predisposes to MH susceptibility in approximately 80% of UK MH families. Ten families with no linkage to chromosome 19 have been investigated for linkage to the other known susceptibility loci and no linkage was found;